

A reversible spherical geometric conversion of protein backbone structure coordinate matrix to three independent vectors of ρ , θ and ϕ : Supplementary information

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Bond ID	Model ID	Atom_Initial	Atom_Final	X _i	Y _i	Z _i	X _f	Y _f	Z _f	ρ (Å)	θ (°)	φ (°)
1	2jsa-1	ARG_A_1_N	ARG_A_1_H	14.733	4.945	1.144	14.853	5.924	1.361	1.01	77.59	83.01
2	2jsa-1	ARG_A_1_N	ARG_A_1_CA	14.733	4.945	1.144	14.178	4.583	-0.15	1.45	152.88	-146.89
3	2jsa-1	ARG_A_1_CA	ARG_A_1_HA	14.178	4.583	-0.15	14.914	3.981	-0.684	1.09	119.32	-39.28
4	2jsa-1	ARG_A_1_CA	ARG_A_1_C	14.178	4.583	-0.15	13.875	5.84	-0.967	1.53	122.29	103.55
5	2jsa-1	ARG_A_1_C	ARG_A_1_O	13.875	5.84	-0.967	14.57	6.135	-1.939	1.23	142.16	23.00
6	2jsa-1	ARG_A_1_C	SER_A_2_N	13.875	5.84	-0.967	12.838	6.548	-0.544	1.32	71.38	145.68
7	2jsa-1	SER_A_2_N	SER_A_2_H	12.838	6.548	-0.544	12.312	6.246	0.264	1.01	36.89	-150.14
8	2jsa-1	SER_A_2_N	SER_A_2_CA	12.838	6.548	-0.544	12.436	7.767	-1.225	1.45	117.95	108.25
9	2jsa-1	SER_A_2_CA	SER_A_2_HA	12.436	7.767	-1.225	11.492	8.102	-0.796	1.09	66.82	160.46
10	2jsa-1	SER_A_2_CA	SER_A_2_C	12.436	7.767	-1.225	12.226	7.489	-2.715	1.53	166.84	-127.07
11	2jsa-1	SER_A_2_C	SER_A_2_O	12.226	7.489	-2.715	13.136	7.682	-3.52	1.23	130.87	11.97
12	2jsa-1	SER_A_2_C	ALA_A_3_N	12.226	7.489	-2.715	11.022	7.04	-3.037	1.32	104.07	-159.55
13	2jsa-1	ALA_A_3_N	ALA_A_3_H	11.022	7.04	-3.037	10.322	6.904	-2.322	1.01	44.92	-169.01
14	2jsa-1	ALA_A_3_N	ALA_A_3_CA	11.022	7.04	-3.037	10.682	6.734	-4.416	1.45	161.65	-138.01
15	2jsa-1	ALA_A_3_CA	ALA_A_3_HA	10.682	6.734	-4.416	10.847	7.624	-5.023	1.09	123.85	79.50
16	2jsa-1	ALA_A_3_CA	ALA_A_3_C	10.682	6.734	-4.416	9.201	6.358	-4.5	1.53	93.15	-165.75
17	2jsa-1	ALA_A_3_C	ALA_A_3_O	9.201	6.358	-4.5	8.384	6.865	-3.733	1.23	51.42	148.18
18	2jsa-1	ALA_A_3_C	LEU_A_4_N	9.201	6.358	-4.5	8.901	5.473	-5.439	1.32	135.14	-108.73
19	2jsa-1	LEU_A_4_N	LEU_A_4_H	8.901	5.473	-5.439	9.626	5.098	-6.034	1.01	126.09	-27.35
20	2jsa-1	LEU_A_4_N	LEU_A_4_CA	8.901	5.473	-5.439	7.533	5.024	-5.634	1.45	97.71	-161.83
21	2jsa-1	LEU_A_4_CA	LEU_A_4_HA	7.533	5.024	-5.634	6.905	5.905	-5.767	1.09	97.01	125.48
22	2jsa-1	LEU_A_4_CA	LEU_A_4_C	7.533	5.024	-5.634	7.055	4.298	-4.374	1.53	34.60	-123.36
23	2jsa-1	LEU_A_4_C	LEU_A_4_O	7.055	4.298	-4.374	5.862	4.047	-4.213	1.23	82.48	-168.12
24	2jsa-1	LEU_A_4_C	SER_A_5_N	7.055	4.298	-4.374	8.012	3.981	-3.514	1.33	49.53	-18.33
25	2jsa-1	SER_A_5_N	SER_A_5_H	8.012	3.981	-3.514	8.974	4.22	-3.711	1.01	101.24	13.95
26	2jsa-1	SER_A_5_N	SER_A_5_CA	8.012	3.981	-3.514	7.704	3.288	-2.274	1.45	31.45	-113.96
27	2jsa-1	SER_A_5_CA	SER_A_5_HA	7.704	3.288	-2.274	7.472	2.25	-2.511	1.09	102.56	-102.60
28	2jsa-1	SER_A_5_C	SER_A_5_O	7.704	3.288	-2.274	6.482	3.925	-1.609	1.53	64.24	152.47
29	2jsa-1	SER_A_5_C	SER_A_5_O	6.482	3.925	-1.609	5.549	3.226	-1.218	1.23	71.46	-143.16
30	2jsa-1	SER_A_5_C	CYS_A_6_N	6.482	3.925	-1.609	6.528	5.245	-1.501	1.33	85.33	88.00
31	2jsa-1	CYS_A_6_N	CYS_A_6_H	6.528	5.245	-1.501	7.328	5.756	-1.845	1.01	109.92	32.57
32	2jsa-1	CYS_A_6_N	CYS_A_6_CA	6.528	5.245	-1.501	5.436	5.984	-0.89	1.45	65.14	145.91
33	2jsa-1	CYS_A_6_CA	CYS_A_6_HA	5.436	5.984	-0.89	5.312	5.629	0.133	1.09	20.18	-109.25
34	2jsa-1	CYS_A_6_CA	CYS_A_6_C	5.436	5.984	-0.89	4.155	5.681	-1.669	1.53	120.62	-166.69
35	2jsa-1	CYS_A_6_C	CYS_A_6_O	4.155	5.681	-1.669	3.163	5.24	-1.091	1.23	61.97	-156.03
36	2jsa-1	CYS_A_6_C	GLN_A_7_N	4.155	5.681	-1.669	4.218	5.929	-2.969	1.32	168.86	75.75
37	2jsa-1	GLN_A_7_N	GLN_A_7_H	4.218	5.929	-2.969	5.068	6.292	-3.377	1.01	113.82	23.13
38	2jsa-1	GLN_A_7_N	GLN_A_7_CA	4.218	5.929	-2.969	3.075	5.688	-3.833	1.45	126.49	-168.09
39	2jsa-1	GLN_A_7_CA	GLN_A_7_HA	3.075	5.688	-3.833	2.417	6.554	-3.77	1.09	86.68	127.23
40	2jsa-1	GLN_A_7_CA	GLN_A_7_C	3.075	5.688	-3.833	2.299	4.459	-3.356	1.53	71.83	-122.27
41	2jsa-1	GLN_A_7_C	GLN_A_7_O	2.299	4.459	-3.356	1.117	4.555	-3.029	1.23	74.58	175.36
42	2jsa-1	GLN_A_7_C	MET_A_8_N	2.299	4.459	-3.356	2.995	3.332	-3.33	1.32	88.88	-58.30
43	2jsa-1	MET_A_8_N	MET_A_8_H	2.995	3.332	-3.33	3.965	3.327	-3.613	1.01	106.26	-0.30
44	2jsa-1	MET_A_8_N	MET_A_8_CA	2.995	3.332	-3.33	2.386	2.085	-2.899	1.45	72.75	-116.03
45	2jsa-1	MET_A_8_CA	MET_A_8_HA	2.386	2.085	-2.899	1.716	1.734	-3.683	1.09	136.03	-152.35
46	2jsa-1	MET_A_8_CA	MET_A_8_C	2.386	2.085	-2.899	1.584	2.284	-1.611	1.53	32.68	166.06
47	2jsa-1	MET_A_8_C	MET_A_8_O	1.584	2.284	-1.611	0.433	1.86	-1.52	1.23	85.76	-159.78
48	2jsa-1	MET_A_8_C	CYS_A_9_N	1.584	2.284	-1.611	2.224	2.929	-0.647	1.32	43.31	45.22
49	2jsa-1	CYS_A_9_N	CYS_A_9_H	2.224	2.929	-0.647	3.171	3.251	-0.791	1.01	98.19	18.78
50	2jsa-1	CYS_A_9_N	CYS_A_9_CA	2.224	2.929	-0.647	1.585	3.189	0.632	1.45	28.34	157.86
51	2jsa-1	CYS_A_9_CA	CYS_A_9_HA	1.585	3.189	0.632	1.35	2.232	1.099	1.09	64.64	-103.80
52	2jsa-1	CYS_A_9_CA	CYS_A_9_C	1.585	3.189	0.632	0.277	3.938	0.372	1.53	99.79	150.20
53	2jsa-1	CYS_A_9_C	CYS_A_9_O	0.277	3.938	0.372	-0.691	3.78	1.113	1.23	52.93	-170.73
54	2jsa-1	CYS_A_9_C	GLU_A_10_N	0.277	3.938	0.372	0.291	4.739	-0.684	1.33	142.81	89.00
55	2jsa-1	GLU_A_10_N	GLU_A_10_H	0.291	4.739	-0.684	1.124	4.82	-1.25	1.01	124.07	5.55
56	2jsa-1	GLU_A_10_N	GLU_A_10_CA	0.291	4.739	-0.684	-0.882	5.513	-1.051	1.45	104.64	146.58
57	2jsa-1	GLU_A_10_CA	GLU_A_10_HA	-0.882	5.513	-1.051	-1.393	5.806	-0.134	1.09	32.71	150.17
58	2jsa-1	GLU_A_10_CA	GLU_A_10_C	-0.882	5.513	-1.051	-1.841	4.661	-1.885	1.53	123.03	-138.38
59	2jsa-1	GLU_A_10_C	GLU_A_10_O	-1.841	4.661	-1.885	-2.935	5.107	-2.228	1.23	106.19	157.82
60	2jsa-1	GLU_A_10_C	LEU_A_11_N	-1.841	4.661	-1.885	-1.395	3.451	-2.188	1.32	103.22	-69.77
61	2jsa-1	LEU_A_11_N	LEU_A_11_H	-1.395	3.451	-2.188	-0.483	3.151	-1.873	1.01	71.84	-18.21
62	2jsa-1	LEU_A_11_N	LEU_A_11_CA	-1.395	3.451	-2.188	-2.2	2.532	-2.975	1.45	122.79	-131.22
63	2jsa-1	LEU_A_11_CA	LEU_A_11_HA	-2.2	2.532	-2.975	-2.895	3.12	-3.573	1.09	123.30	139.77
64	2jsa-1	LEU_A_11_CA	LEU_A_11_C	-2.2	2.532	-2.975	-3.025	1.65	-2.036	1.53	52.13	-133.09
65	2jsa-1	LEU_A_11_C	LEU_A_11_O	-3.025	1.65	-2.036	-4.199	1.39	-2.296	1.23	102.20	-167.51
66	2jsa-1	LEU_A_11_C	VAL_A_12_N	-3.025	1.65	-2.036	-2.379	1.215	-0.965	1.32	36.02	-33.96
67	2jsa-1	VAL_A_12_N	VAL_A_12_H	-2.379	1.215	-0.965	-1.413	1.469	-0.815	1.01	81.46	14.73
68	2jsa-1	VAL_A_12_N	VAL_A_12_CA	-2.379	1.215	-0.965	-3.039	0.367	0.014	1.45	47.66	-127.89
69	2jsa-1	VAL_A_12_CA	VAL_A_12_HA	-3.039	0.367	0.014	-3.582	-0.414	-0.517	1.09	119.17	-124.81
70	2jsa-1	VAL_A_12_CA	VAL_A_12_C	-3.039	0.367	0.014	-4.052	1.199	0.802	1.53	58.99	140.60
71	2jsa-1	VAL_A_12_C	VAL_A_12_O	-4.052	1.199	0.802	-5.206	0.8	0.952	1.23	83.00	-160.93
72	2jsa-1	VAL_A_12_C	VAL_A_13_N	-4.052	1.199	0.802	-3.584	2.341	1.285	1.33	68.63	67.72
73	2jsa-1	VAL_A_13_N	VAL_A_13_H	-3.584	2.341	1.285	-2.623	2.606	1.122	1.01	99.29	15.42
74	2jsa-1	VAL_A_13_N	VAL_A_13_CA	-3.584	2.341	1.285	-4.435	3.233	2.055	1.45	58.01	133.65
75	2jsa-1	VAL_A_13_CA	VAL_A_13_HA	-4.435	3.233	2.055	-4.847	2.676	2.896	1.09	39.48	-126.49
76	2jsa-1	VAL_A_13_CA	VAL_A_13_C	-4.435	3.233	2.055	-5.599	3.701	1.179	1.53	124.92	158.10
77	2jsa-1	VAL_A_13_C	VAL_A_13_O	-5.599	3.701	1.179	-6.762	3.494	1.523	1.23	73.76	-169.91
78	2jsa-1	VAL_A_13_C	LYS_A_14_N	-5.599	3.701	1.179	-5.246	4.324	0.064	1.33	147.29	60.46
79	2jsa-1	LYS_A_14_N	LYS_A_14_H	-5.246	4.324	0.064	-4.269	4.46	-0.155	1.01	102.52	7.92
80	2jsa-1	LYS_A_14_N	LYS_A_14_CA	-5.246	4.324	0.064	-6.247	4.823	-0.863	1.45	129.65	153.50
81	2jsa-1	LYS_A_14_CA	LYS_A_14_HA	-6.247	4.823	-0.863	-6.724	5.691	-0.409	1.09	65.37	118.79
82	2jsa-1	LYS_A_14_CA	LYS_A_14_C	-6.247	4.823	-0.863	-7.323	3.755	-1.069	1.53	97.74	-135.21
83	2jsa-1	LYS_A_14_C	LYS_A_14_O	-7.323	3.755	-1.069	-8.493	4.078	-1.272	1.23	99.49	164.57
84	2jsa-1	LYS_A_14_C	LYS_A_15_N	-7.323	3.755	-1.069	-6.89	2.505	-1.009	1.32	87.40	-70.89
85	2jsa-1	LYS_A_15_N	LYS_A_15_H	-6.89	2.505	-1.009	-5.913	2.313	-0.838	1.01	80.26	-11.12
86	2jsa-1	LYS_A_15_N	LYS_A_15_CA	-6.89	2.505	-1.009	-7.802	1.387	-1.186	1.45	96.99	-129.21
87	2jsa-1	LYS_A_15_CA	LYS_A_15_HA	-7.802	1.387	-1.186	-8.56	1.681	-1.911	1.09	131.72	158.80
88	2jsa-1	LYS_A_15_CA	LYS_A_15_C	-7.802	1.387	-1.186	-8.512	1.1	0.138	1.53	30.05	-157.99
89	2jsa-1	LYS_A_15_C	LYS_A_15_O	-8.512	1.1	0.138	-9.688	0.737	0.15	1.23	89.44	-162.85
90	2jsa-1	LYS_A_15_C	TYR_A_16_N	-8.512	1.1	0.138	-7.769	1.272	1.221	1.32	35.15	13.03
91	2jsa-1	TYR_A_16_N	TYR_A_16_H	-7.769	1.272	1.221	-6.808	1.571	1.136	1.01	94.83	17.28
92	2jsa-1	TYR_A_16_N	TYR_A_16_CA	-7.769								

93	2jsa-1	TYR_A_16_CA	TYR_A_16_HA	-8.313	1.035	2.548	-8.806	0.064	2.586	1.09	88.00	-116.92
94	2jsa-1	TYR_A_16_CA	TYR_A_16_C	-8.313	1.035	2.548	-9.301	2.135	2.94	1.53	75.15	131.93
95	2jsa-1	TYR_A_16_C	TYR_A_16_O	-9.301	2.135	2.94	-10.499	1.884	3.063	1.23	84.26	-168.17
96	2jsa-1	TYR_A_16_C	GLU_A_17_N	-9.301	2.135	2.94	-8.762	3.332	3.124	1.33	82.02	65.76
97	2jsa-1	GLU_A_17_N	GLU_A_17_H	-8.762	3.332	3.124	-7.768	3.466	3.004	1.01	96.82	7.68
98	2jsa-1	GLU_A_17_N	GLU_A_17_CA	-8.762	3.332	3.124	-9.582	4.472	3.499	1.45	75.05	125.73
99	2jsa-1	GLU_A_17_CA	GLU_A_17_HA	-9.582	4.472	3.499	-9.988	4.283	4.493	1.09	24.25	-155.04
100	2jsa-1	GLU_A_17_CA	GLU_A_17_C	-9.582	4.472	3.499	-10.75	4.629	2.524	1.53	129.60	172.34
101	2jsa-1	GLU_A_17_C	GLU_A_17_O	-10.75	4.629	2.524	-11.813	5.122	2.898	1.23	72.30	155.12
102	2jsa-1	GLU_A_17_C	GLY_A_18_N	-10.75	4.629	2.524	-10.513	4.202	1.292	1.33	158.38	-60.97
103	2jsa-1	GLY_A_18_N	GLY_A_18_H	-10.513	4.202	1.292	-9.614	3.808	1.055	1.01	103.57	-23.67
104	2jsa-1	GLY_A_18_N	GLY_A_18_CA	-10.513	4.202	1.292	-11.532	4.29	0.261	1.45	135.23	175.06
105	2jsa-1	GLY_A_18_CA	GLY_A_18_C	-11.532	4.29	0.261	-11.817	2.915	-0.347	1.53	113.41	-101.71
106	2jsa-1	GLY_A_18_C	GLY_A_18_O	-11.817	2.915	-0.347	-11.513	2.673	-1.514	1.23	161.58	-38.52
107	2jsa-1	GLY_A_18_C	SER_A_19_N	-11.817	2.915	-0.347	-12.397	2.05	0.472	1.32	51.82	-123.84
108	2jsa-1	SER_A_19_N	SER_A_19_H	-12.397	2.05	0.472	-12.618	2.317	1.421	1.01	20.06	129.62
109	2jsa-1	SER_A_19_N	SER_A_19_CA	-12.397	2.05	0.472	-12.727	0.706	0.029	1.45	107.75	-103.80
110	2jsa-1	SER_A_19_CA	SER_A_19_HA	-12.727	0.706	0.029	-12.201	0.516	-0.907	1.09	149.14	-19.86
111	2jsa-1	SER_A_19_CA	SER_A_19_C	-12.727	0.706	0.029	-14.232	0.591	-0.222	1.53	99.44	-175.63
112	2jsa-1	SER_A_19_C	SER_A_19_O	-14.232	0.591	-0.222	-14.71	0.918	-1.307	1.23	151.91	145.62
113	2jsa-1	SER_A_19_C	ALA_A_20_N	-14.232	0.591	-0.222	-14.936	0.126	0.799	1.32	39.57	-146.55
114	2jsa-1	ALA_A_20_N	ALA_A_20_H	-14.936	0.126	0.799	-14.475	-0.125	1.662	1.01	31.31	-28.57
115	2jsa-1	ALA_A_20_N	ALA_A_20_CA	-14.936	0.126	0.799	-16.377	-0.035	0.703	1.45	93.79	-173.62
116	2jsa-1	ALA_A_20_CA	ALA_A_20_HA	-16.377	-0.035	0.703	-16.85	0.93	0.881	1.09	80.60	116.11
117	2jsa-1	ALA_A_20_CA	ALA_A_20_C	-16.377	-0.035	0.703	-16.849	-1.012	1.781	1.53	45.19	-115.79
118	2jsa-1	ALA_A_20_C	ALA_A_20_O	-16.849	-1.012	1.781	-17.938	-0.855	2.333	1.23	63.36	171.80
119	2jsa-1	ALA_A_20_C	ASP_A_21_N	-16.849	-1.012	1.781	-16.008	-2.0	2.049	1.32	78.33	-49.60
120	2jsa-1	ASP_A_21_N	ASP_A_21_H	-16.008	-2.0	2.049	-15.129	-2.068	1.555	1.01	119.26	-4.42
121	2jsa-1	ASP_A_21_N	ASP_A_21_CA	-16.008	-2.0	2.049	-16.326	-3.003	3.052	1.45	46.37	-107.59
122	2jsa-1	ASP_A_21_CA	ASP_A_21_HA	-16.326	-3.003	3.052	-17.356	-2.866	3.379	1.09	72.53	172.42
123	2jsa-1	ASP_A_21_CA	ASP_A_21_C	-16.326	-3.003	3.052	-15.378	-2.846	4.242	1.53	38.92	9.40
124	2jsa-1	ASP_A_21_C	ASP_A_21_O	-15.378	-2.846	4.242	-15.634	-3.383	5.319	1.23	28.91	-115.49
125	2jsa-1	ASP_A_21_C	LYS_A_22_N	-15.378	-2.846	4.242	-14.303	-2.108	4.009	1.32	100.13	34.47
126	2jsa-1	LYS_A_22_N	LYS_A_22_H	-14.303	-2.108	4.009	-14.156	-1.696	3.099	1.01	154.33	70.36
127	2jsa-1	LYS_A_22_N	LYS_A_22_CA	-14.303	-2.108	4.009	-13.316	-1.874	5.049	1.45	44.28	13.34
128	2jsa-1	LYS_A_22_CA	LYS_A_22_HA	-13.316	-1.874	5.049	-12.587	-1.158	4.668	1.09	110.45	44.48
129	2jsa-1	LYS_A_22_CA	LYS_A_22_C	-13.316	-1.874	5.049	-12.574	-3.179	5.345	1.53	78.85	-60.38
130	2jsa-1	LYS_A_22_C	LYS_A_22_O	-12.574	-3.179	5.345	-12.164	-3.42	6.479	1.23	22.75	-30.45
131	2jsa-1	LYS_A_22_C	ASP_A_23_N	-12.574	-3.179	5.345	-12.424	-3.986	4.305	1.32	141.72	-79.47
132	2jsa-1	ASP_A_23_N	ASP_A_23_H	-12.424	-3.986	4.305	-12.788	-3.723	3.4	1.01	153.61	144.15
133	2jsa-1	ASP_A_23_N	ASP_A_23_CA	-12.424	-3.986	4.305	-11.738	-5.26	4.44	1.45	84.67	-61.70
134	2jsa-1	ASP_A_23_CA	ASP_A_23_HA	-11.738	-5.26	4.44	-11.841	-5.613	5.466	1.09	19.72	-106.27
135	2jsa-1	ASP_A_23_CA	ASP_A_23_C	-11.738	-5.26	4.44	-10.258	-5.077	4.099	1.53	102.88	7.05
136	2jsa-1	ASP_A_23_C	ASP_A_23_O	-10.258	-5.077	4.099	-9.914	-4.769	2.959	1.23	157.95	41.84
137	2jsa-1	ASP_A_23_C	ALA_A_24_N	-10.258	-5.077	4.099	-9.423	-5.274	5.108	1.32	40.37	-13.27
138	2jsa-1	ALA_A_24_N	ALA_A_24_H	-9.423	-5.274	5.108	-9.777	-5.525	6.02	1.01	25.45	-144.66
139	2jsa-1	ALA_A_24_N	ALA_A_24_CA	-9.423	-5.274	5.108	-7.987	-5.134	4.929	1.45	97.07	5.57
140	2jsa-1	ALA_A_24_CA	ALA_A_24_HA	-7.987	-5.134	4.929	-7.783	-4.168	4.466	1.09	115.12	78.08
141	2jsa-1	ALA_A_24_CA	ALA_A_24_C	-7.987	-5.134	4.929	-7.485	-6.235	3.993	1.53	127.72	-65.49
142	2jsa-1	ALA_A_24_C	ALA_A_24_O	-7.485	-6.235	3.993	-6.337	-6.204	3.552	1.23	111.01	1.55
143	2jsa-1	ALA_A_24_C	ASN_A_25_N	-7.485	-6.235	3.993	-8.369	-7.183	3.718	1.33	101.98	-133.00
144	2jsa-1	ASN_A_25_N	ASN_A_25_H	-8.369	-7.183	3.718	-9.296	-7.145	4.117	1.01	66.73	177.65
145	2jsa-1	ASN_A_25_N	ASN_A_25_CA	-8.369	-7.183	3.718	-8.029	-8.292	2.842	1.45	127.06	-72.96
146	2jsa-1	ASN_A_25_CA	ASN_A_25_HA	-8.029	-8.292	2.842	-6.979	-8.551	2.985	1.09	82.47	-13.86
147	2jsa-1	ASN_A_25_CA	ASN_A_25_C	-8.029	-8.292	2.842	-8.27	-7.88	1.388	1.53	161.83	120.33
148	2jsa-1	ASN_A_25_C	ASN_A_25_O	-8.27	-7.88	1.388	-7.374	-7.99	0.552	1.23	132.80	-7.00
149	2jsa-1	ASN_A_25_C	VAL_A_26_N	-8.27	-7.88	1.388	-9.483	-7.415	1.131	1.32	101.19	159.03
150	2jsa-1	VAL_A_26_N	VAL_A_26_H	-9.483	-7.415	1.131	-10.17	-7.353	1.868	1.01	43.10	174.84
151	2jsa-1	VAL_A_26_N	VAL_A_26_CA	-9.483	-7.415	1.131	-9.852	-6.986	-0.207	1.45	157.08	130.70
152	2jsa-1	VAL_A_26_CA	VAL_A_26_HA	-9.852	-6.986	-0.207	-9.442	-7.699	-0.922	1.09	131.00	-60.10
153	2jsa-1	VAL_A_26_CA	VAL_A_26_C	-9.852	-6.986	-0.207	-9.229	-5.618	-0.49	1.53	100.66	65.52
154	2jsa-1	VAL_A_26_C	VAL_A_26_O	-9.229	-5.618	-0.49	-9.323	-5.108	-1.605	1.23	155.06	100.44
155	2jsa-1	VAL_A_26_C	ILE_A_27_N	-9.229	-5.618	-0.49	-8.604	-5.064	0.539	1.33	39.06	41.55
156	2jsa-1	ILE_A_27_N	ILE_A_27_H	-8.604	-5.064	0.539	-8.563	-5.543	1.428	1.01	28.40	-85.11
157	2jsa-1	ILE_A_27_N	ILE_A_27_CA	-8.604	-5.064	0.539	-7.965	-3.765	0.415	1.45	94.90	63.81
158	2jsa-1	ILE_A_27_CA	ILE_A_27_HA	-7.965	-3.765	0.415	-8.529	-3.179	-0.311	1.09	131.75	133.90
159	2jsa-1	ILE_A_27_CA	ILE_A_27_C	-7.965	-3.765	0.415	-6.549	-3.949	-0.136	1.53	111.10	-7.40
160	2jsa-1	ILE_A_27_C	ILE_A_27_O	-6.549	-3.949	-0.136	-6.175	-3.315	-1.121	1.23	143.23	59.46
161	2jsa-1	ILE_A_27_C	LYS_A_28_N	-6.549	-3.949	-0.136	-5.8	-4.82	0.525	1.33	60.08	-49.31
162	2jsa-1	LYS_A_28_N	LYS_A_28_H	-5.8	-4.82	0.525	-6.173	-5.306	1.328	1.01	37.34	-127.51
163	2jsa-1	LYS_A_28_N	LYS_A_28_CA	-5.8	-4.82	0.525	-4.434	-5.095	0.114	1.45	106.43	-11.38
164	2jsa-1	LYS_A_28_CA	LYS_A_28_HA	-4.434	-5.095	0.114	-3.902	-4.145	0.052	1.09	93.26	60.75
165	2jsa-1	LYS_A_28_CA	LYS_A_28_C	-4.434	-5.095	0.114	-4.442	-5.715	-1.284	1.53	156.08	-90.74
166	2jsa-1	LYS_A_28_C	LYS_A_28_O	-4.442	-5.715	-1.284	-3.454	-5.625	-2.012	1.23	126.27	5.20
167	2jsa-1	LYS_A_28_C	LYS_A_29_N	-4.442	-5.715	-1.284	-5.567	-6.33	-1.618	1.32	104.60	-151.34
168	2jsa-1	LYS_A_29_N	LYS_A_29_H	-5.567	-6.33	-1.618	-6.339	-6.364	-0.968	1.01	49.93	-177.48
169	2jsa-1	LYS_A_29_N	LYS_A_29_CA	-5.567	-6.33	-1.618	-5.716	-6.965	-2.916	1.45	153.32	-103.21
170	2jsa-1	LYS_A_29_CA	LYS_A_29_HA	-5.716	-6.965	-2.916	-4.808	-7.534	-3.119	1.09	100.73	-32.07
171	2jsa-1	LYS_A_29_CA	LYS_A_29_C	-5.716	-6.965	-2.916	-5.841	-5.887	-3.995	1.53	134.84	96.61
172	2jsa-1	LYS_A_29_C	LYS_A_29_O	-5.841	-5.887	-3.995	-5.156	-5.942	-5.015	1.23	146.03	-4.59
173	2jsa-1	LYS_A_29_C	ASP_A_30_N	-5.841	-5.887	-3.995	-6.722	-4.933	-3.733	1.32	78.59	132.72
174	2jsa-1	ASP_A_30_N	ASP_A_30_H	-6.722	-4.933	-3.733	-7.252	-4.952	-2.874	1.01	31.69	-177.95
175	2jsa-1	ASP_A_30_N	ASP_A_30_CA	-6.722	-4.933	-3.733	-6.946	-3.844	-4.668	1.45	130.06	101.62
176	2jsa-1	ASP_A_30_CA	ASP_A_30_HA	-6.946	-3.844	-4.668	-7.455	-4.232	-5.55	1.09	144.03	-142.68
177	2jsa-1	ASP_A_30_CA	ASP_A_30_C	-6.946	-3.844	-4.668	-5.601	-3.237	-5.069	1.53	105.20	24.29
178	2jsa-1	ASP_A_30_C	ASP_A_30_O	-5.601	-3.237	-5.069	-5.381	-2.924	-6.238	1.23	161.88	54.90
179	2jsa-1	ASP_A_30_C	PHE_A_31_N	-5.601	-3.237	-5.069	-4.735	-3.088	-4.077	1.33	41.53	9.76
180	2jsa-1	PHE_A_31_N	PHE_A_31_H	-4.735	-3.088	-4.077	-4.983	-3.367	-3.139	1.01	21.70	-131.63
181	2jsa-1	PHE_A_31_N	PHE_A_31_CA	-4.735	-3.088	-4.077	-3.417	-2.524	-4.312	1.45	99.31	23.17
182	2jsa-1	PHE_A_31_CA	PHE_A_31_HA	-3.417	-2.524	-4.312	-3.509	-1.478	-4.604	1.09	105.54	95.03
183	2jsa-1	PHE_A_31_CA	PHE_A_31_C	-3.417	-2.524	-4.312	-2.675	-3.299</				

186	2jsa-1	ASP_A_32_N	ASP_A_32_H	-2.437	-4.572	-5.121	-2.738	-4.963	-4.24	1.01	29.25	-127.59
187	2jsa-1	ASP_A_32_N	ASP_A_32_CA	-2.437	-4.572	-5.121	-1.741	-5.429	-6.065	1.45	130.53	-50.92
188	2jsa-1	ASP_A_32_CA	ASP_A_32_HA	-1.741	-5.429	-6.065	-0.725	-5.058	-6.2	1.09	97.11	20.06
189	2jsa-1	ASP_A_32_CA	ASP_A_32_C	-1.741	-5.429	-6.065	-2.482	-5.415	-7.403	1.53	151.02	178.92
190	2jsa-1	ASP_A_32_C	ASP_A_32_O	-2.482	-5.415	-7.403	-1.905	-5.737	-8.441	1.23	147.52	-29.16
191	2jsa-1	ASP_A_32_C	ALA_A_33_N	-2.482	-5.415	-7.403	-3.751	-5.038	-7.337	1.33	87.15	163.45
192	2jsa-1	ALA_A_33_N	ALA_A_33_H	-3.751	-5.038	-7.337	-4.161	-4.787	-6.449	1.01	28.43	148.53
193	2jsa-1	ALA_A_33_N	ALA_A_33_CA	-3.751	-5.038	-7.337	-4.577	-4.978	-8.53	1.45	145.23	175.85
194	2jsa-1	ALA_A_33_CA	ALA_A_33_HA	-4.577	-4.978	-8.53	-4.657	-5.98	-8.951	1.09	112.73	-94.56
195	2jsa-1	ALA_A_33_CA	ALA_A_33_C	-4.577	-4.978	-8.53	-3.907	-4.071	-9.564	1.53	132.52	53.55
196	2jsa-1	ALA_A_33_C	ALA_A_33_O	-3.907	-4.071	-9.564	-3.39	-4.549	-10.573	1.23	145.09	-42.76
197	2jsa-1	ALA_A_33_C	GLU_A_34_N	-3.907	-4.071	-9.564	-3.938	-2.778	-9.278	1.32	77.53	91.37
198	2jsa-1	GLU_A_34_N	GLU_A_34_H	-3.938	-2.778	-9.278	-4.38	-2.455	-8.429	1.01	32.81	143.84
199	2jsa-1	GLU_A_34_N	GLU_A_34_CA	-3.938	-2.778	-9.278	-3.34	-1.799	-10.171	1.45	127.90	58.58
200	2jsa-1	GLU_A_34_CA	GLU_A_34_HA	-3.34	-1.799	-10.171	-3.637	-2.046	-11.19	1.09	159.24	-140.25
201	2jsa-1	GLU_A_34_CA	GLU_A_34_C	-3.34	-1.799	-10.171	-1.814	-1.866	-10.085	1.53	86.78	-2.51
202	2jsa-1	GLU_A_34_C	GLU_A_34_O	-1.814	-1.866	-10.085	-1.126	-1.747	-11.098	1.23	145.42	9.81
203	2jsa-1	GLU_A_34_C	CYS_A_35_N	-1.814	-1.866	-10.085	-1.329	-2.056	-8.867	1.32	23.15	-21.39
204	2jsa-1	CYS_A_35_N	CYS_A_35_H	-1.329	-2.056	-8.867	-1.954	-2.147	-8.079	1.01	38.71	-171.72
205	2jsa-1	CYS_A_35_N	CYS_A_35_CA	-1.329	-2.056	-8.867	0.103	-2.139	-8.636	1.45	80.85	-3.32
206	2jsa-1	CYS_A_35_CA	CYS_A_35_HA	0.103	-2.139	-8.636	0.532	-1.146	-8.776	1.09	97.37	66.63
207	2jsa-1	CYS_A_35_CA	CYS_A_35_C	0.103	-2.139	-8.636	0.704	-3.081	-9.682	1.53	133.11	-57.46
208	2jsa-1	CYS_A_35_C	CYS_A_35_O	0.704	-3.081	-9.682	1.888	-2.986	-9.999	1.23	104.94	4.59
209	2jsa-1	CYS_A_35_C	LYS_A_36_N	0.704	-3.081	-9.682	-0.141	-3.967	-10.188	1.32	112.45	-133.64
210	2jsa-1	LYS_A_36_N	LYS_A_36_H	-0.141	-3.967	-10.188	-1.102	-3.987	-9.879	1.01	72.18	-178.81
211	2jsa-1	LYS_A_36_N	LYS_A_36_CA	-0.141	-3.967	-10.188	0.292	-4.925	-11.192	1.45	133.68	-65.68
212	2jsa-1	LYS_A_36_CA	LYS_A_36_HA	0.292	-4.925	-11.192	1.34	-5.161	-11.004	1.09	80.07	-12.69
213	2jsa-1	LYS_A_36_CA	LYS_A_36_C	0.292	-4.925	-11.192	0.202	-4.282	-12.577	1.53	154.88	97.97
214	2jsa-1	LYS_A_36_C	LYS_A_36_O	0.202	-4.282	-12.577	1.207	-4.156	-13.274	1.23	124.53	7.15
215	2jsa-1	LYS_A_36_C	LYS_A_37_N	0.202	-4.282	-12.577	-1.013	-3.891	-12.935	1.33	105.67	162.16
216	2jsa-1	LYS_A_37_N	LYS_A_37_H	-1.013	-3.891	-12.935	-1.795	-4.026	-12.31	1.01	51.78	-170.21
217	2jsa-1	LYS_A_37_N	LYS_A_37_CA	-1.013	-3.891	-12.935	-1.248	-3.264	-14.224	1.45	152.55	110.55
218	2jsa-1	LYS_A_37_CA	LYS_A_37_HA	-1.248	-3.264	-14.224	-0.801	-3.895	-14.992	1.09	134.80	-54.69
219	2jsa-1	LYS_A_37_CA	LYS_A_37_C	-1.248	-3.264	-14.224	-0.537	-1.909	-14.265	1.53	91.53	62.31
220	2jsa-1	LYS_A_37_C	LYS_A_37_O	-0.537	-1.909	-14.265	0.376	-1.707	-15.064	1.23	130.51	12.48
221	2jsa-1	LYS_A_37_C	LEU_A_38_N	-0.537	-1.909	-14.265	-0.983	-1.017	-13.393	1.32	48.83	116.57
222	2jsa-1	LEU_A_38_N	LEU_A_38_H	-0.983	-1.017	-13.393	-1.738	-1.252	-12.765	1.01	51.54	-162.71
223	2jsa-1	LEU_A_38_N	LEU_A_38_CA	-0.983	-1.017	-13.393	-0.401	0.312	-13.319	1.45	87.08	66.35
224	2jsa-1	LEU_A_38_CA	LEU_A_38_HA	-0.401	0.312	-13.319	-0.784	0.895	-14.156	1.09	140.19	123.30
225	2jsa-1	LEU_A_38_CA	LEU_A_38_C	-0.401	0.312	-13.319	1.117	0.21	-13.48	1.53	96.04	-3.84
226	2jsa-1	LEU_A_38_C	LEU_A_38_O	1.117	0.21	-13.48	1.716	0.967	-14.243	1.23	128.32	51.65
227	2jsa-1	LEU_A_38_C	PHE_A_39_N	1.117	0.21	-13.48	1.695	-0.732	-12.75	1.32	56.55	-58.47
228	2jsa-1	PHE_A_39_N	PHE_A_39_H	1.695	-0.732	-12.75	1.14	-1.319	-12.144	1.01	53.12	-133.39
229	2jsa-1	PHE_A_39_N	PHE_A_39_CA	1.695	-0.732	-12.75	3.132	-0.943	-12.803	1.45	92.09	-8.35
230	2jsa-1	PHE_A_39_CA	PHE_A_39_HA	3.132	-0.943	-12.803	3.595	-0.185	-13.436	1.09	125.48	58.58
231	2jsa-1	PHE_A_39_CA	PHE_A_39_C	3.132	-0.943	-12.803	3.462	-2.336	-13.343	1.53	110.67	-76.67
232	2jsa-1	PHE_A_39_C	PHE_A_39_O	3.462	-2.336	-13.343	4.256	-3.064	-12.749	1.23	61.13	-42.52
233	2jsa-1	PHE_A_39_C	HIS_A_40_N	3.462	-2.336	-13.343	2.835	-2.665	-14.463	1.33	147.70	-152.31
234	2jsa-1	HIS_A_40_N	HIS_A_40_H	2.835	-2.665	-14.463	2.194	-2.016	-14.896	1.01	115.39	134.64
235	2jsa-1	HIS_A_40_N	HIS_A_40_CA	2.835	-2.665	-14.463	3.053	-3.958	-15.09	1.45	115.56	-80.43
236	2jsa-1	HIS_A_40_CA	HIS_A_40_HA	3.053	-3.958	-15.09	3.113	-4.709	-14.302	1.09	43.71	-85.43
237	2jsa-1	HIS_A_40_CA	HIS_A_40_C	3.053	-3.958	-15.09	4.39	-3.95	-15.832	1.53	119.03	0.34
238	2jsa-1	HIS_A_40_C	HIS_A_40_O	4.39	-3.95	-15.832	4.976	-5.004	-16.074	1.23	101.35	-60.93
239	2jsa-1	HIS_A_40_C	THR_A_41_N	4.39	-3.95	-15.832	4.835	-2.749	-16.172	1.33	104.87	69.67
240	2jsa-1	THR_A_41_N	THR_A_41_H	4.835	-2.749	-16.172	4.301	-1.924	-15.939	1.01	76.66	122.91
241	2jsa-1	THR_A_41_N	THR_A_41_CA	4.835	-2.749	-16.172	6.093	-2.59	-16.882	1.45	119.25	7.20
242	2jsa-1	THR_A_41_CA	THR_A_41_HA	6.093	-2.59	-16.882	6.457	-3.575	-17.175	1.09	105.59	-69.72
243	2jsa-1	THR_A_41_CA	THR_A_41_C	6.093	-2.59	-16.882	7.143	-1.953	-15.97	1.53	53.40	31.24
244	2jsa-1	THR_A_41_C	THR_A_41_O	7.143	-1.953	-15.97	7.885	-1.069	-16.394	1.23	110.17	49.99
245	2jsa-1	THR_A_41_C	ILE_A_42_N	7.143	-1.953	-15.97	7.172	-2.427	-14.733	1.33	21.00	-86.50
246	2jsa-1	ILE_A_42_N	ILE_A_42_H	7.172	-2.427	-14.733	6.532	-3.156	-14.452	1.01	73.85	-131.28
247	2jsa-1	ILE_A_42_N	ILE_A_42_CA	7.172	-2.427	-14.733	8.119	-1.915	-13.757	1.45	47.80	28.40
248	2jsa-1	ILE_A_42_CA	ILE_A_42_HA	8.119	-1.915	-13.757	8.728	-1.153	-14.245	1.09	116.58	51.37
249	2jsa-1	ILE_A_42_CA	ILE_A_42_C	8.119	-1.915	-13.757	9.052	-3.044	-13.317	1.53	73.28	-50.43
250	2jsa-1	ILE_A_42_C	ILE_A_42_O	9.052	-3.044	-13.317	8.626	-4.191	-13.185	1.23	83.84	-110.38
251	2jsa-1	ILE_A_42_C	PRO_A_43_N	9.052	-3.044	-13.317	10.341	-2.671	-13.096	1.36	80.65	16.14
252	2jsa-1	PRO_A_43_N	PRO_A_43_CA	10.341	-2.671	-13.096	11.339	-3.64	-12.674	1.45	73.12	-44.16
253	2jsa-1	PRO_A_43_CA	PRO_A_43_HA	11.339	-3.64	-12.674	11.253	-4.549	-13.27	1.09	123.13	-95.40
254	2jsa-1	PRO_A_43_CA	PRO_A_43_C	11.339	-3.64	-12.674	11.156	-4.007	-11.2	1.53	15.55	-116.50
255	2jsa-1	PRO_A_43_C	PRO_A_43_O	11.156	-4.007	-11.2	11.515	-3.233	-10.314	1.23	43.92	65.12
256	2jsa-1	PRO_A_43_C	PHE_A_44_N	11.156	-4.007	-11.2	10.599	-5.189	-10.982	1.32	80.53	-115.23
257	2jsa-1	PHE_A_44_N	PHE_A_44_H	10.599	-5.189	-10.982	10.33	-5.775	-11.759	1.01	140.31	-114.66
258	2jsa-1	PHE_A_44_N	PHE_A_44_CA	10.599	-5.189	-10.982	10.364	-5.669	-9.631	1.45	21.58	-116.09
259	2jsa-1	PHE_A_44_CA	PHE_A_44_HA	10.364	-5.669	-9.631	10.203	-6.747	-9.644	1.09	90.68	-98.49
260	2jsa-1	PHE_A_44_CA	PHE_A_44_C	10.364	-5.669	-9.631	9.153	-4.975	-9.005	1.53	65.84	150.18
261	2jsa-1	PHE_A_44_C	PHE_A_44_O	9.153	-4.975	-9.005	8.797	-5.251	-7.861	1.23	21.49	-142.21
262	2jsa-1	PHE_A_44_C	GLY_A_45_N	9.153	-4.975	-9.005	8.552	-4.087	-9.784	1.33	126.00	124.09
263	2jsa-1	GLY_A_45_N	GLY_A_45_H	8.552	-4.087	-9.784	8.899	-3.91	-10.716	1.01	157.32	27.03
264	2jsa-1	GLY_A_45_N	GLY_A_45_CA	8.552	-4.087	-9.784	7.388	-3.351	-9.32	1.45	71.38	147.69
265	2jsa-1	GLY_A_45_CA	GLY_A_45_C	7.388	-3.351	-9.32	6.3	-4.305	-8.821	1.53	70.97	-138.75
266	2jsa-1	GLY_A_45_C	GLY_A_45_O	6.3	-4.305	-8.821	5.969	-4.309	-7.637	1.23	15.62	-179.31
267	2jsa-1	GLY_A_45_C	THR_A_46_N	6.3	-4.305	-8.821	5.774	-5.089	-9.75	1.32	134.54	-123.86
268	2jsa-1	THR_A_46_N	THR_A_46_H	5.774	-5.089	-9.75	6.095	-5.031	-10.706	1.01	161.16	10.24
269	2jsa-1	THR_A_46_N	THR_A_46_CA	5.774	-5.089	-9.75	4.731	-6.045	-9.419	1.45	76.83	-137.49
270	2jsa-1	THR_A_46_CA	THR_A_46_HA	4.731	-6.045	-9.419	3.875	-5.503	-9.019	1.09	68.46	147.66
271	2jsa-1	THR_A_46_CA	THR_A_46_C	4.731	-6.045	-9.419	5.218	-7.016	-8.342	1.53	45.25	-63.36
272	2jsa-1	THR_A_46_C	THR_A_46_O	5.218	-7.016	-8.342	4.428	-7.501	-7.535	1.23	48.96	-148.45
273	2jsa-1	THR_A_46_C	ARG_A_47_N	5.218	-7.016	-8.342	6.518	-7.27	-8.365	1.32	90.99	-11.06
274	2jsa-1	ARG_A_47_N	ARG_A_47_H	6.518	-7.27	-8.365	7.109	-6.835	-9.059	1.01	133.40	36.35
275	2jsa-1	ARG_A_47_N	ARG_A_47_CA	6.518	-7.27	-8.365	7.121	-8.175	-7.401	1.45	48.44	-56.32
276	2jsa-1	ARG_A_47_CA	ARG_A_47_HA	7.121	-8.175							

279	2jsa-1	ARG_A_47_C	GLU_A_48_N	6.99	-7.606	-5.986	7.502	-6.396	-5.82	1.32	82.80	67.06
280	2jsa-1	GLU_A_48_N	GLU_A_48_H	7.502	-6.396	-5.82	7.938	-5.917	-6.595	1.01	140.11	47.69
281	2jsa-1	GLU_A_48_N	GLU_A_48_CA	7.502	-6.396	-5.82	7.449	-5.732	-4.529	1.45	27.29	94.56
282	2jsa-1	GLU_A_48_CA	GLU_A_48_HA	7.449	-5.732	-4.529	7.882	-6.403	-3.787	1.09	47.10	-57.17
283	2jsa-1	GLU_A_48_CA	GLU_A_48_C	7.449	-5.732	-4.529	5.998	-5.451	-4.135	1.53	75.07	169.04
284	2jsa-1	GLU_A_48_C	GLU_A_48_O	5.998	-5.451	-4.135	5.667	-5.419	-2.95	1.23	15.68	174.48
285	2jsa-1	GLU_A_48_C	CYS_A_49_N	5.998	-5.451	-4.135	5.17	-5.255	-5.15	1.32	140.03	166.68
286	2jsa-1	CYS_A_49_N	CYS_A_49_H	5.17	-5.255	-5.15	5.512	-5.296	-6.1	1.01	160.07	-6.84
287	2jsa-1	CYS_A_49_N	CYS_A_49_CA	5.17	-5.255	-5.15	3.761	-4.979	-4.925	1.45	81.09	168.92
288	2jsa-1	CYS_A_49_CA	CYS_A_49_HA	3.761	-4.979	-4.925	3.674	-3.993	-4.468	1.09	65.22	95.04
289	2jsa-1	CYS_A_49_CA	CYS_A_49_C	3.761	-4.979	-4.925	3.218	-6.02	-3.944	1.53	50.12	-117.55
290	2jsa-1	CYS_A_49_C	CYS_A_49_O	3.218	-6.02	-3.944	2.88	-5.691	-2.808	1.23	22.55	135.77
291	2jsa-1	CYS_A_49_C	ASP_A_50_N	3.218	-6.02	-3.944	3.151	-7.255	-4.419	1.32	111.01	-93.11
292	2jsa-1	ASP_A_50_N	ASP_A_50_H	3.151	-7.255	-4.419	3.446	-7.453	-5.365	1.01	159.42	-33.87
293	2jsa-1	ASP_A_50_N	ASP_A_50_CA	3.151	-7.255	-4.419	2.655	-8.347	-3.598	1.45	55.61	-114.43
294	2jsa-1	ASP_A_50_CA	ASP_A_50_HA	2.655	-8.347	-3.598	1.607	-8.166	-3.36	1.09	77.39	170.20
295	2jsa-1	ASP_A_50_CA	ASP_A_50_C	2.655	-8.347	-3.598	3.474	-8.423	-2.309	1.53	32.54	-5.30
296	2jsa-1	ASP_A_50_C	ASP_A_50_O	3.474	-8.423	-2.309	2.994	-8.921	-1.292	1.23	34.22	-133.95
297	2jsa-1	ASP_A_50_C	HIS_A_51_N	3.474	-8.423	-2.309	4.698	-7.922	-2.393	1.33	93.63	22.26
298	2jsa-1	HIS_A_51_N	HIS_A_51_H	4.698	-7.922	-2.393	5.028	-7.528	-3.263	1.01	149.43	50.05
299	2jsa-1	HIS_A_51_N	HIS_A_51_CA	4.698	-7.922	-2.393	5.589	-7.927	-1.245	1.45	37.82	-0.32
300	2jsa-1	HIS_A_51_CA	HIS_A_51_HA	5.589	-7.927	-1.245	5.382	-8.824	-0.662	1.09	57.65	-102.99
301	2jsa-1	HIS_A_51_CA	HIS_A_51_C	5.589	-7.927	-1.245	5.294	-6.713	-0.361	1.53	54.72	103.66
302	2jsa-1	HIS_A_51_C	HIS_A_51_O	5.294	-6.713	-0.361	5.984	-6.481	0.631	1.23	36.27	18.58
303	2jsa-1	HIS_A_51_C	TYR_A_52_N	5.294	-6.713	-0.361	4.268	-5.972	-0.752	1.32	107.17	144.16
304	2jsa-1	TYR_A_52_N	TYR_A_52_H	4.268	-5.972	-0.752	3.746	-6.223	-1.579	1.01	144.99	-154.32
305	2jsa-1	TYR_A_52_N	TYR_A_52_CA	4.268	-5.972	-0.752	3.873	-4.788	-0.007	1.45	59.17	108.45
306	2jsa-1	TYR_A_52_CA	TYR_A_52_HA	3.873	-4.788	-0.007	4.618	-4.554	0.754	1.09	45.74	17.44
307	2jsa-1	TYR_A_52_CA	TYR_A_52_C	3.873	-4.788	-0.007	2.505	-4.985	0.649	1.53	64.61	-171.81
308	2jsa-1	TYR_A_52_C	TYR_A_52_O	2.505	-4.985	0.649	2.321	-4.655	1.82	1.23	17.88	119.14
309	2jsa-1	TYR_A_52_C	VAL_A_53_N	2.505	-4.985	0.649	1.58	-5.52	-0.134	1.32	126.23	-149.96
310	2jsa-1	VAL_A_53_N	VAL_A_53_H	1.58	-5.52	-0.134	1.802	-5.766	-1.088	1.01	160.85	-47.94
311	2jsa-1	VAL_A_53_N	VAL_A_53_CA	1.58	-5.52	-0.134	0.234	-5.764	0.356	1.45	70.29	-169.73
312	2jsa-1	VAL_A_53_CA	VAL_A_53_HA	0.234	-5.764	0.356	-0.201	-4.811	0.657	1.09	73.97	114.53
313	2jsa-1	VAL_A_53_CA	VAL_A_53_C	0.234	-5.764	0.356	0.301	-6.666	1.59	1.53	36.24	-85.75
314	2jsa-1	VAL_A_53_C	VAL_A_53_O	0.301	-6.666	1.59	-0.659	-6.751	2.354	1.23	51.60	-174.94
315	2jsa-1	VAL_A_53_C	ASN_A_54_N	0.301	-6.666	1.59	1.445	-7.317	1.747	1.33	83.20	-29.64
316	2jsa-1	ASN_A_54_N	ASN_A_54_H	1.445	-7.317	1.747	2.194	-7.198	1.079	1.01	131.37	9.03
317	2jsa-1	ASN_A_54_N	ASN_A_54_CA	1.445	-7.317	1.747	1.65	-8.21	2.875	1.45	39.09	-77.07
318	2jsa-1	ASN_A_54_CA	ASN_A_54_HA	1.65	-8.21	2.875	0.889	-8.012	3.63	1.09	46.16	165.42
319	2jsa-1	ASN_A_54_CA	ASN_A_54_C	1.65	-8.21	2.875	3.041	-7.968	3.465	1.53	67.32	9.87
320	2jsa-1	ASN_A_54_C	ASN_A_54_O	3.041	-7.968	3.465	3.923	-8.817	3.352	1.23	95.27	-43.91
321	2jsa-1	ASN_A_54_C	SER_A_55_N	3.041	-7.968	3.465	3.193	-6.805	4.081	1.32	62.29	82.55
322	2jsa-1	SER_A_55_N	SER_A_55_H	3.193	-6.805	4.081	2.423	-6.154	4.136	1.01	86.88	139.79
323	2jsa-1	SER_A_55_N	SER_A_55_CA	3.193	-6.805	4.081	4.461	-6.44	4.689	1.45	65.26	16.06
324	2jsa-1	SER_A_55_CA	SER_A_55_HA	4.461	-6.44	4.689	4.624	-7.084	5.553	1.09	37.56	-75.80
325	2jsa-1	SER_A_55_CA	SER_A_55_C	4.461	-6.44	4.689	4.416	-4.987	5.164	1.53	71.91	91.77
326	2jsa-1	SER_A_55_C	SER_A_55_O	4.416	-4.987	5.164	5.014	-4.644	6.183	1.23	34.08	29.84
327	2jsa-1	SER_A_55_C	LYS_A_56_N	4.416	-4.987	5.164	3.7	-4.171	4.404	1.33	125.00	131.27
328	2jsa-1	LYS_A_56_N	LYS_A_56_H	3.7	-4.171	4.404	3.235	-4.522	3.58	1.01	144.74	-142.95
329	2jsa-1	LYS_A_56_N	LYS_A_56_CA	3.7	-4.171	4.404	3.568	-2.763	4.734	1.45	76.86	95.36
330	2jsa-1	LYS_A_56_CA	LYS_A_56_HA	3.568	-2.763	4.734	3.953	-2.616	5.743	1.09	22.22	20.90
331	2jsa-1	LYS_A_56_CA	LYS_A_56_C	3.568	-2.763	4.734	2.087	-2.381	4.741	1.53	89.74	165.54
332	2jsa-1	LYS_A_56_C	LYS_A_56_O	2.087	-2.381	4.741	1.746	-1.2	4.782	1.23	88.09	106.11
333	2jsa-1	LYS_A_56_C	VAL_A_57_N	2.087	-2.381	4.741	1.245	-3.403	4.699	1.32	91.82	-129.48
334	2jsa-1	VAL_A_57_N	VAL_A_57_H	1.245	-3.403	4.699	1.596	-4.349	4.666	1.01	91.87	-69.64
335	2jsa-1	VAL_A_57_N	VAL_A_57_CA	1.245	-3.403	4.699	-0.192	-3.19	4.7	1.45	89.96	171.57
336	2jsa-1	VAL_A_57_CA	VAL_A_57_HA	-0.192	-3.19	4.7	-0.388	-2.166	4.381	1.09	107.01	100.84
337	2jsa-1	VAL_A_57_CA	VAL_A_57_C	-0.192	-3.19	4.7	-0.728	-3.355	6.123	1.53	21.51	-162.89
338	2jsa-1	VAL_A_57_C	VAL_A_57_O	-0.728	-3.355	6.123	-1.529	-2.545	6.587	1.23	67.84	134.68
339	2jsa-1	VAL_A_57_C	ASP_A_58_N	-0.728	-3.355	6.123	-0.263	-4.409	6.778	1.33	60.38	-66.19
340	2jsa-1	ASP_A_58_N	ASP_A_58_H	-0.263	-4.409	6.778	0.395	-5.034	6.334	1.01	116.07	-43.53
341	2jsa-1	ASP_A_58_N	ASP_A_58_CA	-0.263	-4.409	6.778	-0.685	-4.691	8.139	1.45	20.45	-146.25
342	2jsa-1	ASP_A_58_CA	ASP_A_58_HA	-0.685	-4.691	8.139	-1.745	-4.942	8.138	1.09	90.05	-166.68
343	2jsa-1	ASP_A_58_CA	ASP_A_58_C	-0.685	-4.691	8.139	-0.444	-3.455	9.009	1.53	55.36	78.97
344	2jsa-1	ASP_A_58_C	ASP_A_58_O	-0.444	-3.455	9.009	-1.297	-3.081	9.812	1.23	49.23	156.32
345	2jsa-1	ASP_A_58_C	PRO_A_59_N	-0.444	-3.455	9.009	0.754	-2.841	8.815	1.36	98.20	27.14
346	2jsa-1	PRO_A_59_N	PRO_A_59_CA	0.754	-2.841	8.815	1.118	-1.655	9.572	1.45	58.61	72.94
347	2jsa-1	PRO_A_59_CA	PRO_A_59_HA	1.118	-1.655	9.572	0.876	-1.796	10.625	1.09	14.89	-149.77
348	2jsa-1	PRO_A_59_CA	PRO_A_59_C	1.118	-1.655	9.572	0.365	-0.425	9.062	1.53	109.48	121.47
349	2jsa-1	PRO_A_59_C	PRO_A_59_O	0.365	-0.425	9.062	-0.321	0.249	9.828	1.23	51.46	135.51
350	2jsa-1	PRO_A_59_C	ILE_A_60_N	0.365	-0.425	9.062	0.518	-0.171	7.77	1.33	167.07	58.94
351	2jsa-1	ILE_A_60_N	ILE_A_60_H	0.518	-0.171	7.77	1.097	-0.77	7.199	1.01	124.43	-45.97
352	2jsa-1	ILE_A_60_N	ILE_A_60_CA	0.518	-0.171	7.77	-0.139	0.966	7.149	1.45	115.31	120.02
353	2jsa-1	ILE_A_60_CA	ILE_A_60_HA	-0.139	0.966	7.149	0.342	1.874	7.513	1.09	70.49	62.09
354	2jsa-1	ILE_A_60_CA	ILE_A_60_C	-0.139	0.966	7.149	-1.604	1.007	7.59	1.53	73.25	178.40
355	2jsa-1	ILE_A_60_C	ILE_A_60_O	-1.604	1.007	7.59	-2.069	2.017	8.115	1.23	64.73	114.72
356	2jsa-1	ILE_A_60_C	ILE_A_61_N	-1.604	1.007	7.59	-2.289	-0.104	7.36	1.33	99.99	-121.66
357	2jsa-1	ILE_A_61_N	ILE_A_61_H	-2.289	-0.104	7.36	-1.84	-0.898	6.925	1.01	115.50	-60.51
358	2jsa-1	ILE_A_61_N	ILE_A_61_CA	-2.289	-0.104	7.36	-3.691	-0.207	7.727	1.45	75.37	-175.80
359	2jsa-1	ILE_A_61_CA	ILE_A_61_HA	-3.691	-0.207	7.727	-4.223	0.625	7.266	1.09	115.02	122.60
360	2jsa-1	ILE_A_61_CA	ILE_A_61_C	-3.691	-0.207	7.727	-3.828	-0.063	9.244	1.53	7.46	133.57
361	2jsa-1	ILE_A_61_C	ILE_A_61_O	-3.828	-0.063	9.244	-4.901	0.271	9.744	1.23	66.01	162.71
362	2jsa-1	ILE_A_61_C	HIS_A_62_N	-3.828	-0.063	9.244	-2.727	-0.321	9.933	1.32	58.65	-13.19
363	2jsa-1	HIS_A_62_N	HIS_A_62_H	-2.727	-0.321	9.933	-1.879	-0.591	9.455	1.01	118.24	-17.66
364	2jsa-1	HIS_A_62_N	HIS_A_62_CA	-2.727	-0.321	9.933	-2.711	-0.224	11.383	1.45	3.88	80.63
365	2jsa-1	HIS_A_62_CA	HIS_A_62_HA	-2.711	-0.224	11.383	-3.541	-0.815	11.769	1.09	69.25	-144.55
366	2jsa-1	HIS_A_62_CA	HIS_A_62_C	-2.711	-0.224	11.383	-2.935	1.23	11.802	1.53	74.10	98.76
367	2jsa-1	HIS_A_62_C	HIS_A_62_O	-2.935	1.23	11.802	-3.714	1.504	12.713	1.23	42.19	160.62
368	2jsa-1	HIS_A_62_C	GLU_A_63_N	-2.935	1.23	11.802	-2.237	2.124	11.117	1.33	121.13	52.02
369	2jsa-1	GLU_A_63_N	GLU_A_63_H	-2.237	2.124	11.117	-1.614	1.826	10.379	1.01	136.90	-25.56
370	2jsa-1	GLU_A_63_N	GLU_A_63_CA	-2.237	2.124							

372	2jsa-1	GLU_A_63_CA	GLU_A_63_C	-2.349	3.543	11.407	-3.791	4.014	11.205	1.53	97.58	161.91
373	2jsa-1	GLU_A_63_C	GLU_A_63_O	-3.791	4.014	11.205	-4.429	4.493	12.141	1.23	40.44	143.10
374	2jsa-1	GLU_A_63_C	LEU_A_64_N	-3.791	4.014	11.205	-4.263	3.861	9.976	1.33	158.01	-162.04
375	2jsa-1	LEU_A_64_N	LEU_A_64_H	-4.263	3.861	9.976	-3.681	3.459	9.255	1.01	135.55	-34.63
376	2jsa-1	LEU_A_64_N	LEU_A_64_CA	-4.263	3.861	9.976	-5.617	4.264	9.638	1.45	103.46	163.43
377	2jsa-1	LEU_A_64_CA	LEU_A_64_HA	-5.617	4.264	9.638	-5.718	5.326	9.86	1.09	78.24	95.43
378	2jsa-1	LEU_A_64_CA	LEU_A_64_C	-5.617	4.264	9.638	-6.606	3.506	10.527	1.53	54.49	-142.53
379	2jsa-1	LEU_A_64_C	LEU_A_64_O	-6.606	3.506	10.527	-7.767	3.896	10.641	1.23	84.68	161.43
380	2jsa-1	LEU_A_64_C	GLU_A_65_N	-6.606	3.506	10.527	-6.11	2.437	11.132	1.32	62.82	-65.11
381	2jsa-1	GLU_A_65_N	GLU_A_65_H	-6.11	2.437	11.132	-5.144	2.176	10.992	1.01	97.96	-15.12
382	2jsa-1	GLU_A_65_N	GLU_A_65_CA	-6.11	2.437	11.132	-6.936	1.621	12.006	1.45	53.03	-135.35
383	2jsa-1	GLU_A_65_CA	GLU_A_65_HA	-6.936	1.621	12.006	-7.903	1.483	11.524	1.09	116.26	-171.88
384	2jsa-1	GLU_A_65_CA	GLU_A_65_C	-6.936	1.621	12.006	-7.161	2.334	13.341	1.53	29.25	107.51
385	2jsa-1	GLU_A_65_C	GLU_A_65_O	-7.161	2.334	13.341	-8.207	2.172	13.967	1.23	59.40	-171.20
386	2jsa-1	GLU_A_65_C	GLY_A_66_N	-7.161	2.334	13.341	-6.161	3.109	13.738	1.33	72.58	37.78
387	2jsa-1	GLY_A_66_N	GLY_A_66_H	-6.161	3.109	13.738	-5.329	3.195	13.172	1.01	124.09	5.90
388	2jsa-1	GLY_A_66_N	GLY_A_66_CA	-6.161	3.109	13.738	-6.237	3.847	14.987	1.45	30.71	95.88
389	2jsa-1	GLY_A_66_CA	GLY_A_66_C	-6.237	3.847	14.987	-6.909	5.206	14.781	1.53	97.74	116.31
390	2jsa-1	GLY_A_66_C	GLY_A_66_O	-6.909	5.206	14.781	-7.65	5.673	15.645	1.23	45.39	147.78
391	2jsa-1	GLY_A_66_C	GLY_A_67_N	-6.909	5.206	14.781	-6.627	5.802	13.632	1.32	150.15	64.68
392	2jsa-1	GLY_A_67_N	GLY_A_67_H	-6.627	5.802	13.632	-6.008	5.359	12.968	1.01	131.10	-35.59
393	2jsa-1	GLY_A_67_N	GLY_A_67_CA	-6.627	5.802	13.632	-7.195	7.098	13.301	1.45	103.17	113.67
394	2jsa-1	GLY_A_67_CA	GLY_A_67_C	-7.195	7.098	13.301	-6.14	8.017	12.683	1.53	113.83	41.06
395	2jsa-1	GLY_A_67_C	GLY_A_67_O	-6.14	8.017	12.683	-6.065	9.197	13.021	1.23	74.05	86.36
396	2jsa-1	GLY_A_67_C	THR_A_68_N	-6.14	8.017	12.683	-5.35	7.441	11.788	1.33	132.47	-36.10
397	2jsa-1	THR_A_68_N	THR_A_68_H	-5.35	7.441	11.788	-5.468	6.465	11.558	1.01	103.17	-96.89
398	2jsa-1	THR_A_68_N	THR_A_68_CA	-5.35	7.441	11.788	-4.303	8.195	11.12	1.45	117.37	35.76
399	2jsa-1	THR_A_68_CA	THR_A_68_HA	-4.303	8.195	11.12	-4.204	9.165	11.608	1.09	63.41	84.17
400	2jsa-1	THR_A_68_CA	THR_A_68_C	-4.303	8.195	11.12	-4.673	8.439	9.656	1.53	163.16	146.60
401	2jsa-1	THR_A_68_C	THR_A_68_O	-4.673	8.439	9.656	-5.365	7.628	9.043	1.23	119.90	-130.47
402	2jsa-1	THR_A_68_C	ALA_A_69_N	-4.673	8.439	9.656	-4.196	9.561	9.137	1.33	113.06	66.97
403	2jsa-1	ALA_A_69_N	ALA_A_69_H	-4.196	9.561	9.137	-3.633	10.183	9.701	1.01	56.09	47.85
404	2jsa-1	ALA_A_69_N	ALA_A_69_CA	-4.196	9.561	9.137	-4.468	9.923	7.757	1.45	161.83	126.92
405	2jsa-1	ALA_A_69_CA	ALA_A_69_HA	-4.468	9.923	7.757	-5.483	9.616	7.508	1.09	103.21	-163.17
406	2jsa-1	ALA_A_69_CA	ALA_A_69_C	-4.468	9.923	7.757	-3.498	9.178	6.838	1.53	126.92	-37.53
407	2jsa-1	ALA_A_69_C	ALA_A_69_O	-3.498	9.178	6.838	-2.468	8.68	7.29	1.23	68.44	-25.80
408	2jsa-1	ALA_A_69_C	PRO_A_70_N	-3.498	9.178	6.838	-3.871	9.124	5.531	1.36	163.91	-171.76
409	2jsa-1	PRO_A_70_N	PRO_A_70_CA	-3.871	9.124	5.531	-3.045	8.448	4.545	1.45	132.73	-39.30
410	2jsa-1	PRO_A_70_CA	PRO_A_70_HA	-3.045	8.448	4.545	-2.71	7.487	4.935	1.09	69.03	-70.78
411	2jsa-1	PRO_A_70_CA	PRO_A_70_C	-3.045	8.448	4.545	-1.813	9.285	4.195	1.53	103.22	34.19
412	2jsa-1	PRO_A_70_C	PRO_A_70_O	-1.813	9.285	4.195	-0.944	8.835	3.45	1.23	127.28	-27.38
413	2jsa-1	PRO_A_70_C	LYS_A_71_N	-1.813	9.285	4.195	-1.778	10.488	4.748	1.32	65.32	88.33
414	2jsa-1	LYS_A_71_N	LYS_A_71_H	-1.778	10.488	4.748	-2.529	10.792	5.351	1.01	53.34	157.96
415	2jsa-1	LYS_A_71_N	LYS_A_71_CA	-1.778	10.488	4.748	-0.668	11.393	4.504	1.45	99.67	39.19
416	2jsa-1	LYS_A_71_CA	LYS_A_71_HA	-0.668	11.393	4.504	-0.041	10.955	3.727	1.09	135.45	-34.94
417	2jsa-1	LYS_A_71_CA	LYS_A_71_C	-0.668	11.393	4.504	0.179	11.509	5.773	1.53	33.97	7.80
418	2jsa-1	LYS_A_71_C	LYS_A_71_O	0.179	11.509	5.773	1.163	12.246	5.802	1.23	88.65	36.83
419	2jsa-1	LYS_A_71_C	ASP_A_72_N	0.179	11.509	5.773	-0.236	10.771	6.792	1.32	39.72	-119.35
420	2jsa-1	ASP_A_72_N	ASP_A_72_H	-0.236	10.771	6.792	-1.055	10.189	6.698	1.01	95.34	-144.60
421	2jsa-1	ASP_A_72_N	ASP_A_72_CA	-0.236	10.771	6.792	0.472	10.782	8.061	1.45	29.16	0.89
422	2jsa-1	ASP_A_72_CA	ASP_A_72_HA	0.472	10.782	8.061	1.185	11.607	8.064	1.09	89.84	49.17
423	2jsa-1	ASP_A_72_CA	ASP_A_72_C	0.472	10.782	8.061	1.211	9.455	8.239	1.53	83.32	-60.89
424	2jsa-1	ASP_A_72_C	ASP_A_72_O	1.211	9.455	8.239	2.208	9.387	8.957	1.23	54.30	-3.90
425	2jsa-1	ASP_A_72_C	VAL_A_73_N	1.211	9.455	8.239	0.694	8.432	7.575	1.32	120.08	-116.81
426	2jsa-1	VAL_A_73_N	VAL_A_73_H	0.694	8.432	7.575	-0.129	8.56	7.004	1.01	124.43	171.16
427	2jsa-1	VAL_A_73_N	VAL_A_73_CA	0.694	8.432	7.575	1.293	7.11	7.651	1.45	87.00	-65.62
428	2jsa-1	VAL_A_73_CA	VAL_A_73_HA	1.293	7.11	7.651	1.486	6.879	8.699	1.09	16.03	-50.12
429	2jsa-1	VAL_A_73_CA	VAL_A_73_C	1.293	7.11	7.651	2.633	7.119	6.913	1.53	118.84	0.38
430	2jsa-1	VAL_A_73_C	VAL_A_73_O	2.633	7.119	6.913	3.663	6.76	7.483	1.23	62.41	-19.22
431	2jsa-1	VAL_A_73_C	CYS_A_74_N	2.633	7.119	6.913	2.577	7.533	5.656	1.32	161.62	97.70
432	2jsa-1	CYS_A_74_N	CYS_A_74_H	2.577	7.533	5.656	1.696	7.815	5.252	1.01	113.59	162.25
433	2jsa-1	CYS_A_74_N	CYS_A_74_CA	2.577	7.533	5.656	3.774	7.593	4.834	1.45	124.44	2.87
434	2jsa-1	CYS_A_74_CA	CYS_A_74_HA	3.774	7.593	4.834	4.321	6.658	4.956	1.09	83.57	-59.67
435	2jsa-1	CYS_A_74_CA	CYS_A_74_C	3.774	7.593	4.834	4.65	8.74	5.343	1.53	70.57	52.63
436	2jsa-1	CYS_A_74_C	CYS_A_74_O	4.65	8.74	5.343	4.83	9.742	4.653	1.23	124.13	79.82
437	2jsa-1	CYS_A_74_C	THR_A_75_N	4.65	8.74	5.343	5.17	8.554	6.547	1.32	24.64	-19.68
438	2jsa-1	THR_A_75_N	THR_A_75_H	5.17	8.554	6.547	4.979	7.704	7.058	1.01	59.61	-102.66
439	2jsa-1	THR_A_75_N	THR_A_75_CA	5.17	8.554	6.547	6.023	9.561	7.157	1.45	65.19	49.73
440	2jsa-1	THR_A_75_CA	THR_A_75_HA	6.023	9.561	7.157	6.897	9.711	6.522	1.09	125.61	9.74
441	2jsa-1	THR_A_75_CA	THR_A_75_C	6.023	9.561	7.157	6.512	9.086	8.527	1.53	26.46	-44.17
442	2jsa-1	THR_A_75_C	THR_A_75_O	6.512	9.086	8.527	7.709	8.89	8.729	1.23	80.54	-9.30
443	2jsa-1	THR_A_75_C	LYS_A_76_N	6.512	9.086	8.527	5.56	8.916	9.433	1.33	46.87	-169.88
444	2jsa-1	LYS_A_76_N	LYS_A_76_H	5.56	8.916	9.433	4.595	9.097	9.197	1.01	103.52	169.38
445	2jsa-1	LYS_A_76_N	LYS_A_76_CA	5.56	8.916	9.433	5.879	8.468	10.778	1.45	22.24	-54.55
446	2jsa-1	LYS_A_76_CA	LYS_A_76_HA	5.879	8.468	10.778	6.773	8.999	11.108	1.09	72.39	30.71
447	2jsa-1	LYS_A_76_CA	LYS_A_76_C	5.879	8.468	10.778	6.209	6.975	10.749	1.53	91.09	-77.54
448	2jsa-1	LYS_A_76_C	LYS_A_76_O	6.209	6.975	10.749	6.936	6.479	11.609	1.23	45.66	-34.30
449	2jsa-1	LYS_A_76_C	LEU_A_77_N	6.209	6.975	10.749	5.66	6.299	9.75	1.33	138.92	-129.08
450	2jsa-1	LEU_A_77_N	LEU_A_77_H	5.66	6.299	9.75	5.073	6.772	9.078	1.01	131.71	141.14
451	2jsa-1	LEU_A_77_N	LEU_A_77_CA	5.66	6.299	9.75	5.888	4.872	9.598	1.45	96.00	-80.92
452	2jsa-1	LEU_A_77_CA	LEU_A_77_HA	5.888	4.872	9.598	5.964	4.434	10.594	1.09	24.05	-80.16
453	2jsa-1	LEU_A_77_CA	LEU_A_77_C	5.888	4.872	9.598	7.224	4.646	8.888	1.53	117.65	-9.60
454	2jsa-1	LEU_A_77_C	LEU_A_77_O	7.224	4.646	8.888	7.534	3.527	8.482	1.23	109.27	-74.52
455	2jsa-1	LEU_A_77_C	ASN_A_78_N	7.224	4.646	8.888	7.981	5.726	8.761	1.32	95.50	54.97
456	2jsa-1	ASN_A_78_N	ASN_A_78_H	7.981	5.726	8.761	7.663	6.615	9.12	1.01	69.18	109.68
457	2jsa-1	ASN_A_78_N	ASN_A_78_CA	7.981	5.726	8.761	9.277	5.66	8.108	1.45	116.71	-2.92
458	2jsa-1	ASN_A_78_CA	ASN_A_78_HA	9.277	5.66	8.108	9.562	6.659	7.778	1.09	107.62	74.08
459	2jsa-1	ASN_A_78_CA	ASN_A_78_C	9.277	5.66	8.108	9.189	4.72	6.904	1.53	141.90	-95.35
460	2jsa-1	ASN_A_78_C	ASN_A_78_O	9.189	4.72	6.904	10.158	4.038	6.573	1.23	105.61	-35.14
461	2jsa-1	ASN_A_78_C	GLU_A_79_N	9.189	4.72	6.904	8.019	4.713	6.283	1.32	117.96	-179.66
462	2jsa-1	GLU_A_79_N	GLU_A_79_H	8.019	4.713	6.						

465	2jsa-1	GLU_A_79_CA	GLU_A_79_C	7.792	3.868	5.123	8.022	4.661	3.835	1.53	147.34	73.83
466	2jsa-1	GLU_A_79_C	GLU_A_79_O	8.022	4.661	3.835	8.612	4.151	2.885	1.23	140.62	-40.84
467	2jsa-1	GLU_A_79_C	CYS_A_80_N	8.022	4.661	3.835	7.544	5.897	3.846	1.33	89.52	111.14
468	2jsa-1	CYS_A_80_N	CYS_A_80_H	7.544	5.897	3.846	7.07	6.252	4.664	1.01	35.90	143.17
469	2jsa-1	CYS_A_80_N	CYS_A_80_CA	7.544	5.897	3.846	7.69	6.766	2.69	1.45	142.68	80.46
470	2jsa-1	CYS_A_80_CA	CYS_A_80_HA	7.69	6.766	2.69	7.09	6.359	1.876	1.09	138.31	-145.85
471	2jsa-1	CYS_A_80_CA	CYS_A_80_C	7.69	6.766	2.69	9.16	6.755	2.264	1.53	106.16	-0.43
472	2jsa-1	CYS_A_80_C	CYS_A_80_O	9.16	6.755	2.264	9.467	6.572	1.087	1.23	163.11	-30.80
473	2jsa-1	CYS_A_80_C	PRO_A_81_N	9.16	6.755	2.264	10.051	6.958	3.27	1.36	42.25	12.83
474	2jsa-1	PRO_A_81_N	PRO_A_81_CA	10.051	6.958	3.27	11.481	6.974	3.011	1.45	100.27	0.64
475	2jsa-1	PRO_A_81_CA	PRO_A_81_HA	11.481	6.974	3.011	11.693	7.571	2.124	1.09	144.46	70.45
476	2jsa-1	PRO_A_81_CA	PRO_A_81_C	11.481	6.974	3.011	12.012	5.557	2.781	1.53	98.64	-69.46
477	2jsa-1	PRO_A_81_C	PRO_A_81_O	12.012	5.557	2.781	13.177	5.275	3.054	1.23	77.17	-13.61
1	2jsa-2	ARG_A_1_N	ARG_A_1_H	14.924	2.313	-0.565	14.842	2.65	-1.513	1.01	159.90	103.68
2	2jsa-2	ARG_A_1_N	ARG_A_1_CA	14.924	2.313	-0.565	14.187	3.0	0.482	1.45	43.90	137.01
3	2jsa-2	ARG_A_1_CA	ARG_A_1_HA	14.187	3.0	0.482	13.499	2.29	0.941	1.09	65.10	-134.10
4	2jsa-2	ARG_A_1_CA	ARG_A_1_C	14.187	3.0	0.482	13.384	4.161	-0.108	1.53	112.68	124.67
5	2jsa-2	ARG_A_1_C	ARG_A_1_O	13.384	4.161	-0.108	12.162	4.203	0.019	1.23	84.07	178.03
6	2jsa-2	ARG_A_1_C	SER_A_2_N	13.384	4.161	-0.108	14.105	5.075	-0.74	1.32	118.50	51.73
7	2jsa-2	SER_A_2_N	SER_A_2_H	14.105	5.075	-0.74	15.108	4.976	-0.806	1.01	93.75	-5.64
8	2jsa-2	SER_A_2_N	SER_A_2_CA	14.105	5.075	-0.74	13.475	6.234	-1.35	1.45	114.82	118.53
9	2jsa-2	SER_A_2_CA	SER_A_2_HA	13.475	6.234	-1.35	12.52	6.404	-0.854	1.09	62.92	169.91
10	2jsa-2	SER_A_2_CA	SER_A_2_C	13.475	6.234	-1.35	13.216	5.968	-2.835	1.53	165.96	-134.24
11	2jsa-2	SER_A_2_C	SER_A_2_O	13.216	5.968	-2.835	14.133	6.044	-3.651	1.23	131.57	4.74
12	2jsa-2	SER_A_2_C	ALA_A_3_N	13.216	5.968	-2.835	11.964	5.663	-3.139	1.32	103.27	-166.31
13	2jsa-2	ALA_A_3_N	ALA_A_3_H	11.964	5.663	-3.139	11.262	5.618	-2.414	1.01	44.14	-176.33
14	2jsa-2	ALA_A_3_N	ALA_A_3_CA	11.964	5.663	-3.139	11.572	5.386	-4.51	1.45	160.70	-144.75
15	2jsa-2	ALA_A_3_CA	ALA_A_3_HA	11.572	5.386	-4.51	11.971	6.17	-5.153	1.09	126.16	63.03
16	2jsa-2	ALA_A_3_CA	ALA_A_3_C	11.572	5.386	-4.51	10.047	5.404	-4.616	1.53	93.98	179.32
17	2jsa-2	ALA_A_3_C	ALA_A_3_O	10.047	5.404	-4.616	9.383	6.172	-3.921	1.23	55.61	130.85
18	2jsa-2	ALA_A_3_C	LEU_A_4_N	10.047	5.404	-4.616	9.535	4.549	-5.489	1.32	131.22	-120.91
19	2jsa-2	LEU_A_4_N	LEU_A_4_H	9.535	4.549	-5.489	10.142	3.946	-6.026	1.01	122.11	-44.81
20	2jsa-2	LEU_A_4_N	LEU_A_4_CA	9.535	4.549	-5.489	8.099	4.458	-5.693	1.45	98.07	-176.37
21	2jsa-2	LEU_A_4_CA	LEU_A_4_HA	8.099	4.458	-5.693	7.695	5.47	-5.7	1.09	90.37	111.76
22	2jsa-2	LEU_A_4_CA	LEU_A_4_C	8.099	4.458	-5.693	7.467	3.713	-4.516	1.53	39.69	-130.31
23	2jsa-2	LEU_A_4_C	LEU_A_4_O	7.467	3.713	-4.516	6.247	3.567	-4.451	1.23	86.97	-173.18
24	2jsa-2	LEU_A_4_C	SER_A_5_N	7.467	3.713	-4.516	8.326	3.26	-3.614	1.33	47.11	-27.81
25	2jsa-2	SER_A_5_N	SER_A_5_H	8.326	3.26	-3.614	9.317	3.416	-3.731	1.01	96.65	8.95
26	2jsa-2	SER_A_5_N	SER_A_5_CA	8.326	3.26	-3.614	7.866	2.534	-2.442	1.45	36.25	-122.36
27	2jsa-2	SER_A_5_CA	SER_A_5_HA	7.866	2.534	-2.442	7.398	1.609	-2.776	1.09	107.86	-116.84
28	2jsa-2	SER_A_5_CA	SER_A_5_C	7.866	2.534	-2.442	6.827	3.364	-1.685	1.53	60.35	141.38
29	2jsa-2	SER_A_5_C	SER_A_5_O	6.827	3.364	-1.685	5.828	2.83	-1.21	1.23	67.25	-151.87
30	2jsa-2	SER_A_5_C	CYS_A_6_N	6.827	3.364	-1.685	7.101	4.657	-1.597	1.32	86.19	78.04
31	2jsa-2	CYS_A_6_N	CYS_A_6_H	7.101	4.657	-1.597	7.944	5.028	-2.012	1.01	114.26	23.75
32	2jsa-2	CYS_A_6_N	CYS_A_6_CA	7.101	4.657	-1.597	6.202	5.567	-0.907	1.45	61.66	134.65
33	2jsa-2	CYS_A_6_CA	CYS_A_6_HA	6.202	5.567	-0.907	6.097	5.229	0.124	1.09	18.95	-107.26
34	2jsa-2	CYS_A_6_CA	CYS_A_6_C	6.202	5.567	-0.907	4.833	5.495	-1.585	1.53	116.32	-176.99
35	2jsa-2	CYS_A_6_C	CYS_A_6_O	4.833	5.495	-1.585	3.816	5.307	-0.919	1.23	57.22	-169.53
36	2jsa-2	CYS_A_6_C	GLN_A_7_N	4.833	5.495	-1.585	4.85	5.65	-2.9	1.32	173.24	83.74
37	2jsa-2	GLN_A_7_N	GLN_A_7_H	4.85	5.65	-2.9	5.724	5.803	-3.382	1.01	118.51	9.93
38	2jsa-2	GLN_A_7_N	GLN_A_7_CA	4.85	5.65	-2.9	3.622	5.606	-3.675	1.45	122.24	-177.95
39	2jsa-2	GLN_A_7_CA	GLN_A_7_HA	3.622	5.606	-3.675	3.058	6.514	-3.464	1.09	78.83	121.85
40	2jsa-2	GLN_A_7_CA	GLN_A_7_C	3.622	5.606	-3.675	2.773	4.404	-3.256	1.53	74.11	-125.23
41	2jsa-2	GLN_A_7_C	GLN_A_7_O	2.773	4.404	-3.256	1.585	4.548	-2.972	1.23	76.65	173.09
42	2jsa-2	GLN_A_7_C	MET_A_8_N	2.773	4.404	-3.256	3.415	3.245	-3.231	1.33	88.92	-61.02
43	2jsa-2	MET_A_8_N	MET_A_8_H	3.415	3.245	-3.231	4.393	3.2	-3.48	1.01	104.27	-2.63
44	2jsa-2	MET_A_8_N	MET_A_8_CA	3.415	3.245	-3.231	2.734	2.02	-2.85	1.45	74.79	-119.07
45	2jsa-2	MET_A_8_CA	MET_A_8_HA	2.734	2.02	-2.85	2.061	1.73	-3.656	1.09	137.72	-156.69
46	2jsa-2	MET_A_8_CA	MET_A_8_C	2.734	2.02	-2.85	1.919	2.22	-1.57	1.53	33.25	166.21
47	2jsa-2	MET_A_8_C	MET_A_8_O	1.919	2.22	-1.57	0.776	1.774	-1.483	1.23	85.94	-158.68
48	2jsa-2	MET_A_8_C	CYS_A_9_N	1.919	2.22	-1.57	2.539	2.888	-0.61	1.32	43.51	47.13
49	2jsa-2	CYS_A_9_N	CYS_A_9_H	2.539	2.888	-0.61	3.481	3.225	-0.752	1.01	98.08	19.68
50	2jsa-2	CYS_A_9_N	CYS_A_9_CA	2.539	2.888	-0.61	1.887	3.152	0.66	1.45	28.98	157.96
51	2jsa-2	CYS_A_9_CA	CYS_A_9_HA	1.887	3.152	0.66	1.621	2.197	1.114	1.09	65.39	-105.56
52	2jsa-2	CYS_A_9_CA	CYS_A_9_C	1.887	3.152	0.66	0.601	3.937	0.387	1.53	100.27	148.60
53	2jsa-2	CYS_A_9_C	CYS_A_9_O	0.601	3.937	0.387	-0.371	3.822	1.131	1.23	52.76	-173.25
54	2jsa-2	CYS_A_9_C	GLU_A_10_N	0.601	3.937	0.387	0.639	4.717	-0.685	1.33	143.93	87.21
55	2jsa-2	GLU_A_10_N	GLU_A_10_H	0.639	4.717	-0.685	1.474	4.761	-1.253	1.01	124.19	3.02
56	2jsa-2	GLU_A_10_N	GLU_A_10_CA	0.639	4.717	-0.685	-0.509	5.52	-1.066	1.45	105.21	145.03
57	2jsa-2	GLU_A_10_CA	GLU_A_10_HA	-0.509	5.52	-1.066	-1.0	5.859	-0.154	1.09	33.19	145.38
58	2jsa-2	GLU_A_10_CA	GLU_A_10_C	-0.509	5.52	-1.066	-1.506	4.676	-1.865	1.53	121.45	-139.75
59	2jsa-2	GLU_A_10_C	GLU_A_10_O	-1.506	4.676	-1.865	-2.607	5.131	-2.168	1.23	104.27	157.55
60	2jsa-2	GLU_A_10_C	LEU_A_11_N	-1.506	4.676	-1.865	-1.082	3.461	-2.181	1.33	103.80	-70.76
61	2jsa-2	LEU_A_11_N	LEU_A_11_H	-1.082	3.461	-2.181	-0.163	3.152	-1.897	1.01	73.67	-18.58
62	2jsa-2	LEU_A_11_N	LEU_A_11_CA	-1.082	3.461	-2.181	-1.924	2.549	-2.939	1.45	121.41	-132.71
63	2jsa-2	LEU_A_11_CA	LEU_A_11_HA	-1.924	2.549	-2.939	-2.601	3.144	-3.552	1.09	124.22	138.69
64	2jsa-2	LEU_A_11_CA	LEU_A_11_C	-1.924	2.549	-2.939	-2.775	1.726	-1.971	1.53	50.73	-135.96
65	2jsa-2	LEU_A_11_C	LEU_A_11_O	-2.775	1.726	-1.971	-3.978	1.574	-2.173	1.23	99.46	-172.80
66	2jsa-2	LEU_A_11_C	VAL_A_12_N	-2.775	1.726	-1.971	-2.117	1.216	-0.94	1.33	38.92	-37.78
67	2jsa-2	VAL_A_12_N	VAL_A_12_H	-2.117	1.216	-0.94	-1.126	1.382	-0.836	1.01	84.09	9.51
68	2jsa-2	VAL_A_12_N	VAL_A_12_CA	-2.117	1.216	-0.94	-2.8	0.411	0.059	1.45	46.58	-130.31
69	2jsa-2	VAL_A_12_CA	VAL_A_12_HA	-2.8	0.411	0.059	-3.336	-0.39	-0.45	1.09	117.84	-123.79
70	2jsa-2	VAL_A_12_CA	VAL_A_12_C	-2.8	0.411	0.059	-3.825	1.278	0.793	1.53	61.33	139.77
71	2jsa-2	VAL_A_12_C	VAL_A_12_O	-3.825	1.278	0.793	-4.999	0.921	0.874	1.23	86.22	-163.09
72	2jsa-2	VAL_A_12_C	VAL_A_13_N	-3.825	1.278	0.793	-3.344	2.401	1.307	1.33	67.18	66.81
73	2jsa-2	VAL_A_13_N	VAL_A_13_H	-3.344	2.401	1.307	-2.366	2.631	1.201	1.01	96.02	13.23
74	2jsa-2	VAL_A_13_N	VAL_A_13_CA	-3.344	2.401	1.307	-4.205	3.321	2.03	1.45	60.15	133.10
75	2jsa-2	VAL_A_13_CA	VAL_A_13_HA	-4.205	3.321	2.03	-4.641	2.791	2.877	1.09	39.02	-129.44
76	2jsa-2	VAL_A_13_CA	VAL_A_13_C	-4.205	3.321	2.03	-5.345	3.773	1.114	1.53	126.76	158.37
77	2jsa-2	VAL_A_13_C	VAL_A_13_O	-5.345	3.773	1.114	-6.515	3.574	1.431	1.23	75.05	-170.35
78	2jsa-2	VAL_A_13_C	LYS_A_14_N	-5.345	3.773	1.114	-4.96	4.374	-0.002	1.32	147.40	57.36
79	2jsa-2	LYS_A_14_N	LYS_A_14_H	-4.96	4.374	-0.002	-3.977	4.505	-0.196	1.01	101.07	7.59
80	2jsa-2	LYS_A_14_N	LYS_A_14_CA	-4.96	4.374	-0.002	-5.934					

81	2jsa-2	LYS_A_14_CA	LYS_A_14_HA	-5.934	4.856	-0.966	-6.43	5.727	-0.537	1.09	66.83	119.66
82	2jsa-2	LYS_A_14_CA	LYS_A_14_C	-5.934	4.856	-0.966	-6.998	3.779	-1.192	1.53	98.49	-134.65
83	2jsa-2	LYS_A_14_C	LYS_A_14_O	-6.998	3.779	-1.192	-8.153	4.092	-1.475	1.23	103.31	164.84
84	2jsa-2	LYS_A_14_C	LYS_A_15_N	-6.998	3.779	-1.192	-6.569	2.533	-1.058	1.32	84.19	-71.00
85	2jsa-2	LYS_A_15_N	LYS_A_15_H	-6.569	2.533	-1.058	-5.604	2.35	-0.823	1.01	76.54	-10.74
86	2jsa-2	LYS_A_15_N	LYS_A_15_CA	-6.569	2.533	-1.058	-7.47	1.408	-1.244	1.45	97.35	-128.69
87	2jsa-2	LYS_A_15_CA	LYS_A_15_HA	-7.47	1.408	-1.244	-8.167	1.663	-2.042	1.09	137.08	159.90
88	2jsa-2	LYS_A_15_CA	LYS_A_15_C	-7.47	1.408	-1.244	-8.283	1.194	0.033	1.53	33.36	-165.25
89	2jsa-2	LYS_A_15_C	LYS_A_15_O	-8.283	1.194	0.033	-9.467	0.863	-0.027	1.23	92.79	-164.38
90	2jsa-2	LYS_A_15_C	TYR_A_16_N	-8.283	1.194	0.033	-7.617	1.393	1.162	1.33	31.62	16.64
91	2jsa-2	TYR_A_16_N	TYR_A_16_H	-7.617	1.393	1.162	-6.644	1.663	1.137	1.01	91.42	15.51
92	2jsa-2	TYR_A_16_N	TYR_A_16_CA	-7.617	1.393	1.162	-8.263	1.227	2.451	1.45	27.36	-165.59
93	2jsa-2	TYR_A_16_CA	TYR_A_16_HA	-8.263	1.227	2.451	-8.849	0.308	2.464	1.09	89.32	-122.52
94	2jsa-2	TYR_A_16_CA	TYR_A_16_C	-8.263	1.227	2.451	-9.163	2.421	2.773	1.53	77.85	127.01
95	2jsa-2	TYR_A_16_C	TYR_A_16_O	-9.163	2.421	2.773	-10.385	2.286	2.826	1.23	87.53	-173.70
96	2jsa-2	TYR_A_16_C	GLU_A_17_N	-9.163	2.421	2.773	-8.524	3.564	2.979	1.33	81.06	60.79
97	2jsa-2	GLU_A_17_N	GLU_A_17_H	-8.524	3.564	2.979	-7.516	3.602	2.919	1.01	93.40	2.16
98	2jsa-2	GLU_A_17_N	GLU_A_17_CA	-8.524	3.564	2.979	-9.253	4.781	3.293	1.45	77.52	120.92
99	2jsa-2	GLU_A_17_CA	GLU_A_17_HA	-9.253	4.781	3.293	-9.649	4.686	4.304	1.09	21.94	-166.51
100	2jsa-2	GLU_A_17_CA	GLU_A_17_C	-9.253	4.781	3.293	-10.429	4.96	2.33	1.53	128.99	171.35
101	2jsa-2	GLU_A_17_C	GLU_A_17_O	-10.429	4.96	2.33	-11.492	5.437	2.726	1.23	71.23	155.83
102	2jsa-2	GLU_A_17_C	GLY_A_18_N	-10.429	4.96	2.33	-10.199	4.567	1.086	1.32	159.90	-59.66
103	2jsa-2	GLY_A_18_N	GLY_A_18_H	-10.199	4.567	1.086	-9.3	4.183	0.832	1.01	104.56	-23.13
104	2jsa-2	GLY_A_18_N	GLY_A_18_CA	-10.199	4.567	1.086	-11.226	4.678	0.065	1.45	134.67	173.83
105	2jsa-2	GLY_A_18_CA	GLY_A_18_C	-11.226	4.678	0.065	-11.643	3.298	-0.446	1.53	109.52	-106.81
106	2jsa-2	GLY_A_18_C	GLY_A_18_O	-11.643	3.298	-0.446	-11.715	3.074	-1.653	1.23	168.97	-107.82
107	2jsa-2	GLY_A_18_C	SER_A_19_N	-11.643	3.298	-0.446	-11.906	2.407	0.699	1.33	44.51	-106.45
108	2jsa-2	SER_A_19_N	SER_A_19_H	-11.906	2.407	0.699	-11.826	2.661	1.474	1.01	15.28	72.52
109	2jsa-2	SER_A_19_N	SER_A_19_CA	-11.906	2.407	0.699	-12.314	1.054	0.16	1.45	103.49	-106.78
110	2jsa-2	SER_A_19_CA	SER_A_19_HA	-12.314	1.054	0.16	-12.005	0.851	-0.865	1.09	160.17	-33.30
111	2jsa-2	SER_A_19_CA	SER_A_19_C	-12.314	1.054	0.16	-13.836	0.929	0.247	1.53	86.74	-175.30
112	2jsa-2	SER_A_19_C	SER_A_19_O	-13.836	0.929	0.247	-14.481	0.482	-0.701	1.23	140.38	-145.28
113	2jsa-2	SER_A_19_C	ALA_A_20_N	-13.836	0.929	0.247	-14.367	1.331	1.392	1.32	30.19	142.87
114	2jsa-2	ALA_A_20_N	ALA_A_20_H	-14.367	1.331	1.392	-13.775	1.687	2.129	1.01	43.15	31.02
115	2jsa-2	ALA_A_20_N	ALA_A_20_CA	-14.367	1.331	1.392	-15.801	1.269	1.615	1.45	81.17	-177.52
116	2jsa-2	ALA_A_20_CA	ALA_A_20_HA	-15.801	1.269	1.615	-16.06	1.956	2.421	1.09	42.33	110.66
117	2jsa-2	ALA_A_20_CA	ALA_A_20_C	-15.801	1.269	1.615	-16.186	-0.148	2.044	1.53	73.71	-105.20
118	2jsa-2	ALA_A_20_C	ALA_A_20_O	-16.186	-0.148	2.044	-17.342	-0.409	2.375	1.23	74.39	-167.28
119	2jsa-2	ALA_A_20_C	ASP_A_21_N	-16.186	-0.148	2.044	-15.194	-1.027	2.025	1.33	90.82	-41.54
120	2jsa-2	ASP_A_21_N	ASP_A_21_H	-15.194	-1.027	2.025	-14.267	-0.742	1.742	1.01	106.27	17.09
121	2jsa-2	ASP_A_21_N	ASP_A_21_CA	-15.194	-1.027	2.025	-15.414	-2.412	2.408	1.45	74.72	-99.03
122	2jsa-2	ASP_A_21_CA	ASP_A_21_HA	-15.414	-2.412	2.408	-16.486	-2.605	2.446	1.09	88.00	-169.79
123	2jsa-2	ASP_A_21_CA	ASP_A_21_C	-15.414	-2.412	2.408	-14.792	-2.661	3.783	1.53	25.98	-21.82
124	2jsa-2	ASP_A_21_C	ASP_A_21_O	-14.792	-2.661	3.783	-15.082	-3.67	4.426	1.23	58.51	-106.04
125	2jsa-2	ASP_A_21_C	LYS_A_22_N	-14.792	-2.661	3.783	-13.949	-1.725	4.195	1.33	71.89	47.99
126	2jsa-2	LYS_A_22_N	LYS_A_22_H	-13.949	-1.725	4.195	-13.758	-0.921	3.614	1.01	125.11	76.64
127	2jsa-2	LYS_A_22_N	LYS_A_22_CA	-13.949	-1.725	4.195	-13.283	-1.83	5.482	1.45	27.65	-8.96
128	2jsa-2	LYS_A_22_CA	LYS_A_22_HA	-13.283	-1.83	5.482	-12.45	-1.126	5.491	1.09	89.53	40.20
129	2jsa-2	LYS_A_22_CA	LYS_A_22_C	-13.283	-1.83	5.482	-12.705	-3.238	5.638	1.53	84.15	-67.68
130	2jsa-2	LYS_A_22_C	LYS_A_22_O	-12.705	-3.238	5.638	-12.825	-3.849	6.699	1.23	30.41	-101.11
131	2jsa-2	LYS_A_22_C	ASP_A_23_N	-12.705	-3.238	5.638	-12.088	-3.713	4.565	1.33	144.03	-37.59
132	2jsa-2	ASP_A_23_N	ASP_A_23_H	-12.088	-3.713	4.565	-12.026	-3.155	3.725	1.01	146.24	83.66
133	2jsa-2	ASP_A_23_N	ASP_A_23_CA	-12.088	-3.713	4.565	-11.49	-5.037	4.569	1.45	89.84	-65.69
134	2jsa-2	ASP_A_23_CA	ASP_A_23_HA	-11.49	-5.037	4.569	-11.565	-5.459	5.571	1.09	23.16	-100.08
135	2jsa-2	ASP_A_23_CA	ASP_A_23_C	-11.49	-5.037	4.569	-10.02	-4.929	4.16	1.53	105.51	4.20
136	2jsa-2	ASP_A_23_C	ASP_A_23_O	-10.02	-4.929	4.16	-9.712	-4.52	3.041	1.23	155.41	53.02
137	2jsa-2	ASP_A_23_C	ALA_A_24_N	-10.02	-4.929	4.16	-9.151	-5.303	5.086	1.32	45.61	-23.29
138	2jsa-2	ALA_A_24_N	ALA_A_24_H	-9.151	-5.303	5.086	-9.475	-5.629	5.985	1.01	27.08	-134.82
139	2jsa-2	ALA_A_24_N	ALA_A_24_CA	-9.151	-5.303	5.086	-7.721	-5.253	4.836	1.45	99.91	2.00
140	2jsa-2	ALA_A_24_CA	ALA_A_24_HA	-7.721	-5.253	4.836	-7.478	-4.295	4.377	1.09	114.91	75.77
141	2jsa-2	ALA_A_24_CA	ALA_A_24_C	-7.721	-5.253	4.836	-7.339	-6.369	3.86	1.53	129.61	-71.10
142	2jsa-2	ALA_A_24_C	ALA_A_24_O	-7.339	-6.369	3.86	-6.194	-6.449	3.421	1.23	110.93	-4.00
143	2jsa-2	ALA_A_24_C	ASN_A_25_N	-7.339	-6.369	3.86	-8.322	-7.201	3.55	1.32	103.53	-139.76
144	2jsa-2	ASN_A_25_N	ASN_A_25_H	-8.322	-7.201	3.55	-9.241	-7.074	3.949	1.01	66.73	172.13
145	2jsa-2	ASN_A_25_N	ASN_A_25_CA	-8.322	-7.201	3.55	-8.104	-8.308	2.635	1.45	129.04	-78.86
146	2jsa-2	ASN_A_25_CA	ASN_A_25_HA	-8.104	-8.308	2.635	-7.078	-8.661	2.74	1.09	84.47	-18.99
147	2jsa-2	ASN_A_25_CA	ASN_A_25_C	-8.104	-8.308	2.635	-8.346	-7.834	1.201	1.53	159.64	117.05
148	2jsa-2	ASN_A_25_C	ASN_A_25_O	-8.346	-7.834	1.201	-7.507	-8.038	0.326	1.23	135.38	-13.67
149	2jsa-2	ASN_A_25_C	VAL_A_26_N	-8.346	-7.834	1.201	-9.498	-7.21	1.004	1.32	98.55	151.56
150	2jsa-2	VAL_A_26_N	VAL_A_26_H	-9.498	-7.21	1.004	-10.141	-7.078	1.771	1.01	40.56	168.40
151	2jsa-2	VAL_A_26_N	VAL_A_26_CA	-9.498	-7.21	1.004	-9.862	-6.704	-0.309	1.45	154.60	125.73
152	2jsa-2	VAL_A_26_CA	VAL_A_26_HA	-9.862	-6.704	-0.309	-9.54	-7.428	-1.058	1.09	133.39	-66.02
153	2jsa-2	VAL_A_26_CA	VAL_A_26_C	-9.862	-6.704	-0.309	-9.121	-5.391	-0.569	1.53	99.78	60.56
154	2jsa-2	VAL_A_26_C	VAL_A_26_O	-9.121	-5.391	-0.569	-9.145	-4.87	-1.682	1.23	154.89	92.64
155	2jsa-2	VAL_A_26_C	ILE_A_27_N	-9.121	-5.391	-0.569	-8.48	-4.893	0.479	1.33	37.76	37.84
156	2jsa-2	ILE_A_27_N	ILE_A_27_H	-8.48	-4.893	0.479	-8.503	-5.376	1.366	1.01	28.60	-92.73
157	2jsa-2	ILE_A_27_N	ILE_A_27_CA	-8.48	-4.893	0.479	-7.733	-3.651	0.379	1.45	93.95	58.98
158	2jsa-2	ILE_A_27_CA	ILE_A_27_HA	-7.733	-3.651	0.379	-8.237	-3.012	-0.346	1.09	131.70	128.26
159	2jsa-2	ILE_A_27_CA	ILE_A_27_C	-7.733	-3.651	0.379	-6.332	-3.946	-0.158	1.53	110.56	-11.89
160	2jsa-2	ILE_A_27_C	ILE_A_27_O	-6.332	-3.946	-0.158	-5.99	-3.541	-1.269	1.23	154.49	49.82
161	2jsa-2	ILE_A_27_C	LYS_A_28_N	-6.332	-3.946	-0.158	-5.556	-4.647	0.656	1.33	52.10	-42.09
162	2jsa-2	LYS_A_28_N	LYS_A_28_H	-5.556	-4.647	0.656	-5.902	-4.946	1.557	1.01	26.91	-139.17
163	2jsa-2	LYS_A_28_N	LYS_A_28_CA	-5.556	-4.647	0.656	-4.199	-5.0	0.276	1.45	105.16	-14.58
164	2jsa-2	LYS_A_28_CA	LYS_A_28_HA	-4.199	-5.0	0.276	-3.624	-4.079	0.181	1.09	95.00	58.02
165	2jsa-2	LYS_A_28_CA	LYS_A_28_C	-4.199	-5.0	0.276	-4.218	-5.679	-1.095	1.53	153.64	-91.60
166	2jsa-2	LYS_A_28_C	LYS_A_28_O	-4.218	-5.679	-1.095	-3.295	-5.504	-1.89	1.23	130.24	10.74
167	2jsa-2	LYS_A_28_C	LYS_A_29_N	-4.218	-5.679	-1.095	-5.276	-6.439	-1.328	1.32	100.14	-144.31
168	2jsa-2	LYS_A_29_N	LYS_A_29_H	-5.276	-6.439	-1.328	-5.995	-6.538	-0.626	1.01	45.95	-172.16
169	2jsa-2	LYS_A_29_N	LYS_A_29_CA	-5.276	-6.439	-1.328	-5.427	-7.145	-2.59	1.45	150.23	-102.07
170	2jsa-2	LYS_A_29_CA	LYS_A_29_HA	-5.427	-7.145	-2.59	-4.504	-7.692	-2.783	1.09	100.20	-30.65
171	2jsa-2	LYS_A_29_CA	LYS_A_29_C	-5.427	-7.145	-2.59	-5.611	-6.1				

174	2jsa-2	ASP_A_30_N	ASP_A_30_H	-6.432	-5.127	-3.443	-6.885	-5.074	-2.542	1.01	26.85	173.33
175	2jsa-2	ASP_A_30_N	ASP_A_30_CA	-6.432	-5.127	-3.443	-6.7	-4.088	-4.423	1.45	132.41	104.46
176	2jsa-2	ASP_A_30_CA	ASP_A_30_HA	-6.7	-4.088	-4.423	-7.214	-4.528	-5.277	1.09	141.61	-139.44
177	2jsa-2	ASP_A_30_CA	ASP_A_30_C	-6.7	-4.088	-4.423	-5.378	-3.466	-4.875	1.53	107.19	25.20
178	2jsa-2	ASP_A_30_C	ASP_A_30_O	-5.378	-3.466	-4.875	-5.133	-3.322	-6.071	1.23	166.63	30.45
179	2jsa-2	ASP_A_30_C	PHE_A_31_N	-5.378	-3.466	-4.875	-4.561	-3.112	-3.894	1.32	42.23	23.43
180	2jsa-2	PHE_A_31_N	PHE_A_31_H	-4.561	-3.112	-3.894	-4.829	-3.259	-2.931	1.01	17.61	-151.25
181	2jsa-2	PHE_A_31_N	PHE_A_31_CA	-4.561	-3.112	-3.894	-3.269	-2.509	-4.175	1.45	101.15	25.02
182	2jsa-2	PHE_A_31_CA	PHE_A_31_HA	-3.269	-2.509	-4.175	-3.402	-1.467	-4.466	1.09	105.48	97.27
183	2jsa-2	PHE_A_31_CA	PHE_A_31_C	-3.269	-2.509	-4.175	-2.542	-3.265	-5.289	1.53	136.73	-46.12
184	2jsa-2	PHE_A_31_C	PHE_A_31_O	-2.542	-3.265	-5.289	-2.128	-2.669	-6.282	1.23	143.84	55.21
185	2jsa-2	PHE_A_31_C	ASP_A_32_N	-2.542	-3.265	-5.289	-2.409	-4.567	-5.087	1.32	81.23	-84.17
186	2jsa-2	ASP_A_32_N	ASP_A_32_H	-2.409	-4.567	-5.087	-2.774	-4.991	-4.246	1.01	33.63	-130.72
187	2jsa-2	ASP_A_32_N	ASP_A_32_CA	-2.409	-4.567	-5.087	-1.739	-5.412	-6.06	1.45	132.06	-51.59
188	2jsa-2	ASP_A_32_CA	ASP_A_32_HA	-1.739	-5.412	-6.06	-0.71	-5.072	-6.177	1.09	96.16	18.28
189	2jsa-2	ASP_A_32_CA	ASP_A_32_C	-1.739	-5.412	-6.06	-2.473	-5.321	-7.399	1.53	151.09	172.93
190	2jsa-2	ASP_A_32_C	ASP_A_32_O	-2.473	-5.321	-7.399	-1.887	-5.573	-8.451	1.23	148.77	-23.27
191	2jsa-2	ASP_A_32_C	ALA_A_33_N	-2.473	-5.321	-7.399	-3.746	-4.959	-7.316	1.33	86.41	164.13
192	2jsa-2	ALA_A_33_N	ALA_A_33_H	-3.746	-4.959	-7.316	-4.163	-4.767	-6.416	1.01	27.03	155.28
193	2jsa-2	ALA_A_33_N	ALA_A_33_CA	-3.746	-4.959	-7.316	-4.566	-4.832	-8.509	1.45	145.18	171.20
194	2jsa-2	ALA_A_33_CA	ALA_A_33_HA	-4.566	-4.832	-8.509	-4.401	-5.703	-9.143	1.09	125.57	-79.27
195	2jsa-2	ALA_A_33_CA	ALA_A_33_C	-4.566	-4.832	-8.509	-4.141	-3.582	-9.283	1.53	120.38	71.22
196	2jsa-2	ALA_A_33_C	ALA_A_33_O	-4.141	-3.582	-9.283	-3.575	-3.684	-10.371	1.23	152.14	-10.22
197	2jsa-2	ALA_A_33_C	GLU_A_34_N	-4.141	-3.582	-9.283	-4.432	-2.432	-8.694	1.32	63.59	104.20
198	2jsa-2	GLU_A_34_N	GLU_A_34_H	-4.432	-2.432	-8.694	-4.9	-2.423	-7.799	1.01	27.61	178.90
199	2jsa-2	GLU_A_34_N	GLU_A_34_CA	-4.432	-2.432	-8.694	-4.087	-1.165	-9.315	1.45	115.31	74.77
200	2jsa-2	GLU_A_34_CA	GLU_A_34_HA	-4.087	-1.165	-9.315	-4.659	-1.075	-10.238	1.09	147.90	171.06
201	2jsa-2	GLU_A_34_CA	GLU_A_34_C	-4.087	-1.165	-9.315	-2.599	-1.133	-9.668	1.53	103.34	1.23
202	2jsa-2	GLU_A_34_C	GLU_A_34_O	-2.599	-1.133	-9.668	-2.195	-0.454	-10.611	1.23	140.04	59.25
203	2jsa-2	GLU_A_34_C	CYS_A_35_N	-2.599	-1.133	-9.668	-1.824	-1.878	-8.893	1.33	54.21	-43.87
204	2jsa-2	CYS_A_35_N	CYS_A_35_H	-1.824	-1.878	-8.893	-2.225	-2.412	-8.136	1.01	41.42	-126.90
205	2jsa-2	CYS_A_35_N	CYS_A_35_CA	-1.824	-1.878	-8.893	-0.389	-1.945	-9.112	1.45	98.67	-2.67
206	2jsa-2	CYS_A_35_CA	CYS_A_35_HA	-0.389	-1.945	-9.112	-0.021	-0.934	-9.29	1.09	99.39	70.00
207	2jsa-2	CYS_A_35_CA	CYS_A_35_C	-0.389	-1.945	-9.112	-0.133	-2.784	-10.365	1.53	145.01	-73.03
208	2jsa-2	CYS_A_35_C	CYS_A_35_O	-0.133	-2.784	-10.365	0.658	-2.397	-11.224	1.23	134.29	26.07
209	2jsa-2	CYS_A_35_C	LYS_A_36_N	-0.133	-2.784	-10.365	-0.817	-3.916	-10.43	1.32	92.81	-121.14
210	2jsa-2	LYS_A_36_N	LYS_A_36_H	-0.817	-3.916	-10.43	-1.45	-4.171	-9.686	1.01	42.53	-158.06
211	2jsa-2	LYS_A_36_N	LYS_A_36_CA	-0.817	-3.916	-10.43	-0.674	-4.813	-11.565	1.45	141.33	-80.94
212	2jsa-2	LYS_A_36_CA	LYS_A_36_HA	-0.674	-4.813	-11.565	0.353	-5.178	-11.578	1.09	90.68	-19.57
213	2jsa-2	LYS_A_36_CA	LYS_A_36_C	-0.674	-4.813	-11.565	-0.906	-4.033	-12.86	1.53	147.85	106.56
214	2jsa-2	LYS_A_36_C	LYS_A_36_O	-0.906	-4.033	-12.86	-0.49	-4.465	-13.933	1.23	150.80	-46.08
215	2jsa-2	LYS_A_36_C	LYS_A_37_N	-0.906	-4.033	-12.86	-1.569	-2.895	-12.716	1.32	83.76	120.23
216	2jsa-2	LYS_A_37_N	LYS_A_37_H	-1.569	-2.895	-12.716	-1.88	-2.6	-11.802	1.01	25.13	136.51
217	2jsa-2	LYS_A_37_N	LYS_A_37_CA	-1.569	-2.895	-12.716	-1.862	-2.049	-13.861	1.45	141.98	109.10
218	2jsa-2	LYS_A_37_CA	LYS_A_37_HA	-1.862	-2.049	-13.861	-1.611	-2.605	-14.764	1.09	145.96	-65.70
219	2jsa-2	LYS_A_37_CA	LYS_A_37_C	-1.862	-2.049	-13.861	-0.968	-0.809	-13.815	1.53	88.28	54.21
220	2jsa-2	LYS_A_37_C	LYS_A_37_O	-0.968	-0.809	-13.815	-0.412	-0.401	-14.834	1.23	145.91	36.27
221	2jsa-2	LYS_A_37_C	LEU_A_38_N	-0.968	-0.809	-13.815	-0.858	-0.241	-12.622	1.33	25.87	79.04
222	2jsa-2	LEU_A_38_N	LEU_A_38_H	-0.858	-0.241	-12.622	-1.344	-0.629	-11.827	1.01	38.03	-141.40
223	2jsa-2	LEU_A_38_N	LEU_A_38_CA	-0.858	-0.241	-12.622	-0.041	0.945	-12.43	1.45	82.41	55.44
224	2jsa-2	LEU_A_38_CA	LEU_A_38_HA	-0.041	0.945	-12.43	-0.349	1.689	-13.164	1.09	132.35	112.49
225	2jsa-2	LEU_A_38_CA	LEU_A_38_C	-0.041	0.945	-12.43	1.425	0.6	-12.704	1.53	100.31	-13.24
226	2jsa-2	LEU_A_38_C	LEU_A_38_O	1.425	0.6	-12.704	2.021	1.114	-13.65	1.23	140.24	40.78
227	2jsa-2	LEU_A_38_C	PHE_A_39_N	1.425	0.6	-12.704	1.962	-0.269	-11.86	1.33	50.44	-58.29
228	2jsa-2	PHE_A_39_N	PHE_A_39_H	1.962	-0.269	-11.86	1.412	-0.652	-11.105	1.01	41.60	-145.15
229	2jsa-2	PHE_A_39_N	PHE_A_39_CA	1.962	-0.269	-11.86	3.346	-0.689	-12.0	1.45	95.53	-16.88
230	2jsa-2	PHE_A_39_CA	PHE_A_39_HA	3.346	-0.689	-12.0	3.943	0.132	-12.398	1.09	111.41	53.98
231	2jsa-2	PHE_A_39_CA	PHE_A_39_C	3.346	-0.689	-12.0	3.461	-1.903	-12.923	1.53	127.12	-84.59
232	2jsa-2	PHE_A_39_C	PHE_A_39_O	3.461	-1.903	-12.923	4.327	-2.755	-12.731	1.23	81.02	-44.53
233	2jsa-2	PHE_A_39_C	HIS_A_40_N	3.461	-1.903	-12.923	2.574	-1.944	-13.907	1.33	137.94	-177.35
234	2jsa-2	HIS_A_40_N	HIS_A_40_H	2.574	-1.944	-13.907	1.889	-1.208	-14.005	1.01	95.57	132.94
235	2jsa-2	HIS_A_40_N	HIS_A_40_CA	2.574	-1.944	-13.907	2.564	-3.039	-14.861	1.45	131.06	-90.52
236	2jsa-2	HIS_A_40_CA	HIS_A_40_HA	2.564	-3.039	-14.861	2.587	-3.973	-14.3	1.09	59.02	-88.59
237	2jsa-2	HIS_A_40_CA	HIS_A_40_C	2.564	-3.039	-14.861	3.825	-2.979	-15.725	1.53	124.39	2.72
238	2jsa-2	HIS_A_40_C	HIS_A_40_O	3.825	-2.979	-15.725	4.24	-3.988	-16.294	1.23	117.54	-67.64
239	2jsa-2	HIS_A_40_C	THR_A_41_N	3.825	-2.979	-15.725	4.399	-1.787	-15.794	1.32	92.99	64.29
240	2jsa-2	THR_A_41_N	THR_A_41_H	4.399	-1.787	-15.794	4.003	-1.001	-15.298	1.01	60.60	116.74
241	2jsa-2	THR_A_41_N	THR_A_41_CA	4.399	-1.787	-15.794	5.606	-1.582	-16.579	1.45	122.67	9.64
242	2jsa-2	THR_A_41_CA	THR_A_41_HA	5.606	-1.582	-16.579	5.871	-2.52	-17.066	1.09	116.55	-74.22
243	2jsa-2	THR_A_41_CA	THR_A_41_C	5.606	-1.582	-16.579	6.769	-1.178	-15.672	1.53	53.62	19.16
244	2jsa-2	THR_A_41_C	THR_A_41_O	6.769	-1.178	-15.672	7.328	-0.092	-15.819	1.23	96.86	62.76
245	2jsa-2	THR_A_41_C	ILE_A_42_N	6.769	-1.178	-15.672	7.101	-2.074	-14.755	1.32	46.18	-69.67
246	2jsa-2	ILE_A_42_N	ILE_A_42_H	7.101	-2.074	-14.755	6.599	-2.948	-14.692	1.01	86.42	-119.87
247	2jsa-2	ILE_A_42_N	ILE_A_42_CA	7.101	-2.074	-14.755	8.189	-1.824	-13.824	1.45	50.17	12.94
248	2jsa-2	ILE_A_42_CA	ILE_A_42_HA	8.189	-1.824	-13.824	9.909	-1.168	-14.314	1.09	116.71	42.34
249	2jsa-2	ILE_A_42_CA	ILE_A_42_C	8.189	-1.824	-13.824	8.9	-3.143	-13.511	1.53	78.20	-61.67
250	2jsa-2	ILE_A_42_C	ILE_A_42_O	8.9	-3.143	-13.511	8.261	-4.191	-13.42	1.23	85.76	-121.37
251	2jsa-2	ILE_A_42_C	PRO_A_43_N	8.9	-3.143	-13.511	10.247	-3.046	-13.352	1.36	83.29	4.12
252	2jsa-2	PRO_A_43_N	PRO_A_43_CA	10.247	-3.046	-13.352	11.051	-4.218	-13.052	1.45	78.08	-55.55
253	2jsa-2	PRO_A_43_CA	PRO_A_43_HA	11.051	-4.218	-13.052	10.756	-5.048	-13.694	1.09	126.09	-109.57
254	2jsa-2	PRO_A_43_CA	PRO_A_43_C	11.051	-4.218	-13.052	10.874	-4.646	-11.593	1.53	17.61	-112.47
255	2jsa-2	PRO_A_43_C	PRO_A_43_O	10.874	-4.646	-11.593	11.385	-3.991	-10.685	1.23	42.46	52.04
256	2jsa-2	PRO_A_43_C	PHE_A_44_N	10.874	-4.646	-11.593	10.151	-5.741	-11.414	1.32	82.23	-123.44
257	2jsa-2	PHE_A_44_N	PHE_A_44_H	10.151	-5.741	-11.414	9.763	-6.229	-12.208	1.01	141.86	-128.49
258	2jsa-2	PHE_A_44_N	PHE_A_44_CA	10.151	-5.741	-11.414	9.901	-6.263	-10.082	1.45	23.49	-115.59
259	2jsa-2	PHE_A_44_CA	PHE_A_44_HA	9.901	-6.263	-10.082	9.588	-7.305	-10.146	1.09	93.37	-106.72
260	2jsa-2	PHE_A_44_CA	PHE_A_44_C	9.901	-6.263	-10.082	8.825	-5.445	-9.365	1.53	62.06	142.76
261	2jsa-2	PHE_A_44_C	PHE_A_44_O	8.825	-5.445	-9.365	8.445	-5.762	-8.24	1.23	23.74	-140.16
262	2jsa-2	PHE_A_44_C	GLY_A_45_N	8.825	-5.445	-9.365	8.364	-4.406	-10.047	1.33	120.96	113.93
263	2jsa-2	GLY_A_45_N	GLY_A_45_H	8.364	-4.406	-10.047	8.724	-4.203	-10.969	1.01	155.86	29.42
264	2jsa-2	GLY_A_45_N	GLY_A_45_CA	8.364	-4.406	-10.047						

267	2jsa-2	GLY_A_45_C	THR_A_46_N	6.149	-4.356	-8.981	5.733	-5.311	-9.8	1.33	128.18	-113.54
268	2jsa-2	THR_A_46_N	THR_A_46_H	5.733	-5.311	-9.8	6.195	-5.457	-10.686	1.01	151.33	-17.54
269	2jsa-2	THR_A_46_N	THR_A_46_CA	5.733	-5.311	-9.8	4.612	-6.165	-9.445	1.45	75.86	-142.70
270	2jsa-2	THR_A_46_CA	THR_A_46_HA	4.612	-6.165	-9.445	3.798	-5.539	-9.08	1.09	70.43	142.44
271	2jsa-2	THR_A_46_CA	THR_A_46_C	4.612	-6.165	-9.445	5.007	-7.125	-8.322	1.53	42.75	-67.63
272	2jsa-2	THR_A_46_C	THR_A_46_O	5.007	-7.125	-8.322	4.175	-7.494	-7.496	1.23	47.78	-156.08
273	2jsa-2	THR_A_46_C	ARG_A_47_N	5.007	-7.125	-8.322	6.277	-7.502	-8.329	1.32	90.30	-16.53
274	2jsa-2	ARG_A_47_N	ARG_A_47_H	6.277	-7.502	-8.329	6.906	-7.158	-9.041	1.01	134.80	28.67
275	2jsa-2	ARG_A_47_N	ARG_A_47_CA	6.277	-7.502	-8.329	6.792	-8.413	-7.321	1.45	46.07	-60.52
276	2jsa-2	ARG_A_47_CA	ARG_A_47_HA	6.792	-8.413	-7.321	6.164	-9.304	-7.31	1.09	89.42	-125.18
277	2jsa-2	ARG_A_47_CA	ARG_A_47_C	6.792	-8.413	-7.321	6.748	-7.756	-5.939	1.53	25.48	93.83
278	2jsa-2	ARG_A_47_C	ARG_A_47_O	6.748	-7.756	-5.939	6.075	-8.247	-5.035	1.23	42.66	-143.89
279	2jsa-2	ARG_A_47_C	GLU_A_48_N	6.748	-7.756	-5.939	7.476	-6.655	-5.821	1.33	84.89	56.53
280	2jsa-2	GLU_A_48_N	GLU_A_48_H	7.476	-6.655	-5.821	8.006	-6.308	-6.608	1.01	141.17	33.21
281	2jsa-2	GLU_A_48_N	GLU_A_48_CA	7.476	-6.655	-5.821	7.529	-5.925	-4.565	1.45	30.23	85.85
282	2jsa-2	GLU_A_48_CA	GLU_A_48_HA	7.529	-5.925	-4.565	8.009	-6.564	-3.823	1.09	47.13	-53.09
283	2jsa-2	GLU_A_48_CA	GLU_A_48_C	7.529	-5.925	-4.565	6.115	-5.603	-4.079	1.53	71.47	167.17
284	2jsa-2	GLU_A_48_C	GLU_A_48_O	6.115	-5.603	-4.079	5.879	-5.491	-2.876	1.23	12.25	154.61
285	2jsa-2	GLU_A_48_C	CYS_A_49_N	6.115	-5.603	-4.079	5.211	-5.463	-5.037	1.32	136.32	171.20
286	2jsa-2	CYS_A_49_N	CYS_A_49_H	5.211	-5.463	-5.037	5.476	-5.57	-6.006	1.01	163.57	-21.99
287	2jsa-2	CYS_A_49_N	CYS_A_49_CA	5.211	-5.463	-5.037	3.827	-5.156	-4.721	1.45	77.43	167.49
288	2jsa-2	CYS_A_49_CA	CYS_A_49_HA	3.827	-5.156	-4.721	3.806	-4.243	-4.125	1.09	56.87	91.32
289	2jsa-2	CYS_A_49_CA	CYS_A_49_C	3.827	-5.156	-4.721	3.261	-6.3	-3.877	1.53	56.53	-116.32
290	2jsa-2	CYS_A_49_C	CYS_A_49_O	3.261	-6.3	-3.877	2.73	-6.072	-2.791	1.23	28.02	156.76
291	2jsa-2	CYS_A_49_C	ASP_A_50_N	3.261	-6.3	-3.877	3.395	-7.506	-4.409	1.32	113.67	-83.66
292	2jsa-2	ASP_A_50_N	ASP_A_50_H	3.395	-7.506	-4.409	3.843	-7.619	-5.307	1.01	152.77	-14.16
293	2jsa-2	ASP_A_50_N	ASP_A_50_CA	3.395	-7.506	-4.409	2.904	-8.687	-3.719	1.45	61.65	-112.58
294	2jsa-2	ASP_A_50_CA	ASP_A_50_HA	2.904	-8.687	-3.719	1.842	-8.561	-3.51	1.09	78.94	173.23
295	2jsa-2	ASP_A_50_CA	ASP_A_50_C	2.904	-8.687	-3.719	3.674	-8.863	-2.409	1.53	31.09	-12.88
296	2jsa-2	ASP_A_50_C	ASP_A_50_O	3.674	-8.863	-2.409	3.283	-9.661	-1.558	1.23	46.24	-116.10
297	2jsa-2	ASP_A_50_C	HIS_A_51_N	3.674	-8.863	-2.409	4.756	-8.109	-2.289	1.32	84.80	34.87
298	2jsa-2	HIS_A_51_N	HIS_A_51_H	4.756	-8.109	-2.289	5.02	-7.476	-3.031	1.01	137.25	67.36
299	2jsa-2	HIS_A_51_N	HIS_A_51_CA	4.756	-8.109	-2.289	5.585	-8.173	-1.097	1.45	34.90	-4.41
300	2jsa-2	HIS_A_51_CA	HIS_A_51_HA	5.585	-8.173	-1.097	5.282	-9.048	-0.522	1.09	58.16	-109.10
301	2jsa-2	HIS_A_51_CA	HIS_A_51_C	5.585	-8.173	-1.097	5.338	-6.934	-0.234	1.53	55.66	101.27
302	2jsa-2	HIS_A_51_C	HIS_A_51_O	5.338	-6.934	-0.234	5.975	-6.759	0.804	1.23	32.47	15.36
303	2jsa-2	HIS_A_51_C	TYR_A_52_N	5.338	-6.934	-0.234	4.411	-6.106	-0.694	1.33	110.31	138.23
304	2jsa-2	TYR_A_52_N	TYR_A_52_H	4.411	-6.106	-0.694	3.927	-6.313	-1.556	1.01	148.59	-156.84
305	2jsa-2	TYR_A_52_N	TYR_A_52_CA	4.411	-6.106	-0.694	4.072	-4.889	0.024	1.45	60.39	105.57
306	2jsa-2	TYR_A_52_CA	TYR_A_52_HA	4.072	-4.889	0.024	4.83	-4.672	0.778	1.09	46.28	15.98
307	2jsa-2	TYR_A_52_CA	TYR_A_52_C	4.072	-4.889	0.024	2.698	-5.008	0.687	1.53	64.32	-175.05
308	2jsa-2	TYR_A_52_C	TYR_A_52_O	2.698	-5.008	0.687	2.527	-4.621	1.842	1.23	20.12	113.84
309	2jsa-2	TYR_A_52_C	VAL_A_53_N	2.698	-5.008	0.687	1.755	-5.547	-0.072	1.33	124.95	-150.25
310	2jsa-2	VAL_A_53_N	VAL_A_53_H	1.755	-5.547	-0.072	1.968	-5.844	-1.013	1.01	158.77	-54.35
311	2jsa-2	VAL_A_53_N	VAL_A_53_CA	1.755	-5.547	-0.072	0.401	-5.722	0.429	1.45	69.85	-172.64
312	2jsa-2	VAL_A_53_CA	VAL_A_53_HA	0.401	-5.722	0.429	-0.005	-4.741	0.675	1.09	76.95	112.48
313	2jsa-2	VAL_A_53_CA	VAL_A_53_C	0.401	-5.722	0.429	0.441	-6.554	1.711	1.53	33.01	-87.25
314	2jsa-2	VAL_A_53_C	VAL_A_53_O	0.441	-6.554	1.711	-0.516	-6.552	2.486	1.23	51.00	179.88
315	2jsa-2	VAL_A_53_C	ASN_A_54_N	0.441	-6.554	1.711	1.555	-7.246	1.897	1.32	81.93	-31.85
316	2jsa-2	ASN_A_54_N	ASN_A_54_H	1.555	-7.246	1.897	2.301	-7.2	1.218	1.01	132.25	3.53
317	2jsa-2	ASN_A_54_N	ASN_A_54_CA	1.555	-7.246	1.897	1.731	-8.081	3.073	1.45	35.97	-78.10
318	2jsa-2	ASN_A_54_CA	ASN_A_54_HA	1.731	-8.081	3.073	0.961	-7.835	3.804	1.09	47.88	162.28
319	2jsa-2	ASN_A_54_CA	ASN_A_54_C	1.731	-8.081	3.073	3.116	-7.825	3.672	1.53	66.96	10.47
320	2jsa-2	ASN_A_54_C	ASN_A_54_O	3.116	-7.825	3.672	3.894	-8.757	3.867	1.23	80.88	-50.15
321	2jsa-2	ASN_A_54_C	SER_A_55_N	3.116	-7.825	3.672	3.381	-6.556	3.948	1.33	77.98	78.20
322	2jsa-2	SER_A_55_N	SER_A_55_H	3.381	-6.556	3.948	2.693	-5.84	3.762	1.01	100.61	133.86
323	2jsa-2	SER_A_55_N	SER_A_55_CA	3.381	-6.556	3.948	4.657	-6.166	4.521	1.45	66.76	17.00
324	2jsa-2	SER_A_55_CA	SER_A_55_HA	4.657	-6.166	4.521	4.89	-6.853	5.335	1.09	41.71	-71.27
325	2jsa-2	SER_A_55_CA	SER_A_55_C	4.657	-6.166	4.521	4.565	-4.749	5.088	1.53	68.23	93.71
326	2jsa-2	SER_A_55_C	SER_A_55_O	4.565	-4.749	5.088	4.938	-4.51	6.237	1.23	21.08	32.65
327	2jsa-2	SER_A_55_C	LYS_A_56_N	4.565	-4.749	5.088	4.066	-3.845	4.258	1.32	128.79	118.90
328	2jsa-2	LYS_A_56_N	LYS_A_56_H	4.066	-3.845	4.258	3.78	-4.112	3.327	1.01	157.20	-136.97
329	2jsa-2	LYS_A_56_N	LYS_A_56_CA	4.066	-3.845	4.258	3.92	-2.456	4.663	1.45	73.83	96.00
330	2jsa-2	LYS_A_56_CA	LYS_A_56_HA	3.92	-2.456	4.663	4.331	-2.352	5.667	1.09	22.89	14.20
331	2jsa-2	LYS_A_56_CA	LYS_A_56_C	3.92	-2.456	4.663	2.433	-2.104	4.73	1.53	87.49	166.68
332	2jsa-2	LYS_A_56_C	LYS_A_56_O	2.433	-2.104	4.73	2.074	-0.933	4.853	1.23	84.27	107.04
333	2jsa-2	LYS_A_56_C	VAL_A_57_N	2.433	-2.104	4.73	1.608	-3.137	4.646	1.32	93.64	-128.61
334	2jsa-2	VAL_A_57_N	VAL_A_57_H	1.608	-3.137	4.646	1.974	-4.073	4.546	1.01	95.68	-68.64
335	2jsa-2	VAL_A_57_N	VAL_A_57_CA	1.608	-3.137	4.646	0.168	-2.949	4.695	1.45	88.07	172.56
336	2jsa-2	VAL_A_57_CA	VAL_A_57_HA	0.168	-2.949	4.695	-0.055	-1.919	4.415	1.09	104.88	102.22
337	2jsa-2	VAL_A_57_CA	VAL_A_57_C	0.168	-2.949	4.695	-0.322	-3.17	6.129	1.53	20.55	-155.72
338	2jsa-2	VAL_A_57_C	VAL_A_57_O	-0.322	-3.17	6.129	-1.045	-2.339	6.675	1.23	63.63	131.02
339	2jsa-2	VAL_A_57_C	ASP_A_58_N	-0.322	-3.17	6.129	0.092	-4.293	6.696	1.32	64.65	-69.76
340	2jsa-2	ASP_A_58_N	ASP_A_58_H	0.092	-4.293	6.696	0.686	-4.932	6.186	1.01	120.31	-47.09
341	2jsa-2	ASP_A_58_N	ASP_A_58_CA	0.092	-4.293	6.696	-0.295	-4.632	8.054	1.45	20.75	-138.78
342	2jsa-2	ASP_A_58_CA	ASP_A_58_HA	-0.295	-4.632	8.054	-1.347	-4.916	8.064	1.09	89.47	-164.89
343	2jsa-2	ASP_A_58_CA	ASP_A_58_C	-0.295	-4.632	8.054	-0.075	-3.419	8.961	1.53	53.66	79.72
344	2jsa-2	ASP_A_58_C	ASP_A_58_O	-0.075	-3.419	8.961	-0.929	-3.09	9.781	1.23	48.14	158.93
345	2jsa-2	ASP_A_58_C	PRO_A_59_N	-0.075	-3.419	8.961	1.106	-2.771	8.777	1.36	97.78	28.75
346	2jsa-2	PRO_A_59_N	PRO_A_59_CA	1.106	-2.771	8.777	1.45	-1.601	9.568	1.45	57.03	73.62
347	2jsa-2	PRO_A_59_CA	PRO_A_59_HA	1.45	-1.601	9.568	1.221	-1.78	10.619	1.09	15.46	-141.99
348	2jsa-2	PRO_A_59_CA	PRO_A_59_C	1.45	-1.601	9.568	0.663	-0.374	9.102	1.53	107.73	122.68
349	2jsa-2	PRO_A_59_C	PRO_A_59_O	0.663	-0.374	9.102	0.006	0.288	9.905	1.23	49.27	134.78
350	2jsa-2	PRO_A_59_C	ILE_A_60_N	0.663	-0.374	9.102	0.756	-0.108	7.807	1.33	167.72	70.73
351	2jsa-2	ILE_A_60_N	ILE_A_60_H	0.756	-0.108	7.807	1.314	-0.696	7.205	1.01	126.60	-46.50
352	2jsa-2	ILE_A_60_N	ILE_A_60_CA	0.756	-0.108	7.807	0.061	1.028	7.226	1.45	113.57	121.46
353	2jsa-2	ILE_A_60_CA	ILE_A_60_HA	0.061	1.028	7.226	0.53	1.938	7.601	1.09	69.88	62.73
354	2jsa-2	ILE_A_60_CA	ILE_A_60_C	0.061	1.028	7.226	-1.395	1.027	7.697	1.53	72.07	-179.96
355	2jsa-2	ILE_A_60_C	ILE_A_60_O	-1.395	1.027	7.697	-1.854	1.991	8.306	1.23	60.30	115.46
356	2jsa-2	ILE_A_60_C	ILE_A_61_N	-1.395	1.027	7.697	-2.079	-0.068	7.397	1.33	103.08	-121.99
357	2jsa-2	ILE_A_61_N	ILE_A_61_H	-2.079	-0.068	7.397	-1.635	-0.824	6.895	1.01	119.79	-59.57
358	2jsa-2	ILE_A_61_N	ILE_A_61_CA</									

360	2jsa-2	ILE_A_61_CA	ILE_A_61_C	-3.473	-0.207	7.782	-3.592	-0.088	9.303	1.53	6.31	135.00
361	2jsa-2	ILE_A_61_C	ILE_A_61_O	-3.592	-0.088	9.303	-4.663	0.221	9.823	1.23	64.99	163.91
362	2jsa-2	ILE_A_61_C	HIS_A_62_N	-3.592	-0.088	9.303	-2.476	-0.338	9.973	1.33	59.64	-12.63
363	2jsa-2	HIS_A_62_N	HIS_A_62_H	-2.476	-0.338	9.973	-1.63	-0.586	9.479	1.01	119.26	-16.34
364	2jsa-2	HIS_A_62_N	HIS_A_62_CA	-2.476	-0.338	9.973	-2.442	-0.263	11.424	1.45	3.25	65.61
365	2jsa-2	HIS_A_62_CA	HIS_A_62_HA	-2.442	-0.263	11.424	-3.236	-0.9	11.813	1.09	69.09	-141.26
366	2jsa-2	HIS_A_62_CA	HIS_A_62_C	-2.442	-0.263	11.424	-2.73	1.172	11.87	1.53	73.05	161.35
367	2jsa-2	HIS_A_62_C	HIS_A_62_O	-2.73	1.172	11.87	-3.35	1.39	12.909	1.23	32.31	160.63
368	2jsa-2	HIS_A_62_C	GLU_A_63_N	-2.73	1.172	11.87	-2.265	2.113	11.061	1.33	127.62	63.70
369	2jsa-2	GLU_A_63_N	GLU_A_63_H	-2.265	2.113	11.061	-1.763	1.86	10.222	1.01	146.18	-26.75
370	2jsa-2	GLU_A_63_N	GLU_A_63_CA	-2.265	2.113	11.061	-2.465	3.521	11.36	1.45	78.13	98.08
371	2jsa-2	GLU_A_63_CA	GLU_A_63_HA	-2.465	3.521	11.36	-2.348	3.658	12.435	1.09	9.51	49.50
372	2jsa-2	GLU_A_63_CA	GLU_A_63_C	-2.465	3.521	11.36	-3.881	3.951	10.972	1.53	104.69	163.11
373	2jsa-2	GLU_A_63_C	GLU_A_63_O	-3.881	3.951	10.972	-4.631	4.453	11.808	1.23	47.19	146.20
374	2jsa-2	GLU_A_63_C	LEU_A_64_N	-3.881	3.951	10.972	-4.204	3.736	9.705	1.33	162.97	-146.35
375	2jsa-2	LEU_A_64_N	LEU_A_64_H	-4.204	3.736	9.705	-3.536	3.317	9.074	1.01	128.67	-32.10
376	2jsa-2	LEU_A_64_N	LEU_A_64_CA	-4.204	3.736	9.705	-5.517	4.095	9.197	1.45	110.47	161.71
377	2jsa-2	LEU_A_64_CA	LEU_A_64_HA	-5.517	4.095	9.197	-5.568	5.182	9.134	1.09	93.31	92.69
378	2jsa-2	LEU_A_64_CA	LEU_A_64_C	-5.517	4.095	9.197	-6.586	3.636	10.189	1.53	49.55	-156.76
379	2jsa-2	LEU_A_64_C	LEU_A_64_O	-6.586	3.636	10.189	-7.537	4.366	10.466	1.23	76.99	142.49
380	2jsa-2	LEU_A_64_C	GLU_A_65_N	-6.586	3.636	10.189	-6.396	2.427	10.697	1.33	67.46	-81.07
381	2jsa-2	GLU_A_65_N	GLU_A_65_H	-6.396	2.427	10.697	-5.59	1.882	10.424	1.01	105.67	-34.07
382	2jsa-2	GLU_A_65_N	GLU_A_65_CA	-6.396	2.427	10.697	-7.333	1.861	11.652	1.45	48.90	-148.87
383	2jsa-2	GLU_A_65_CA	GLU_A_65_HA	-7.333	1.861	11.652	-8.325	1.879	11.203	1.09	114.35	178.96
384	2jsa-2	GLU_A_65_CA	GLU_A_65_C	-7.333	1.861	11.652	-7.366	2.706	12.928	1.53	33.53	92.24
385	2jsa-2	GLU_A_65_C	GLU_A_65_O	-7.366	2.706	12.928	-8.43	2.925	13.505	1.23	62.02	168.37
386	2jsa-2	GLU_A_65_C	GLY_A_66_N	-7.366	2.706	12.928	-6.187	3.16	13.33	1.33	72.35	21.06
387	2jsa-2	GLY_A_66_N	GLY_A_66_H	-6.187	3.16	13.33	-5.352	2.942	12.805	1.01	121.31	-14.63
388	2jsa-2	GLY_A_66_N	GLY_A_66_CA	-6.187	3.16	13.33	-6.068	3.976	14.526	1.45	34.59	81.70
389	2jsa-2	GLY_A_66_CA	GLY_A_66_C	-6.068	3.976	14.526	-6.851	5.283	14.378	1.53	95.55	120.93
390	2jsa-2	GLY_A_66_C	GLY_A_66_O	-6.851	5.283	14.378	-7.452	5.763	15.338	1.23	38.70	141.39
391	2jsa-2	GLY_A_66_C	GLY_A_67_N	-6.851	5.283	14.378	-6.818	5.821	13.168	1.32	155.99	86.49
392	2jsa-2	GLY_A_67_N	GLY_A_67_H	-6.818	5.821	13.168	-6.302	5.371	12.425	1.01	137.34	-41.09
393	2jsa-2	GLY_A_67_N	GLY_A_67_CA	-6.818	5.821	13.168	-7.517	7.063	12.881	1.45	101.39	119.37
394	2jsa-2	GLY_A_67_CA	GLY_A_67_C	-7.517	7.063	12.881	-6.668	7.979	11.997	1.53	125.29	47.17
395	2jsa-2	GLY_A_67_C	GLY_A_67_O	-6.668	7.979	11.997	-7.148	9.005	11.519	1.23	112.88	115.07
396	2jsa-2	GLY_A_67_C	THR_A_68_N	-6.668	7.979	11.997	-5.421	7.573	11.805	1.33	98.33	-18.03
397	2jsa-2	THR_A_68_N	THR_A_68_H	-5.421	7.573	11.805	-5.093	6.717	12.229	1.01	65.18	-69.03
398	2jsa-2	THR_A_68_N	THR_A_68_CA	-5.421	7.573	11.805	-4.502	8.343	10.986	1.45	124.34	39.96
399	2jsa-2	THR_A_68_CA	THR_A_68_HA	-4.502	8.343	10.986	-4.426	9.35	11.398	1.09	67.81	85.68
400	2jsa-2	THR_A_68_CA	THR_A_68_C	-4.502	8.343	10.986	-5.03	8.459	9.555	1.53	159.30	167.61
401	2jsa-2	THR_A_68_C	THR_A_68_O	-5.03	8.459	9.555	-5.896	7.688	9.145	1.23	109.47	-138.32
402	2jsa-2	THR_A_68_C	ALA_A_69_N	-5.03	8.459	9.555	-4.487	9.429	8.834	1.32	122.97	60.76
403	2jsa-2	ALA_A_69_N	ALA_A_69_H	-4.487	9.429	8.834	-3.78	10.028	9.237	1.01	66.50	40.27
404	2jsa-2	ALA_A_69_N	ALA_A_69_CA	-4.487	9.429	8.834	-4.892	9.655	7.457	1.45	161.39	150.84
405	2jsa-2	ALA_A_69_CA	ALA_A_69_HA	-4.892	9.655	7.457	-5.957	9.446	7.367	1.09	94.74	-168.90
406	2jsa-2	ALA_A_69_CA	ALA_A_69_C	-4.892	9.655	7.457	-4.131	8.695	6.541	1.53	126.79	-51.60
407	2jsa-2	ALA_A_69_C	ALA_A_69_O	-4.131	8.695	6.541	-3.109	8.135	6.934	1.23	71.36	-28.72
408	2jsa-2	ALA_A_69_C	PRO_A_70_N	-4.131	8.695	6.541	-4.674	8.528	5.305	1.36	155.32	-162.90
409	2jsa-2	PRO_A_70_N	PRO_A_70_CA	-4.674	8.528	5.305	-4.058	7.644	4.331	1.45	132.11	-55.13
410	2jsa-2	PRO_A_70_CA	PRO_A_70_HA	-4.058	7.644	4.331	-3.776	6.704	4.805	1.09	64.22	-73.30
411	2jsa-2	PRO_A_70_CA	PRO_A_70_C	-4.058	7.644	4.331	-2.802	8.28	3.73	1.53	113.12	26.86
412	2jsa-2	PRO_A_70_C	PRO_A_70_O	-2.802	8.28	3.73	-2.072	7.634	2.979	1.23	127.61	-41.51
413	2jsa-2	PRO_A_70_C	LYS_A_71_N	-2.802	8.28	3.73	-2.588	9.538	4.085	1.32	74.45	80.35
414	2jsa-2	LYS_A_71_N	LYS_A_71_H	-2.588	9.538	4.085	-3.23	10.007	4.708	1.01	51.92	143.85
415	2jsa-2	LYS_A_71_N	LYS_A_71_CA	-2.588	9.538	4.085	-1.433	10.27	3.592	1.45	109.83	32.37
416	2jsa-2	LYS_A_71_CA	LYS_A_71_HA	-1.433	10.27	3.592	-0.86	9.602	2.948	1.09	126.19	-49.38
417	2jsa-2	LYS_A_71_CA	LYS_A_71_C	-1.433	10.27	3.592	-0.538	10.659	4.77	1.53	39.64	23.49
418	2jsa-2	LYS_A_71_C	LYS_A_71_O	-0.538	10.659	4.77	0.464	11.347	4.592	1.23	98.33	34.47
419	2jsa-2	LYS_A_71_C	ASP_A_72_N	-0.538	10.659	4.77	-0.935	10.2	5.949	1.33	27.24	-130.86
420	2jsa-2	ASP_A_72_N	ASP_A_72_H	-0.935	10.2	5.949	-1.772	9.639	6.022	1.01	85.86	-146.17
421	2jsa-2	ASP_A_72_N	ASP_A_72_CA	-0.935	10.2	5.949	-0.182	10.491	7.156	1.45	33.78	21.13
422	2jsa-2	ASP_A_72_CA	ASP_A_72_HA	-0.182	10.491	7.156	0.602	11.211	6.922	1.09	102.40	42.56
423	2jsa-2	ASP_A_72_CA	ASP_A_72_C	-0.182	10.491	7.156	0.441	9.199	7.688	1.53	69.65	-64.26
424	2jsa-2	ASP_A_72_C	ASP_A_72_O	0.441	9.199	7.688	1.499	9.228	8.316	1.23	59.32	1.57
425	2jsa-2	ASP_A_72_C	VAL_A_73_N	0.441	9.199	7.688	-0.241	8.096	7.417	1.32	101.80	-121.73
426	2jsa-2	VAL_A_73_N	VAL_A_73_H	-0.241	8.096	7.417	-1.104	8.147	6.896	1.01	121.08	176.62
427	2jsa-2	VAL_A_73_N	VAL_A_73_CA	-0.241	8.096	7.417	0.233	6.796	7.86	1.45	72.25	-69.97
428	2jsa-2	VAL_A_73_CA	VAL_A_73_HA	0.233	6.796	7.86	0.099	6.731	8.94	1.09	7.85	-154.12
429	2jsa-2	VAL_A_73_CA	VAL_A_73_C	0.233	6.796	7.86	1.728	6.672	7.559	1.53	101.35	-4.74
430	2jsa-2	VAL_A_73_C	VAL_A_73_O	1.728	6.672	7.559	2.562	7.092	8.359	1.23	49.41	26.73
431	2jsa-2	VAL_A_73_C	CYS_A_74_N	1.728	6.672	7.559	2.02	6.095	6.403	1.32	150.78	-63.16
432	2jsa-2	CYS_A_74_N	CYS_A_74_H	2.02	6.095	6.403	1.282	5.775	5.793	1.01	127.17	-156.56
433	2jsa-2	CYS_A_74_N	CYS_A_74_CA	2.02	6.095	6.403	3.4	5.911	5.987	1.45	106.64	-7.59
434	2jsa-2	CYS_A_74_CA	CYS_A_74_HA	3.4	5.911	5.987	3.789	5.016	6.473	1.09	63.53	-66.51
435	2jsa-2	CYS_A_74_CA	CYS_A_74_C	3.4	5.911	5.987	4.212	7.116	6.466	1.53	71.76	56.03
436	2jsa-2	CYS_A_74_C	CYS_A_74_O	4.212	7.116	6.466	5.289	6.956	7.037	1.23	62.33	-8.45
437	2jsa-2	CYS_A_74_C	THR_A_75_N	4.212	7.116	6.466	3.662	8.296	6.216	1.33	100.87	114.99
438	2jsa-2	THR_A_75_N	THR_A_75_H	3.662	8.296	6.216	2.772	8.352	5.743	1.01	117.94	176.40
439	2jsa-2	THR_A_75_N	THR_A_75_CA	3.662	8.296	6.216	4.321	9.527	6.614	1.45	74.09	61.84
440	2jsa-2	THR_A_75_CA	THR_A_75_HA	4.321	9.527	6.614	5.092	9.764	5.88	1.09	132.30	17.09
441	2jsa-2	THR_A_75_CA	THR_A_75_C	4.321	9.527	6.614	5.002	9.353	7.973	1.53	27.35	-14.33
442	2jsa-2	THR_A_75_C	THR_A_75_O	5.002	9.353	7.973	6.23	9.306	8.055	1.23	86.18	-2.19
443	2jsa-2	THR_A_75_C	LYS_A_76_N	5.002	9.353	7.973	4.177	9.259	9.005	1.32	38.82	-173.50
444	2jsa-2	LYS_A_76_N	LYS_A_76_H	4.177	9.259	9.005	3.178	9.304	8.863	1.01	98.08	177.42
445	2jsa-2	LYS_A_76_N	LYS_A_76_CA	4.177	9.259	9.005	4.684	9.091	10.356	1.45	21.57	-18.33
446	2jsa-2	LYS_A_76_CA	LYS_A_76_HA	4.684	9.091	10.356	5.459	9.84	10.522	1.09	81.24	44.02
447	2jsa-2	LYS_A_76_CA	LYS_A_76_C	4.684	9.091	10.356	5.336	7.712	10.483	1.53	85.24	-64.69
448	2jsa-2	LYS_A_76_C	LYS_A_76_O	5.336	7.712	10.483	6.222	7.514	11.312	1.23	47.60	-12.60
449	2jsa-2	LYS_A_76_C	LEU_A_77_N	5.336	7.712	10.483	4.87	6.793	9.649	1.33	128.99	-116.89
450	2jsa-2	LEU_A_77_N	LEU_A_77_H	4.87	6.793	9.649	4.					

453	2jsa-2	LEU_A_77_CA	LEU_A_77_C	5.395	5.439	9.657	6.722	5.407	8.896	1.53	119.83	-1.38
454	2jsa-2	LEU_A_77_C	LEU_A_77_O	6.722	5.407	8.896	7.258	4.334	8.621	1.23	102.91	-63.46
455	2jsa-2	LEU_A_77_C	ASN_A_78_N	6.722	5.407	8.896	7.213	6.596	8.577	1.33	103.93	67.56
456	2jsa-2	ASN_A_78_N	ASN_A_78_H	7.213	6.596	8.577	6.718	7.437	8.836	1.01	75.14	120.48
457	2jsa-2	ASN_A_78_N	ASN_A_78_CA	7.213	6.596	8.577	8.468	6.717	7.853	1.45	119.87	5.51
458	2jsa-2	ASN_A_78_CA	ASN_A_78_HA	8.468	6.717	7.853	8.535	7.715	7.42	1.09	113.41	86.16
459	2jsa-2	ASN_A_78_CA	ASN_A_78_C	8.468	6.717	7.853	8.515	5.664	6.743	1.53	136.48	-87.44
460	2jsa-2	ASN_A_78_C	ASN_A_78_O	8.515	5.664	6.743	9.591	5.212	6.357	1.23	108.30	-22.79
461	2jsa-2	ASN_A_78_C	GLU_A_79_N	8.515	5.664	6.743	7.334	5.303	6.263	1.32	111.24	-163.00
462	2jsa-2	GLU_A_79_N	GLU_A_79_H	7.334	5.303	6.263	6.489	5.716	6.63	1.01	68.68	153.95
463	2jsa-2	GLU_A_79_N	GLU_A_79_CA	7.334	5.303	6.263	7.227	4.313	5.205	1.45	136.74	-96.17
464	2jsa-2	GLU_A_79_CA	GLU_A_79_HA	7.227	4.313	5.205	8.203	3.843	5.084	1.09	96.37	-25.71
465	2jsa-2	GLU_A_79_CA	GLU_A_79_C	7.227	4.313	5.205	6.85	4.985	3.884	1.53	149.75	119.29
466	2jsa-2	GLU_A_79_C	GLU_A_79_O	6.85	4.985	3.884	5.756	4.768	3.362	1.23	115.08	-168.78
467	2jsa-2	GLU_A_79_C	CYS_A_80_N	6.85	4.985	3.884	7.775	5.787	3.379	1.32	112.42	40.93
468	2jsa-2	CYS_A_80_N	CYS_A_80_H	7.775	5.787	3.379	8.653	5.918	3.861	1.01	61.50	8.49
469	2jsa-2	CYS_A_80_N	CYS_A_80_CA	7.775	5.787	3.379	7.553	6.492	2.128	1.45	149.42	107.48
470	2jsa-2	CYS_A_80_CA	CYS_A_80_HA	7.553	6.492	2.128	7.615	5.771	1.313	1.09	138.40	-85.09
471	2jsa-2	CYS_A_80_CA	CYS_A_80_C	7.553	6.492	2.128	8.67	7.523	1.952	1.53	96.60	42.71
472	2jsa-2	CYS_A_80_C	CYS_A_80_O	8.67	7.523	1.952	9.354	7.534	0.93	1.23	146.20	0.92
473	2jsa-2	CYS_A_80_C	PRO_A_81_N	8.67	7.523	1.952	8.824	8.387	2.992	1.36	40.16	79.89
474	2jsa-2	PRO_A_81_N	PRO_A_81_CA	8.824	8.387	2.992	9.845	9.419	2.963	1.45	91.14	45.31
475	2jsa-2	PRO_A_81_CA	PRO_A_81_HA	9.845	9.419	2.963	9.848	9.914	1.992	1.09	152.99	89.65
476	2jsa-2	PRO_A_81_CA	PRO_A_81_C	9.845	9.419	2.963	11.233	8.823	3.207	1.53	80.82	-23.24
477	2jsa-2	PRO_A_81_C	PRO_A_81_O	11.233	8.823	3.207	11.821	9.025	4.269	1.23	30.35	18.96
1	2jsa-3	ARG_A_1_N	ARG_A_1_H	14.994	0.726	-3.438	15.81	1.274	-3.203	1.01	76.55	33.88
2	2jsa-3	ARG_A_1_N	ARG_A_1_CA	14.994	0.726	-3.438	13.682	1.257	-3.109	1.45	76.91	157.97
3	2jsa-3	ARG_A_1_CA	ARG_A_1_HA	13.682	1.257	-3.109	13.116	1.371	-4.033	1.09	148.00	168.61
4	2jsa-3	ARG_A_1_CA	ARG_A_1_C	13.682	1.257	-3.109	13.816	2.625	-2.435	1.53	63.88	84.41
5	2jsa-3	ARG_A_1_C	ARG_A_1_O	13.816	2.625	-2.435	14.679	2.818	-1.58	1.23	45.97	12.61
6	2jsa-3	ARG_A_1_C	SER_A_2_N	13.816	2.625	-2.435	12.949	3.538	-2.847	1.32	108.12	133.52
7	2jsa-3	SER_A_2_N	SER_A_2_H	12.949	3.538	-2.847	12.266	3.309	-3.555	1.01	134.50	-161.46
8	2jsa-3	SER_A_2_N	SER_A_2_CA	12.949	3.538	-2.847	12.959	4.882	-2.294	1.45	67.64	89.57
9	2jsa-3	SER_A_2_CA	SER_A_2_HA	12.959	4.882	-2.294	12.692	4.82	-1.239	1.09	14.56	-166.93
10	2jsa-3	SER_A_2_CA	SER_A_2_C	12.959	4.882	-2.294	11.925	5.751	-3.011	1.53	117.96	139.96
11	2jsa-3	SER_A_2_C	SER_A_2_O	11.925	5.751	-3.011	12.216	6.883	-3.391	1.23	108.01	75.58
12	2jsa-3	SER_A_2_C	ALA_A_3_N	11.925	5.751	-3.011	10.736	5.187	-3.172	1.33	96.98	-154.62
13	2jsa-3	ALA_A_3_N	ALA_A_3_H	10.736	5.187	-3.172	10.568	4.251	-2.833	1.01	70.38	-100.18
14	2jsa-3	ALA_A_3_N	ALA_A_3_CA	10.736	5.187	-3.172	9.655	5.896	-3.836	1.45	117.19	146.74
15	2jsa-3	ALA_A_3_CA	ALA_A_3_HA	9.655	5.896	-3.836	9.388	6.767	-3.238	1.09	56.72	107.04
16	2jsa-3	ALA_A_3_CA	ALA_A_3_C	9.655	5.896	-3.836	8.433	4.981	-3.93	1.53	93.52	-143.18
17	2jsa-3	ALA_A_3_C	ALA_A_3_O	8.433	4.981	-3.93	7.393	5.267	-3.339	1.23	61.28	164.62
18	2jsa-3	ALA_A_3_C	LEU_A_4_N	8.433	4.981	-3.93	8.599	3.9	-4.678	1.32	124.37	-81.27
19	2jsa-3	LEU_A_4_N	LEU_A_4_H	8.599	3.9	-4.678	9.483	3.728	-5.135	1.01	116.91	-11.01
20	2jsa-3	LEU_A_4_N	LEU_A_4_CA	8.599	3.9	-4.678	7.521	2.942	-4.857	1.45	97.08	-138.37
21	2jsa-3	LEU_A_4_CA	LEU_A_4_HA	7.521	2.942	-4.857	6.75	3.412	-5.467	1.09	124.04	148.63
22	2jsa-3	LEU_A_4_CA	LEU_A_4_C	7.521	2.942	-4.857	6.904	2.615	-3.496	1.53	27.16	-152.08
23	2jsa-3	LEU_A_4_C	LEU_A_4_O	6.904	2.615	-3.496	5.71	2.825	-3.285	1.23	80.13	170.02
24	2jsa-3	LEU_A_4_C	SER_A_5_N	6.904	2.615	-3.496	7.745	2.106	-2.607	1.33	47.88	-31.18
25	2jsa-3	SER_A_5_N	SER_A_5_H	7.745	2.106	-2.607	8.715	1.961	-2.849	1.01	103.86	-8.50
26	2jsa-3	SER_A_5_N	SER_A_5_CA	7.745	2.106	-2.607	7.296	1.748	-1.273	1.45	23.29	-141.43
27	2jsa-3	SER_A_5_CA	SER_A_5_HA	7.296	1.748	-1.273	6.827	0.766	-1.323	1.09	92.63	-115.53
28	2jsa-3	SER_A_5_CA	SER_A_5_C	7.296	1.748	-1.273	6.262	2.762	-0.778	1.53	71.13	135.56
29	2jsa-3	SER_A_5_C	SER_A_5_O	6.262	2.762	-0.778	5.193	2.381	-0.301	1.23	67.20	-160.38
30	2jsa-3	SER_A_5_C	CYS_A_6_N	6.262	2.762	-0.778	6.615	4.032	-0.91	1.32	95.72	74.47
31	2jsa-3	CYS_A_6_N	CYS_A_6_H	6.615	4.032	-0.91	7.51	4.272	-1.313	1.01	113.50	15.01
32	2jsa-3	CYS_A_6_N	CYS_A_6_CA	6.615	4.032	-0.91	5.731	5.103	-0.483	1.45	72.91	129.54
33	2jsa-3	CYS_A_6_CA	CYS_A_6_HA	5.731	5.103	-0.483	5.443	4.918	0.552	1.09	18.30	-147.28
34	2jsa-3	CYS_A_6_CA	CYS_A_6_C	5.731	5.103	-0.483	4.473	5.062	-1.354	1.53	124.68	-178.13
35	2jsa-3	CYS_A_6_C	CYS_A_6_O	4.473	5.062	-1.354	3.38	4.791	-0.861	1.23	66.36	-166.07
36	2jsa-3	CYS_A_6_C	GLN_A_7_N	4.473	5.062	-1.354	4.67	5.339	-2.635	1.33	165.14	54.58
37	2jsa-3	GLN_A_7_N	GLN_A_7_H	4.67	5.339	-2.635	5.598	5.556	-2.971	1.01	109.42	13.16
38	2jsa-3	GLN_A_7_N	GLN_A_7_CA	4.67	5.339	-2.635	3.566	5.339	-3.579	1.45	130.53	180.00
39	2jsa-3	GLN_A_7_CA	GLN_A_7_HA	3.566	5.339	-3.579	3.031	6.282	-3.471	1.09	84.31	119.57
40	2jsa-3	GLN_A_7_CA	GLN_A_7_C	3.566	5.339	-3.579	2.598	4.197	-3.263	1.53	78.08	-130.29
41	2jsa-3	GLN_A_7_C	GLN_A_7_O	2.598	4.197	-3.263	1.398	4.42	-3.114	1.23	83.04	169.47
42	2jsa-3	GLN_A_7_C	MET_A_8_N	2.598	4.197	-3.263	3.156	2.999	-3.171	1.32	86.02	-65.03
43	2jsa-3	MET_A_8_N	MET_A_8_H	3.156	2.999	-3.171	4.151	2.89	-3.308	1.01	97.79	-6.25
44	2jsa-3	MET_A_8_N	MET_A_8_CA	3.156	2.999	-3.171	2.357	1.822	-2.875	1.45	78.25	-124.17
45	2jsa-3	MET_A_8_CA	MET_A_8_HA	2.357	1.822	-2.875	1.717	1.61	-3.731	1.09	141.78	-161.67
46	2jsa-3	MET_A_8_CA	MET_A_8_C	2.357	1.822	-2.875	1.479	2.05	-1.643	1.53	36.36	165.44
47	2jsa-3	MET_A_8_C	MET_A_8_O	1.479	2.05	-1.643	0.35	1.565	-1.581	1.23	87.11	-156.75
48	2jsa-3	MET_A_8_C	CYS_A_9_N	1.479	2.05	-1.643	2.031	2.79	-0.692	1.33	44.15	53.28
49	2jsa-3	CYS_A_9_N	CYS_A_9_H	2.031	2.79	-0.692	2.965	3.158	-0.81	1.01	96.70	21.50
50	2jsa-3	CYS_A_9_N	CYS_A_9_CA	2.031	2.79	-0.692	1.312	3.089	0.535	1.45	32.40	157.42
51	2jsa-3	CYS_A_9_CA	CYS_A_9_HA	1.312	3.089	0.535	1.03	2.147	1.005	1.09	64.45	-106.67
52	2jsa-3	CYS_A_9_CA	CYS_A_9_C	1.312	3.089	0.535	0.038	3.853	0.172	1.53	103.73	149.05
53	2jsa-3	CYS_A_9_C	CYS_A_9_O	0.038	3.853	0.172	-0.99	3.703	0.83	1.23	57.65	-171.70
54	2jsa-3	CYS_A_9_C	GLU_A_10_N	0.038	3.853	0.172	0.147	4.657	-0.876	1.33	142.25	82.28
55	2jsa-3	GLU_A_10_N	GLU_A_10_H	0.147	4.657	-0.876	1.024	4.73	-1.371	1.01	119.36	4.76
56	2jsa-3	GLU_A_10_N	GLU_A_10_CA	0.147	4.657	-0.876	-0.984	5.446	-1.335	1.45	108.41	145.10
57	2jsa-3	GLU_A_10_CA	GLU_A_10_HA	-0.984	5.446	-1.335	-1.522	5.806	-0.458	1.09	36.43	146.21
58	2jsa-3	GLU_A_10_CA	GLU_A_10_C	-0.984	5.446	-1.335	-1.936	4.579	-2.162	1.53	122.71	-137.68
59	2jsa-3	GLU_A_10_C	GLU_A_10_O	-1.936	4.579	-2.162	-3.031	5.014	-2.513	1.23	106.59	158.33
60	2jsa-3	GLU_A_10_C	LEU_A_11_N	-1.936	4.579	-2.162	-1.481	3.367	-2.449	1.33	102.50	-69.42
61	2jsa-3	LEU_A_11_N	LEU_A_11_H	-1.481	3.367	-2.449	-0.568	3.076	-2.128	1.01	71.48	-17.68
62	2jsa-3	LEU_A_11_N	LEU_A_11_CA	-1.481	3.367	-2.449	-2.279	2.435	-3.227	1.45	122.38	-130.57
63	2jsa-3	LEU_A_11_CA	LEU_A_11_HA	-2.279	2.435	-3.227	-2.954	3.014	-3.857	1.09	125.31	139.38
64	2jsa-3	LEU_A_11_CA	LEU_A_11_C	-2.279	2.435	-3.227	-3.136	1.589	-2.282	1.53	51.88	-135.37
65	2jsa-3	LEU_A_11_C	LEU_A_11_O	-3.136	1.589	-2.282	-4.298	1.313	-2.572	1.23	103.65	-166.64
66	2jsa-3	LEU_A_11_C	VAL_A_12_N	-3.136	1.589	-2.282	-2.526	1.202	-1.172	1.32	33.06	-32.39
67	2jsa-3	VAL_A_12_N	VAL_A_12_H	-2.526	1.202	-1.172	-1.566	1.466	-1.0	1.01	80.20	15.38
68	2jsa-3	VAL_A_12										

69	2jsa-3	VAL_A_12_CA	VAL_A_12_HA	-3.218	0.393	-0.182	-3.766	-0.392	-0.702	1.09	118.51	-124.92
70	2jsa-3	VAL_A_12_CA	VAL_A_12_C	-3.218	0.393	-0.182	-4.23	1.265	0.566	1.53	60.75	139.25
71	2jsa-3	VAL_A_12_C	VAL_A_12_O	-4.23	1.265	0.566	-5.393	0.89	0.707	1.23	83.42	-162.13
72	2jsa-3	VAL_A_12_C	VAL_A_13_N	-4.23	1.265	0.566	-3.75	2.412	1.024	1.33	69.78	67.29
73	2jsa-3	VAL_A_13_N	VAL_A_13_H	-3.75	2.412	1.024	-2.782	2.656	0.871	1.01	98.71	14.15
74	2jsa-3	VAL_A_13_N	VAL_A_13_CA	-3.75	2.412	1.024	-4.598	3.34	1.753	1.45	59.89	132.42
75	2jsa-3	VAL_A_13_CA	VAL_A_13_HA	-4.598	3.34	1.753	-4.98	2.833	2.639	1.09	35.62	-127.00
76	2jsa-3	VAL_A_13_CA	VAL_A_13_C	-4.598	3.34	1.753	-5.791	3.73	0.877	1.53	124.91	161.90
77	2jsa-3	VAL_A_13_C	VAL_A_13_O	-5.791	3.73	0.877	-6.941	3.517	1.257	1.23	72.00	-169.51
78	2jsa-3	VAL_A_13_C	LYS_A_14_N	-5.791	3.73	0.877	-5.475	4.296	-0.278	1.32	150.70	60.83
79	2jsa-3	LYS_A_14_N	LYS_A_14_H	-5.475	4.296	-0.278	-4.506	4.442	-0.525	1.01	104.15	8.57
80	2jsa-3	LYS_A_14_N	LYS_A_14_CA	-5.475	4.296	-0.278	-6.506	4.718	-1.212	1.45	129.98	157.74
81	2jsa-3	LYS_A_14_CA	LYS_A_14_HA	-6.506	4.718	-1.212	-6.988	5.606	-0.803	1.09	67.96	118.49
82	2jsa-3	LYS_A_14_CA	LYS_A_14_C	-6.506	4.718	-1.212	-7.567	3.622	-1.323	1.53	94.16	-134.07
83	2jsa-3	LYS_A_14_C	LYS_A_14_O	-7.567	3.622	-1.323	-8.75	3.913	-1.492	1.23	97.90	166.18
84	2jsa-3	LYS_A_14_C	LYS_A_15_N	-7.567	3.622	-1.323	-7.106	2.383	-1.221	1.33	85.59	-69.59
85	2jsa-3	LYS_A_15_N	LYS_A_15_H	-7.106	2.383	-1.221	-6.119	2.217	-1.08	1.01	81.98	-9.55
86	2jsa-3	LYS_A_15_N	LYS_A_15_CA	-7.106	2.383	-1.221	-8.001	1.242	-1.308	1.45	93.43	-128.11
87	2jsa-3	LYS_A_15_CA	LYS_A_15_HA	-8.001	1.242	-1.308	-8.74	1.451	-2.081	1.09	135.19	164.21
88	2jsa-3	LYS_A_15_CA	LYS_A_15_C	-8.001	1.242	-1.308	-8.748	1.083	0.017	1.53	29.96	-167.98
89	2jsa-3	LYS_A_15_C	LYS_A_15_O	-8.748	1.083	0.017	-9.937	0.769	0.031	1.23	89.35	-165.21
90	2jsa-3	LYS_A_15_C	TYR_A_16_N	-8.748	1.083	0.017	-8.019	1.306	1.011	1.33	35.12	17.01
91	2jsa-3	TYR_A_16_N	TYR_A_16_H	-8.019	1.306	1.101	-7.045	1.56	1.015	1.01	94.88	14.62
92	2jsa-3	TYR_A_16_N	TYR_A_16_CA	-8.019	1.306	1.101	-8.596	1.191	2.429	1.45	23.89	-168.73
93	2jsa-3	TYR_A_16_CA	TYR_A_16_HA	-8.596	1.191	2.429	-9.175	0.271	2.51	1.09	85.74	-122.18
94	2jsa-3	TYR_A_16_CA	TYR_A_16_C	-8.596	1.191	2.429	-9.486	2.395	2.746	1.53	78.05	126.47
95	2jsa-3	TYR_A_16_C	TYR_A_16_O	-9.486	2.395	2.746	-10.704	2.259	2.863	1.23	84.55	-173.63
96	2jsa-3	TYR_A_16_C	GLU_A_17_N	-9.486	2.395	2.746	-8.844	3.547	2.876	1.33	84.37	60.87
97	2jsa-3	GLU_A_17_N	GLU_A_17_H	-8.844	3.547	2.876	-7.84	3.585	2.766	1.01	96.25	2.17
98	2jsa-3	GLU_A_17_N	GLU_A_17_CA	-8.844	3.547	2.876	-9.561	4.774	3.176	1.45	78.08	120.30
99	2jsa-3	GLU_A_17_CA	GLU_A_17_HA	-9.561	4.774	3.176	-9.788	4.779	4.242	1.09	12.02	178.74
100	2jsa-3	GLU_A_17_CA	GLU_A_17_C	-9.561	4.774	3.176	-10.881	4.821	2.402	1.53	120.37	177.96
101	2jsa-3	GLU_A_17_C	GLU_A_17_O	-10.881	4.821	2.402	-11.904	5.243	2.939	1.23	64.11	157.58
102	2jsa-3	GLU_A_17_C	GLY_A_18_N	-10.881	4.821	2.402	-10.814	4.38	1.155	1.32	160.32	-81.36
103	2jsa-3	GLY_A_18_N	GLY_A_18_H	-10.814	4.38	1.155	-9.937	4.046	0.78	1.01	111.78	-20.85
104	2jsa-3	GLY_A_18_N	GLY_A_18_CA	-10.814	4.38	1.155	-11.992	4.366	0.303	1.45	125.87	-179.32
105	2jsa-3	GLY_A_18_CA	GLY_A_18_C	-11.992	4.366	0.303	-12.343	2.94	-0.124	1.53	106.21	-103.83
106	2jsa-3	GLY_A_18_C	GLY_A_18_O	-12.343	2.94	-0.124	-12.578	2.681	-1.303	1.23	163.48	-132.22
107	2jsa-3	GLY_A_18_C	SER_A_19_N	-12.343	2.94	-0.124	-12.367	2.051	0.859	1.33	42.14	-91.55
108	2jsa-3	SER_A_19_N	SER_A_19_H	-12.367	2.051	0.859	-12.163	2.335	1.807	1.01	20.25	54.31
109	2jsa-3	SER_A_19_N	SER_A_19_CA	-12.367	2.051	0.859	-12.686	0.658	0.599	1.45	100.31	-102.90
110	2jsa-3	SER_A_19_CA	SER_A_19_HA	-12.686	0.658	0.599	-12.237	0.376	-0.354	1.09	150.91	-32.13
111	2jsa-3	SER_A_19_CA	SER_A_19_C	-12.686	0.658	0.599	-14.202	0.477	0.501	1.53	93.67	-173.19
112	2jsa-3	SER_A_19_C	SER_A_19_O	-14.202	0.477	0.501	-14.707	-0.026	-0.502	1.23	144.60	-135.11
113	2jsa-3	SER_A_19_C	ALA_A_20_N	-14.202	0.477	0.501	-14.886	0.898	1.555	1.33	37.31	148.39
114	2jsa-3	ALA_A_20_N	ALA_A_20_H	-14.886	0.898	1.555	-14.404	1.302	2.346	1.01	38.49	39.97
115	2jsa-3	ALA_A_20_N	ALA_A_20_CA	-14.886	0.898	1.555	-16.335	0.789	1.599	1.45	88.27	-175.70
116	2jsa-3	ALA_A_20_CA	ALA_A_20_HA	-16.335	0.789	1.599	-16.719	1.515	2.316	1.09	48.88	117.88
117	2jsa-3	ALA_A_20_CA	ALA_A_20_C	-16.335	0.789	1.599	-16.722	-0.613	2.074	1.53	71.91	-105.43
118	2jsa-3	ALA_A_20_C	ALA_A_20_O	-16.722	-0.613	2.074	-17.895	-0.886	2.323	1.23	78.32	-166.90
119	2jsa-3	ALA_A_20_C	ASP_A_21_N	-16.722	-0.613	2.074	-15.713	-1.465	2.186	1.33	85.15	-40.18
120	2jsa-3	ASP_A_21_N	ASP_A_21_H	-15.713	-1.465	2.186	-14.772	-1.172	1.963	1.01	102.75	17.30
121	2jsa-3	ASP_A_21_N	ASP_A_21_CA	-15.713	-1.465	2.186	-15.934	-2.832	2.628	1.45	72.30	-99.18
122	2jsa-3	ASP_A_21_CA	ASP_A_21_HA	-15.934	-2.832	2.628	-17.005	-3.004	2.733	1.09	84.47	-170.88
123	2jsa-3	ASP_A_21_CA	ASP_A_21_C	-15.934	-2.832	2.628	-15.238	-3.048	3.972	1.53	28.47	-17.24
124	2jsa-3	ASP_A_21_C	ASP_A_21_O	-15.238	-3.048	3.972	-15.465	-4.057	4.639	1.23	57.18	-102.68
125	2jsa-3	ASP_A_21_C	LYS_A_22_N	-15.238	-3.048	3.972	-14.405	-2.082	4.333	1.33	74.20	49.23
126	2jsa-3	LYS_A_22_N	LYS_A_22_H	-14.405	-2.082	4.333	-14.267	-1.279	3.736	1.01	126.23	80.25
127	2jsa-3	LYS_A_22_N	LYS_A_22_CA	-14.405	-2.082	4.333	-13.675	-2.154	5.588	1.45	30.31	-5.63
128	2jsa-3	LYS_A_22_CA	LYS_A_22_HA	-13.675	-2.154	5.588	-12.866	-1.424	5.55	1.09	92.00	42.06
129	2jsa-3	LYS_A_22_CA	LYS_A_22_C	-13.675	-2.154	5.588	-13.044	-3.54	5.727	1.53	84.78	-65.52
130	2jsa-3	LYS_A_22_C	LYS_A_22_O	-13.044	-3.54	5.727	-13.365	-4.282	6.654	1.23	41.09	-113.39
131	2jsa-3	LYS_A_22_C	ASP_A_23_N	-13.044	-3.54	5.727	-12.156	-3.848	4.792	1.33	134.85	-19.13
132	2jsa-3	ASP_A_23_N	ASP_A_23_H	-12.156	-3.848	4.792	-11.94	-3.188	4.058	1.01	136.59	71.88
133	2jsa-3	ASP_A_23_N	ASP_A_23_CA	-12.156	-3.848	4.792	-11.477	-5.133	4.799	1.45	89.72	-62.15
134	2jsa-3	ASP_A_23_CA	ASP_A_23_HA	-11.477	-5.133	4.799	-11.466	-5.525	5.816	1.09	21.09	-88.39
135	2jsa-3	ASP_A_23_CA	ASP_A_23_C	-11.477	-5.133	4.799	-10.043	-4.949	4.298	1.53	109.11	7.31
136	2jsa-3	ASP_A_23_C	ASP_A_23_O	-10.043	-4.949	4.298	-9.827	-4.497	3.174	1.23	155.98	64.46
137	2jsa-3	ASP_A_23_C	ALA_A_24_N	-10.043	-4.949	4.298	-9.099	-5.308	5.156	1.33	49.65	-20.82
138	2jsa-3	ALA_A_24_N	ALA_A_24_H	-9.099	-5.308	5.156	-9.349	-5.67	6.065	1.01	25.83	-124.63
139	2jsa-3	ALA_A_24_N	ALA_A_24_CA	-9.099	-5.308	5.156	-7.693	-5.189	4.814	1.45	103.62	4.84
140	2jsa-3	ALA_A_24_CA	ALA_A_24_HA	-7.693	-5.189	4.814	-7.535	-4.238	4.306	1.09	117.79	80.57
141	2jsa-3	ALA_A_24_CA	ALA_A_24_C	-7.693	-5.189	4.814	-7.307	-6.319	3.856	1.53	128.74	-71.14
142	2jsa-3	ALA_A_24_C	ALA_A_24_O	-7.307	-6.319	3.856	-6.164	-6.395	3.41	1.23	111.27	-3.80
143	2jsa-3	ALA_A_24_C	ASN_A_25_N	-7.307	-6.319	3.856	-8.283	-7.168	3.57	1.32	102.47	-138.98
144	2jsa-3	ASN_A_25_N	ASN_A_25_H	-8.283	-7.168	3.57	-9.2	-7.043	3.974	1.01	66.42	172.24
145	2jsa-3	ASN_A_25_N	ASN_A_25_CA	-8.283	-7.168	3.57	-8.06	-8.29	2.675	1.45	128.04	-78.76
146	2jsa-3	ASN_A_25_CA	ASN_A_25_HA	-8.06	-8.29	2.675	-7.035	-8.643	2.794	1.09	83.74	-19.00
147	2jsa-3	ASN_A_25_CA	ASN_A_25_C	-8.06	-8.29	2.675	-8.29	-7.838	1.231	1.53	160.65	116.97
148	2jsa-3	ASN_A_25_C	ASN_A_25_O	-8.29	-7.838	1.231	-7.481	-8.127	0.35	1.23	135.72	-19.66
149	2jsa-3	ASN_A_25_C	VAL_A_26_N	-8.29	-7.838	1.231	-9.396	-7.136	1.034	1.32	98.55	147.60
150	2jsa-3	VAL_A_26_N	VAL_A_26_H	-9.396	-7.136	1.034	-10.015	-6.935	1.806	1.01	40.13	162.01
151	2jsa-3	VAL_A_26_N	VAL_A_26_CA	-9.396	-7.136	1.034	-9.742	-6.641	-0.288	1.45	155.45	124.95
152	2jsa-3	VAL_A_26_CA	VAL_A_26_HA	-9.742	-6.641	-0.288	-9.481	-7.405	-1.021	1.09	132.24	-71.14
153	2jsa-3	VAL_A_26_CA	VAL_A_26_C	-9.742	-6.641	-0.288	-8.916	-5.39	-0.592	1.53	101.46	56.56
154	2jsa-3	VAL_A_26_C	VAL_A_26_O	-8.916	-5.39	-0.592	-8.815	-4.974	-1.745	1.23	159.63	76.35
155	2jsa-3	VAL_A_26_C	ILE_A_27_N	-8.916	-5.39	-0.592	-8.347	-4.826	0.462	1.32	37.24	44.75
156	2jsa-3	ILE_A_27_N	ILE_A_27_H	-8.347	-4.826	0.462	-8.472	-5.224	1.382	1.01	24.39	-107.44
157	2jsa-3	ILE_A_27_N	ILE_A_27_CA	-8.347	-4.826	0.462	-7.532	-3.629	0.323	1.45	95.48	55.75
158	2jsa-3	ILE_A_27_CA	ILE_A_27_HA	-7.532	-3.629	0.323	-8.011	-2.977	-0.407	1.09	132.06	126.30
159	2jsa-3	ILE_A_27_CA	ILE_A_27_C	-7.532	-3.629	0.323	-6.158	-4.016	-0.23	1.53		

162	2jsa-3	LYS_A_28_N	LYS_A_28_H	-5.401	-4.724	0.594	-5.742	-4.971	1.512	1.01	24.64	-144.08
163	2jsa-3	LYS_A_28_N	LYS_A_28_CA	-5.401	-4.724	0.594	-4.073	-5.16	0.203	1.45	105.63	-18.18
164	2jsa-3	LYS_A_28_CA	LYS_A_28_HA	-4.073	-5.16	0.203	-3.449	-4.274	0.08	1.09	96.48	54.84
165	2jsa-3	LYS_A_28_CA	LYS_A_28_C	-4.073	-5.16	0.203	-4.151	-5.866	-1.152	1.53	152.34	-96.30
166	2jsa-3	LYS_A_28_C	LYS_A_28_O	-4.151	-5.866	-1.152	-3.228	-5.774	-1.959	1.23	131.02	5.69
167	2jsa-3	LYS_A_28_C	LYS_A_29_N	-4.151	-5.866	-1.152	-5.263	-6.557	-1.36	1.33	99.03	-148.14
168	2jsa-3	LYS_A_29_N	LYS_A_29_H	-5.263	-6.557	-1.36	-5.981	-6.589	-0.651	1.01	45.39	-177.45
169	2jsa-3	LYS_A_29_N	LYS_A_29_CA	-5.263	-6.557	-1.36	-5.474	-7.279	-2.603	1.45	148.82	-106.29
170	2jsa-3	LYS_A_29_CA	LYS_A_29_HA	-5.474	-7.279	-2.603	-4.582	-7.872	-2.804	1.09	100.63	-33.62
171	2jsa-3	LYS_A_29_CA	LYS_A_29_C	-5.474	-7.279	-2.603	-5.635	-6.277	-3.749	1.53	138.47	99.13
172	2jsa-3	LYS_A_29_C	LYS_A_29_O	-5.635	-6.277	-3.749	-4.806	-6.227	-4.655	1.23	137.49	3.45
173	2jsa-3	LYS_A_29_C	ASP_A_30_N	-5.635	-6.277	-3.749	-6.707	-5.504	-3.67	1.32	86.58	144.21
174	2jsa-3	ASP_A_30_N	ASP_A_30_H	-6.707	-5.504	-3.67	-7.347	-5.601	-2.895	1.01	39.87	-171.38
175	2jsa-3	ASP_A_30_N	ASP_A_30_CA	-6.707	-5.504	-3.67	-6.988	-4.506	-4.688	1.45	134.48	105.73
176	2jsa-3	ASP_A_30_CA	ASP_A_30_HA	-6.988	-4.506	-4.688	-7.411	-5.0	-5.563	1.09	143.38	-130.57
177	2jsa-3	ASP_A_30_CA	ASP_A_30_C	-6.988	-4.506	-4.688	-5.689	-3.794	-5.07	1.53	104.46	28.73
178	2jsa-3	ASP_A_30_C	ASP_A_30_O	-5.689	-3.794	-5.07	-5.369	-3.67	-6.251	1.23	163.80	21.18
179	2jsa-3	ASP_A_30_C	PHE_A_31_N	-5.689	-3.794	-5.07	-4.974	-3.346	-4.049	1.32	39.57	32.07
180	2jsa-3	PHE_A_31_N	PHE_A_31_H	-4.974	-3.346	-4.049	-5.297	-3.485	-3.102	1.01	20.37	-156.72
181	2jsa-3	PHE_A_31_N	PHE_A_31_CA	-4.974	-3.346	-4.049	-3.717	-2.65	-4.263	1.45	98.47	28.97
182	2jsa-3	PHE_A_31_CA	PHE_A_31_HA	-3.717	-2.65	-4.263	-3.91	-1.617	-4.551	1.09	105.33	100.58
183	2jsa-3	PHE_A_31_CA	PHE_A_31_C	-3.717	-2.65	-4.263	-2.886	-3.34	-5.347	1.53	135.10	-39.70
184	2jsa-3	PHE_A_31_C	PHE_A_31_O	-2.886	-3.34	-5.347	-2.531	-2.721	-6.349	1.23	144.54	60.17
185	2jsa-3	PHE_A_31_C	ASP_A_32_N	-2.886	-3.34	-5.347	-2.6	-4.611	-5.11	1.32	79.69	-77.32
186	2jsa-3	ASP_A_32_N	ASP_A_32_H	-2.6	-4.611	-5.11	-2.923	-5.055	-4.263	1.01	32.95	-126.04
187	2jsa-3	ASP_A_32_N	ASP_A_32_CA	-2.6	-4.611	-5.11	-1.819	-5.392	-6.054	1.45	130.52	-45.00
188	2jsa-3	ASP_A_32_CA	ASP_A_32_HA	-1.819	-5.392	-6.054	-0.805	-4.994	-6.092	1.09	92.00	21.43
189	2jsa-3	ASP_A_32_CA	ASP_A_32_C	-1.819	-5.392	-6.054	-2.464	-5.305	-7.439	1.53	154.83	172.32
190	2jsa-3	ASP_A_32_C	ASP_A_32_O	-2.464	-5.305	-7.439	-1.775	-5.382	-8.454	1.23	145.67	-6.38
191	2jsa-3	ASP_A_32_C	ALA_A_33_N	-2.464	-5.305	-7.439	-3.779	-5.145	-7.433	1.32	89.74	173.06
192	2jsa-3	ALA_A_33_N	ALA_A_33_H	-3.779	-5.145	-7.433	-4.281	-5.09	-6.558	1.01	29.99	173.75
193	2jsa-3	ALA_A_33_N	ALA_A_33_CA	-3.779	-5.145	-7.433	-4.525	-5.046	-8.678	1.45	148.85	172.44
194	2jsa-3	ALA_A_33_CA	ALA_A_33_HA	-4.525	-5.046	-8.678	-4.32	-5.93	-9.281	1.09	123.60	-76.94
195	2jsa-3	ALA_A_33_CA	ALA_A_33_C	-4.525	-5.046	-8.678	-4.057	-3.814	-9.452	1.53	120.43	69.20
196	2jsa-3	ALA_A_33_C	ALA_A_33_O	-4.057	-3.814	-9.452	-3.694	-3.913	-10.624	1.23	162.20	-15.26
197	2jsa-3	ALA_A_33_C	GLU_A_34_N	-4.057	-3.814	-9.452	-4.078	-2.68	-8.767	1.32	58.87	91.06
198	2jsa-3	GLU_A_34_N	GLU_A_34_H	-4.078	-2.68	-8.767	-4.386	-2.673	-7.805	1.01	17.76	178.70
199	2jsa-3	GLU_A_34_N	GLU_A_34_CA	-4.078	-2.68	-8.767	-3.66	-1.429	-9.376	1.45	114.78	71.52
200	2jsa-3	GLU_A_34_CA	GLU_A_34_HA	-3.66	-1.429	-9.376	-4.02	-1.418	-10.404	1.09	160.69	178.25
201	2jsa-3	GLU_A_34_CA	GLU_A_34_C	-3.66	-1.429	-9.376	-2.133	-1.335	-9.401	1.53	90.94	3.52
202	2jsa-3	GLU_A_34_C	GLU_A_34_O	-2.133	-1.335	-9.401	-1.573	-0.418	-10.001	1.23	119.18	58.59
203	2jsa-3	GLU_A_34_C	CYS_A_35_N	-2.133	-1.335	-9.401	-1.502	-2.296	-8.742	1.33	60.18	-56.71
204	2jsa-3	CYS_A_35_N	CYS_A_35_H	-1.502	-2.296	-8.742	-2.026	-3.019	-8.271	1.01	62.19	-125.93
205	2jsa-3	CYS_A_35_N	CYS_A_35_CA	-1.502	-2.296	-8.742	-0.051	-2.334	-8.682	1.45	87.63	-1.50
206	2jsa-3	CYS_A_35_CA	CYS_A_35_HA	-0.051	-2.334	-8.682	0.314	-1.314	-8.556	1.09	83.37	70.31
207	2jsa-3	CYS_A_35_CA	CYS_A_35_C	-0.051	-2.334	-8.682	0.472	-2.876	-10.013	1.53	150.50	-46.02
208	2jsa-3	CYS_A_35_C	CYS_A_35_O	0.472	-2.876	-10.013	1.347	-2.273	-10.633	1.23	120.26	34.57
209	2jsa-3	CYS_A_35_C	LYS_A_36_N	0.472	-2.876	-10.013	-0.086	-4.009	-10.415	1.33	107.66	-116.22
210	2jsa-3	LYS_A_36_N	LYS_A_36_H	-0.086	-4.009	-10.415	-0.801	-4.45	-9.854	1.01	56.26	-148.33
211	2jsa-3	LYS_A_36_N	LYS_A_36_CA	-0.086	-4.009	-10.415	0.313	-4.64	-11.661	1.45	149.07	-57.69
212	2jsa-3	LYS_A_36_CA	LYS_A_36_HA	0.313	-4.64	-11.661	1.401	-4.718	-11.667	1.09	90.32	-4.10
213	2jsa-3	LYS_A_36_CA	LYS_A_36_C	0.313	-4.64	-11.661	-0.095	-3.746	-12.833	1.53	140.02	114.53
214	2jsa-3	LYS_A_36_C	LYS_A_36_O	-0.095	-3.746	-12.833	0.531	-3.779	-13.891	1.23	149.35	-3.02
215	2jsa-3	LYS_A_36_C	LYS_A_37_N	-0.095	-3.746	-12.833	-1.143	-2.967	-12.606	1.33	80.14	143.38
216	2jsa-3	LYS_A_37_N	LYS_A_37_H	-1.143	-2.967	-12.606	-1.61	-2.991	-11.711	1.01	27.59	-177.06
217	2jsa-3	LYS_A_37_N	LYS_A_37_CA	-1.143	-2.967	-12.606	-1.642	-2.066	-13.63	1.45	134.83	118.98
218	2jsa-3	LYS_A_37_CA	LYS_A_37_HA	-1.642	-2.066	-13.63	-1.517	-2.552	-14.597	1.09	152.57	-75.58
219	2jsa-3	LYS_A_37_CA	LYS_A_37_C	-1.642	-2.066	-13.63	-0.796	-0.79	-13.637	1.53	90.26	56.46
220	2jsa-3	LYS_A_37_C	LYS_A_37_O	-0.796	-0.79	-13.637	-0.238	-0.417	-14.668	1.23	146.94	33.76
221	2jsa-3	LYS_A_37_C	LEU_A_38_N	-0.796	-0.79	-13.637	-0.728	-0.157	-12.475	1.32	28.72	83.87
222	2jsa-3	LEU_A_38_N	LEU_A_38_H	-0.728	-0.157	-12.475	-1.212	-0.522	-11.667	1.01	36.88	-142.98
223	2jsa-3	LEU_A_38_N	LEU_A_38_CA	-0.728	-0.157	-12.475	0.04	1.068	-12.335	1.45	84.47	57.91
224	2jsa-3	LEU_A_38_CA	LEU_A_38_HA	0.04	1.068	-12.335	-0.3	1.769	-13.097	1.09	134.36	115.87
225	2jsa-3	LEU_A_38_CA	LEU_A_38_C	0.04	1.068	-12.335	1.517	0.772	-12.602	1.53	100.05	-11.33
226	2jsa-3	LEU_A_38_C	LEU_A_38_O	1.517	0.772	-12.602	2.123	1.371	-13.489	1.23	136.15	44.67
227	2jsa-3	LEU_A_38_C	PHE_A_39_N	1.517	0.772	-12.602	2.054	-0.152	-11.82	1.32	53.81	-59.84
228	2jsa-3	PHE_A_39_N	PHE_A_39_H	2.054	-0.152	-11.82	1.495	-0.605	-11.111	1.01	45.42	-140.98
229	2jsa-3	PHE_A_39_N	PHE_A_39_CA	2.054	-0.152	-11.82	3.449	-0.535	-11.96	1.45	95.53	-15.35
230	2jsa-3	PHE_A_39_CA	PHE_A_39_HA	3.449	-0.535	-11.96	4.047	0.336	-12.228	1.09	104.23	55.53
231	2jsa-3	PHE_A_39_CA	PHE_A_39_C	3.449	-0.535	-11.96	3.614	-1.62	-13.025	1.53	134.14	-81.35
232	2jsa-3	PHE_A_39_C	PHE_A_39_O	3.614	-1.62	-13.025	4.52	-2.448	-12.938	1.23	85.95	-42.42
233	2jsa-3	PHE_A_39_C	HIS_A_40_N	3.614	-1.62	-13.025	2.725	-1.583	-14.007	1.33	137.82	177.62
234	2jsa-3	HIS_A_40_N	HIS_A_40_H	2.725	-1.583	-14.007	2.006	-0.874	-14.015	1.01	90.45	135.40
235	2jsa-3	HIS_A_40_N	HIS_A_40_CA	2.725	-1.583	-14.007	2.761	-2.553	-15.087	1.45	138.05	-87.87
236	2jsa-3	HIS_A_40_CA	HIS_A_40_HA	2.761	-2.553	-15.087	2.663	-3.547	-14.65	1.09	66.37	-95.63
237	2jsa-3	HIS_A_40_CA	HIS_A_40_C	2.761	-2.553	-15.087	4.115	-2.483	-15.795	1.53	117.57	2.96
238	2jsa-3	HIS_A_40_C	HIS_A_40_O	4.115	-2.483	-15.795	4.596	-3.484	-16.325	1.23	115.51	-64.33
239	2jsa-3	HIS_A_40_C	THR_A_41_N	4.115	-2.483	-15.795	4.694	-1.291	-15.78	1.33	89.35	64.09
240	2jsa-3	THR_A_41_N	THR_A_41_H	4.694	-1.291	-15.78	4.243	-0.512	-15.323	1.01	63.08	120.07
241	2jsa-3	THR_A_41_N	THR_A_41_CA	4.694	-1.291	-15.78	5.983	-1.078	-16.415	1.45	115.92	9.38
242	2jsa-3	THR_A_41_CA	THR_A_41_HA	5.983	-1.078	-16.415	6.33	-2.024	-16.83	1.09	112.38	-69.86
243	2jsa-3	THR_A_41_CA	THR_A_41_C	5.983	-1.078	-16.415	7.013	-0.609	-15.384	1.53	47.67	24.48
244	2jsa-3	THR_A_41_C	THR_A_41_O	7.013	-0.609	-15.384	7.431	0.548	-15.4	1.23	90.75	70.14
245	2jsa-3	THR_A_41_C	ILE_A_42_N	7.013	-0.609	-15.384	7.392	-1.531	-14.512	1.32	48.82	-67.65
246	2jsa-3	ILE_A_42_N	ILE_A_42_H	7.392	-1.531	-14.512	7.007	-2.463	-14.558	1.01	92.61	-112.45
247	2jsa-3	ILE_A_42_N	ILE_A_42_CA	7.392	-1.531	-14.512	8.364	-1.228	-13.476	1.45	44.50	17.31
248	2jsa-3	ILE_A_42_CA	ILE_A_42_HA	8.364	-1.228	-13.476	9.043	-0.468	-13.863	1.09	110.79	48.22
249	2jsa-3	ILE_A_42_CA	ILE_A_42_C	8.364	-1.228	-13.476	9.191	-2.479	-13.176	1.53	78.69	-56.53
250	2jsa-3	ILE_A_42_C	ILE_A_42_O	9.191	-2.479	-13.176	8.667	-3.592	-13.187	1.23	90.51	-115.21
251	2jsa-3	ILE_A_42_C	PRO_A_43_N	9.191	-2.479	-13.176	10.505	-2.25	-12.907	1.36	78.60	9.89
252	2jsa-3	PRO_A_43_N	PRO_A_43_CA	10.505	-2.25	-12.907	11.409	-3.34				

255	2jsa-3	PRO_A_43_C	PRO_A_43_O	11.175	-3.874	-11.187	11.654	-3.289	-10.216	1.23	37.91	50.69
256	2jsa-3	PRO_A_43_C	PHE_A_44_N	11.175	-3.874	-11.187	10.441	-4.974	-11.113	1.32	86.80	-123.71
257	2jsa-3	PHE_A_44_N	PHE_A_44_H	10.441	-4.974	-11.113	10.081	-5.402	-11.953	1.01	146.34	-130.07
258	2jsa-3	PHE_A_44_N	PHE_A_44_CA	10.441	-4.974	-11.113	10.138	-5.587	-9.83	1.45	28.06	-116.30
259	2jsa-3	PHE_A_44_CA	PHE_A_44_HA	10.138	-5.587	-9.83	9.811	-6.616	-9.979	1.09	97.86	-107.63
260	2jsa-3	PHE_A_44_CA	PHE_A_44_C	10.138	-5.587	-9.83	9.051	-4.803	-9.09	1.53	61.10	144.20
261	2jsa-3	PHE_A_44_C	PHE_A_44_O	9.051	-4.803	-9.09	8.672	-5.162	-7.977	1.23	25.13	-136.55
262	2jsa-3	PHE_A_44_C	GLY_A_45_N	9.051	-4.803	-9.09	8.582	-3.748	-9.74	1.32	119.38	113.97
263	2jsa-3	GLY_A_45_N	GLY_A_45_H	8.582	-3.748	-9.74	8.942	-3.513	-10.654	1.01	154.81	33.14
264	2jsa-3	GLY_A_45_N	GLY_A_45_CA	8.582	-3.748	-9.74	7.547	-2.91	-9.159	1.45	66.43	141.00
265	2jsa-3	GLY_A_45_CA	GLY_A_45_C	7.547	-2.91	-9.159	6.416	-3.762	-8.577	1.53	67.66	-143.01
266	2jsa-3	GLY_A_45_C	GLY_A_45_O	6.416	-3.762	-8.577	6.128	-3.687	-7.383	1.23	14.00	165.40
267	2jsa-3	GLY_A_45_C	THR_A_46_N	6.416	-3.762	-8.577	5.805	-4.55	-9.447	1.32	131.10	-127.79
268	2jsa-3	THR_A_46_N	THR_A_46_H	5.805	-4.55	-9.447	6.095	-4.559	-10.415	1.01	163.31	-1.78
269	2jsa-3	THR_A_46_N	THR_A_46_CA	5.805	-4.55	-9.447	4.712	-5.416	-9.036	1.45	73.58	-141.61
270	2jsa-3	THR_A_46_CA	THR_A_46_HA	4.712	-5.416	-9.036	3.949	-4.808	-8.55	1.09	63.52	141.45
271	2jsa-3	THR_A_46_CA	THR_A_46_C	4.712	-5.416	-9.036	5.203	-6.451	-8.024	1.53	48.54	-64.62
272	2jsa-3	THR_A_46_C	THR_A_46_O	5.203	-6.451	-8.024	4.508	-6.757	-7.056	1.23	38.11	-156.24
273	2jsa-3	THR_A_46_C	ARG_A_47_N	5.203	-6.451	-8.024	6.399	-6.962	-8.281	1.33	101.18	-23.13
274	2jsa-3	ARG_A_47_N	ARG_A_47_H	6.399	-6.962	-8.281	6.916	-6.663	-9.096	1.01	143.77	30.04
275	2jsa-3	ARG_A_47_N	ARG_A_47_CA	6.399	-6.962	-8.281	6.992	-7.958	-7.403	1.45	52.86	-59.23
276	2jsa-3	ARG_A_47_CA	ARG_A_47_HA	6.992	-7.958	-7.403	6.386	-8.863	-7.45	1.09	92.47	-123.81
277	2jsa-3	ARG_A_47_CA	ARG_A_47_C	6.992	-7.958	-7.403	7.015	-7.448	-5.962	1.53	19.51	87.42
278	2jsa-3	ARG_A_47_C	ARG_A_47_O	7.015	-7.448	-5.962	6.829	-8.22	-5.023	1.23	40.22	-103.55
279	2jsa-3	ARG_A_47_C	GLU_A_48_N	7.015	-7.448	-5.962	7.245	-6.149	-5.83	1.33	84.29	79.96
280	2jsa-3	GLU_A_48_N	GLU_A_48_H	7.245	-6.149	-5.83	7.388	-5.573	-6.647	1.01	144.00	76.06
281	2jsa-3	GLU_A_48_N	GLU_A_48_CA	7.245	-6.149	-5.83	7.296	-5.527	-4.519	1.45	25.46	85.31
282	2jsa-3	GLU_A_48_CA	GLU_A_48_HA	7.296	-5.527	-4.519	7.818	-6.205	-3.844	1.09	51.73	-52.41
283	2jsa-3	GLU_A_48_CA	GLU_A_48_C	7.296	-5.527	-4.519	5.881	-5.307	-3.98	1.53	69.37	171.16
284	2jsa-3	GLU_A_48_C	GLU_A_48_O	5.881	-5.307	-3.98	5.645	-5.426	-2.778	1.23	12.40	-153.24
285	2jsa-3	GLU_A_48_C	CYS_A_49_N	5.881	-5.307	-3.98	4.976	-4.992	-4.895	1.32	133.68	160.81
286	2jsa-3	CYS_A_49_N	CYS_A_49_H	4.976	-4.992	-4.895	5.241	-4.913	-5.866	1.01	164.10	16.60
287	2jsa-3	CYS_A_49_N	CYS_A_49_CA	4.976	-4.992	-4.895	3.59	-4.755	-4.527	1.45	75.33	170.30
288	2jsa-3	CYS_A_49_CA	CYS_A_49_HA	3.59	-4.755	-4.527	3.555	-3.893	-3.86	1.09	52.29	92.33
289	2jsa-3	CYS_A_49_CA	CYS_A_49_C	3.59	-4.755	-4.527	3.079	-5.981	-3.767	1.53	60.22	-112.63
290	2jsa-3	CYS_A_49_C	CYS_A_49_O	3.079	-5.981	-3.767	2.377	-5.846	-2.765	1.23	35.51	169.11
291	2jsa-3	CYS_A_49_C	ASP_A_50_N	3.079	-5.981	-3.767	3.452	-7.148	-4.27	1.32	112.32	-72.27
292	2jsa-3	ASP_A_50_N	ASP_A_50_H	3.452	-7.148	-4.27	4.032	-7.184	-5.097	1.01	144.91	-3.55
293	2jsa-3	ASP_A_50_N	ASP_A_50_CA	3.452	-7.148	-4.27	3.04	-8.396	-3.651	1.45	64.78	-108.27
294	2jsa-3	ASP_A_50_CA	ASP_A_50_HA	3.04	-8.396	-3.651	1.955	-8.403	-3.553	1.09	84.84	-179.63
295	2jsa-3	ASP_A_50_CA	ASP_A_50_C	3.04	-8.396	-3.651	3.688	-8.513	-2.27	1.53	25.49	-10.23
296	2jsa-3	ASP_A_50_C	ASP_A_50_O	3.688	-8.513	-2.27	3.063	-8.991	-1.325	1.23	39.78	-142.59
297	2jsa-3	ASP_A_50_C	HIS_A_51_N	3.688	-8.513	-2.27	4.934	-8.069	-2.196	1.32	86.80	19.61
298	2jsa-3	HIS_A_51_N	HIS_A_51_H	4.934	-8.069	-2.196	5.388	-7.689	-3.014	1.01	144.10	39.93
299	2jsa-3	HIS_A_51_N	HIS_A_51_CA	4.934	-8.069	-2.196	5.674	-8.118	-0.947	1.45	30.70	-3.79
300	2jsa-3	HIS_A_51_CA	HIS_A_51_HA	5.674	-8.118	-0.947	5.329	-8.986	-0.385	1.09	58.97	-111.68
301	2jsa-3	HIS_A_51_CA	HIS_A_51_C	5.674	-8.118	-0.947	5.367	-6.869	-0.119	1.53	57.23	103.81
302	2jsa-3	HIS_A_51_C	HIS_A_51_O	5.367	-6.869	-0.119	6.05	-6.588	0.865	1.23	36.89	22.36
303	2jsa-3	HIS_A_51_C	TYR_A_52_N	5.367	-6.869	-0.119	4.338	-6.152	-0.548	1.33	108.88	145.13
304	2jsa-3	TYR_A_52_N	TYR_A_52_H	4.338	-6.152	-0.548	3.822	-6.442	-1.366	1.01	144.11	-150.66
305	2jsa-3	TYR_A_52_N	TYR_A_52_CA	4.338	-6.152	-0.548	3.932	-4.939	0.142	1.45	61.66	108.51
306	2jsa-3	TYR_A_52_CA	TYR_A_52_HA	3.932	-4.939	0.142	4.686	-4.651	0.875	1.09	47.76	20.91
307	2jsa-3	TYR_A_52_CA	TYR_A_52_C	3.932	-4.939	0.142	2.581	-5.129	0.834	1.53	63.10	-171.99
308	2jsa-3	TYR_A_52_C	TYR_A_52_O	2.581	-5.129	0.834	2.429	-4.796	2.009	1.23	17.30	114.53
309	2jsa-3	TYR_A_52_C	VAL_A_53_N	2.581	-5.129	0.834	1.633	-5.66	0.077	1.32	124.86	-150.75
310	2jsa-3	VAL_A_53_N	VAL_A_53_H	1.633	-5.66	0.077	1.829	-5.907	-0.882	1.01	161.80	-51.57
311	2jsa-3	VAL_A_53_N	VAL_A_53_CA	1.633	-5.66	0.077	0.3	-5.898	0.602	1.45	68.81	-169.88
312	2jsa-3	VAL_A_53_CA	VAL_A_53_HA	0.3	-5.898	0.602	-0.146	-4.936	0.854	1.09	76.63	114.87
313	2jsa-3	VAL_A_53_CA	VAL_A_53_C	0.3	-5.898	0.602	0.401	-6.725	1.885	1.53	33.00	-83.04
314	2jsa-3	VAL_A_53_C	VAL_A_53_O	0.401	-6.725	1.885	-0.528	-6.746	2.69	1.23	49.10	-178.71
315	2jsa-3	VAL_A_53_C	ASN_A_54_N	0.401	-6.725	1.885	1.54	-7.388	2.035	1.33	83.51	-30.20
316	2jsa-3	ASN_A_54_N	ASN_A_54_H	1.54	-7.388	2.035	2.262	-7.324	1.332	1.01	134.12	5.07
317	2jsa-3	ASN_A_54_N	ASN_A_54_CA	1.54	-7.388	2.035	1.775	-8.215	3.205	1.45	36.31	-74.14
318	2jsa-3	ASN_A_54_CA	ASN_A_54_HA	1.775	-8.215	3.205	1.042	-7.965	3.972	1.09	45.28	161.17
319	2jsa-3	ASN_A_54_CA	ASN_A_54_C	1.775	-8.215	3.205	3.188	-7.954	3.733	1.53	69.82	10.47
320	2jsa-3	ASN_A_54_C	ASN_A_54_O	3.188	-7.954	3.733	4.061	-8.816	3.634	1.23	94.61	-44.64
321	2jsa-3	ASN_A_54_C	SER_A_55_N	3.188	-7.954	3.733	3.369	-6.763	4.283	1.32	65.46	81.36
322	2jsa-3	SER_A_55_N	SER_A_55_H	3.369	-6.763	4.283	2.605	-6.104	4.333	1.01	87.16	139.22
323	2jsa-3	SER_A_55_N	SER_A_55_CA	3.369	-6.763	4.283	4.661	-6.377	4.826	1.45	68.07	16.63
324	2jsa-3	SER_A_55_CA	SER_A_55_HA	4.661	-6.377	4.826	4.843	-6.965	5.726	1.09	34.37	-72.80
325	2jsa-3	SER_A_55_CA	SER_A_55_C	4.661	-6.377	4.826	4.649	-4.895	5.204	1.53	75.69	90.46
326	2jsa-3	SER_A_55_C	SER_A_55_O	4.649	-4.895	5.204	5.299	-4.492	6.167	1.23	38.46	31.80
327	2jsa-3	SER_A_55_C	LYS_A_56_N	4.649	-4.895	5.204	3.903	-4.126	4.426	1.32	125.99	134.13
328	2jsa-3	LYS_A_56_N	LYS_A_56_H	3.903	-4.126	4.426	3.395	-4.527	3.651	1.01	140.13	-141.71
329	2jsa-3	LYS_A_56_N	LYS_A_56_CA	3.903	-4.126	4.426	3.798	-2.696	4.667	1.45	80.46	94.20
330	2jsa-3	LYS_A_56_CA	LYS_A_56_HA	3.798	-2.696	4.667	4.214	-2.489	5.654	1.09	25.21	26.45
331	2jsa-3	LYS_A_56_CA	LYS_A_56_C	3.798	-2.696	4.667	2.322	-2.294	4.691	1.53	89.10	164.76
332	2jsa-3	LYS_A_56_C	LYS_A_56_O	2.322	-2.294	4.691	1.998	-1.112	4.783	1.23	85.71	105.33
333	2jsa-3	LYS_A_56_C	VAL_A_57_N	2.322	-2.294	4.691	1.466	-3.302	4.605	1.33	93.72	-130.34
334	2jsa-3	VAL_A_57_N	VAL_A_57_H	1.466	-3.302	4.605	1.804	-4.251	4.53	1.01	94.26	-70.40
335	2jsa-3	VAL_A_57_N	VAL_A_57_CA	1.466	-3.302	4.605	0.032	-3.069	4.616	1.45	89.57	170.77
336	2jsa-3	VAL_A_57_CA	VAL_A_57_HA	0.032	-3.069	4.616	-0.151	-2.039	4.309	1.09	106.35	100.07
337	2jsa-3	VAL_A_57_CA	VAL_A_57_C	0.032	-3.069	4.616	-0.499	-3.241	6.04	1.53	21.40	-162.05
338	2jsa-3	VAL_A_57_C	VAL_A_57_O	-0.499	-3.241	6.04	-1.285	-2.423	6.516	1.23	67.24	133.86
339	2jsa-3	VAL_A_57_C	ASP_A_58_N	-0.499	-3.241	6.04	-0.047	-4.309	6.681	1.33	61.07	-67.06
340	2jsa-3	ASP_A_58_N	ASP_A_58_H	-0.047	-4.309	6.681	0.599	-4.939	6.227	1.01	116.71	-44.28
341	2jsa-3	ASP_A_58_N	ASP_A_58_CA	-0.047	-4.309	6.681	-0.466	-4.599	8.041	1.45	20.54	-145.31
342	2jsa-3	ASP_A_58_CA	ASP_A_58_HA	-0.466	-4.599	8.041	-1.516	-4.891	8.035	1.09	90.32	-164.46
343	2jsa-3	ASP_A_58_CA	ASP_A_58_C	-0.466	-4.599	8.041	-0.279	-3.35	8.905	1.53	55.62	81.48
344	2jsa-3	ASP_A_58_C	ASP_A_58_O	-0.279	-3.35	8.905	-1.158	-2.994	9.688	1.23	50.46	157.95
345	2jsa-3	ASP_A_58_C	PRO_A_59_N	-0.279	-3.35	8.905	0.904	-2.702	8.729	1.36	97.43	28.71
346	2jsa-3	PRO_A_59_N	PRO									

348	2jsa-3	PRO_A_59_CA	PRO_A_59_C	1.218	-1.501	9.483	0.44	-0.298	8.948	1.53	110.48	122.89
349	2jsa-3	PRO_A_59_C	PRO_A_59_O	0.44	-0.298	8.948	-0.292	0.353	9.69	1.23	52.86	138.35
350	2jsa-3	PRO_A_59_C	ILE_A_60_N	0.44	-0.298	8.948	0.625	-0.038	7.662	1.32	166.06	54.57
351	2jsa-3	ILE_A_60_N	ILE_A_60_H	0.625	-0.038	7.662	1.243	-0.616	7.11	1.01	123.12	-43.08
352	2jsa-3	ILE_A_60_N	ILE_A_60_CA	0.625	-0.038	7.662	-0.051	1.076	7.018	1.45	116.30	121.25
353	2jsa-3	ILE_A_60_CA	ILE_A_60_HA	-0.051	1.076	7.018	0.401	2.0	7.38	1.09	70.61	63.93
354	2jsa-3	ILE_A_60_CA	ILE_A_60_C	-0.051	1.076	7.018	-1.523	1.084	7.436	1.53	74.15	179.69
355	2jsa-3	ILE_A_60_C	ILE_A_60_O	-1.523	1.084	7.436	-2.008	2.069	7.989	1.23	63.27	116.21
356	2jsa-3	ILE_A_60_C	ILE_A_61_N	-1.523	1.084	7.436	-2.19	-0.025	7.156	1.32	102.21	-121.02
357	2jsa-3	ILE_A_61_N	ILE_A_61_H	-2.19	-0.025	7.156	-1.725	-0.797	6.701	1.01	116.79	-58.94
358	2jsa-3	ILE_A_61_N	ILE_A_61_CA	-2.19	-0.025	7.156	-3.597	-0.158	7.496	1.45	76.47	-174.60
359	2jsa-3	ILE_A_61_CA	ILE_A_61_HA	-3.597	-0.158	7.496	-4.14	0.65	7.006	1.09	116.72	123.90
360	2jsa-3	ILE_A_61_CA	ILE_A_61_C	-3.597	-0.158	7.496	-3.77	0.014	9.007	1.53	9.17	135.17
361	2jsa-3	ILE_A_61_C	ILE_A_61_O	-3.77	0.014	9.007	-4.853	0.364	9.475	1.23	67.65	162.09
362	2jsa-3	ILE_A_61_C	HIS_A_62_N	-3.77	0.014	9.007	-2.687	-0.238	9.727	1.32	57.08	-13.10
363	2jsa-3	HIS_A_62_N	HIS_A_62_H	-2.687	-0.238	9.727	-1.829	-0.521	9.274	1.01	116.63	-18.25
364	2jsa-3	HIS_A_62_N	HIS_A_62_C	-2.687	-0.238	9.727	-2.706	-0.115	11.174	1.45	4.92	98.78
365	2jsa-3	HIS_A_62_C	HIS_A_62_HA	-2.706	-0.115	11.174	-3.541	-0.705	11.551	1.09	69.76	-144.76
366	2jsa-3	HIS_A_62_C	HIS_A_62_O	-2.706	-0.115	11.174	-2.949	1.346	11.562	1.53	75.32	99.44
367	2jsa-3	HIS_A_62_C	HIS_A_62_H	-2.949	1.346	11.562	-3.769	1.632	12.433	1.23	44.92	160.77
368	2jsa-3	HIS_A_62_C	GLU_A_63_N	-2.949	1.346	11.562	-2.221	2.23	10.897	1.32	120.14	50.53
369	2jsa-3	GLU_A_63_N	GLU_A_63_H	-2.221	2.23	10.897	-1.565	1.922	10.193	1.01	134.17	-25.15
370	2jsa-3	GLU_A_63_N	GLU_A_63_CA	-2.221	2.23	10.897	-2.346	3.653	11.16	1.45	79.57	95.02
371	2jsa-3	GLU_A_63_CA	GLU_A_63_HA	-2.346	3.653	11.16	-2.131	3.821	12.216	1.09	14.49	38.00
372	2jsa-3	GLU_A_63_CA	GLU_A_63_C	-2.346	3.653	11.16	-3.776	4.12	10.88	1.53	100.54	161.91
373	2jsa-3	GLU_A_63_C	GLU_A_63_O	-3.776	4.12	10.88	-4.399	4.767	11.72	1.23	46.92	133.92
374	2jsa-3	GLU_A_63_C	LEU_A_64_N	-3.776	4.12	10.88	-4.255	3.775	9.693	1.33	153.56	-144.24
375	2jsa-3	LEU_A_64_N	LEU_A_64_H	-4.255	3.775	9.693	-3.686	3.243	9.05	1.01	129.54	-43.08
376	2jsa-3	LEU_A_64_N	LEU_A_64_C	-4.255	3.775	9.693	-5.599	4.151	9.291	1.45	106.07	164.37
377	2jsa-3	LEU_A_64_C	LEU_A_64_HA	-5.599	4.151	9.291	-5.678	5.236	9.354	1.09	86.69	94.16
378	2jsa-3	LEU_A_64_C	LEU_A_64_C	-5.599	4.151	9.291	-6.608	3.554	10.274	1.53	50.02	-149.39
379	2jsa-3	LEU_A_64_C	LEU_A_64_O	-6.608	3.554	10.274	-7.609	4.188	10.604	1.23	74.44	147.65
380	2jsa-3	LEU_A_64_C	GLU_A_65_N	-6.608	3.554	10.274	-6.309	2.34	10.714	1.33	70.61	-76.16
381	2jsa-3	GLU_A_65_N	GLU_A_65_H	-6.309	2.34	10.714	-5.467	1.878	10.4	1.01	108.10	-28.75
382	2jsa-3	GLU_A_65_N	GLU_A_65_C	-6.309	2.34	10.714	-7.177	1.65	11.653	1.45	49.74	-141.52
383	2jsa-3	GLU_A_65_C	GLU_A_65_HA	-7.177	1.65	11.653	-8.161	1.556	11.196	1.09	114.81	-174.54
384	2jsa-3	GLU_A_65_C	GLU_A_65_C	-7.177	1.65	11.653	-7.321	2.464	12.94	1.53	32.71	100.03
385	2jsa-3	GLU_A_65_C	GLU_A_65_O	-7.321	2.464	12.94	-8.433	2.7	13.408	1.23	67.62	168.02
386	2jsa-3	GLU_A_65_C	GLY_A_66_N	-7.321	2.464	12.94	-6.179	2.871	13.475	1.33	66.19	19.62
387	2jsa-3	GLY_A_66_N	GLY_A_66_H	-6.179	2.871	13.475	-5.3	2.64	13.035	1.01	115.83	-14.72
388	2jsa-3	GLY_A_66_N	GLY_A_66_C	-6.179	2.871	13.475	-6.164	3.655	14.7	1.45	32.62	88.90
389	2jsa-3	GLY_A_66_C	GLY_A_66_C	-6.164	3.655	14.7	-6.888	4.988	14.506	1.53	97.29	118.51
390	2jsa-3	GLY_A_66_C	GLY_A_66_O	-6.888	4.988	14.506	-7.685	5.393	15.35	1.23	46.65	153.06
391	2jsa-3	GLY_A_66_C	GLY_A_67_N	-6.888	4.988	14.506	-6.585	5.633	13.39	1.32	147.44	64.84
392	2jsa-3	GLY_A_67_N	GLY_A_67_H	-6.585	5.633	13.39	-5.919	5.24	12.741	1.01	130.01	-30.54
393	2jsa-3	GLY_A_67_N	GLY_A_67_C	-6.585	5.633	13.39	-7.198	6.913	13.074	1.45	102.55	115.59
394	2jsa-3	GLY_A_67_C	GLY_A_67_C	-7.198	6.913	13.074	-6.157	7.906	12.554	1.53	109.87	43.65
395	2jsa-3	GLY_A_67_C	GLY_A_67_O	-6.157	7.906	12.554	-6.159	9.073	12.941	1.23	71.65	90.10
396	2jsa-3	GLY_A_67_C	THR_A_68_N	-6.157	7.906	12.554	-5.291	7.405	11.686	1.32	130.94	-30.05
397	2jsa-3	THR_A_68_N	THR_A_68_H	-5.291	7.405	11.686	-5.348	6.434	11.413	1.01	105.68	-93.36
398	2jsa-3	THR_A_68_N	THR_A_68_C	-5.291	7.405	11.686	-4.245	8.234	11.108	1.45	113.42	38.40
399	2jsa-3	THR_A_68_C	THR_A_68_HA	-4.245	8.234	11.108	-4.284	9.22	11.571	1.09	64.86	92.27
400	2jsa-3	THR_A_68_C	THR_A_68_C	-4.245	8.234	11.108	-4.473	8.409	9.606	1.53	169.17	142.49
401	2jsa-3	THR_A_68_C	THR_A_68_O	-4.473	8.409	9.606	-4.7	7.434	8.891	1.23	125.54	-103.11
402	2jsa-3	THR_A_68_C	ALA_A_69_N	-4.473	8.409	9.606	-4.404	9.658	9.171	1.32	109.18	86.84
403	2jsa-3	ALA_A_69_N	ALA_A_69_H	-4.404	9.658	9.171	-4.214	10.411	9.817	1.01	50.25	75.84
404	2jsa-3	ALA_A_69_N	ALA_A_69_C	-4.404	9.658	9.171	-4.599	9.974	7.766	1.45	165.20	121.68
405	2jsa-3	ALA_A_69_C	ALA_A_69_HA	-4.599	9.974	7.766	-5.607	9.677	7.477	1.09	105.38	-163.58
406	2jsa-3	ALA_A_69_C	ALA_A_69_C	-4.599	9.974	7.766	-3.6	9.178	6.925	1.53	123.36	-38.55
407	2jsa-3	ALA_A_69_C	ALA_A_69_O	-3.6	9.178	6.925	-2.606	8.674	7.448	1.23	64.86	-26.89
408	2jsa-3	ALA_A_69_C	PRO_A_70_N	-3.6	9.178	6.925	-3.904	9.087	5.603	1.36	166.50	-163.34
409	2jsa-3	PRO_A_70_N	PRO_A_70_C	-3.904	9.087	5.603	-3.044	8.361	4.684	1.45	129.23	-40.17
410	2jsa-3	PRO_A_70_C	PRO_A_70_HA	-3.044	8.361	4.684	-2.752	7.406	5.122	1.09	66.32	-73.00
411	2jsa-3	PRO_A_70_C	PRO_A_70_C	-3.044	8.361	4.684	-1.776	9.159	4.373	1.53	101.73	32.18
412	2jsa-3	PRO_A_70_C	PRO_A_70_O	-1.776	9.159	4.373	-0.803	8.611	3.857	1.23	114.80	-29.39
413	2jsa-3	PRO_A_70_C	LYS_A_71_N	-1.776	9.159	4.373	-1.827	10.442	4.702	1.33	75.63	92.28
414	2jsa-3	LYS_A_71_N	LYS_A_71_H	-1.827	10.442	4.702	-2.659	10.826	5.125	1.01	65.22	155.22
415	2jsa-3	LYS_A_71_N	LYS_A_71_CA	-1.827	10.442	4.702	-0.695	11.321	4.464	1.45	99.43	37.83
416	2jsa-3	LYS_A_71_CA	LYS_A_71_HA	-0.695	11.321	4.464	-0.067	10.864	3.699	1.09	134.57	-36.04
417	2jsa-3	LYS_A_71_CA	LYS_A_71_C	-0.695	11.321	4.464	0.138	11.431	5.742	1.53	33.32	7.52
418	2jsa-3	LYS_A_71_C	LYS_A_71_O	0.138	11.431	5.742	1.112	12.181	5.791	1.23	87.72	37.60
419	2jsa-3	LYS_A_71_C	ASP_A_72_N	0.138	11.431	5.742	-0.277	10.674	6.747	1.32	40.66	-118.73
420	2jsa-3	ASP_A_72_N	ASP_A_72_H	-0.277	10.674	6.747	-1.088	10.082	6.637	1.01	96.25	-143.87
421	2jsa-3	ASP_A_72_N	ASP_A_72_CA	-0.277	10.674	6.747	0.418	10.677	8.024	1.45	28.56	0.25
422	2jsa-3	ASP_A_72_CA	ASP_A_72_HA	0.418	10.677	8.024	1.113	11.517	8.05	1.09	88.63	50.40
423	2jsa-3	ASP_A_72_CA	ASP_A_72_C	0.418	10.677	8.024	1.184	9.362	8.185	1.53	83.96	-59.78
424	2jsa-3	ASP_A_72_C	ASP_A_72_O	1.184	9.362	8.185	2.246	9.331	8.805	1.23	59.73	-1.67
425	2jsa-3	ASP_A_72_C	VAL_A_73_N	1.184	9.362	8.185	0.616	8.309	7.616	1.32	115.43	-118.34
426	2jsa-3	VAL_A_73_N	VAL_A_73_H	0.616	8.309	7.616	-0.258	8.409	7.121	1.01	119.37	173.47
427	2jsa-3	VAL_A_73_N	VAL_A_73_CA	0.616	8.309	7.616	1.232	6.995	7.69	1.45	87.08	-64.88
428	2jsa-3	VAL_A_73_CA	VAL_A_73_HA	1.232	6.995	7.69	1.501	6.798	8.728	1.09	17.81	-36.22
429	2jsa-3	VAL_A_73_CA	VAL_A_73_C	1.232	6.995	7.69	2.516	6.993	6.858	1.53	122.94	-0.09
430	2jsa-3	VAL_A_73_C	VAL_A_73_O	2.516	6.993	6.858	3.556	6.522	7.317	1.23	68.10	-24.37
431	2jsa-3	VAL_A_73_C	CYS_A_74_N	2.516	6.993	6.858	2.401	7.522	5.649	1.32	155.88	102.26
432	2jsa-3	CYS_A_74_N	CYS_A_74_H	2.401	7.522	5.649	1.514	7.89	5.337	1.01	108.00	157.47
433	2jsa-3	CYS_A_74_N	CYS_A_74_CA	2.401	7.522	5.649	3.54	7.586	4.749	1.45	128.27	3.22
434	2jsa-3	CYS_A_74_CA	CYS_A_74_HA	3.54	7.586	4.749	4.122	6.671	4.866	1.09	83.84	-57.54
435	2jsa-3	CYS_A_74_CA	CYS_A_74_C	3.54	7.586	4.749	4.412	8.773	5.161	1.53	74.37	53.70
436	2jsa-3	CYS_A_74_C	CYS_A_74_O	4.412	8.773	5.161	4.52	9.754	4.426	1.23	126.68	83.72
437	2jsa-3	CYS_A_74_C	THR_A_75_N	4.412	8.773	5.161	5.013	8.647	6.335	1.32	27.61	-11.84
438	2jsa-3	THR_A_75_N	THR_A_75_H	5.013	8.647	6.335	4.88	7.812				

441	2jsa-3	THR_A_75_CA	THR_A_75_C	5.873	9.697	6.854	6.496	9.268	8.184	1.53	29.63	-34.55
442	2jsa-3	THR_A_75_O	THR_A_75_O	6.496	9.268	8.184	7.718	9.215	8.311	1.23	84.07	-2.48
443	2jsa-3	THR_A_75_C	LYS_A_76_N	6.496	9.268	8.184	5.628	8.972	9.14	1.32	43.81	-161.17
444	2jsa-3	LYS_A_76_N	LYS_A_76_H	5.628	8.972	9.14	4.636	9.038	8.964	1.01	100.04	176.19
445	2jsa-3	LYS_A_76_N	LYS_A_76_CA	5.628	8.972	9.14	6.079	8.549	10.455	1.45	25.18	-43.17
446	2jsa-3	LYS_A_76_CA	LYS_A_76_HA	6.079	8.549	10.455	6.93	9.17	10.736	1.09	75.07	36.12
447	2jsa-3	LYS_A_76_CA	LYS_A_76_C	6.079	8.549	10.455	6.565	7.1	10.381	1.53	92.77	-71.46
448	2jsa-3	LYS_A_76_C	LYS_A_76_O	6.565	7.1	10.381	7.406	6.682	11.175	1.23	49.79	-26.43
449	2jsa-3	LYS_A_76_C	LEU_A_77_N	6.565	7.1	10.381	6.014	6.373	9.42	1.33	136.49	-127.16
450	2jsa-3	LEU_A_77_N	LEU_A_77_H	6.014	6.373	9.42	5.328	6.783	8.802	1.01	127.71	149.13
451	2jsa-3	LEU_A_77_N	LEU_A_77_CA	6.014	6.373	9.42	6.38	4.979	9.232	1.45	97.43	-75.29
452	2jsa-3	LEU_A_77_CA	LEU_A_77_HA	6.38	4.979	9.232	6.633	4.562	10.207	1.09	26.58	-58.75
453	2jsa-3	LEU_A_77_CA	LEU_A_77_C	6.38	4.979	9.232	7.631	4.9	8.354	1.53	125.01	-3.61
454	2jsa-3	LEU_A_77_C	LEU_A_77_O	7.631	4.9	8.354	8.007	3.821	7.899	1.23	111.71	-70.79
455	2jsa-3	LEU_A_77_O	ASN_A_78_N	7.631	4.9	8.354	8.242	6.057	8.142	1.33	99.20	62.16
456	2jsa-3	ASN_A_78_N	ASN_A_78_H	8.242	6.057	8.142	7.878	6.907	8.549	1.01	66.24	113.18
457	2jsa-3	ASN_A_78_N	ASN_A_78_CA	8.242	6.057	8.142	9.442	6.131	7.327	1.45	124.13	3.53
458	2jsa-3	ASN_A_78_CA	ASN_A_78_HA	9.442	6.131	7.327	9.647	7.175	7.088	1.09	102.66	78.89
459	2jsa-3	ASN_A_78_CA	ASN_A_78_C	9.442	6.131	7.327	9.229	5.336	6.038	1.53	147.44	-105.00
460	2jsa-3	ASN_A_78_C	ASN_A_78_O	9.229	5.336	6.038	10.163	4.732	5.515	1.23	115.18	-32.89
461	2jsa-3	ASN_A_78_C	GLU_A_79_N	9.229	5.336	6.038	7.992	5.362	5.563	1.33	111.00	178.80
462	2jsa-3	GLU_A_79_N	GLU_A_79_H	7.992	5.362	5.563	7.273	5.881	6.046	1.01	61.42	144.18
463	2jsa-3	GLU_A_79_N	GLU_A_79_CA	7.992	5.362	5.563	7.642	4.651	4.344	1.45	146.97	-116.21
464	2jsa-3	GLU_A_79_CA	GLU_A_79_HA	7.642	4.651	4.344	8.492	4.03	4.061	1.09	105.05	-36.15
465	2jsa-3	GLU_A_79_CA	GLU_A_79_C	7.642	4.651	4.344	7.373	5.642	3.211	1.53	137.81	105.19
466	2jsa-3	GLU_A_79_C	GLU_A_79_O	7.373	5.642	3.211	6.839	5.268	2.168	1.23	147.99	-144.99
467	2jsa-3	GLU_A_79_O	CYS_A_80_N	7.373	5.642	3.211	7.754	6.888	3.453	1.33	79.48	73.00
468	2jsa-3	CYS_A_80_N	CYS_A_80_H	7.754	6.888	3.453	8.189	7.126	4.334	1.01	29.37	28.68
469	2jsa-3	CYS_A_80_N	CYS_A_80_CA	7.754	6.888	3.453	7.559	7.935	2.465	1.45	132.85	100.55
470	2jsa-3	CYS_A_80_CA	CYS_A_80_HA	7.559	7.935	2.465	8.101	7.658	1.56	1.09	146.08	-27.07
471	2jsa-3	CYS_A_80_CA	CYS_A_80_C	7.559	7.935	2.465	8.159	9.232	3.014	1.53	68.98	65.17
472	2jsa-3	CYS_A_80_C	CYS_A_80_O	8.159	9.232	3.014	7.509	9.947	3.775	1.23	51.78	132.27
473	2jsa-3	CYS_A_80_C	PRO_A_81_N	8.159	9.232	3.014	9.426	9.5	2.598	1.36	107.81	11.94
474	2jsa-3	PRO_A_81_N	PRO_A_81_CA	9.426	9.5	2.598	10.12	10.697	3.04	1.45	72.28	59.90
475	2jsa-3	PRO_A_81_CA	PRO_A_81_HA	10.12	10.697	3.04	9.986	10.832	4.113	1.09	10.05	134.79
476	2jsa-3	PRO_A_81_CA	PRO_A_81_C	10.12	10.697	3.04	9.584	11.939	2.324	1.53	117.89	113.34
477	2jsa-3	PRO_A_81_C	PRO_A_81_O	9.584	11.939	2.324	8.715	12.635	2.848	1.23	64.80	141.31
1	2jsa-4	ARG_A_1_N	ARG_A_1_H	16.266	6.009	2.145	16.103	6.862	1.629	1.01	120.72	100.82
2	2jsa-4	ARG_A_1_N	ARG_A_1_CA	16.266	6.009	2.145	15.125	5.18	2.495	1.45	76.06	-144.00
3	2jsa-4	ARG_A_1_CA	ARG_A_1_HA	15.125	5.18	2.495	15.256	4.201	2.033	1.09	115.07	-82.38
4	2jsa-4	ARG_A_1_CA	ARG_A_1_C	15.125	5.18	2.495	13.831	5.809	1.973	1.53	109.94	154.08
5	2jsa-4	ARG_A_1_C	ARG_A_1_O	13.831	5.809	1.973	13.117	6.48	2.718	1.23	52.75	136.78
6	2jsa-4	ARG_A_1_C	SER_A_2_N	13.831	5.809	1.973	13.569	5.572	0.696	1.32	164.54	-137.87
7	2jsa-4	SER_A_2_N	SER_A_2_H	13.569	5.572	0.696	14.201	5.011	0.143	1.01	123.20	-41.59
8	2jsa-4	SER_A_2_N	SER_A_2_CA	13.569	5.572	0.696	12.375	6.108	0.065	1.45	115.74	155.82
9	2jsa-4	SER_A_2_CA	SER_A_2_HA	12.375	6.108	0.065	11.505	5.686	0.567	1.09	62.56	-154.12
10	2jsa-4	SER_A_2_CA	SER_A_2_C	12.375	6.108	0.065	12.335	5.701	-1.41	1.53	164.50	-95.61
11	2jsa-4	SER_A_2_C	SER_A_2_O	12.335	5.701	-1.41	13.316	5.872	-2.131	1.23	125.91	9.89
12	2jsa-4	SER_A_2_C	ALA_A_3_N	12.335	5.701	-1.41	11.19	5.171	-1.813	1.32	107.71	-155.16
13	2jsa-4	ALA_A_3_N	ALA_A_3_H	11.19	5.171	-1.813	10.425	5.059	-1.163	1.01	49.95	-171.67
14	2jsa-4	ALA_A_3_N	ALA_A_3_CA	11.19	5.171	-1.813	11.009	4.74	-3.189	1.45	161.24	-112.78
15	2jsa-4	ALA_A_3_CA	ALA_A_3_HA	11.009	4.74	-3.189	11.197	5.586	-3.85	1.09	127.33	77.47
16	2jsa-4	ALA_A_3_CA	ALA_A_3_C	11.009	4.74	-3.189	9.563	4.281	-3.389	1.53	97.51	-162.39
17	2jsa-4	ALA_A_3_C	ALA_A_3_O	9.563	4.281	-3.389	8.662	4.733	-2.685	1.23	55.07	153.36
18	2jsa-4	ALA_A_3_C	LEU_A_4_N	9.563	4.281	-3.389	9.387	3.389	-4.353	1.33	136.68	-101.16
19	2jsa-4	LEU_A_4_N	LEU_A_4_H	9.387	3.389	-4.353	10.175	3.062	-4.893	1.01	122.33	-22.54
20	2jsa-4	LEU_A_4_N	LEU_A_4_CA	9.387	3.389	-4.353	8.066	2.864	-4.654	1.45	101.96	-158.33
21	2jsa-4	LEU_A_4_CA	LEU_A_4_HA	8.066	2.864	-4.654	7.516	3.63	-5.201	1.09	120.12	125.68
22	2jsa-4	LEU_A_4_CA	LEU_A_4_C	8.066	2.864	-4.654	7.318	2.598	-3.348	1.53	31.29	-160.42
23	2jsa-4	LEU_A_4_C	LEU_A_4_O	7.318	2.598	-3.348	6.115	2.84	-3.257	1.23	85.76	168.63
24	2jsa-4	LEU_A_4_C	SER_A_5_N	7.318	2.598	-3.348	8.059	2.103	-2.367	1.33	42.25	-33.74
25	2jsa-4	SER_A_5_N	SER_A_5_H	8.059	2.103	-2.367	9.044	1.93	-2.512	1.01	98.25	-9.96
26	2jsa-4	SER_A_5_N	SER_A_5_CA	8.059	2.103	-2.367	7.481	1.801	-1.07	1.45	26.69	-152.41
27	2jsa-4	SER_A_5_CA	SER_A_5_HA	7.481	1.801	-1.07	6.94	0.859	-1.149	1.09	94.16	-119.87
28	2jsa-4	SER_A_5_CA	SER_A_5_C	7.481	1.801	-1.07	6.496	2.9	-0.667	1.53	74.73	131.87
29	2jsa-4	SER_A_5_C	SER_A_5_O	6.496	2.9	-0.667	5.327	2.626	-0.404	1.23	77.64	-166.81
30	2jsa-4	SER_A_5_C	CYS_A_6_N	6.496	2.9	-0.667	7.006	4.123	-0.632	1.33	88.49	67.36
31	2jsa-4	CYS_A_6_N	CYS_A_6_H	7.006	4.123	-0.632	7.978	4.276	-0.863	1.01	103.21	8.95
32	2jsa-4	CYS_A_6_N	CYS_A_6_CA	7.006	4.123	-0.632	6.187	5.265	-0.265	1.45	75.36	125.65
33	2jsa-4	CYS_A_6_CA	CYS_A_6_HA	6.187	5.265	-0.265	5.887	5.152	0.777	1.09	17.10	-159.36
34	2jsa-4	CYS_A_6_CA	CYS_A_6_C	6.187	5.265	-0.265	4.93	5.255	-1.138	1.53	124.78	-179.54
35	2jsa-4	CYS_A_6_C	CYS_A_6_O	4.93	5.255	-1.138	3.823	5.07	-0.636	1.23	65.90	-170.51
36	2jsa-4	CYS_A_6_C	GLN_A_7_N	4.93	5.255	-1.138	5.145	5.456	-2.43	1.33	167.17	43.07
37	2jsa-4	GLN_A_7_N	GLN_A_7_H	5.145	5.456	-2.43	6.084	5.602	-2.773	1.01	109.85	8.84
38	2jsa-4	GLN_A_7_N	GLN_A_7_CA	5.145	5.456	-2.43	4.043	5.473	-3.378	1.45	130.70	179.12
39	2jsa-4	GLN_A_7_CA	GLN_A_7_HA	4.043	5.473	-3.378	3.515	6.419	-3.264	1.09	83.99	119.17
40	2jsa-4	GLN_A_7_CA	GLN_A_7_C	4.043	5.473	-3.378	3.066	4.336	-3.075	1.53	78.57	-130.67
41	2jsa-4	GLN_A_7_C	GLN_A_7_O	3.066	4.336	-3.075	1.873	4.572	-2.885	1.23	81.12	168.81
42	2jsa-4	GLN_A_7_C	MET_A_8_N	3.066	4.336	-3.075	3.606	3.127	-3.038	1.32	88.40	-65.93
43	2jsa-4	MET_A_8_N	MET_A_8_H	3.606	3.127	-3.038	4.595	3.007	-3.204	1.01	99.46	-6.92
44	2jsa-4	MET_A_8_N	MET_A_8_CA	3.606	3.127	-3.038	2.796	1.953	-2.761	1.45	79.01	-124.60
45	2jsa-4	MET_A_8_CA	MET_A_8_HA	2.796	1.953	-2.761	2.143	1.77	-3.614	1.09	141.51	-164.34
46	2jsa-4	MET_A_8_CA	MET_A_8_C	2.796	1.953	-2.761	1.936	2.163	-1.513	1.53	35.35	166.28
47	2jsa-4	MET_A_8_C	MET_A_8_O	1.936	2.163	-1.513	0.869	1.563	-1.381	1.23	83.85	-150.65
48	2jsa-4	MET_A_8_C	CYS_A_9_N	1.936	2.163	-1.513	2.43	3.015	-0.628	1.32	48.06	59.89
49	2jsa-4	CYS_A_9_N	CYS_A_9_H	2.43	3.015	-0.628	3.314	3.473	-0.802	1.01	99.91	27.39
50	2jsa-4	CYS_A_9_N	CYS_A_9_CA	2.43	3.015	-0.628	1.721	3.312	0.604	1.45	31.96	157.27
51	2jsa-4	CYS_A_9_CA	CYS_A_9_HA	1.721	3.312	0.604	1.461	2.369	1.086	1.09	63.77	-105.41
52	2jsa-4	CYS_A_9_CA	CYS_A_9_C	1.721	3.312	0.604	0.429	4.05	0.249	1.53	103.42	150.26
53	2jsa-4	CYS_A_9_C	CYS_A_9_O	0.429	4.05	0.249	-0.587	3.891	0.925	1.23	56.68	-171.11
54	2jsa-4	CYS_A_9_C	GLU_A_10_N	0.429	4.05	0.249	0.509	4.84	-0.811	1.32	143.16	84.22
55	2jsa-4	GLU_A_10_N	GLU_A_10_H	0.509	4.84	-0.811	1.378	4.921	-1.32	1.01	120.25	5.33
56	2jsa-4	GLU_A										

57	2jsa-4	GLU_A_10_CA	GLU_A_10_HA	-0.641	5.603	-1.265	-1.17	5.97	-0.385	1.09	36.19	145.25
58	2jsa-4	GLU_A_10_CA	GLU_A_10_C	-0.641	5.603	-1.265	-1.593	4.707	-2.06	1.53	121.30	-136.74
59	2jsa-4	GLU_A_10_C	GLU_A_10_O	-1.593	4.707	-2.06	-2.704	5.117	-2.395	1.23	105.80	159.74
60	2jsa-4	GLU_A_10_C	LEU_A_11_N	-1.593	4.707	-2.06	-1.125	3.499	-2.338	1.32	102.11	-68.82
61	2jsa-4	LEU_A_11_N	LEU_A_11_H	-1.125	3.499	-2.338	-0.202	3.228	-2.029	1.01	72.19	-16.36
62	2jsa-4	LEU_A_11_N	LEU_A_11_CA	-1.125	3.499	-2.338	-1.919	2.541	-3.087	1.45	121.05	-129.65
63	2jsa-4	LEU_A_11_CA	LEU_A_11_HA	-1.919	2.541	-3.087	-2.602	3.098	-3.728	1.09	126.03	140.80
64	2jsa-4	LEU_A_11_CA	LEU_A_11_C	-1.919	2.541	-3.087	-2.764	1.715	-2.115	1.53	50.56	-135.65
65	2jsa-4	LEU_A_11_C	LEU_A_11_O	-2.764	1.715	-2.115	-3.947	1.48	-2.358	1.23	101.39	-168.76
66	2jsa-4	LEU_A_11_C	VAL_A_12_N	-2.764	1.715	-2.115	-2.123	1.295	-1.033	1.33	35.31	-33.23
67	2jsa-4	VAL_A_12_N	VAL_A_12_H	-2.123	1.295	-1.033	-1.148	1.525	-0.898	1.01	82.32	13.27
68	2jsa-4	VAL_A_12_N	VAL_A_12_CA	-2.123	1.295	-1.033	-2.8	0.501	-0.023	1.45	45.93	-130.45
69	2jsa-4	VAL_A_12_CA	VAL_A_12_HA	-2.8	0.501	-0.023	-3.308	-0.325	-0.519	1.09	117.09	-121.59
70	2jsa-4	VAL_A_12_CA	VAL_A_12_C	-2.8	0.501	-0.023	-3.858	1.361	0.672	1.53	62.99	140.89
71	2jsa-4	VAL_A_12_C	VAL_A_12_O	-3.858	1.361	0.672	-5.019	0.966	0.768	1.23	85.52	-161.21
72	2jsa-4	VAL_A_12_C	VAL_A_13_N	-3.858	1.361	0.672	-3.419	2.521	1.138	1.32	69.41	69.27
73	2jsa-4	VAL_A_13_N	VAL_A_13_H	-3.419	2.521	1.138	-2.45	2.782	1.022	1.01	96.59	15.07
74	2jsa-4	VAL_A_13_N	VAL_A_13_CA	-3.419	2.521	1.138	-4.314	3.439	1.822	1.45	61.92	134.27
75	2jsa-4	VAL_A_13_CA	VAL_A_13_HA	-4.314	3.439	1.822	-4.739	2.927	2.685	1.09	37.63	-129.70
76	2jsa-4	VAL_A_13_CA	VAL_A_13_C	-4.314	3.439	1.822	-5.46	3.821	0.883	1.53	127.86	161.57
77	2jsa-4	VAL_A_13_C	VAL_A_13_O	-5.46	3.821	0.883	-6.629	3.616	1.21	1.23	74.60	-170.05
78	2jsa-4	VAL_A_13_C	LYS_A_14_N	-5.46	3.821	0.883	-5.087	4.367	-0.264	1.32	150.04	55.66
79	2jsa-4	LYS_A_14_N	LYS_A_14_H	-5.087	4.367	-0.264	-4.107	4.504	-0.466	1.01	101.54	7.96
80	2jsa-4	LYS_A_14_N	LYS_A_14_CA	-5.087	4.367	-0.264	-6.069	4.779	-1.252	1.45	132.85	157.24
81	2jsa-4	LYS_A_14_CA	LYS_A_14_HA	-6.069	4.779	-1.252	-6.586	5.658	-0.867	1.09	69.32	120.46
82	2jsa-4	LYS_A_14_CA	LYS_A_14_C	-6.069	4.779	-1.252	-7.106	3.668	-1.428	1.53	96.61	-133.03
83	2jsa-4	LYS_A_14_C	LYS_A_14_O	-7.106	3.668	-1.428	-8.27	3.94	-1.719	1.23	103.68	166.85
84	2jsa-4	LYS_A_14_C	LYS_A_15_N	-7.106	3.668	-1.428	-6.648	2.439	-1.242	1.32	81.93	-69.56
85	2jsa-4	LYS_A_15_N	LYS_A_15_H	-6.648	2.439	-1.242	-5.678	2.289	-1.003	1.01	76.31	-8.79
86	2jsa-4	LYS_A_15_N	LYS_A_15_CA	-6.648	2.439	-1.242	-7.521	1.285	-1.376	1.45	95.29	-127.11
87	2jsa-4	LYS_A_15_CA	LYS_A_15_HA	-7.521	1.285	-1.376	-8.242	1.498	-2.165	1.09	136.38	163.54
88	2jsa-4	LYS_A_15_CA	LYS_A_15_C	-7.521	1.285	-1.376	-8.301	1.088	-0.075	1.53	31.73	-165.83
89	2jsa-4	LYS_A_15_C	LYS_A_15_O	-8.301	1.088	-0.075	-9.475	0.723	-0.099	1.23	91.12	-162.73
90	2jsa-4	LYS_A_15_C	TYR_A_16_N	-8.301	1.088	-0.075	-7.616	1.339	1.032	1.33	33.39	20.12
91	2jsa-4	TYR_A_16_N	TYR_A_16_H	-7.616	1.339	1.032	-6.652	1.636	0.977	1.01	93.12	17.12
92	2jsa-4	TYR_A_16_N	TYR_A_16_CA	-7.616	1.339	1.032	-8.229	1.192	2.341	1.45	25.71	-166.51
93	2jsa-4	TYR_A_16_CA	TYR_A_16_HA	-8.229	1.192	2.341	-8.736	0.23	2.415	1.09	86.11	-117.79
94	2jsa-4	TYR_A_16_CA	TYR_A_16_C	-8.229	1.192	2.341	-9.222	2.325	2.61	1.53	79.88	131.23
95	2jsa-4	TYR_A_16_C	TYR_A_16_O	-9.222	2.325	2.61	-10.425	2.091	2.71	1.23	85.34	-168.99
96	2jsa-4	TYR_A_16_C	GLU_A_17_N	-9.222	2.325	2.61	-8.68	3.53	2.72	1.33	85.24	65.78
97	2jsa-4	GLU_A_17_N	GLU_A_17_H	-8.68	3.53	2.72	-7.681	3.649	2.626	1.01	95.34	6.79
98	2jsa-4	GLU_A_17_N	GLU_A_17_CA	-8.68	3.53	2.72	-9.503	4.7	2.976	1.45	79.85	125.12
99	2jsa-4	GLU_A_17_CA	GLU_A_17_HA	-9.503	4.7	2.976	-9.833	4.66	4.014	1.09	17.76	-173.09
100	2jsa-4	GLU_A_17_CA	GLU_A_17_C	-9.503	4.7	2.976	-10.74	4.686	2.077	1.53	126.01	-179.35
101	2jsa-4	GLU_A_17_C	GLU_A_17_O	-10.74	4.686	2.077	-11.844	4.985	2.529	1.23	68.44	164.85
102	2jsa-4	GLU_A_17_C	GLY_A_18_N	-10.74	4.686	2.077	-10.515	4.334	0.819	1.33	161.63	-57.41
103	2jsa-4	GLY_A_18_N	GLY_A_18_H	-10.515	4.334	0.819	-9.58	4.101	0.516	1.01	107.46	-13.99
104	2jsa-4	GLY_A_18_N	GLY_A_18_CA	-10.515	4.334	0.819	-11.598	4.276	-0.147	1.45	131.69	-176.93
105	2jsa-4	GLY_A_18_CA	GLY_A_18_C	-11.598	4.276	-0.147	-11.824	2.843	-0.633	1.53	108.52	-98.96
106	2jsa-4	GLY_A_18_C	GLY_A_18_O	-11.824	2.843	-0.633	-11.864	2.59	-1.836	1.23	167.98	-98.98
107	2jsa-4	GLY_A_18_C	SER_A_19_N	-11.824	2.843	-0.633	-11.966	1.942	0.328	1.32	43.51	-98.96
108	2jsa-4	SER_A_19_N	SER_A_19_H	-11.966	1.942	0.328	-11.922	2.221	1.298	1.01	16.23	81.04
109	2jsa-4	SER_A_19_N	SER_A_19_CA	-11.966	1.942	0.328	-12.188	0.541	0.012	1.45	102.56	-99.00
110	2jsa-4	SER_A_19_CA	SER_A_19_HA	-12.188	0.541	0.012	-11.7	0.324	-0.938	1.09	150.66	-23.97
111	2jsa-4	SER_A_19_CA	SER_A_19_C	-12.188	0.541	0.012	-13.686	0.267	-0.132	1.53	95.40	-169.63
112	2jsa-4	SER_A_19_C	SER_A_19_O	-13.686	0.267	-0.132	-14.116	-0.346	-1.109	1.23	142.53	-125.05
113	2jsa-4	SER_A_19_C	ALA_A_20_N	-13.686	0.267	-0.132	-14.438	0.733	0.853	1.32	41.93	148.21
114	2jsa-4	ALA_A_20_N	ALA_A_20_H	-14.438	0.733	0.853	-14.015	1.227	1.626	1.01	40.08	49.43
115	2jsa-4	ALA_A_20_N	ALA_A_20_CA	-14.438	0.733	0.853	-15.879	0.546	0.847	1.45	90.24	-172.61
116	2jsa-4	ALA_A_20_CA	ALA_A_20_HA	-15.879	0.546	0.847	-16.337	1.337	1.441	1.09	56.98	120.07
117	2jsa-4	ALA_A_20_CA	ALA_A_20_C	-15.879	0.546	0.847	-16.217	-0.799	1.491	1.53	65.09	-104.11
118	2jsa-4	ALA_A_20_C	ALA_A_20_O	-16.217	-0.799	1.491	-16.842	-1.653	0.864	1.23	120.65	-126.20
119	2jsa-4	ALA_A_20_C	ASP_A_21_N	-16.217	-0.799	1.491	-15.788	-0.948	2.736	1.33	20.04	-19.15
120	2jsa-4	ASP_A_21_N	ASP_A_21_H	-15.788	-0.948	2.736	-15.278	-0.204	3.191	1.01	63.23	55.57
121	2jsa-4	ASP_A_21_N	ASP_A_21_CA	-15.788	-0.948	2.736	-16.037	-2.176	3.472	1.45	59.57	-101.46
122	2jsa-4	ASP_A_21_CA	ASP_A_21_HA	-16.037	-2.176	3.472	-17.069	-2.177	3.823	1.09	71.22	-179.94
123	2jsa-4	ASP_A_21_CA	ASP_A_21_C	-16.037	-2.176	3.472	-15.082	-2.253	4.664	1.53	38.79	-4.61
124	2jsa-4	ASP_A_21_C	ASP_A_21_O	-15.082	-2.253	4.664	-15.386	-2.899	5.667	1.23	35.44	-115.20
125	2jsa-4	ASP_A_21_C	LYS_A_22_N	-15.082	-2.253	4.664	-13.947	-1.587	4.517	1.32	96.37	30.40
126	2jsa-4	LYS_A_22_N	LYS_A_22_H	-13.947	-1.587	4.517	-13.763	-1.078	3.665	1.01	147.57	70.13
127	2jsa-4	LYS_A_22_N	LYS_A_22_CA	-13.947	-1.587	4.517	-12.946	-1.572	5.57	1.45	43.55	0.86
128	2jsa-4	LYS_A_22_CA	LYS_A_22_HA	-12.946	-1.572	5.57	-12.13	-0.924	5.251	1.09	107.02	38.45
129	2jsa-4	LYS_A_22_CA	LYS_A_22_C	-12.946	-1.572	5.57	-12.378	-2.982	5.747	1.53	83.36	-68.06
130	2jsa-4	LYS_A_22_C	LYS_A_22_O	-12.378	-2.982	5.747	-12.278	-3.478	6.868	1.23	24.29	-78.60
131	2jsa-4	LYS_A_22_C	ASP_A_23_N	-12.378	-2.982	5.747	-12.018	-3.586	4.623	1.33	147.97	-59.20
132	2jsa-4	ASP_A_23_N	ASP_A_23_H	-12.018	-3.586	4.623	-12.127	-3.117	3.735	1.01	151.53	103.08
133	2jsa-4	ASP_A_23_N	ASP_A_23_CA	-12.018	-3.586	4.623	-11.463	-4.928	4.641	1.45	89.29	-67.53
134	2jsa-4	ASP_A_23_CA	ASP_A_23_HA	-11.463	-4.928	4.641	-11.531	-5.328	5.653	1.09	21.85	-99.65
135	2jsa-4	ASP_A_23_CA	ASP_A_23_C	-11.463	-4.928	4.641	-9.999	-4.875	4.2	1.53	106.75	2.07
136	2jsa-4	ASP_A_23_C	ASP_A_23_O	-9.999	-4.875	4.2	-9.706	-4.598	3.038	1.23	160.86	43.39
137	2jsa-4	ASP_A_23_C	ALA_A_24_N	-9.999	-4.875	4.2	-9.118	-5.145	5.153	1.33	44.04	-17.04
138	2jsa-4	ALA_A_24_N	ALA_A_24_H	-9.118	-5.145	5.153	-9.431	-5.364	6.088	1.01	22.22	-145.02
139	2jsa-4	ALA_A_24_N	ALA_A_24_CA	-9.118	-5.145	5.153	-7.691	-5.131	4.878	1.45	100.91	0.56
140	2jsa-4	ALA_A_24_CA	ALA_A_24_HA	-7.691	-5.131	4.878	-7.434	-4.185	4.401	1.09	115.95	74.80
141	2jsa-4	ALA_A_24_CA	ALA_A_24_C	-7.691	-5.131	4.878	-7.352	-6.268	3.912	1.53	129.15	-73.40
142	2jsa-4	ALA_A_24_C	ALA_A_24_O	-7.352	-6.268	3.912	-6.222	-6.363	3.433	1.23	112.90	-4.81
143	2jsa-4	ALA_A_24_C	ASN_A_25_N	-7.352	-6.268	3.912	-8.349	-7.1	3.654	1.32	101.24	-140.15
144	2jsa-4	ASN_A_25_N	ASN_A_25_H	-8.349	-7.1	3.654	-9.252	-6.959	4.083	1.01	64.85	171.13
145	2jsa-4	ASN_A_25_N	ASN_A_25_CA	-8.349	-7.1	3.654	-8.17	-8.227	2.755	1.45	128.23	-80.98
146	2jsa-4	ASN_A_25_CA	ASN_A_25_HA	-8.17	-8.227	2.755	-7.155	-8.611	2.863	1.09	84.32	-20.72
147	2jsa-4	ASN_A_25_CA	ASN_A_25_C	-8.17	-8.227	2.755	-8.401	-7.765	1.314	1.53	160.28</	

150	2jsa-4	VAL_A_26_N	VAL_A_26_H	-9.577	-7.196	1.091	-10.244	-7.094	1.843	1.01	41.90	171.31
151	2jsa-4	VAL_A_26_N	VAL_A_26_CA	-9.577	-7.196	1.091	-9.932	-6.709	-0.231	1.45	155.49	126.09
152	2jsa-4	VAL_A_26_CA	VAL_A_26_HA	-9.932	-6.709	-0.231	-9.634	-7.458	-0.965	1.09	132.32	-68.30
153	2jsa-4	VAL_A_26_CA	VAL_A_26_C	-9.932	-6.709	-0.231	-9.156	-5.423	-0.523	1.53	101.00	58.89
154	2jsa-4	VAL_A_26_C	VAL_A_26_O	-9.156	-5.423	-0.523	-9.202	-4.906	-1.638	1.23	155.04	95.08
155	2jsa-4	VAL_A_26_C	ILE_A_27_N	-9.156	-5.423	-0.523	-8.461	-4.945	0.499	1.33	39.53	34.52
156	2jsa-4	ILE_A_27_N	ILE_A_27_H	-8.461	-4.945	0.499	-8.468	-5.424	1.388	1.01	28.32	-90.84
157	2jsa-4	ILE_A_27_N	ILE_A_27_CA	-8.461	-4.945	0.499	-7.676	-3.73	0.366	1.45	95.25	57.13
158	2jsa-4	ILE_A_27_CA	ILE_A_27_HA	-7.676	-3.73	0.366	-8.162	-3.092	-0.372	1.09	132.62	127.30
159	2jsa-4	ILE_A_27_CA	ILE_A_27_C	-7.676	-3.73	0.366	-6.286	-4.082	-0.168	1.53	110.43	-14.21
160	2jsa-4	ILE_A_27_C	ILE_A_27_O	-6.286	-4.082	-0.168	-5.997	-3.869	-1.344	1.23	163.02	36.39
161	2jsa-4	ILE_A_27_C	LYS_A_28_N	-6.286	-4.082	-0.168	-5.462	-4.614	0.723	1.33	47.75	-32.85
162	2jsa-4	LYS_A_28_N	LYS_A_28_H	-5.462	-4.614	0.723	-5.767	-4.76	1.674	1.01	19.57	-154.42
163	2jsa-4	LYS_A_28_N	LYS_A_28_CA	-5.462	-4.614	0.723	-4.109	-4.997	0.357	1.45	104.59	-15.81
164	2jsa-4	LYS_A_28_CA	LYS_A_28_HA	-4.109	-4.997	0.357	-3.514	-4.088	0.262	1.09	95.00	56.79
165	2jsa-4	LYS_A_28_CA	LYS_A_28_C	-4.109	-4.997	0.357	-4.131	-5.684	-1.011	1.53	153.32	-91.83
166	2jsa-4	LYS_A_28_C	LYS_A_28_O	-4.131	-5.684	-1.011	-3.233	-5.48	-1.826	1.23	131.51	12.80
167	2jsa-4	LYS_A_28_C	LYS_A_29_N	-4.131	-5.684	-1.011	-5.167	-6.483	-1.22	1.32	99.08	-142.36
168	2jsa-4	LYS_A_29_N	LYS_A_29_H	-5.167	-6.483	-1.22	-5.869	-6.603	-0.504	1.01	44.85	-170.30
169	2jsa-4	LYS_A_29_N	LYS_A_29_CA	-5.167	-6.483	-1.22	-5.318	-7.201	-2.474	1.45	149.67	-101.88
170	2jsa-4	LYS_A_29_CA	LYS_A_29_HA	-5.318	-7.201	-2.474	-4.388	-7.736	-2.671	1.09	100.40	-29.91
171	2jsa-4	LYS_A_29_CA	LYS_A_29_C	-5.318	-7.201	-2.474	-5.527	-6.196	-3.609	1.53	137.87	101.75
172	2jsa-4	LYS_A_29_C	LYS_A_29_O	-5.527	-6.196	-3.609	-4.894	-6.3	-4.658	1.23	148.55	-9.33
173	2jsa-4	LYS_A_29_C	ASP_A_30_N	-5.527	-6.196	-3.609	-6.417	-5.247	-3.36	1.32	79.17	133.16
174	2jsa-4	ASP_A_30_N	ASP_A_30_H	-6.417	-5.247	-3.36	-6.9	-5.223	-2.473	1.01	28.60	177.16
175	2jsa-4	ASP_A_30_N	ASP_A_30_CA	-6.417	-5.247	-3.36	-6.718	-4.226	-4.349	1.45	132.90	106.43
176	2jsa-4	ASP_A_30_CA	ASP_A_30_HA	-6.718	-4.226	-4.349	-7.25	-4.683	-5.183	1.09	139.94	-139.34
177	2jsa-4	ASP_A_30_CA	ASP_A_30_C	-6.718	-4.226	-4.349	-5.412	-3.602	-4.844	1.53	108.88	25.54
178	2jsa-4	ASP_A_30_C	ASP_A_30_O	-5.412	-3.602	-4.844	-5.171	-3.531	-6.049	1.23	168.22	16.42
179	2jsa-4	ASP_A_30_C	PHE_A_31_N	-5.412	-3.602	-4.844	-4.602	-3.166	-3.891	1.32	43.99	28.29
180	2jsa-4	PHE_A_31_N	PHE_A_31_H	-4.602	-3.166	-3.891	-4.864	-3.257	-2.92	1.01	15.94	-160.85
181	2jsa-4	PHE_A_31_N	PHE_A_31_CA	-4.602	-3.166	-3.891	-3.326	-2.551	-4.215	1.45	102.88	25.73
182	2jsa-4	PHE_A_31_CA	PHE_A_31_HA	-3.326	-2.551	-4.215	-3.484	-1.528	-4.556	1.09	108.23	98.78
183	2jsa-4	PHE_A_31_CA	PHE_A_31_C	-3.326	-2.551	-4.215	-2.593	-3.346	-5.298	1.53	135.04	-47.32
184	2jsa-4	PHE_A_31_C	PHE_A_31_O	-2.593	-3.346	-5.298	-2.175	-2.785	-6.309	1.23	145.32	53.31
185	2jsa-4	PHE_A_31_C	ASP_A_32_N	-2.593	-3.346	-5.298	-2.461	-4.64	-5.049	1.32	79.16	-84.18
186	2jsa-4	ASP_A_32_N	ASP_A_32_H	-2.461	-4.64	-5.049	-2.829	-5.034	-4.195	1.01	32.26	-133.05
187	2jsa-4	ASP_A_32_N	ASP_A_32_CA	-2.461	-4.64	-5.049	-1.787	-5.519	-5.99	1.45	130.35	-52.52
188	2jsa-4	ASP_A_32_CA	ASP_A_32_HA	-1.787	-5.519	-5.99	-0.761	-5.176	-6.125	1.09	97.11	18.49
189	2jsa-4	ASP_A_32_CA	ASP_A_32_C	-1.787	-5.519	-5.99	-2.526	-5.488	-7.33	1.53	151.10	177.60
190	2jsa-4	ASP_A_32_C	ASP_A_32_O	-2.526	-5.488	-7.33	-1.911	-5.634	-8.385	1.23	149.07	-13.35
191	2jsa-4	ASP_A_32_C	ALA_A_33_N	-2.526	-5.488	-7.33	-3.834	-5.297	-7.242	1.32	86.19	171.69
192	2jsa-4	ALA_A_33_N	ALA_A_33_H	-3.834	-5.297	-7.242	-4.272	-5.185	-6.339	1.01	26.60	165.66
193	2jsa-4	ALA_A_33_N	ALA_A_33_CA	-3.834	-5.297	-7.242	-4.664	-5.245	-8.435	1.45	145.12	176.42
194	2jsa-4	ALA_A_33_CA	ALA_A_33_HA	-4.664	-5.245	-8.435	-4.508	-6.157	-9.01	1.09	121.86	-80.29
195	2jsa-4	ALA_A_33_CA	ALA_A_33_C	-4.664	-5.245	-8.435	-4.24	-4.053	-9.294	1.53	124.18	70.42
196	2jsa-4	ALA_A_33_C	ALA_A_33_O	-4.24	-4.053	-9.294	-3.682	-4.23	-10.376	1.23	151.59	-17.60
197	2jsa-4	ALA_A_33_C	GLU_A_34_N	-4.24	-4.053	-9.294	-4.52	-2.864	-8.781	1.32	67.22	103.25
198	2jsa-4	GLU_A_34_N	GLU_A_34_H	-4.52	-2.864	-8.781	-4.98	-2.793	-7.885	1.01	27.45	171.23
199	2jsa-4	GLU_A_34_N	GLU_A_34_CA	-4.52	-2.864	-8.781	-4.174	-1.643	-9.488	1.45	119.12	74.18
200	2jsa-4	GLU_A_34_CA	GLU_A_34_HA	-4.174	-1.643	-9.488	-4.832	-1.556	-10.352	1.09	142.47	172.47
201	2jsa-4	GLU_A_34_CA	GLU_A_34_C	-4.174	-1.643	-9.488	-2.73	-1.709	-9.989	1.53	109.12	-2.62
202	2jsa-4	GLU_A_34_C	GLU_A_34_O	-2.73	-1.709	-9.989	-2.482	-1.629	-11.191	1.23	167.77	17.88
203	2jsa-4	GLU_A_34_C	CYS_A_35_N	-2.73	-1.709	-9.989	-1.815	-1.856	-9.042	1.33	44.38	-9.13
204	2jsa-4	CYS_A_35_N	CYS_A_35_H	-1.815	-1.856	-9.042	-2.091	-1.916	-8.072	1.01	16.23	-167.74
205	2jsa-4	CYS_A_35_N	CYS_A_35_CA	-1.815	-1.856	-9.042	-0.403	-1.935	-9.371	1.45	103.10	-3.20
206	2jsa-4	CYS_A_35_CA	CYS_A_35_HA	-0.403	-1.935	-9.371	-0.065	-0.944	-9.675	1.09	106.19	71.17
207	2jsa-4	CYS_A_35_CA	CYS_A_35_C	-0.403	-1.935	-9.371	-0.238	-2.89	-10.555	1.53	140.70	-80.20
208	2jsa-4	CYS_A_35_C	CYS_A_35_O	-0.238	-2.89	-10.555	0.312	-2.514	-11.589	1.23	147.20	34.36
209	2jsa-4	CYS_A_35_C	LYS_A_36_N	-0.238	-2.89	-10.555	-0.726	-4.107	-10.365	1.32	81.75	-111.85
210	2jsa-4	LYS_A_36_N	LYS_A_36_H	-0.726	-4.107	-10.365	-1.166	-4.347	-9.488	1.01	29.75	-151.39
211	2jsa-4	LYS_A_36_N	LYS_A_36_CA	-0.726	-4.107	-10.365	-0.64	-5.119	-11.405	1.45	135.68	-85.14
212	2jsa-4	LYS_A_36_CA	LYS_A_36_HA	-0.64	-5.119	-11.405	0.379	-5.506	-11.416	1.09	90.58	-20.80
213	2jsa-4	LYS_A_36_CA	LYS_A_36_C	-0.64	-5.119	-11.405	-0.906	-4.47	-12.765	1.53	152.72	112.29
214	2jsa-4	LYS_A_36_C	LYS_A_36_O	-0.906	-4.47	-12.765	-0.389	-4.924	-13.785	1.23	146.00	-41.29
215	2jsa-4	LYS_A_36_C	LYS_A_37_N	-0.906	-4.47	-12.765	-1.71	-3.418	-12.735	1.32	88.70	127.39
216	2jsa-4	LYS_A_37_N	LYS_A_37_H	-1.71	-3.418	-12.735	-2.099	-3.099	-11.859	1.01	29.87	140.65
217	2jsa-4	LYS_A_37_N	LYS_A_37_CA	-1.71	-3.418	-12.735	-2.049	-2.702	-13.954	1.45	146.98	115.34
218	2jsa-4	LYS_A_37_CA	LYS_A_37_HA	-2.049	-2.702	-13.954	-1.817	-3.348	-14.801	1.09	140.98	-70.25
219	2jsa-4	LYS_A_37_CA	LYS_A_37_C	-2.049	-2.702	-13.954	-1.173	-1.453	-14.068	1.53	94.27	54.96
220	2jsa-4	LYS_A_37_C	LYS_A_37_O	-1.173	-1.453	-14.068	-0.493	-1.258	-15.074	1.23	144.89	16.00
221	2jsa-4	LYS_A_37_C	LEU_A_38_N	-1.173	-1.453	-14.068	-1.217	-0.64	-13.022	1.33	37.90	93.10
222	2jsa-4	LEU_A_38_N	LEU_A_38_H	-1.217	-0.64	-13.022	-1.799	-0.863	-12.228	1.01	38.13	-159.04
223	2jsa-4	LEU_A_38_N	LEU_A_38_CA	-1.217	-0.64	-13.022	-0.434	0.583	-12.993	1.45	88.86	57.37
224	2jsa-4	LEU_A_38_CA	LEU_A_38_HA	-0.434	0.583	-12.993	-0.846	1.265	-13.737	1.09	133.04	121.14
225	2jsa-4	LEU_A_38_CA	LEU_A_38_C	-0.434	0.583	-12.993	1.008	0.272	-13.396	1.53	105.28	-12.17
226	2jsa-4	LEU_A_38_C	LEU_A_38_O	1.008	0.272	-13.396	1.608	1.001	-14.186	1.23	129.92	50.54
227	2jsa-4	LEU_A_38_C	PHE_A_39_N	1.008	0.272	-13.396	1.525	-0.812	-12.837	1.32	65.04	-64.50
228	2jsa-4	PHE_A_39_N	PHE_A_39_H	1.525	-0.812	-12.837	0.974	-1.365	-12.196	1.01	50.61	-134.90
229	2jsa-4	PHE_A_39_N	PHE_A_39_CA	1.525	-0.812	-12.837	2.886	-1.23	-13.128	1.45	101.55	-17.07
230	2jsa-4	PHE_A_39_CA	PHE_A_39_HA	2.886	-1.23	-13.128	3.371	-0.492	-13.767	1.09	125.89	56.69
231	2jsa-4	PHE_A_39_CA	PHE_A_39_C	2.886	-1.23	-13.128	2.905	-2.596	-13.815	1.53	116.70	-89.20
232	2jsa-4	PHE_A_39_C	PHE_A_39_O	2.905	-2.596	-13.815	3.681	-3.473	-13.437	1.23	72.11	-48.50
233	2jsa-4	PHE_A_39_C	HIS_A_40_N	2.905	-2.596	-13.815	2.042	-2.736	-14.81	1.32	138.70	-170.79
234	2jsa-4	HIS_A_40_N	HIS_A_40_H	2.042	-2.736	-14.81	1.433	-1.972	-15.065	1.01	104.63	128.56
235	2jsa-4	HIS_A_40_N	HIS_A_40_CA	2.042	-2.736	-14.81	1.95	-3.981	-15.553	1.45	120.76	-94.23
236	2jsa-4	HIS_A_40_CA	HIS_A_40_HA	1.95	-3.981	-15.553	1.865	-4.796	-14.834	1.09	48.73	-95.95
237	2jsa-4	HIS_A_40_CA	HIS_A_40_C	1.95	-3.981	-15.553	3.234	-4.196	-16.355	1.53	121.63	-9.51
238	2jsa-4	HIS_A_40_C	HIS_A_40_O	3.234	-4.196	-16.355	3.678	-5.329	-16.532	1.23	98.28	-68.60
239	2jsa-4	HIS_A_40_C	THR_A_41_N	3.234	-4.196	-16.355	3.797	-3.089	-16.818	1.33	110.45	63.04
240	2jsa-4	THR_A_41_N	THR_A_41_H	3.797	-3.089	-16.818	3.378					

243	2jsa-4	THR_A_41_CA	THR_A_41_C	5.022	-3.143	-17.597	6.229	-3.357	-16.681	1.53	53.23	-10.05
244	2jsa-4	THR_A_41_C	THR_A_41_O	6.229	-3.357	-16.681	7.098	-4.176	-16.975	1.23	103.83	-43.30
245	2jsa-4	THR_A_41_C	ILE_A_42_N	6.229	-3.357	-16.681	6.243	-2.606	-15.589	1.33	34.52	88.93
246	2jsa-4	ILE_A_42_N	ILE_A_42_H	6.243	-2.606	-15.589	5.494	-1.953	-15.411	1.01	79.84	138.92
247	2jsa-4	ILE_A_42_N	ILE_A_42_CA	6.243	-2.606	-15.589	7.327	-2.704	-14.628	1.45	48.56	-5.17
248	2jsa-4	ILE_A_42_CA	ILE_A_42_HA	7.327	-2.704	-14.628	8.234	-2.33	-15.104	1.09	115.88	22.41
249	2jsa-4	ILE_A_42_CA	ILE_A_42_C	7.327	-2.704	-14.628	7.56	-4.175	-14.276	1.53	76.70	-81.00
250	2jsa-4	ILE_A_42_C	ILE_A_42_O	7.56	-4.175	-14.276	6.61	-4.948	-14.168	1.23	84.96	-140.87
251	2jsa-4	ILE_A_42_C	PRO_A_43_N	7.56	-4.175	-14.276	8.863	-4.525	-14.101	1.36	82.61	-15.04
252	2jsa-4	PRO_A_43_N	PRO_A_43_CA	8.863	-4.525	-14.101	9.232	-5.889	-13.763	1.45	76.55	-74.86
253	2jsa-4	PRO_A_43_CA	PRO_A_43_HA	9.232	-5.889	-13.763	8.681	-6.591	-14.388	1.09	125.01	-128.13
254	2jsa-4	PRO_A_43_CA	PRO_A_43_C	9.232	-5.889	-13.763	8.919	-6.195	-12.298	1.53	16.64	-135.65
255	2jsa-4	PRO_A_43_C	PRO_A_43_O	8.919	-6.195	-12.298	7.793	-6.564	-11.964	1.23	74.26	-161.86
256	2jsa-4	PRO_A_43_C	PHE_A_44_N	8.919	-6.195	-12.298	9.932	-6.03	-11.461	1.32	50.80	9.25
257	2jsa-4	PHE_A_44_N	PHE_A_44_H	9.932	-6.03	-11.461	10.831	-5.724	-11.805	1.01	109.91	18.80
258	2jsa-4	PHE_A_44_N	PHE_A_44_CA	9.932	-6.03	-11.461	9.778	-6.283	-10.038	1.45	11.76	-121.33
259	2jsa-4	PHE_A_44_CA	PHE_A_44_HA	9.778	-6.283	-10.038	9.679	-7.354	-9.861	1.09	80.65	-95.28
260	2jsa-4	PHE_A_44_CA	PHE_A_44_C	9.778	-6.283	-10.038	8.554	-5.554	-9.481	1.53	68.65	149.22
261	2jsa-4	PHE_A_44_C	PHE_A_44_O	8.554	-5.554	-9.481	7.974	-5.981	-8.483	1.23	35.82	-143.64
262	2jsa-4	PHE_A_44_C	GLY_A_45_N	8.554	-5.554	-9.481	8.196	-4.468	-10.15	1.32	120.33	108.24
263	2jsa-4	GLY_A_45_N	GLY_A_45_H	8.196	-4.468	-10.15	8.719	-4.177	-10.964	1.01	143.67	29.09
264	2jsa-4	GLY_A_45_N	GLY_A_45_CA	8.196	-4.468	-10.15	7.052	-3.675	-9.733	1.45	73.32	145.27
265	2jsa-4	GLY_A_45_CA	GLY_A_45_C	7.052	-3.675	-9.733	5.947	-4.567	-9.162	1.53	68.10	-141.09
266	2jsa-4	GLY_A_45_C	GLY_A_45_O	5.947	-4.567	-9.162	5.585	-4.441	-7.994	1.23	18.17	160.81
267	2jsa-4	GLY_A_45_C	THR_A_46_N	5.947	-4.567	-9.162	5.442	-5.448	-10.013	1.32	129.96	-119.82
268	2jsa-4	THR_A_46_N	THR_A_46_H	5.442	-5.448	-10.013	5.79	-5.496	-10.96	1.01	159.65	-7.85
269	2jsa-4	THR_A_46_N	THR_A_46_CA	5.442	-5.448	-10.013	4.386	-6.359	-9.609	1.45	73.84	-139.22
270	2jsa-4	THR_A_46_CA	THR_A_46_HA	4.386	-6.359	-9.609	3.527	-5.774	-9.279	1.09	72.38	145.74
271	2jsa-4	THR_A_46_CA	THR_A_46_C	4.386	-6.359	-9.609	4.848	-7.222	-8.433	1.53	39.77	-61.84
272	2jsa-4	THR_A_46_C	THR_A_46_O	4.848	-7.222	-8.433	4.072	-7.502	-7.52	1.23	42.10	-160.16
273	2jsa-4	THR_A_46_C	ARG_A_47_N	4.848	-7.222	-8.433	6.11	-7.621	-8.494	1.32	92.64	-17.55
274	2jsa-4	ARG_A_47_N	ARG_A_47_H	6.11	-7.621	-8.494	6.691	-7.354	-9.276	1.01	140.73	24.68
275	2jsa-4	ARG_A_47_N	ARG_A_47_CA	6.11	-7.621	-8.494	6.686	-8.447	-7.446	1.45	43.86	-55.11
276	2jsa-4	ARG_A_47_CA	ARG_A_47_HA	6.686	-8.447	-7.446	6.061	-9.331	-7.322	1.09	83.47	-125.26
277	2jsa-4	ARG_A_47_CA	ARG_A_47_C	6.686	-8.447	-7.446	6.726	-7.676	-6.125	1.53	30.30	87.03
278	2jsa-4	ARG_A_47_C	ARG_A_47_O	6.726	-7.676	-6.125	6.142	-8.108	-5.132	1.23	36.19	-143.51
279	2jsa-4	ARG_A_47_C	GLU_A_48_N	6.726	-7.676	-6.125	7.421	-6.548	-6.154	1.33	91.25	58.36
280	2jsa-4	GLU_A_48_N	GLU_A_48_H	7.421	-6.548	-6.154	7.876	-6.253	-7.006	1.01	147.52	32.96
281	2jsa-4	GLU_A_48_N	GLU_A_48_CA	7.421	-6.548	-6.154	7.544	-5.714	-4.971	1.45	35.47	81.61
282	2jsa-4	GLU_A_48_CA	GLU_A_48_HA	7.544	-5.714	-4.971	8.066	-6.289	-4.205	1.09	45.39	-47.77
283	2jsa-4	GLU_A_48_CA	GLU_A_48_C	7.544	-5.714	-4.971	6.16	-5.345	-4.435	1.53	69.48	165.07
284	2jsa-4	GLU_A_48_C	GLU_A_48_O	6.16	-5.345	-4.435	5.948	-5.315	-3.224	1.23	10.03	171.95
285	2jsa-4	GLU_A_48_C	CYS_A_49_N	6.16	-5.345	-4.435	5.254	-5.073	-5.363	1.33	134.45	163.29
286	2jsa-4	CYS_A_49_N	CYS_A_49_H	5.254	-5.073	-5.363	5.499	-5.118	-6.342	1.01	165.72	-10.41
287	2jsa-4	CYS_A_49_N	CYS_A_49_CA	5.254	-5.073	-5.363	3.896	-4.707	-4.999	1.45	75.49	164.92
288	2jsa-4	CYS_A_49_CA	CYS_A_49_HA	3.896	-4.707	-4.999	3.942	-3.863	-4.31	1.09	50.82	86.88
289	2jsa-4	CYS_A_49_CA	CYS_A_49_C	3.896	-4.707	-4.999	3.257	-5.894	-4.275	1.53	61.76	-118.29
290	2jsa-4	CYS_A_49_C	CYS_A_49_O	3.257	-5.894	-4.275	2.57	-5.716	-3.27	1.23	35.23	165.47
291	2jsa-4	CYS_A_49_C	ASP_A_50_N	3.257	-5.894	-4.275	3.505	-7.079	-4.814	1.33	114.00	-78.18
292	2jsa-4	ASP_A_50_N	ASP_A_50_H	3.505	-7.079	-4.814	4.078	-7.151	-5.643	1.01	145.14	-7.16
293	2jsa-4	ASP_A_50_N	ASP_A_50_CA	3.505	-7.079	-4.814	2.962	-8.294	-4.231	1.45	66.34	-114.08
294	2jsa-4	ASP_A_50_CA	ASP_A_50_HA	2.962	-8.294	-4.231	1.902	-8.148	-4.027	1.09	79.21	172.16
295	2jsa-4	ASP_A_50_CA	ASP_A_50_C	2.962	-8.294	-4.231	3.704	-8.607	-2.931	1.53	31.78	-22.87
296	2jsa-4	ASP_A_50_C	ASP_A_50_O	3.704	-8.607	-2.931	3.344	-9.541	-2.216	1.23	54.46	-111.08
297	2jsa-4	ASP_A_50_C	HIS_A_51_N	3.704	-8.607	-2.931	4.726	-7.808	-2.664	1.32	78.37	38.02
298	2jsa-4	HIS_A_51_N	HIS_A_51_H	4.726	-7.808	-2.664	4.966	-7.059	-3.298	1.01	128.87	72.23
299	2jsa-4	HIS_A_51_N	HIS_A_51_CA	4.726	-7.808	-2.664	5.522	-7.988	-1.461	1.45	34.15	-12.74
300	2jsa-4	HIS_A_51_CA	HIS_A_51_HA	5.522	-7.988	-1.461	5.165	-8.883	-0.952	1.09	62.16	-111.75
301	2jsa-4	HIS_A_51_CA	HIS_A_51_C	5.522	-7.988	-1.461	5.311	-6.799	-0.522	1.53	52.13	100.06
302	2jsa-4	HIS_A_51_C	HIS_A_51_O	5.311	-6.799	-0.522	5.92	-6.728	0.544	1.23	29.91	6.65
303	2jsa-4	HIS_A_51_C	TYR_A_52_N	5.311	-6.799	-0.522	4.447	-5.892	-0.954	1.33	109.03	133.61
304	2jsa-4	TYR_A_52_N	TYR_A_52_H	4.447	-5.892	-0.954	3.985	-6.013	-1.843	1.01	151.75	-165.32
305	2jsa-4	TYR_A_52_N	TYR_A_52_CA	4.447	-5.892	-0.954	4.148	-4.709	-0.166	1.45	57.15	104.18
306	2jsa-4	TYR_A_52_CA	TYR_A_52_HA	4.148	-4.709	-0.166	4.944	-4.525	0.556	1.09	48.53	13.02
307	2jsa-4	TYR_A_52_CA	TYR_A_52_C	4.148	-4.709	-0.166	2.809	-4.858	0.562	1.53	61.62	-173.65
308	2jsa-4	TYR_A_52_C	TYR_A_52_O	2.809	-4.858	0.562	2.682	-4.466	1.72	1.23	19.59	107.95
309	2jsa-4	TYR_A_52_C	VAL_A_53_N	2.809	-4.858	0.562	1.846	-5.426	-0.148	1.32	122.42	-149.47
310	2jsa-4	VAL_A_53_N	VAL_A_53_H	1.846	-5.426	-0.148	2.023	-5.724	-1.096	1.01	159.92	-59.29
311	2jsa-4	VAL_A_53_N	VAL_A_53_CA	1.846	-5.426	-0.148	0.523	-5.632	0.415	1.45	67.19	-171.15
312	2jsa-4	VAL_A_53_CA	VAL_A_53_HA	0.523	-5.632	0.415	0.105	-4.66	0.677	1.09	76.09	113.27
313	2jsa-4	VAL_A_53_CA	VAL_A_53_C	0.523	-5.632	0.415	0.643	-6.459	1.697	1.53	33.10	-81.74
314	2jsa-4	VAL_A_53_C	VAL_A_53_O	0.643	-6.459	1.697	-0.283	-6.493	2.507	1.23	48.84	-177.90
315	2jsa-4	VAL_A_53_C	ASN_A_54_N	0.643	-6.459	1.697	1.79	-7.106	1.841	1.32	83.76	-29.43
316	2jsa-4	ASN_A_54_N	ASN_A_54_H	1.79	-7.106	1.841	2.508	-7.033	1.134	1.01	134.41	5.81
317	2jsa-4	ASN_A_54_N	ASN_A_54_CA	1.79	-7.106	1.841	2.043	-7.93	3.011	1.45	36.38	-72.93
318	2jsa-4	ASN_A_54_CA	ASN_A_54_HA	2.043	-7.93	3.011	1.318	-7.682	3.786	1.09	44.67	161.12
319	2jsa-4	ASN_A_54_CA	ASN_A_54_C	2.043	-7.93	3.011	3.46	-7.662	3.522	1.53	70.49	10.71
320	2jsa-4	ASN_A_54_C	ASN_A_54_O	3.46	-7.662	3.522	4.31	-8.551	3.498	1.23	91.12	-46.28
321	2jsa-4	ASN_A_54_C	SER_A_55_N	3.46	-7.662	3.522	3.669	-6.434	3.973	1.32	70.10	80.34
322	2jsa-4	SER_A_55_N	SER_A_55_H	3.669	-6.434	3.973	2.922	-5.754	3.964	1.01	90.51	137.69
323	2jsa-4	SER_A_55_N	SER_A_55_CA	3.669	-6.434	3.973	4.968	-6.038	4.489	1.45	69.19	16.95
324	2jsa-4	SER_A_55_CA	SER_A_55_HA	4.968	-6.038	4.489	5.238	-6.72	5.296	1.09	42.27	-68.40
325	2jsa-4	SER_A_55_CA	SER_A_55_C	4.968	-6.038	4.489	4.897	-4.617	5.052	1.53	68.41	92.86
326	2jsa-4	SER_A_55_C	SER_A_55_O	4.897	-4.617	5.052	5.482	-4.327	6.093	1.23	32.10	26.37
327	2jsa-4	SER_A_55_C	LYS_A_56_N	4.897	-4.617	5.052	4.173	-3.767	4.337	1.33	122.63	130.42
328	2jsa-4	LYS_A_56_N	LYS_A_56_H	4.173	-3.767	4.337	3.718	-4.074	3.49	1.01	147.06	-145.99
329	2jsa-4	LYS_A_56_N	LYS_A_56_CA	4.173	-3.767	4.337	4.018	-2.384	4.751	1.45	73.43	96.39
330	2jsa-4	LYS_A_56_CA	LYS_A_56_HA	4.018	-2.384	4.751	4.39	-2.294	5.772	1.09	20.55	13.60
331	2jsa-4	LYS_A_56_CA	LYS_A_56_C	4.018	-2.384	4.751	2.53	-2.023	4.764	1.53	89.51	166.36
332	2jsa-4	LYS_A_56_C	LYS_A_56_O	2.53	-2.023	4.764	2.172	-0.856	4.904	1.23	83.46	107.05
333	2jsa-4	LYS_A_56_C	VAL_A_57_N	2.53	-2.023	4.764	1.704	-3.049	4.615	1.33	96.45	-128.84

336	2jsa-4	VAL_A_57_CA	VAL_A_57_HA	0.265	-2.856	4.608	0.058	-1.821	4.336	1.09	104.45	101.31
337	2jsa-4	VAL_A_57_CA	VAL_A_57_C	0.265	-2.856	4.608	-0.285	-3.096	6.015	1.53	23.10	-156.43
338	2jsa-4	VAL_A_57_C	VAL_A_57_O	-0.285	-3.096	6.015	-1.075	-2.3	6.521	1.23	65.72	134.78
339	2jsa-4	VAL_A_57_C	ASP_A_58_N	-0.285	-3.096	6.015	0.154	-4.197	6.607	1.32	63.46	-68.26
340	2jsa-4	ASP_A_58_N	ASP_A_58_H	0.154	-4.197	6.607	0.802	-4.808	6.13	1.01	118.17	-43.32
341	2jsa-4	ASP_A_58_N	ASP_A_58_CA	0.154	-4.197	6.607	-0.284	-4.551	7.947	1.45	22.80	-141.05
342	2jsa-4	ASP_A_58_CA	ASP_A_58_HA	-0.284	-4.551	7.947	-1.333	-4.845	7.912	1.09	91.84	-164.34
343	2jsa-4	ASP_A_58_CA	ASP_A_58_C	-0.284	-4.551	7.947	-0.113	-3.344	8.872	1.53	52.81	81.94
344	2jsa-4	ASP_A_58_C	ASP_A_58_O	-0.113	-3.344	8.872	-1.004	-3.03	9.66	1.23	50.17	160.59
345	2jsa-4	ASP_A_58_C	PRO_A_59_N	-0.113	-3.344	8.872	1.067	-2.682	8.741	1.36	95.53	29.29
346	2jsa-4	PRO_A_59_N	PRO_A_59_CA	1.067	-2.682	8.741	1.366	-1.516	9.554	1.45	55.96	75.62
347	2jsa-4	PRO_A_59_CA	PRO_A_59_HA	1.366	-1.516	9.554	1.096	-1.706	10.593	1.09	17.63	-144.87
348	2jsa-4	PRO_A_59_CA	PRO_A_59_C	1.366	-1.516	9.554	0.586	-0.293	9.067	1.53	108.56	122.53
349	2jsa-4	PRO_A_59_C	PRO_A_59_O	0.586	-0.293	9.067	-0.17	0.309	9.828	1.23	51.78	141.47
350	2jsa-4	PRO_A_59_C	ILE_A_60_N	0.586	-0.293	9.067	0.798	0.038	7.802	1.32	162.74	57.36
351	2jsa-4	ILE_A_60_N	ILE_A_60_H	0.798	0.038	7.802	1.435	-0.503	7.234	1.01	124.20	-40.34
352	2jsa-4	ILE_A_60_N	ILE_A_60_CA	0.798	0.038	7.802	0.124	1.178	7.204	1.45	114.30	120.59
353	2jsa-4	ILE_A_60_CA	ILE_A_60_HA	0.124	1.178	7.204	0.566	2.085	7.617	1.09	67.74	64.02
354	2jsa-4	ILE_A_60_CA	ILE_A_60_C	0.124	1.178	7.204	-1.353	1.158	7.601	1.53	74.96	-179.22
355	2jsa-4	ILE_A_60_C	ILE_A_60_O	-1.353	1.158	7.601	-1.845	2.099	8.223	1.23	59.64	117.60
356	2jsa-4	ILE_A_60_C	ILE_A_61_N	-1.353	1.158	7.601	-2.019	0.076	7.225	1.33	106.49	-121.61
357	2jsa-4	ILE_A_61_N	ILE_A_61_H	-2.019	0.076	7.225	-1.549	-0.659	6.716	1.01	120.26	-57.40
358	2jsa-4	ILE_A_61_N	ILE_A_61_CA	-2.019	0.076	7.225	-3.43	-0.079	7.534	1.45	77.72	-173.73
359	2jsa-4	ILE_A_61_CA	ILE_A_61_HA	-3.43	-0.079	7.534	-3.971	0.739	7.058	1.09	115.89	123.48
360	2jsa-4	ILE_A_61_CA	ILE_A_61_C	-3.43	-0.079	7.534	-3.634	0.047	9.046	1.53	9.01	148.30
361	2jsa-4	ILE_A_61_C	ILE_A_61_O	-3.634	0.047	9.046	-4.727	0.377	9.503	1.23	68.19	163.20
362	2jsa-4	ILE_A_61_C	HIS_A_62_N	-3.634	0.047	9.046	-2.564	-0.223	9.779	1.32	56.41	-14.16
363	2jsa-4	HIS_A_62_N	HIS_A_62_H	-2.564	-0.223	9.779	-1.697	-0.49	9.335	1.01	116.08	-17.12
364	2jsa-4	HIS_A_62_N	HIS_A_62_CA	-2.564	-0.223	9.779	-2.612	-0.143	11.229	1.45	3.68	120.96
365	2jsa-4	HIS_A_62_CA	HIS_A_62_HA	-2.612	-0.143	11.229	-3.493	-0.688	11.567	1.09	71.93	-148.26
366	2jsa-4	HIS_A_62_CA	HIS_A_62_C	-2.612	-0.143	11.229	-2.769	1.316	11.658	1.53	73.70	96.14
367	2jsa-4	HIS_A_62_C	HIS_A_62_O	-2.769	1.316	11.658	-3.284	1.597	12.74	1.23	28.47	151.38
368	2jsa-4	HIS_A_62_C	GLU_A_63_N	-2.769	1.316	11.658	-2.316	2.208	10.789	1.33	130.98	63.08
369	2jsa-4	GLU_A_63_N	GLU_A_63_H	-2.316	2.208	10.789	-1.904	1.905	9.918	1.01	149.58	-36.33
370	2jsa-4	GLU_A_63_N	GLU_A_63_CA	-2.316	2.208	10.789	-2.401	3.632	11.065	1.45	79.05	93.42
371	2jsa-4	GLU_A_63_CA	GLU_A_63_HA	-2.401	3.632	11.065	-2.137	3.789	12.111	1.09	16.36	30.74
372	2jsa-4	GLU_A_63_CA	GLU_A_63_C	-2.401	3.632	11.065	-3.831	4.131	10.85	1.53	98.08	160.76
373	2jsa-4	GLU_A_63_C	GLU_A_63_O	-3.831	4.131	10.85	-4.403	4.781	11.723	1.23	44.76	131.35
374	2jsa-4	GLU_A_63_C	LEU_A_64_N	-3.831	4.131	10.85	-4.367	3.806	9.683	1.32	151.76	-148.77
375	2jsa-4	LEU_A_64_N	LEU_A_64_H	-4.367	3.806	9.683	-3.837	3.268	9.012	1.01	131.62	-45.43
376	2jsa-4	LEU_A_64_N	LEU_A_64_CA	-4.367	3.806	9.683	-5.72	4.213	9.342	1.45	103.57	163.26
377	2jsa-4	LEU_A_64_CA	LEU_A_64_HA	-5.72	4.213	9.342	-5.799	5.288	9.503	1.09	81.50	94.20
378	2jsa-4	LEU_A_64_CA	LEU_A_64_C	-5.72	4.213	9.342	-6.708	3.527	10.287	1.53	51.84	-145.23
379	2jsa-4	LEU_A_64_C	LEU_A_64_O	-6.708	3.527	10.287	-7.788	4.054	10.552	1.23	77.56	153.99
380	2jsa-4	LEU_A_64_C	GLU_A_65_N	-6.708	3.527	10.287	-6.303	2.361	10.77	1.33	68.63	-70.85
381	2jsa-4	GLU_A_65_N	GLU_A_65_H	-6.303	2.361	10.77	-5.401	1.988	10.509	1.01	104.97	-22.47
382	2jsa-4	GLU_A_65_N	GLU_A_65_CA	-6.303	2.361	10.77	-7.139	1.597	11.68	1.45	51.22	-137.58
383	2jsa-4	GLU_A_65_CA	GLU_A_65_HA	-7.139	1.597	11.68	-8.126	1.499	11.229	1.09	114.45	-174.33
384	2jsa-4	GLU_A_65_CA	GLU_A_65_C	-7.139	1.597	11.68	-7.29	2.337	13.011	1.53	29.57	101.53
385	2jsa-4	GLU_A_65_C	GLU_A_65_O	-7.29	2.337	13.011	-8.399	2.484	13.522	1.23	65.45	172.45
386	2jsa-4	GLU_A_65_C	GLY_A_66_N	-7.29	2.337	13.011	-6.157	2.784	13.534	1.33	66.76	21.53
387	2jsa-4	GLY_A_66_N	GLY_A_66_H	-6.157	2.784	13.534	-5.28	2.627	13.058	1.01	118.11	-10.15
388	2jsa-4	GLY_A_66_N	GLY_A_66_CA	-6.157	2.784	13.534	-6.149	3.505	14.795	1.45	29.76	89.36
389	2jsa-4	GLY_A_66_CA	GLY_A_66_C	-6.149	3.505	14.795	-6.874	4.847	14.665	1.53	94.87	118.38
390	2jsa-4	GLY_A_66_C	GLY_A_66_O	-6.874	4.847	14.665	-7.818	5.121	15.404	1.23	53.06	163.81
391	2jsa-4	GLY_A_66_C	GLY_A_67_N	-6.874	4.847	14.665	-6.406	5.647	13.718	1.33	135.62	59.67
392	2jsa-4	GLY_A_67_N	GLY_A_67_H	-6.406	5.647	13.718	-5.626	5.355	13.146	1.01	124.48	-20.52
393	2jsa-4	GLY_A_67_N	GLY_A_67_CA	-6.406	5.647	13.718	-6.997	6.953	13.481	1.45	99.39	114.35
394	2jsa-4	GLY_A_67_CA	GLY_A_67_C	-6.997	6.953	13.481	-5.999	7.892	12.801	1.53	116.39	43.26
395	2jsa-4	GLY_A_67_C	GLY_A_67_O	-5.999	7.892	12.801	-5.887	9.059	13.174	1.23	72.35	84.52
396	2jsa-4	GLY_A_67_C	THR_A_68_N	-5.999	7.892	12.801	-5.298	7.347	11.818	1.32	137.91	-37.86
397	2jsa-4	THR_A_68_N	THR_A_68_H	-5.298	7.347	11.818	-5.441	6.38	11.566	1.01	104.46	-98.41
398	2jsa-4	THR_A_68_N	THR_A_68_CA	-5.298	7.347	11.818	-4.313	8.122	11.083	1.45	120.39	38.20
399	2jsa-4	THR_A_68_CA	THR_A_68_HA	-4.313	8.122	11.083	-4.256	9.12	11.519	1.09	66.43	86.73
400	2jsa-4	THR_A_68_CA	THR_A_68_C	-4.313	8.122	11.083	-4.734	8.271	9.62	1.53	163.02	160.51
401	2jsa-4	THR_A_68_C	THR_A_68_O	-4.734	8.271	9.62	-5.17	7.305	8.994	1.23	120.57	-114.29
402	2jsa-4	THR_A_68_C	ALA_A_69_N	-4.734	8.271	9.62	-4.589	9.487	9.116	1.32	112.37	83.20
403	2jsa-4	ALA_A_69_N	ALA_A_69_H	-4.589	9.487	9.116	-4.224	10.234	9.689	1.01	55.43	63.96
404	2jsa-4	ALA_A_69_N	ALA_A_69_CA	-4.589	9.487	9.116	-4.949	9.775	7.738	1.45	161.50	141.34
405	2jsa-4	ALA_A_69_CA	ALA_A_69_HA	-4.949	9.775	7.738	-5.968	9.432	7.564	1.09	99.19	-161.40
406	2jsa-4	ALA_A_69_CA	ALA_A_69_C	-4.949	9.775	7.738	-4.014	9.008	6.8	1.53	127.80	-39.36
407	2jsa-4	ALA_A_69_C	ALA_A_69_O	-4.014	9.008	6.8	-3.023	8.429	7.243	1.23	68.89	-30.30
408	2jsa-4	ALA_A_69_C	PRO_A_70_N	-4.014	9.008	6.8	-4.369	9.032	5.488	1.36	164.83	176.13
409	2jsa-4	PRO_A_70_N	PRO_A_70_CA	-4.369	9.032	5.488	-3.573	8.347	4.484	1.45	133.71	-40.71
410	2jsa-4	PRO_A_70_CA	PRO_A_70_HA	-3.573	8.347	4.484	-3.304	7.351	4.836	1.09	71.16	-74.89
411	2jsa-4	PRO_A_70_CA	PRO_A_70_C	-3.573	8.347	4.484	-2.286	9.119	4.185	1.53	101.27	30.96
412	2jsa-4	PRO_A_70_C	PRO_A_70_O	-2.286	9.119	4.185	-1.323	8.551	3.671	1.23	114.69	-30.53
413	2jsa-4	PRO_A_70_C	LYS_A_71_N	-2.286	9.119	4.185	-2.311	10.401	4.52	1.33	75.36	91.12
414	2jsa-4	LYS_A_71_N	LYS_A_71_H	-2.311	10.401	4.52	-3.137	10.801	4.94	1.01	65.41	154.16
415	2jsa-4	LYS_A_71_N	LYS_A_71_CA	-2.311	10.401	4.52	-1.158	11.255	4.293	1.45	98.99	36.53
416	2jsa-4	LYS_A_71_CA	LYS_A_71_HA	-1.158	11.255	4.293	-0.547	10.799	3.514	1.09	135.62	-36.73
417	2jsa-4	LYS_A_71_CA	LYS_A_71_C	-1.158	11.255	4.293	-0.315	11.317	5.569	1.53	33.52	4.21
418	2jsa-4	LYS_A_71_C	LYS_A_71_O	-0.315	11.317	5.569	0.785	11.867	5.565	1.23	90.19	26.57
419	2jsa-4	LYS_A_71_C	ASP_A_72_N	-0.315	11.317	5.569	-0.864	10.744	6.63	1.32	36.79	-133.77
420	2jsa-4	ASP_A_72_N	ASP_A_72_H	-0.864	10.744	6.63	-1.773	10.31	6.561	1.01	93.92	-154.48
421	2jsa-4	ASP_A_72_N	ASP_A_72_CA	-0.864	10.744	6.63	-0.176	10.727	7.91	1.45	28.27	-1.42
422	2jsa-4	ASP_A_72_CA	ASP_A_72_HA	-0.176	10.727	7.91	0.556	11.535	7.933	1.09	88.79	47.83
423	2jsa-4	ASP_A_72_CA	ASP_A_72_C	-0.176	10.727	7.91	0.528	9.381	8.087	1.53	83.35	-62.39
424	2jsa-4	ASP_A_72_C	ASP_A_72_O	0.528	9.381	8.087	1.631	9.32	8.628	1.23	63.91	-3.17
425	2jsa-4	ASP_A_72_C	VAL_A_73_N	0.528	9.381	8.087	-0.137	8.334	7.621	1.32	110.59	-122.42
426	2jsa-4	VAL_A_73_N	VAL_A_73_H	-0.137	8.334	7.621	-1.04					

429	2jsa-4	VAL_A_73_CA	VAL_A_73_C	0.412	6.992	7.721	1.847	6.993	7.189	1.53	110.34	0.04
430	2jsa-4	VAL_A_73_O	VAL_A_73_O	1.847	6.993	7.189	2.769	6.566	7.882	1.23	55.70	-24.85
431	2jsa-4	VAL_A_73_C	CYS_A_74_N	1.847	6.993	7.189	1.989	7.476	5.964	1.32	157.66	73.62
432	2jsa-4	CYS_A_74_N	CYS_A_74_H	1.989	7.476	5.964	1.185	7.811	5.453	1.01	120.40	157.38
433	2jsa-4	CYS_A_74_N	CYS_A_74_CA	1.989	7.476	5.964	3.296	7.537	5.33	1.45	115.85	2.67
434	2jsa-4	CYS_A_74_CA	CYS_A_74_HA	3.296	7.537	5.33	3.868	6.662	5.638	1.09	73.58	-56.83
435	2jsa-4	CYS_A_74_CA	CYS_A_74_C	3.296	7.537	5.33	4.015	8.791	5.834	1.53	70.78	60.17
436	2jsa-4	CYS_A_74_C	CYS_A_74_O	4.015	8.791	5.834	4.454	9.62	5.039	1.23	130.28	62.10
437	2jsa-4	CYS_A_74_C	THR_A_75_N	4.015	8.791	5.834	4.114	8.889	7.151	1.32	6.04	44.71
438	2jsa-4	THR_A_75_N	THR_A_75_H	4.114	8.889	7.151	3.731	8.168	7.745	1.01	53.96	-117.98
439	2jsa-4	THR_A_75_N	THR_A_75_CA	4.114	8.889	7.151	4.772	10.026	7.77	1.45	64.77	59.94
440	2jsa-4	THR_A_75_CA	THR_A_75_HA	4.772	10.026	7.77	5.513	10.423	7.075	1.09	129.58	28.18
441	2jsa-4	THR_A_75_CA	THR_A_75_C	4.772	10.026	7.77	5.504	9.592	9.041	1.53	33.80	-30.66
442	2jsa-4	THR_A_75_C	THR_A_75_O	5.504	9.592	9.041	6.711	9.798	9.167	1.23	84.12	9.69
443	2jsa-4	THR_A_75_C	LYS_A_76_N	5.504	9.592	9.041	4.744	9.001	9.95	1.32	46.64	-142.13
444	2jsa-4	LYS_A_76_N	LYS_A_76_H	4.744	9.001	9.95	3.758	8.865	9.779	1.01	99.75	-172.15
445	2jsa-4	LYS_A_76_N	LYS_A_76_CA	4.744	9.001	9.95	5.307	8.537	11.208	1.45	30.11	-39.49
446	2jsa-4	LYS_A_76_CA	LYS_A_76_HA	5.307	8.537	11.208	6.098	9.228	11.501	1.09	74.41	41.14
447	2jsa-4	LYS_A_76_CA	LYS_A_76_C	5.307	8.537	11.208	5.944	7.162	10.999	1.53	97.85	-65.14
448	2jsa-4	LYS_A_76_C	LYS_A_76_O	5.944	7.162	10.999	6.858	6.781	11.728	1.23	53.64	-22.63
449	2jsa-4	LYS_A_76_C	LEU_A_77_N	5.944	7.162	10.999	5.438	6.455	10.0	1.32	138.97	-125.59
450	2jsa-4	LEU_A_77_N	LEU_A_77_H	5.438	6.455	10.0	4.686	6.832	9.441	1.01	123.60	153.37
451	2jsa-4	LEU_A_77_N	LEU_A_77_CA	5.438	6.455	10.0	5.947	5.131	9.685	1.45	102.52	-68.97
452	2jsa-4	LEU_A_77_CA	LEU_A_77_HA	5.947	5.131	9.685	6.15	4.616	10.624	1.09	30.52	-68.49
453	2jsa-4	LEU_A_77_CA	LEU_A_77_C	5.947	5.131	9.685	7.272	5.264	8.933	1.53	119.45	5.73
454	2jsa-4	LEU_A_77_C	LEU_A_77_O	7.272	5.264	8.933	7.875	4.264	8.548	1.23	108.25	-58.91
455	2jsa-4	LEU_A_77_C	ASN_A_78_N	7.272	5.264	8.933	7.688	6.509	8.749	1.33	97.98	71.52
456	2jsa-4	ASN_A_78_N	ASN_A_78_H	7.688	6.509	8.749	7.142	7.285	9.096	1.01	69.91	125.13
457	2jsa-4	ASN_A_78_N	ASN_A_78_CA	7.688	6.509	8.749	8.931	6.786	8.049	1.45	118.80	12.56
458	2jsa-4	ASN_A_78_CA	ASN_A_78_HA	8.931	6.786	8.049	9.048	7.865	7.944	1.09	95.53	83.81
459	2jsa-4	ASN_A_78_CA	ASN_A_78_C	8.931	6.786	8.049	8.893	6.13	6.667	1.53	154.57	-93.32
460	2jsa-4	ASN_A_78_C	ASN_A_78_O	8.893	6.13	6.667	9.928	5.965	6.025	1.23	121.49	-9.06
461	2jsa-4	ASN_A_78_C	GLU_A_79_N	8.893	6.13	6.667	7.686	5.772	6.251	1.33	108.29	-163.48
462	2jsa-4	GLU_A_79_N	GLU_A_79_H	7.686	5.772	6.251	6.878	5.938	6.833	1.01	54.79	168.39
463	2jsa-4	GLU_A_79_N	GLU_A_79_CA	7.686	5.772	6.251	7.498	5.138	4.958	1.45	152.91	-106.52
464	2jsa-4	GLU_A_79_CA	GLU_A_79_HA	7.498	5.138	4.958	8.462	4.749	4.63	1.09	107.51	-21.98
465	2jsa-4	GLU_A_79_CA	GLU_A_79_C	7.498	5.138	4.958	7.018	6.162	3.928	1.53	132.33	115.11
466	2jsa-4	GLU_A_79_C	GLU_A_79_O	7.018	6.162	3.928	5.967	5.986	3.316	1.23	119.87	-170.49
467	2jsa-4	GLU_A_79_C	CYS_A_80_N	7.018	6.162	3.928	7.812	7.212	3.771	1.33	96.80	52.90
468	2jsa-4	CYS_A_80_N	CYS_A_80_H	7.812	7.212	3.771	8.663	7.292	4.31	1.01	57.76	5.37
469	2jsa-4	CYS_A_80_N	CYS_A_80_CA	7.812	7.212	3.771	7.481	8.265	2.826	1.45	130.57	107.45
470	2jsa-4	CYS_A_80_CA	CYS_A_80_HA	7.481	8.265	2.826	7.702	7.906	1.821	1.09	157.24	-58.38
471	2jsa-4	CYS_A_80_CA	CYS_A_80_C	7.481	8.265	2.826	8.375	9.472	3.119	1.53	78.96	53.47
472	2jsa-4	CYS_A_80_C	CYS_A_80_O	8.375	9.472	3.119	8.782	9.685	4.26	1.23	21.93	27.62
473	2jsa-4	CYS_A_80_C	PRO_A_81_N	8.375	9.472	3.119	8.663	10.25	2.042	1.36	142.39	69.69
474	2jsa-4	PRO_A_81_N	PRO_A_81_CA	8.663	10.25	2.042	9.5	11.429	2.171	1.45	84.90	54.63
475	2jsa-4	PRO_A_81_CA	PRO_A_81_HA	9.5	11.429	2.171	10.376	11.199	2.778	1.09	56.17	-14.71
476	2jsa-4	PRO_A_81_CA	PRO_A_81_C	9.5	11.429	2.171	8.736	12.575	2.838	1.53	64.16	123.69
477	2jsa-4	PRO_A_81_C	PRO_A_81_O	8.736	12.575	2.838	8.285	12.447	3.975	1.23	22.41	-164.16
1	2jsa-5	ARG_A_1_N	ARG_A_1_H	14.073	1.616	-0.782	14.844	2.125	-1.191	1.01	113.88	33.43
2	2jsa-5	ARG_A_1_N	ARG_A_1_CA	14.073	1.616	-0.782	12.928	2.365	-0.295	1.45	70.41	146.81
3	2jsa-5	ARG_A_1_CA	ARG_A_1_HA	12.928	2.365	-0.295	12.046	2.042	-0.848	1.09	120.49	-159.89
4	2jsa-5	ARG_A_1_CA	ARG_A_1_C	12.928	2.365	-0.295	13.136	3.863	-0.521	1.53	98.50	82.09
5	2jsa-5	ARG_A_1_C	ARG_A_1_O	13.136	3.863	-0.521	14.159	4.275	-1.066	1.23	116.30	21.94
6	2jsa-5	ARG_A_1_C	SER_A_2_N	13.136	3.863	-0.521	12.151	4.637	-0.092	1.32	71.10	141.84
7	2jsa-5	SER_A_2_N	SER_A_2_H	12.151	4.637	-0.092	11.339	4.229	0.348	1.01	64.16	-153.32
8	2jsa-5	SER_A_2_N	SER_A_2_CA	12.151	4.637	-0.092	12.213	6.081	-0.24	1.45	95.85	87.54
9	2jsa-5	SER_A_2_CA	SER_A_2_HA	12.213	6.081	-0.24	11.486	6.526	0.439	1.09	51.46	148.53
10	2jsa-5	SER_A_2_CA	SER_A_2_C	12.213	6.081	-0.24	11.851	6.475	-1.674	1.53	159.54	132.58
11	2jsa-5	SER_A_2_C	SER_A_2_O	11.851	6.475	-1.674	12.578	7.232	-2.316	1.23	121.45	46.16
12	2jsa-5	SER_A_2_C	ALA_A_3_N	11.851	6.475	-1.674	10.728	5.943	-2.134	1.33	110.31	-154.65
13	2jsa-5	ALA_A_3_N	ALA_A_3_H	10.728	5.943	-2.134	10.181	5.327	-1.55	1.01	54.67	-131.60
14	2jsa-5	ALA_A_3_N	ALA_A_3_CA	10.728	5.943	-2.134	10.261	6.23	-3.48	1.45	157.84	148.43
15	2jsa-5	ALA_A_3_CA	ALA_A_3_HA	10.261	6.23	-3.48	10.086	7.302	-3.569	1.09	94.68	99.27
16	2jsa-5	ALA_A_3_CA	ALA_A_3_C	10.261	6.23	-3.48	8.937	5.501	-3.722	1.53	99.10	-151.16
17	2jsa-5	ALA_A_3_C	ALA_A_3_O	8.937	5.501	-3.722	7.865	6.087	-3.569	1.23	82.86	151.34
18	2jsa-5	ALA_A_3_C	LEU_A_4_N	8.937	5.501	-3.722	9.054	4.236	-4.095	1.32	106.36	-84.72
19	2jsa-5	LEU_A_4_N	LEU_A_4_H	9.054	4.236	-4.095	9.968	3.819	-4.201	1.01	96.02	-24.52
20	2jsa-5	LEU_A_4_N	LEU_A_4_CA	9.054	4.236	-4.095	7.88	3.422	-4.359	1.45	100.47	-145.26
21	2jsa-5	LEU_A_4_CA	LEU_A_4_HA	7.88	3.422	-4.359	7.173	4.025	-4.929	1.09	121.53	139.54
22	2jsa-5	LEU_A_4_CA	LEU_A_4_C	7.88	3.422	-4.359	7.213	3.052	-3.033	1.53	29.91	-150.98
23	2jsa-5	LEU_A_4_C	LEU_A_4_O	7.213	3.052	-3.033	5.987	3.011	-2.941	1.23	85.71	-178.08
24	2jsa-5	LEU_A_4_C	SER_A_5_N	7.213	3.052	-3.033	8.049	2.789	-2.04	1.32	41.43	-17.46
25	2jsa-5	SER_A_5_N	SER_A_5_H	8.049	2.789	-2.04	9.047	2.841	-2.188	1.01	98.42	2.98
26	2jsa-5	SER_A_5_N	SER_A_5_CA	8.049	2.789	-2.04	7.556	2.423	-0.723	1.45	25.00	-143.41
27	2jsa-5	SER_A_5_CA	SER_A_5_HA	7.556	2.423	-0.723	7.079	1.446	-0.796	1.09	93.84	-116.02
28	2jsa-5	SER_A_5_CA	SER_A_5_C	7.556	2.423	-0.723	6.516	3.442	-0.252	1.53	72.07	135.58
29	2jsa-5	SER_A_5_C	SER_A_5_O	6.516	3.442	-0.252	5.507	3.073	0.346	1.23	60.90	-159.91
30	2jsa-5	SER_A_5_C	CYS_A_6_N	6.516	3.442	-0.252	6.799	4.704	-0.539	1.32	102.51	77.36
31	2jsa-5	CYS_A_6_N	CYS_A_6_H	6.799	4.704	-0.539	7.649	4.935	-1.034	1.01	119.33	15.20
32	2jsa-5	CYS_A_6_N	CYS_A_6_CA	6.799	4.704	-0.539	5.901	5.779	-0.152	1.45	74.56	129.87
33	2jsa-5	CYS_A_6_CA	CYS_A_6_HA	5.901	5.779	-0.152	5.624	5.635	0.892	1.09	16.65	-152.53
34	2jsa-5	CYS_A_6_CA	CYS_A_6_C	5.901	5.779	-0.152	4.638	5.682	-1.009	1.53	124.08	-175.61
35	2jsa-5	CYS_A_6_C	CYS_A_6_O	4.638	5.682	-1.009	3.535	5.539	-0.484	1.23	64.73	-172.61
36	2jsa-5	CYS_A_6_C	GLN_A_7_N	4.638	5.682	-1.009	4.841	5.763	-2.317	1.33	170.51	21.75
37	2jsa-5	GLN_A_7_N	GLN_A_7_H	4.841	5.763	-2.317	5.776	5.881	-2.68	1.01	111.07	7.19
38	2jsa-5	GLN_A_7_N	GLN_A_7_CA	4.841	5.763	-2.317	3.732	5.686	-3.252	1.45	130.07	-176.03
39	2jsa-5	GLN_A_7_CA	GLN_A_7_HA	3.732	5.686	-3.252	3.123	6.581	-3.126	1.09	83.36	124.23
40	2jsa-5	GLN_A_7_CA	GLN_A_7_C	3.732	5.686	-3.252	2.863	4.465	-2.946	1.53	78.46	-125.44
41	2jsa-5	GLN_A_7_C	GLN_A_7_O	2.863	4.465	-2.946	1.656	4.592	-2.746	1.23	80.64	173.99
42	2jsa-5	GLN_A_7_C	MET_A_8_N	2.863	4.465	-2.946	3.509	3.309	-2.918	1.32	88.79	-60.80
43	2jsa-5	MET_A_8_N	MET_A_8_H	3.509	3.309	-2.918	4.504	3.279	-3.093	1.01	99.97</	

45	2jsa-5	MET_A_8_CA	MET_A_8_HA	2.811	2.066	-2.639	2.2	1.807	-3.503	1.09	142.47	-157.03
46	2jsa-5	MET_A_8_CA	MET_A_8_C	2.811	2.066	-2.639	1.905	2.21	-1.414	1.53	36.83	170.97
47	2jsa-5	MET_A_8_C	MET_A_8_O	1.905	2.21	-1.414	0.766	1.747	-1.423	1.23	90.42	-157.88
48	2jsa-5	MET_A_8_C	CYS_A_9_N	1.905	2.21	-1.414	2.446	2.853	-0.39	1.32	39.37	49.92
49	2jsa-5	CYS_A_9_N	CYS_A_9_H	2.446	2.853	-0.39	3.39	3.208	-0.453	1.01	93.57	20.61
50	2jsa-5	CYS_A_9_N	CYS_A_9_CA	2.446	2.853	-0.39	1.7	3.063	0.84	1.45	32.21	164.28
51	2jsa-5	CYS_A_9_CA	CYS_A_9_HA	1.7	3.063	0.84	1.414	2.09	1.239	1.09	68.52	-106.38
52	2jsa-5	CYS_A_9_CA	CYS_A_9_C	1.7	3.063	0.84	0.428	3.845	0.503	1.53	102.72	148.42
53	2jsa-5	CYS_A_9_C	CYS_A_9_O	0.428	3.845	0.503	-0.597	3.683	1.163	1.23	57.54	-171.02
54	2jsa-5	CYS_A_9_C	GLU_A_10_N	0.428	3.845	0.503	0.538	4.675	-0.524	1.33	140.81	82.45
55	2jsa-5	GLU_A_10_N	GLU_A_10_H	0.538	4.675	-0.524	1.413	4.756	-1.022	1.01	119.54	5.29
56	2jsa-5	GLU_A_10_N	GLU_A_10_CA	0.538	4.675	-0.524	-0.591	5.482	-0.955	1.45	107.25	144.44
57	2jsa-5	GLU_A_10_CA	GLU_A_10_HA	-0.591	5.482	-0.955	-1.122	5.823	-0.066	1.09	35.37	147.29
58	2jsa-5	GLU_A_10_CA	GLU_A_10_C	-0.591	5.482	-0.955	-1.553	4.641	-1.798	1.53	123.41	-138.84
59	2jsa-5	GLU_A_10_C	GLU_A_10_O	-1.553	4.641	-1.798	-2.652	5.09	-2.125	1.23	105.40	157.78
60	2jsa-5	GLU_A_10_C	LEU_A_11_N	-1.553	4.641	-1.798	-1.106	3.438	-2.125	1.32	104.29	-69.62
61	2jsa-5	LEU_A_11_N	LEU_A_11_H	-1.106	3.438	-2.125	-0.191	3.135	-1.821	1.01	72.49	-18.32
62	2jsa-5	LEU_A_11_N	LEU_A_11_CA	-1.106	3.438	-2.125	-1.913	2.531	-2.923	1.45	123.32	-131.66
63	2jsa-5	LEU_A_11_CA	LEU_A_11_HA	-1.913	2.531	-2.923	-2.597	3.129	-3.525	1.09	123.53	138.84
64	2jsa-5	LEU_A_11_CA	LEU_A_11_C	-1.913	2.531	-2.923	-2.755	1.654	-1.995	1.53	52.65	-133.83
65	2jsa-5	LEU_A_11_C	LEU_A_11_O	-2.755	1.654	-1.995	-3.92	1.384	-2.278	1.23	103.31	-166.95
66	2jsa-5	LEU_A_11_C	VAL_A_12_N	-2.755	1.654	-1.995	-2.131	1.233	-0.904	1.33	34.60	-34.01
67	2jsa-5	VAL_A_12_N	VAL_A_12_H	-2.131	1.233	-0.904	-1.17	1.494	-0.735	1.01	80.37	15.19
68	2jsa-5	VAL_A_12_N	VAL_A_12_CA	-2.131	1.233	-0.904	-2.809	0.392	0.068	1.45	48.02	-128.88
69	2jsa-5	VAL_A_12_CA	VAL_A_12_HA	-2.809	0.392	0.068	-3.352	-0.386	-0.469	1.09	119.51	-124.91
70	2jsa-5	VAL_A_12_CA	VAL_A_12_C	-2.809	0.392	0.068	-3.825	1.232	0.844	1.53	59.52	140.42
71	2jsa-5	VAL_A_12_C	VAL_A_12_O	-3.825	1.232	0.844	-4.972	0.823	1.016	1.23	81.96	-160.37
72	2jsa-5	VAL_A_12_C	VAL_A_13_N	-3.825	1.232	0.844	-3.368	2.394	1.289	1.33	70.38	68.53
73	2jsa-5	VAL_A_13_N	VAL_A_13_H	-3.368	2.394	1.289	-2.412	2.668	1.109	1.01	100.26	15.99
74	2jsa-5	VAL_A_13_N	VAL_A_13_CA	-3.368	2.394	1.289	-4.224	3.295	2.041	1.45	58.82	133.53
75	2jsa-5	VAL_A_13_CA	VAL_A_13_HA	-4.224	3.295	2.041	-4.621	2.755	2.901	1.09	37.93	-126.32
76	2jsa-5	VAL_A_13_CA	VAL_A_13_C	-4.224	3.295	2.041	-5.401	3.724	1.166	1.53	124.93	159.97
77	2jsa-5	VAL_A_13_C	VAL_A_13_O	-5.401	3.724	1.166	-6.557	3.486	1.511	1.23	73.71	-168.37
78	2jsa-5	VAL_A_13_C	LYS_A_14_N	-5.401	3.724	1.166	-5.068	4.35	0.046	1.33	147.66	61.99
79	2jsa-5	LYS_A_14_N	LYS_A_14_H	-5.068	4.35	0.046	-4.096	4.512	-0.176	1.01	102.70	9.46
80	2jsa-5	LYS_A_14_N	LYS_A_14_CA	-5.068	4.35	0.046	-6.084	4.815	-0.883	1.45	129.74	155.41
81	2jsa-5	LYS_A_14_CA	LYS_A_14_HA	-6.084	4.815	-0.883	-6.587	5.671	-0.432	1.09	65.57	120.44
82	2jsa-5	LYS_A_14_CA	LYS_A_14_C	-6.084	4.815	-0.883	-7.128	3.714	-1.084	1.53	97.55	-133.48
83	2jsa-5	LYS_A_14_C	LYS_A_14_O	-7.128	3.714	-1.084	-8.303	4.001	-1.302	1.23	100.22	166.27
84	2jsa-5	LYS_A_14_C	LYS_A_15_N	-7.128	3.714	-1.084	-6.659	2.477	-1.002	1.33	86.45	-69.24
85	2jsa-5	LYS_A_15_N	LYS_A_15_H	-6.659	2.477	-1.002	-5.679	2.316	-0.819	1.01	79.56	-9.33
86	2jsa-5	LYS_A_15_N	LYS_A_15_CA	-6.659	2.477	-1.002	-7.537	1.332	-1.172	1.45	96.72	-127.48
87	2jsa-5	LYS_A_15_CA	LYS_A_15_HA	-7.537	1.332	-1.172	-8.247	1.566	-0.964	1.09	136.65	161.76
88	2jsa-5	LYS_A_15_CA	LYS_A_15_C	-7.537	1.332	-1.172	-8.333	1.11	-1.116	1.53	32.68	-164.42
89	2jsa-5	LYS_A_15_C	LYS_A_15_O	-8.333	1.11	0.116	-9.523	0.802	0.068	1.23	92.24	-165.49
90	2jsa-5	LYS_A_15_C	TYR_A_16_N	-8.333	1.11	0.116	-7.644	1.275	1.235	1.32	32.34	13.47
91	2jsa-5	TYR_A_16_N	TYR_A_16_H	-7.644	1.275	1.235	-6.666	1.528	1.198	1.01	92.10	14.50
92	2jsa-5	TYR_A_16_N	TYR_A_16_CA	-7.644	1.275	1.235	-8.272	1.096	2.534	1.45	26.69	-164.09
93	2jsa-5	TYR_A_16_CA	TYR_A_16_HA	-8.272	1.096	2.534	-8.897	0.203	2.532	1.09	90.11	-124.99
94	2jsa-5	TYR_A_16_CA	TYR_A_16_C	-8.272	1.096	2.534	-9.113	2.318	2.908	1.53	75.85	124.54
95	2jsa-5	TYR_A_16_C	TYR_A_16_O	-9.113	2.318	2.908	-10.341	2.253	2.909	1.23	89.95	-176.97
96	2jsa-5	TYR_A_16_C	GLU_A_17_N	-9.113	2.318	2.908	-8.419	3.403	3.219	1.32	76.42	57.40
97	2jsa-5	GLU_A_17_N	GLU_A_17_H	-8.419	3.403	3.219	-7.409	3.384	3.197	1.01	91.25	-1.08
98	2jsa-5	GLU_A_17_N	GLU_A_17_CA	-8.419	3.403	3.219	-9.086	4.637	3.595	1.45	74.99	118.39
99	2jsa-5	GLU_A_17_CA	GLU_A_17_HA	-9.086	4.637	3.595	-9.427	4.536	4.625	1.09	19.05	-163.50
100	2jsa-5	GLU_A_17_CA	GLU_A_17_C	-9.086	4.637	3.595	-10.309	4.872	2.704	1.53	125.58	169.12
101	2jsa-5	GLU_A_17_C	GLU_A_17_O	-10.309	4.872	2.704	-11.333	5.37	3.168	1.23	67.83	154.07
102	2jsa-5	GLU_A_17_C	GLY_A_18_N	-10.309	4.872	2.704	-10.16	4.502	1.44	1.33	162.49	-68.07
103	2jsa-5	GLY_A_18_N	GLY_A_18_H	-10.16	4.502	1.44	-9.288	4.099	1.127	1.01	108.05	-24.80
104	2jsa-5	GLY_A_18_N	GLY_A_18_CA	-10.16	4.502	1.44	-11.239	4.666	0.481	1.45	131.31	171.36
105	2jsa-5	GLY_A_18_CA	GLY_A_18_C	-11.239	4.666	0.481	-11.682	3.314	-0.082	1.53	111.59	-108.14
106	2jsa-5	GLY_A_18_C	GLY_A_18_O	-11.682	3.314	-0.082	-11.847	3.165	-1.291	1.23	169.58	-137.92
107	2jsa-5	GLY_A_18_C	SER_A_19_N	-11.682	3.314	-0.082	-11.863	2.363	0.823	1.33	46.93	-100.78
108	2jsa-5	SER_A_19_N	SER_A_19_H	-11.863	2.363	0.823	-11.709	2.557	1.802	1.01	14.20	51.56
109	2jsa-5	SER_A_19_N	SER_A_19_CA	-11.863	2.363	0.823	-12.285	1.028	0.432	1.45	105.60	-107.54
110	2jsa-5	SER_A_19_CA	SER_A_19_HA	-12.285	1.028	0.432	-11.978	0.861	-0.6	1.09	161.29	-28.55
111	2jsa-5	SER_A_19_CA	SER_A_19_C	-12.285	1.028	0.432	-13.808	0.916	0.515	1.53	86.89	-175.79
112	2jsa-5	SER_A_19_C	SER_A_19_O	-13.808	0.916	0.515	-14.455	0.489	-0.44	1.23	140.93	-146.58
113	2jsa-5	SER_A_19_C	ALA_A_20_N	-13.808	0.916	0.515	-14.337	1.305	1.666	1.33	29.70	143.67
114	2jsa-5	ALA_A_20_N	ALA_A_20_H	-14.337	1.305	1.666	-13.743	1.644	2.41	1.01	42.59	29.71
115	2jsa-5	ALA_A_20_N	ALA_A_20_CA	-14.337	1.305	1.666	-15.773	1.253	1.886	1.45	81.30	-177.93
116	2jsa-5	ALA_A_20_CA	ALA_A_20_HA	-15.773	1.253	1.886	-16.018	1.871	2.75	1.09	37.58	111.63
117	2jsa-5	ALA_A_20_CA	ALA_A_20_C	-15.773	1.253	1.886	-16.185	-0.189	2.189	1.53	78.58	-105.95
118	2jsa-5	ALA_A_20_C	ALA_A_20_O	-16.185	-0.189	2.189	-17.364	-0.47	2.398	1.23	80.22	-166.59
119	2jsa-5	ALA_A_20_C	ASP_A_21_N	-16.185	-0.189	2.189	-15.191	-1.065	2.204	1.33	89.35	-41.39
120	2jsa-5	ASP_A_21_N	ASP_A_21_H	-15.191	-1.065	2.204	-14.244	-0.763	2.023	1.01	100.32	17.69
121	2jsa-5	ASP_A_21_N	ASP_A_21_CA	-15.191	-1.065	2.204	-15.436	-2.47	2.478	1.45	79.12	-99.89
122	2jsa-5	ASP_A_21_CA	ASP_A_21_HA	-15.436	-2.47	2.478	-16.511	-2.645	2.505	1.09	88.58	-170.75
123	2jsa-5	ASP_A_21_CA	ASP_A_21_C	-15.436	-2.47	2.478	-14.816	-2.838	3.828	1.53	28.11	-30.69
124	2jsa-5	ASP_A_21_C	ASP_A_21_O	-14.816	-2.838	3.828	-15.078	-3.915	4.362	1.23	64.28	-103.67
125	2jsa-5	ASP_A_21_C	LYS_A_22_N	-14.816	-2.838	3.828	-14.006	-1.923	4.339	1.32	67.31	48.48
126	2jsa-5	LYS_A_22_N	LYS_A_22_H	-14.006	-1.923	4.339	-13.836	-1.059	3.844	1.01	119.34	78.87
127	2jsa-5	LYS_A_22_N	LYS_A_22_CA	-14.006	-1.923	4.339	-13.347	-2.139	5.617	1.45	28.49	-18.15
128	2jsa-5	LYS_A_22_CA	LYS_A_22_HA	-13.347	-2.139	5.617	-12.507	-1.447	5.685	1.09	86.42	39.48
129	2jsa-5	LYS_A_22_CA	LYS_A_22_C	-13.347	-2.139	5.617	-12.782	-3.559	5.661	1.53	88.35	-68.30
130	2jsa-5	LYS_A_22_C	LYS_A_22_O	-12.782	-3.559	5.661	-13.02	-4.295	6.617	1.23	38.98	-107.92
131	2jsa-5	LYS_A_22_C	ASP_A_23_N	-12.782	-3.559	5.661	-12.046	-3.902	4.615	1.32	142.18	-24.99
132	2jsa-5	ASP_A_23_N	ASP_A_23_H	-12.046	-3.902	4.615	-11.892	-3.245	3.863	1.01	138.10	76.81
133	2jsa-5	ASP_A_23_N	ASP_A_23_CA	-12.046	-3.902	4.615	-11.446	-5.223	4.523	1.45	93.63	-65.57
134	2jsa-5	ASP_A_23_CA	ASP_A_23_HA	-11.446	-5.223	4.523	-11.474	-5.696	5.505	1.09	25.76	-93.39
135	2jsa-5	ASP_A_23_CA	ASP_A_23_C	-11.446	-5.223	4.523	-9.997	-5.088	4.052	1.53	107.93	5.32
13												

138	2jsa-5	ALA_A_24_N	ALA_A_24_H	-9.081	-5.32	4.982	-9.36	-5.565	5.921	1.01	21.58	-138.71
139	2jsa-5	ALA_A_24_N	ALA_A_24_CA	-9.081	-5.32	4.982	-7.663	-5.227	4.676	1.45	102.15	3.75
140	2jsa-5	ALA_A_24_CA	ALA_A_24_HA	-7.663	-5.227	4.676	-7.46	-4.246	4.245	1.09	113.28	78.31
141	2jsa-5	ALA_A_24_CA	ALA_A_24_C	-7.663	-5.227	4.676	-7.299	-6.296	3.642	1.53	132.48	-71.20
142	2jsa-5	ALA_A_24_C	ALA_A_24_O	-7.299	-6.296	3.642	-6.2	-6.279	3.09	1.23	116.67	0.89
143	2jsa-5	ALA_A_24_C	ASN_A_25_N	-7.299	-6.296	3.642	-8.242	-7.198	3.413	1.32	99.95	-136.27
144	2jsa-5	ASN_A_25_N	ASN_A_25_H	-8.242	-7.198	3.413	-9.123	-7.149	3.905	1.01	60.86	176.82
145	2jsa-5	ASN_A_25_N	ASN_A_25_CA	-8.242	-7.198	3.413	-8.033	-8.271	2.456	1.45	131.20	-78.98
146	2jsa-5	ASN_A_25_CA	ASN_A_25_HA	-8.033	-8.271	2.456	-7.006	-8.627	2.538	1.09	85.69	-19.12
147	2jsa-5	ASN_A_25_CA	ASN_A_25_C	-8.033	-8.271	2.456	-8.289	-7.745	1.043	1.53	157.51	-115.95
148	2jsa-5	ASN_A_25_C	ASN_A_25_O	-8.289	-7.745	1.043	-7.467	-7.932	0.148	1.23	136.71	-12.82
149	2jsa-5	ASN_A_25_C	VAL_A_26_N	-8.289	-7.745	1.043	-9.434	-7.096	0.885	1.33	96.85	150.45
150	2jsa-5	VAL_A_26_N	VAL_A_26_H	-9.434	-7.096	0.885	-10.064	-6.979	1.666	1.01	39.37	169.48
151	2jsa-5	VAL_A_26_N	VAL_A_26_CA	-9.434	-7.096	0.885	-9.808	-6.541	-0.405	1.45	152.58	123.98
152	2jsa-5	VAL_A_26_CA	VAL_A_26_HA	-9.808	-6.541	-0.405	-9.537	-7.258	-1.18	1.09	135.32	-69.30
153	2jsa-5	VAL_A_26_CA	VAL_A_26_C	-9.808	-6.541	-0.405	-9.018	-5.255	-0.651	1.53	99.26	58.44
154	2jsa-5	VAL_A_26_C	VAL_A_26_O	-9.018	-5.255	-0.651	-9.067	-4.691	-1.743	1.23	152.60	94.97
155	2jsa-5	VAL_A_26_C	ILE_A_27_N	-9.018	-5.255	-0.651	-8.305	-4.83	0.383	1.33	38.76	30.80
156	2jsa-5	ILE_A_27_N	ILE_A_27_H	-8.305	-4.83	0.383	-8.309	-5.346	1.251	1.01	30.73	-90.44
157	2jsa-5	ILE_A_27_N	ILE_A_27_CA	-8.305	-4.83	0.383	-7.505	-3.621	0.292	1.45	93.59	56.51
158	2jsa-5	ILE_A_27_CA	ILE_A_27_HA	-7.505	-3.621	0.292	-7.969	-2.964	-0.443	1.09	132.42	125.23
159	2jsa-5	ILE_A_27_CA	ILE_A_27_C	-7.505	-3.621	0.292	-6.108	-3.976	-0.22	1.53	109.56	-14.26
160	2jsa-5	ILE_A_27_C	ILE_A_27_O	-6.108	-3.976	-0.22	-5.72	-3.567	-1.313	1.23	152.72	46.51
161	2jsa-5	ILE_A_27_C	LYS_A_28_N	-6.108	-3.976	-0.22	-5.389	-4.735	0.596	1.33	52.03	-46.55
162	2jsa-5	LYS_A_28_N	LYS_A_28_H	-5.389	-4.735	0.596	-5.771	-5.035	1.481	1.01	28.76	-141.86
163	2jsa-5	LYS_A_28_N	LYS_A_28_CA	-5.389	-4.735	0.596	-4.044	-5.15	0.239	1.45	104.23	-17.15
164	2jsa-5	LYS_A_28_CA	LYS_A_28_HA	-4.044	-5.15	0.239	-3.416	-4.26	0.197	1.09	92.21	54.79
165	2jsa-5	LYS_A_28_CA	LYS_A_28_C	-4.044	-5.15	0.239	-4.06	-5.774	-1.158	1.53	155.92	-91.47
166	2jsa-5	LYS_A_28_C	LYS_A_28_O	-4.06	-5.774	-1.158	-3.152	-5.543	-1.955	1.23	130.39	14.27
167	2jsa-5	LYS_A_28_C	LYS_A_29_N	-4.06	-5.774	-1.158	-5.103	-6.552	-1.412	1.33	101.05	-143.28
168	2jsa-5	LYS_A_29_N	LYS_A_29_H	-5.103	-6.552	-1.412	-5.812	-6.697	-0.708	1.01	45.79	-168.44
169	2jsa-5	LYS_A_29_N	LYS_A_29_CA	-5.103	-6.552	-1.412	-5.249	-7.21	-2.699	1.45	152.36	-102.51
170	2jsa-5	LYS_A_29_CA	LYS_A_29_HA	-5.249	-7.21	-2.699	-4.321	-7.741	-2.914	1.09	101.37	-29.78
171	2jsa-5	LYS_A_29_CA	LYS_A_29_C	-5.249	-7.21	-2.699	-5.443	-6.154	-3.789	1.53	135.43	100.41
172	2jsa-5	LYS_A_29_C	LYS_A_29_O	-5.443	-6.154	-3.789	-4.793	-6.206	-4.831	1.23	147.96	-4.57
173	2jsa-5	LYS_A_29_C	ASP_A_30_N	-5.443	-6.154	-3.789	-6.341	-5.22	-3.509	1.33	77.81	133.87
174	2jsa-5	ASP_A_30_N	ASP_A_30_H	-6.341	-5.22	-3.509	-6.84	-5.24	-2.631	1.01	29.63	-177.70
175	2jsa-5	ASP_A_30_N	ASP_A_30_CA	-6.341	-5.22	-3.509	-6.628	-4.153	-4.452	1.45	130.48	105.06
176	2jsa-5	ASP_A_30_CA	ASP_A_30_HA	-6.628	-4.153	-4.452	-7.164	-4.567	-5.306	1.09	141.58	-142.32
177	2jsa-5	ASP_A_30_CA	ASP_A_30_C	-6.628	-4.153	-4.452	-5.314	-3.523	-4.919	1.53	107.77	25.62
178	2jsa-5	ASP_A_30_C	ASP_A_30_O	-5.314	-3.523	-4.919	-5.071	-3.404	-6.119	1.23	167.29	26.09
179	2jsa-5	ASP_A_30_C	PHE_A_31_N	-5.314	-3.523	-4.919	-4.502	-3.135	-3.947	1.32	42.80	25.54
180	2jsa-5	PHE_A_31_N	PHE_A_31_H	-4.502	-3.135	-3.947	-4.768	-3.263	-2.981	1.01	16.99	-154.30
181	2jsa-5	PHE_A_31_N	PHE_A_31_CA	-4.502	-3.135	-3.947	-3.219	-2.521	-4.243	1.45	101.76	25.57
182	2jsa-5	PHE_A_31_CA	PHE_A_31_HA	-3.219	-2.521	-4.243	-3.366	-1.485	-4.549	1.09	106.30	98.08
183	2jsa-5	PHE_A_31_CA	PHE_A_31_C	-3.219	-2.521	-4.243	-2.487	-3.285	-5.349	1.53	136.27	-46.23
184	2jsa-5	PHE_A_31_C	PHE_A_31_O	-2.487	-3.285	-5.349	-2.126	-2.707	-6.374	1.23	146.38	58.01
185	2jsa-5	PHE_A_31_C	ASP_A_32_N	-2.487	-3.285	-5.349	-2.291	-4.572	-5.104	1.32	79.34	-81.34
186	2jsa-5	ASP_A_32_N	ASP_A_32_H	-2.291	-4.572	-5.104	-2.614	-4.98	-4.239	1.01	31.03	-128.37
187	2jsa-5	ASP_A_32_N	ASP_A_32_CA	-2.291	-4.572	-5.104	-1.61	-5.421	-6.066	1.45	131.47	-51.27
188	2jsa-5	ASP_A_32_CA	ASP_A_32_HA	-1.61	-5.421	-6.066	-0.604	-5.035	-6.232	1.09	98.76	20.99
189	2jsa-5	ASP_A_32_CA	ASP_A_32_C	-1.61	-5.421	-6.066	-2.39	-5.423	-7.383	1.53	149.36	-179.85
190	2jsa-5	ASP_A_32_C	ASP_A_32_O	-2.39	-5.423	-7.383	-1.828	-5.703	-8.44	1.23	149.29	-26.48
191	2jsa-5	ASP_A_32_C	ALA_A_33_N	-2.39	-5.423	-7.383	-3.672	-5.106	-7.274	1.33	85.28	166.11
192	2jsa-5	ALA_A_33_N	ALA_A_33_H	-3.672	-5.106	-7.274	-4.067	-4.888	-6.37	1.01	26.52	151.11
193	2jsa-5	ALA_A_33_N	ALA_A_33_CA	-3.672	-5.106	-7.274	-4.535	-5.066	-8.443	1.45	143.53	177.35
194	2jsa-5	ALA_A_33_CA	ALA_A_33_HA	-4.535	-5.066	-8.443	-4.374	-5.971	-9.029	1.09	122.52	-79.91
195	2jsa-5	ALA_A_33_CA	ALA_A_33_C	-4.535	-5.066	-8.443	-4.162	-3.858	-9.306	1.53	124.32	72.84
196	2jsa-5	ALA_A_33_C	ALA_A_33_O	-4.162	-3.858	-9.306	-3.727	-4.017	-10.446	1.23	157.89	-20.08
197	2jsa-5	ALA_A_33_C	GLU_A_34_N	-4.162	-3.858	-9.306	-4.346	-2.68	-8.73	1.32	64.21	98.88
198	2jsa-5	GLU_A_34_N	GLU_A_34_H	-4.346	-2.68	-8.73	-4.707	-2.626	-7.788	1.01	21.18	171.49
199	2jsa-5	GLU_A_34_N	GLU_A_34_CA	-4.346	-2.68	-8.73	-4.035	-1.447	-9.431	1.45	118.87	75.84
200	2jsa-5	GLU_A_34_CA	GLU_A_34_HA	-4.035	-1.447	-9.431	-4.676	-1.388	-10.31	1.09	143.78	174.74
201	2jsa-5	GLU_A_34_CA	GLU_A_34_C	-4.035	-1.447	-9.431	-2.579	-1.456	-9.899	1.53	107.82	-0.35
202	2jsa-5	GLU_A_34_C	GLU_A_34_O	-2.579	-1.456	-9.899	-2.29	-1.13	-11.051	1.23	159.28	48.44
203	2jsa-5	GLU_A_34_C	CYS_A_35_N	-2.579	-1.456	-9.899	-1.698	-1.832	-8.983	1.33	46.28	-23.11
204	2jsa-5	CYS_A_35_N	CYS_A_35_H	-1.698	-1.832	-8.983	-2.005	-2.087	-8.055	1.01	23.27	-140.29
205	2jsa-5	CYS_A_35_N	CYS_A_35_CA	-1.698	-1.832	-8.983	-0.278	-1.887	-9.289	1.45	102.15	-2.22
206	2jsa-5	CYS_A_35_CA	CYS_A_35_HA	-0.278	-1.887	-9.289	0.046	-0.892	-9.596	1.09	106.35	71.96
207	2jsa-5	CYS_A_35_CA	CYS_A_35_C	-0.278	-1.887	-9.289	-0.076	-2.849	-10.461	1.53	140.01	-78.14
208	2jsa-5	CYS_A_35_C	CYS_A_35_O	-0.076	-2.849	-10.461	0.617	-2.523	-11.424	1.23	141.51	25.19
209	2jsa-5	CYS_A_35_C	LYS_A_36_N	-0.076	-2.849	-10.461	-0.694	-4.016	-10.342	1.33	84.85	-117.90
210	2jsa-5	LYS_A_36_N	LYS_A_36_H	-0.694	-4.016	-10.342	-1.248	-4.217	-9.522	1.01	35.70	-160.06
211	2jsa-5	LYS_A_36_N	LYS_A_36_CA	-0.694	-4.016	-10.342	-0.59	-5.026	-11.38	1.45	135.63	-84.12
212	2jsa-5	LYS_A_36_CA	LYS_A_36_HA	-0.59	-5.026	-11.38	0.392	-5.493	-11.3	1.09	85.79	-25.43
213	2jsa-5	LYS_A_36_CA	LYS_A_36_C	-0.59	-5.026	-11.38	-0.674	-4.353	-12.752	1.53	153.70	97.11
214	2jsa-5	LYS_A_36_C	LYS_A_36_O	-0.674	-4.353	-12.752	0.014	-4.759	-13.688	1.23	139.52	-30.55
215	2jsa-5	LYS_A_36_C	LYS_A_37_N	-0.674	-4.353	-12.752	-1.521	-3.338	-12.826	1.32	93.20	129.84
216	2jsa-5	LYS_A_37_N	LYS_A_37_H	-1.521	-3.338	-12.826	-2.054	-3.06	-12.014	1.01	36.51	152.45
217	2jsa-5	LYS_A_37_N	LYS_A_37_CA	-1.521	-3.338	-12.826	-1.703	-2.605	-14.068	1.45	148.70	103.94
218	2jsa-5	LYS_A_37_CA	LYS_A_37_HA	-1.703	-2.605	-14.068	-1.39	-3.25	-14.889	1.09	138.87	-64.11
219	2jsa-5	LYS_A_37_CA	LYS_A_37_C	-1.703	-2.605	-14.068	-0.791	-1.376	-14.069	1.53	90.04	53.42
220	2jsa-5	LYS_A_37_C	LYS_A_37_O	-0.791	-1.376	-14.069	0.001	-1.186	-14.991	1.23	138.54	13.49
221	2jsa-5	LYS_A_37_C	LEU_A_38_N	-0.791	-1.376	-14.069	-0.933	-0.574	-13.024	1.32	37.93	100.04
222	2jsa-5	LEU_A_38_N	LEU_A_38_H	-0.933	-0.574	-13.024	-1.604	-0.792	-12.302	1.01	44.34	-162.00
223	2jsa-5	LEU_A_38_N	LEU_A_38_CA	-0.933	-0.574	-13.024	-0.131	0.631	-12.892	1.45	84.79	56.35
224	2jsa-5	LEU_A_38_CA	LEU_A_38_HA	-0.131	0.631	-12.892	-0.478	1.35	-13.634	1.09	132.90	115.76
225	2jsa-5	LEU_A_38_CA	LEU_A_38_C	-0.131	0.631	-12.892	1.329	0.305	-13.209	1.53	101.96	-12.59
226	2jsa-5	LEU_A_38_C	LEU_A_38_O	1.329	0.305	-13.209	1.98	1.025	-13.965	1.23	127.91	47.88
227	2jsa-5	LEU_A_38_C	PHE_A_39_N	1.329	0.305	-13.209	1.802	-0.782	-12.617	1.33	63.46	-66.48
228	2jsa-5	PHE_A_39_N	PHE_A_39_H	1.802	-0.782	-12.617	1.21	-1.328	-12.008	1		

231	2jsa-5	PHE_A_39_CA	PHE_A_39_C	3.174	-1.212	-12.828	3.22	-2.591	-13.49	1.53	115.63	-88.09
232	2jsa-5	PHE_A_39_C	PHE_A_39_O	3.22	-2.591	-13.49	4.019	-3.443	-13.102	1.23	71.62	-46.84
233	2jsa-5	PHE_A_39_C	HIS_A_40_N	3.22	-2.591	-13.49	2.353	-2.768	-14.477	1.33	138.12	-168.46
234	2jsa-5	HIS_A_40_N	HIS_A_40_H	2.353	-2.768	-14.477	1.725	-2.023	-14.742	1.01	105.21	130.13
235	2jsa-5	HIS_A_40_N	HIS_A_40_CA	2.353	-2.768	-14.477	2.286	-4.029	-15.195	1.45	119.62	-93.04
236	2jsa-5	HIS_A_40_CA	HIS_A_40_HA	2.286	-4.029	-15.195	2.237	-4.833	-14.46	1.09	47.62	-93.49
237	2jsa-5	HIS_A_40_CA	HIS_A_40_C	2.286	-4.029	-15.195	3.562	-4.221	-16.016	1.53	122.47	-8.56
238	2jsa-5	HIS_A_40_C	HIS_A_40_O	3.562	-4.221	-16.016	3.925	-5.347	-16.352	1.23	105.85	-72.13
239	2jsa-5	HIS_A_40_C	THR_A_41_N	3.562	-4.221	-16.016	4.209	-3.104	-16.315	1.33	103.04	59.92
240	2jsa-5	THR_A_41_N	THR_A_41_H	4.209	-3.104	-16.315	3.853	-2.211	-16.004	1.01	72.07	111.74
241	2jsa-5	THR_A_41_N	THR_A_41_CA	4.209	-3.104	-16.315	5.437	-3.135	-17.09	1.45	122.25	-1.45
242	2jsa-5	THR_A_41_CA	THR_A_41_HA	5.437	-3.135	-17.09	5.424	-4.017	-17.73	1.09	125.96	-90.84
243	2jsa-5	THR_A_41_CA	THR_A_41_C	5.437	-3.135	-17.09	6.65	-3.243	-16.164	1.53	52.75	-5.09
244	2jsa-5	THR_A_41_C	THR_A_41_O	6.65	-3.243	-16.164	7.562	-4.03	-16.418	1.23	101.91	-40.79
245	2jsa-5	THR_A_41_C	ILE_A_42_N	6.65	-3.243	-16.164	6.622	-2.442	-15.109	1.32	37.22	92.00
246	2jsa-5	ILE_A_42_N	ILE_A_42_H	6.622	-2.442	-15.109	5.839	-1.821	-14.962	1.01	81.63	141.58
247	2jsa-5	ILE_A_42_N	ILE_A_42_CA	6.622	-2.442	-15.109	7.708	-2.438	-14.143	1.45	48.35	0.21
248	2jsa-5	ILE_A_42_CA	ILE_A_42_HA	7.708	-2.438	-14.143	8.535	-1.869	-14.567	1.09	112.90	34.53
249	2jsa-5	ILE_A_42_CA	ILE_A_42_C	7.708	-2.438	-14.143	8.195	-3.871	-13.924	1.53	81.77	-71.23
250	2jsa-5	ILE_A_42_C	ILE_A_42_O	8.195	-3.871	-13.924	7.395	-4.805	-13.893	1.23	88.56	-130.58
251	2jsa-5	ILE_A_42_C	PRO_A_43_N	8.195	-3.871	-13.924	9.54	-4.005	-13.772	1.36	83.58	-5.69
252	2jsa-5	PRO_A_43_N	PRO_A_43_CA	9.54	-4.005	-13.772	10.143	-5.309	-13.557	1.45	81.49	-65.18
253	2jsa-5	PRO_A_43_CA	PRO_A_43_HA	10.143	-5.309	-13.557	9.716	-6.036	-14.247	1.09	129.30	-120.43
254	2jsa-5	PRO_A_43_CA	PRO_A_43_C	10.143	-5.309	-13.557	9.9	-5.796	-12.127	1.53	20.84	-116.52
255	2jsa-5	PRO_A_43_C	PRO_A_43_O	9.9	-5.796	-12.127	9.437	-6.917	-11.919	1.23	80.27	-112.44
256	2jsa-5	PRO_A_43_C	PHE_A_44_N	9.9	-5.796	-12.127	10.222	-4.929	-11.178	1.33	44.26	69.63
257	2jsa-5	PHE_A_44_N	PHE_A_44_H	10.222	-4.929	-11.178	10.598	-4.024	-11.422	1.01	103.98	67.44
258	2jsa-5	PHE_A_44_N	PHE_A_44_CA	10.222	-4.929	-11.178	10.044	-5.257	-9.773	1.45	14.88	-118.49
259	2jsa-5	PHE_A_44_CA	PHE_A_44_HA	10.044	-5.257	-9.773	9.866	-6.326	-9.662	1.09	84.15	-99.45
260	2jsa-5	PHE_A_44_CA	PHE_A_44_C	10.044	-5.257	-9.773	8.874	-4.475	-9.172	1.53	66.87	146.24
261	2jsa-5	PHE_A_44_C	PHE_A_44_O	8.874	-4.475	-9.172	8.905	-4.113	-7.996	1.23	17.17	85.11
262	2jsa-5	PHE_A_44_C	GLY_A_45_N	8.874	-4.475	-9.172	7.874	-4.235	-10.005	1.32	129.01	166.50
263	2jsa-5	GLY_A_45_N	GLY_A_45_H	7.874	-4.235	-10.005	7.919	-4.561	-10.96	1.01	160.99	-82.14
264	2jsa-5	GLY_A_45_N	GLY_A_45_CA	7.874	-4.235	-10.005	6.696	-3.502	-9.57	1.45	72.59	148.11
265	2jsa-5	GLY_A_45_CA	GLY_A_45_C	6.696	-3.502	-9.57	5.622	-4.454	-9.04	1.53	69.73	-138.45
266	2jsa-5	GLY_A_45_C	GLY_A_45_O	5.622	-4.454	-9.04	5.132	-4.285	-7.925	1.23	24.93	160.97
267	2jsa-5	GLY_A_45_C	THR_A_46_N	5.622	-4.454	-9.04	5.286	-5.434	-9.867	1.33	128.60	-108.92
268	2jsa-5	THR_A_46_N	THR_A_46_H	5.286	-5.434	-9.867	5.731	-5.512	-10.771	1.01	153.45	-9.94
269	2jsa-5	THR_A_46_N	THR_A_46_CA	5.286	-5.434	-9.867	4.278	-6.413	-9.496	1.45	75.21	-135.84
270	2jsa-5	THR_A_46_CA	THR_A_46_HA	4.278	-6.413	-9.496	3.418	-5.889	-9.078	1.09	67.46	148.65
271	2jsa-5	THR_A_46_CA	THR_A_46_C	4.278	-6.413	-9.496	4.822	-7.357	-8.422	1.53	45.41	-60.05
272	2jsa-5	THR_A_46_C	THR_A_46_O	4.822	-7.357	-8.422	4.073	-7.831	-7.57	1.23	46.13	-147.67
273	2jsa-5	THR_A_46_C	ARG_A_47_N	4.822	-7.357	-8.422	6.122	-7.602	-8.498	1.33	93.29	-10.67
274	2jsa-5	ARG_A_47_N	ARG_A_47_H	6.122	-7.602	-8.498	6.678	-7.177	-9.226	1.01	136.13	37.39
275	2jsa-5	ARG_A_47_N	ARG_A_47_CA	6.122	-7.602	-8.498	6.775	-8.482	-7.544	1.45	48.96	-53.42
276	2jsa-5	ARG_A_47_CA	ARG_A_47_HA	6.775	-8.482	-7.544	6.207	-9.41	-7.487	1.09	87.00	-121.47
277	2jsa-5	ARG_A_47_CA	ARG_A_47_C	6.775	-8.482	-7.544	6.807	-7.831	-6.159	1.53	25.20	87.19
278	2jsa-5	ARG_A_47_C	ARG_A_47_O	6.807	-7.831	-6.159	6.289	-8.391	-5.193	1.23	38.30	-132.77
279	2jsa-5	ARG_A_47_C	GLU_A_48_N	6.807	-7.831	-6.159	7.421	-6.658	-6.105	1.33	87.66	62.37
280	2jsa-5	GLU_A_48_N	GLU_A_48_H	7.421	-6.658	-6.105	7.824	-6.256	-6.939	1.01	145.69	44.93
281	2jsa-5	GLU_A_48_N	GLU_A_48_CA	7.421	-6.658	-6.105	7.528	-5.926	-4.856	1.45	30.64	81.68
282	2jsa-5	GLU_A_48_CA	GLU_A_48_HA	7.528	-5.926	-4.856	8.012	-6.574	-4.125	1.09	47.89	-53.24
283	2jsa-5	GLU_A_48_CA	GLU_A_48_C	7.528	-5.926	-4.856	6.137	-5.565	-4.332	1.53	69.97	165.45
284	2jsa-5	GLU_A_48_C	GLU_A_48_O	6.137	-5.565	-4.332	5.927	-5.481	-3.122	1.23	10.59	158.20
285	2jsa-5	GLU_A_48_C	CYS_A_49_N	6.137	-5.565	-4.332	5.222	-5.359	-5.268	1.33	134.94	167.31
286	2jsa-5	CYS_A_49_N	CYS_A_49_H	5.222	-5.359	-5.268	5.465	-5.444	-6.244	1.01	165.22	-19.28
287	2jsa-5	CYS_A_49_N	CYS_A_49_CA	5.222	-5.359	-5.268	3.856	-5.009	-4.915	1.45	75.95	165.63
288	2jsa-5	CYS_A_49_CA	CYS_A_49_HA	3.856	-5.009	-4.915	3.885	-4.153	-4.24	1.09	51.76	88.06
289	2jsa-5	CYS_A_49_CA	CYS_A_49_C	3.856	-5.009	-4.915	3.233	-6.193	-4.173	1.53	60.99	-117.75
290	2jsa-5	CYS_A_49_C	CYS_A_49_O	3.233	-6.193	-4.173	2.688	-6.029	-3.082	1.23	27.55	163.25
291	2jsa-5	CYS_A_49_C	ASP_A_50_N	3.233	-6.193	-4.173	3.334	-7.358	-4.795	1.32	118.01	-85.05
292	2jsa-5	ASP_A_50_N	ASP_A_50_H	3.334	-7.358	-4.795	3.796	-7.418	-5.691	1.01	152.53	-7.40
293	2jsa-5	ASP_A_50_N	ASP_A_50_CA	3.334	-7.358	-4.795	2.786	-8.57	-4.207	1.45	66.15	-114.33
294	2jsa-5	ASP_A_50_CA	ASP_A_50_HA	2.786	-8.57	-4.207	1.72	-8.429	-4.029	1.09	80.60	172.47
295	2jsa-5	ASP_A_50_CA	ASP_A_50_C	2.786	-8.57	-4.207	3.5	-8.858	-2.884	1.53	30.20	-21.97
296	2jsa-5	ASP_A_50_C	ASP_A_50_O	3.5	-8.858	-2.884	3.034	-9.67	-2.088	1.23	49.63	-119.85
297	2jsa-5	ASP_A_50_C	HIS_A_51_N	3.5	-8.858	-2.884	4.619	-8.176	-2.693	1.32	81.71	31.36
298	2jsa-5	HIS_A_51_N	HIS_A_51_H	4.619	-8.176	-2.693	4.944	-7.524	-3.393	1.01	133.86	63.51
299	2jsa-5	HIS_A_51_N	HIS_A_51_CA	4.619	-8.176	-2.693	5.403	-8.348	-1.48	1.45	33.49	-12.37
300	2jsa-5	HIS_A_51_CA	HIS_A_51_HA	5.403	-8.348	-1.48	5.035	-9.234	-0.964	1.09	61.73	-112.56
301	2jsa-5	HIS_A_51_CA	HIS_A_51_C	5.403	-8.348	-1.48	5.191	-7.146	-0.558	1.53	52.93	100.00
302	2jsa-5	HIS_A_51_C	HIS_A_51_O	5.191	-7.146	-0.558	5.783	-7.073	0.517	1.23	29.02	7.03
303	2jsa-5	HIS_A_51_C	TYR_A_52_N	5.191	-7.146	-0.558	4.346	-6.233	-1.014	1.32	110.13	132.78
304	2jsa-5	TYR_A_52_N	TYR_A_52_H	4.346	-6.233	-1.014	3.897	-6.358	-1.91	1.01	152.52	-164.44
305	2jsa-5	TYR_A_52_N	TYR_A_52_CA	4.346	-6.233	-1.014	4.049	-5.037	-0.242	1.45	57.93	103.95
306	2jsa-5	TYR_A_52_CA	TYR_A_52_HA	4.049	-5.037	-0.242	4.819	-4.874	0.513	1.09	46.19	11.95
307	2jsa-5	TYR_A_52_CA	TYR_A_52_C	4.049	-5.037	-0.242	2.679	-5.144	0.429	1.53	63.97	-175.53
308	2jsa-5	TYR_A_52_C	TYR_A_52_O	2.679	-5.144	0.429	2.518	-4.752	1.585	1.23	20.13	112.33
309	2jsa-5	TYR_A_52_C	VAL_A_53_N	2.679	-5.144	0.429	1.727	-5.677	-0.322	1.32	124.54	-150.76
310	2jsa-5	VAL_A_53_N	VAL_A_53_H	1.727	-5.677	-0.322	1.932	-5.978	-1.264	1.01	158.86	-55.74
311	2jsa-5	VAL_A_53_N	VAL_A_53_CA	1.727	-5.677	-0.322	0.376	-5.84	0.187	1.45	69.49	-173.12
312	2jsa-5	VAL_A_53_CA	VAL_A_53_HA	0.376	-5.84	0.187	-0.021	-4.855	0.433	1.09	76.96	111.95
313	2jsa-5	VAL_A_53_CA	VAL_A_53_C	0.376	-5.84	0.187	0.416	-6.669	1.471	1.53	32.88	-87.24
314	2jsa-5	VAL_A_53_C	VAL_A_53_O	0.416	-6.669	1.471	-0.537	-6.662	2.249	1.23	50.77	179.58
315	2jsa-5	VAL_A_53_C	ASN_A_54_N	0.416	-6.669	1.471	1.529	-7.364	1.655	1.33	82.02	-31.98
316	2jsa-5	ASN_A_54_N	ASN_A_54_H	1.529	-7.364	1.655	2.274	-7.322	0.974	1.01	132.38	3.23
317	2jsa-5	ASN_A_54_N	ASN_A_54_CA	1.529	-7.364	1.655	1.705	-8.197	2.833	1.45	35.86	-78.07
318	2jsa-5	ASN_A_54_CA	ASN_A_54_HA	1.705	-8.197	2.833	0.976	-7.905	3.589	1.09	46.09	158.17
319	2jsa-5	ASN_A_54_CA	ASN_A_54_C	1.705	-8.197	2.833	3.123	-8.009	3.377	1.53	69.18	7.55
320	2jsa-5	ASN_A_54_C	ASN_A_54_O	3.123	-8.009	3.377	3.947	-8.919	3.3	1.23	93.59	-47.84
321	2jsa-5	ASN_A_54_C	SER_A_55_N	3.123	-8.009	3.377	3.363	-6.822	3.915	1.33	66.05	78.57

324	2jsa-5	SER_A_55_CA	SER_A_55_HA	4.667	-6.504	4.472	4.863	-7.189	5.297	1.09	40.81	-74.03
325	2jsa-5	SER_A_55_CA	SER_A_55_C	4.667	-6.504	4.472	4.669	-5.072	5.012	1.53	69.34	89.92
326	2jsa-5	SER_A_55_C	SER_A_55_O	4.669	-5.072	5.012	5.311	-4.786	6.022	1.23	34.83	24.01
327	2jsa-5	SER_A_55_C	LYS_A_56_N	4.669	-5.072	5.012	3.945	-4.209	4.314	1.33	121.78	129.99
328	2jsa-5	LYS_A_56_N	LYS_A_56_H	3.945	-4.209	4.314	3.444	-4.514	3.492	1.01	144.49	-148.67
329	2jsa-5	LYS_A_56_N	LYS_A_56_CA	3.945	-4.209	4.314	3.855	-2.814	4.71	1.45	74.18	93.69
330	2jsa-5	LYS_A_56_CA	LYS_A_56_HA	3.855	-2.814	4.71	4.222	-2.73	5.733	1.09	20.20	12.89
331	2jsa-5	LYS_A_56_CA	LYS_A_56_C	3.855	-2.814	4.71	2.389	-2.38	4.706	1.53	90.15	163.51
332	2jsa-5	LYS_A_56_C	LYS_A_56_O	2.389	-2.38	4.706	2.089	-1.193	4.823	1.23	84.54	104.18
333	2jsa-5	LYS_A_56_C	VAL_A_57_N	2.389	-2.38	4.706	1.514	-3.365	4.567	1.32	96.02	-131.62
334	2jsa-5	VAL_A_57_N	VAL_A_57_H	1.514	-3.365	4.567	1.833	-4.319	4.474	1.01	95.28	-71.51
335	2jsa-5	VAL_A_57_N	VAL_A_57_CA	1.514	-3.365	4.567	0.085	-3.1	4.545	1.45	90.87	169.49
336	2jsa-5	VAL_A_57_CA	VAL_A_57_HA	0.085	-3.1	4.545	-0.067	-2.052	4.285	1.09	103.79	98.25
337	2jsa-5	VAL_A_57_CA	VAL_A_57_C	0.085	-3.1	4.545	-0.493	-3.331	5.942	1.53	24.02	-158.22
338	2jsa-5	VAL_A_57_C	VAL_A_57_O	-0.493	-3.331	5.942	-1.29	-2.528	6.429	1.23	66.71	134.79
339	2jsa-5	VAL_A_57_C	ASP_A_58_N	-0.493	-3.331	5.942	-0.072	-4.431	6.548	1.32	62.77	-69.06
340	2jsa-5	ASP_A_58_N	ASP_A_58_H	-0.072	-4.431	6.548	0.583	-5.047	6.087	1.01	117.14	-43.24
341	2jsa-5	ASP_A_58_N	ASP_A_58_CA	-0.072	-4.431	6.548	-0.538	-4.777	7.88	1.45	23.54	-143.41
342	2jsa-5	ASP_A_58_CA	ASP_A_58_HA	-0.538	-4.777	7.88	-1.599	-5.023	7.833	1.09	92.47	-166.95
343	2jsa-5	ASP_A_58_CA	ASP_A_58_C	-0.538	-4.777	7.88	-0.321	-3.587	8.817	1.53	52.24	79.67
344	2jsa-5	ASP_A_58_C	ASP_A_58_O	-0.321	-3.587	8.817	-1.204	-3.24	9.6	1.23	50.47	158.55
345	2jsa-5	ASP_A_58_C	PRO_A_59_N	-0.321	-3.587	8.817	0.891	-2.981	8.705	1.36	94.72	26.57
346	2jsa-5	PRO_A_59_N	PRO_A_59_CA	0.891	-2.981	8.705	1.236	-1.837	9.533	1.45	55.28	73.22
347	2jsa-5	PRO_A_59_CA	PRO_A_59_HA	1.236	-1.837	9.533	0.947	-2.024	10.567	1.09	18.41	-147.09
348	2jsa-5	PRO_A_59_CA	PRO_A_59_C	1.236	-1.837	9.533	0.52	-0.575	9.049	1.53	108.45	119.57
349	2jsa-5	PRO_A_59_C	PRO_A_59_O	0.52	-0.575	9.049	-0.157	0.096	9.828	1.23	50.74	135.26
350	2jsa-5	PRO_A_59_C	ILE_A_60_N	0.52	-0.575	9.049	0.693	-0.288	7.767	1.33	165.35	58.92
351	2jsa-5	ILE_A_60_N	ILE_A_60_H	0.693	-0.288	7.767	1.263	-0.885	7.185	1.01	125.19	-46.33
352	2jsa-5	ILE_A_60_N	ILE_A_60_CA	0.693	-0.288	7.767	0.072	0.882	7.171	1.45	114.23	117.96
353	2jsa-5	ILE_A_60_CA	ILE_A_60_HA	0.072	0.882	7.171	0.592	1.766	7.542	1.09	70.11	59.53
354	2jsa-5	ILE_A_60_CA	ILE_A_60_C	0.072	0.882	7.171	-1.385	0.971	7.631	1.53	72.51	176.50
355	2jsa-5	ILE_A_60_C	ILE_A_60_O	-1.385	0.971	7.631	-1.807	1.993	8.172	1.23	63.93	112.44
356	2jsa-5	ILE_A_60_C	ILE_A_61_N	-1.385	0.971	7.631	-2.112	-0.111	7.401	1.32	100.01	-123.90
357	2jsa-5	ILE_A_61_N	ILE_A_61_H	-2.112	-0.111	7.401	-1.698	-0.916	6.953	1.01	116.33	-62.78
358	2jsa-5	ILE_A_61_N	ILE_A_61_CA	-2.112	-0.111	7.401	-3.512	-0.168	7.785	1.45	74.67	-177.67
359	2jsa-5	ILE_A_61_CA	ILE_A_61_HA	-3.512	-0.168	7.785	-4.031	0.653	7.291	1.09	116.96	122.30
360	2jsa-5	ILE_A_61_CA	ILE_A_61_C	-3.512	-0.168	7.785	-3.631	0.048	9.295	1.53	9.28	118.85
361	2jsa-5	ILE_A_61_C	ILE_A_61_O	-3.631	0.048	9.295	-4.667	0.5	9.781	1.23	66.73	156.43
362	2jsa-5	ILE_A_61_C	HIS_A_62_N	-3.631	0.048	9.295	-2.556	-0.285	9.994	1.32	58.15	-17.21
363	2jsa-5	HIS_A_62_N	HIS_A_62_H	-2.556	-0.285	9.994	-1.738	-0.651	9.527	1.01	117.52	-24.11
364	2jsa-5	HIS_A_62_N	HIS_A_62_CA	-2.556	-0.285	9.994	-2.527	-0.133	11.439	1.45	6.11	79.20
365	2jsa-5	HIS_A_62_CA	HIS_A_62_HA	-2.527	-0.133	11.439	-3.427	-0.595	11.844	1.09	68.18	-152.83
366	2jsa-5	HIS_A_62_CA	HIS_A_62_C	-2.527	-0.133	11.439	-2.559	1.354	11.8	1.53	76.36	91.23
367	2jsa-5	HIS_A_62_C	HIS_A_62_O	-2.559	1.354	11.8	-2.922	1.718	12.916	1.23	24.73	134.92
368	2jsa-5	HIS_A_62_C	GLU_A_63_N	-2.559	1.354	11.8	-2.175	2.173	10.832	1.32	136.94	64.88
369	2jsa-5	GLU_A_63_N	GLU_A_63_H	-2.175	2.173	10.832	-1.89	1.803	9.936	1.01	152.47	-52.39
370	2jsa-5	GLU_A_63_N	GLU_A_63_CA	-2.175	2.173	10.832	-2.155	3.612	11.033	1.45	82.05	89.20
371	2jsa-5	GLU_A_63_CA	GLU_A_63_HA	-2.155	3.612	11.033	-1.941	3.803	12.085	1.09	15.25	41.75
372	2jsa-5	GLU_A_63_CA	GLU_A_63_C	-2.155	3.612	11.033	-3.522	4.213	10.703	1.53	102.46	156.27
373	2jsa-5	GLU_A_63_C	GLU_A_63_O	-3.522	4.213	10.703	-4.024	5.064	11.436	1.23	53.43	120.54
374	2jsa-5	GLU_A_63_C	LEU_A_64_N	-3.522	4.213	10.703	-4.087	3.748	9.599	1.32	146.46	-140.55
375	2jsa-5	LEU_A_64_N	LEU_A_64_H	-4.087	3.748	9.599	-3.616	3.048	9.043	1.01	123.38	-56.07
376	2jsa-5	LEU_A_64_N	LEU_A_64_CA	-4.087	3.748	9.599	-5.387	4.228	9.163	1.45	107.46	159.73
377	2jsa-5	LEU_A_64_CA	LEU_A_64_HA	-5.387	4.228	9.163	-5.357	5.318	9.151	1.09	90.63	88.42
378	2jsa-5	LEU_A_64_CA	LEU_A_64_C	-5.387	4.228	9.163	-6.45	3.804	10.178	1.53	48.43	-158.25
379	2jsa-5	LEU_A_64_C	LEU_A_64_O	-6.45	3.804	10.178	-7.342	4.584	10.511	1.23	74.30	138.83
380	2jsa-5	LEU_A_64_C	GLU_A_65_N	-6.45	3.804	10.178	-6.319	2.57	10.643	1.33	69.46	-83.94
381	2jsa-5	GLU_A_65_N	GLU_A_65_H	-6.319	2.57	10.643	-5.559	1.985	10.326	1.01	108.29	-37.59
382	2jsa-5	GLU_A_65_N	GLU_A_65_CA	-6.319	2.57	10.643	-7.258	2.033	11.614	1.45	48.09	-150.24
383	2jsa-5	GLU_A_65_CA	GLU_A_65_HA	-7.258	2.033	11.614	-8.267	2.215	11.245	1.09	109.79	169.78
384	2jsa-5	GLU_A_65_CA	GLU_A_65_C	-7.258	2.033	11.614	-7.101	2.75	12.957	1.53	28.66	77.65
385	2jsa-5	GLU_A_65_C	GLU_A_65_O	-7.101	2.75	12.957	-8.074	2.927	13.687	1.23	53.57	169.69
386	2jsa-5	GLU_A_65_C	GLY_A_66_N	-7.101	2.75	12.957	-5.868	3.142	13.241	1.32	77.62	17.64
387	2jsa-5	GLY_A_66_N	GLY_A_66_H	-5.868	3.142	13.241	-5.114	2.961	12.593	1.01	129.88	-13.50
388	2jsa-5	GLY_A_66_N	GLY_A_66_CA	-5.868	3.142	13.241	-5.571	3.836	14.482	1.45	31.31	66.83
389	2jsa-5	GLY_A_66_CA	GLY_A_66_C	-5.571	3.836	14.482	-6.2	5.231	14.495	1.53	89.51	114.27
390	2jsa-5	GLY_A_66_C	GLY_A_66_O	-6.2	5.231	14.495	-6.854	5.612	15.464	1.23	37.99	149.78
391	2jsa-5	GLY_A_66_C	GLY_A_67_N	-6.2	5.231	14.495	-5.978	5.955	13.407	1.33	145.16	72.95
392	2jsa-5	GLY_A_67_N	GLY_A_67_H	-5.978	5.955	13.407	-5.428	5.578	12.648	1.01	138.70	-34.43
393	2jsa-5	GLY_A_67_N	GLY_A_67_CA	-5.978	5.955	13.407	-6.516	7.299	13.281	1.45	94.97	111.82
394	2jsa-5	GLY_A_67_CA	GLY_A_67_C	-6.516	7.299	13.281	-5.772	8.087	12.201	1.53	134.90	46.65
395	2jsa-5	GLY_A_67_C	GLY_A_67_O	-5.772	8.087	12.201	-6.316	9.033	11.632	1.23	117.54	119.90
396	2jsa-5	GLY_A_67_C	THR_A_68_N	-5.772	8.087	12.201	-4.54	7.668	11.95	1.33	100.92	-18.78
397	2jsa-5	THR_A_68_N	THR_A_68_H	-4.54	7.668	11.95	-4.157	6.882	12.456	1.01	59.94	-64.02
398	2jsa-5	THR_A_68_N	THR_A_68_CA	-4.54	7.668	11.95	-3.716	8.324	10.948	1.45	133.57	38.52
399	2jsa-5	THR_A_68_CA	THR_A_68_HA	-3.716	8.324	10.948	-3.524	9.348	11.268	1.09	72.93	79.38
400	2jsa-5	THR_A_68_CA	THR_A_68_C	-3.716	8.324	10.948	-4.451	8.379	9.607	1.53	151.21	175.72
401	2jsa-5	THR_A_68_C	THR_A_68_O	-4.451	8.379	9.607	-5.257	7.503	9.301	1.23	104.42	-132.62
402	2jsa-5	THR_A_68_C	ALA_A_69_N	-4.451	8.379	9.607	-4.144	9.417	8.844	1.32	125.18	73.52
403	2jsa-5	ALA_A_69_N	ALA_A_69_H	-4.144	9.417	8.844	-3.471	10.1	9.161	1.01	71.71	45.42
404	2jsa-5	ALA_A_69_N	ALA_A_69_CA	-4.144	9.417	8.844	-4.765	9.597	7.542	1.45	153.59	163.84
405	2jsa-5	ALA_A_69_CA	ALA_A_69_HA	-4.765	9.597	7.542	-5.776	9.191	7.576	1.09	88.21	-158.12
406	2jsa-5	ALA_A_69_CA	ALA_A_69_C	-4.765	9.597	7.542	-3.968	8.823	6.49	1.53	133.44	-44.16
407	2jsa-5	ALA_A_69_C	ALA_A_69_O	-3.968	8.823	6.49	-2.851	8.381	6.753	1.23	77.65	-21.59
408	2jsa-5	ALA_A_69_C	PRO_A_70_N	-3.968	8.823	6.49	-4.59	8.679	5.289	1.36	152.00	-166.97
409	2jsa-5	PRO_A_70_N	PRO_A_70_CA	-4.59	8.679	5.289	-3.952	7.965	4.197	1.45	138.75	-48.22
410	2jsa-5	PRO_A_70_CA	PRO_A_70_HA	-3.952	7.965	4.197	-3.51	7.039	4.564	1.09	70.32	-64.48
411	2jsa-5	PRO_A_70_CA	PRO_A_70_C	-3.952	7.965	4.197	-2.847	8.811	3.562	1.53	114.53	37.44
412	2jsa-5	PRO_A_70_C	PRO_A_70_O	-2.847	8.811	3.562	-2.177	8.367	2.63	1.23	139.23	-33.53
413	2jsa-5	PRO_A_70_C	LYS_A_71_N	-2.847	8.811	3.562	-2.689	10.017	4.091	1.33	66.49	82.54
414	2jsa-5	LYS_A_71_N	LYS_A_71_H	-2.689	10.017	4.091	-3.275	10.318				

417	2jsa-5	LYS_A_71_CA	LYS_A_71_C	-1.677	10.928	3.587	-0.667	11.225	4.697	1.53	43.48	16.39
418	2jsa-5	LYS_A_71_C	LYS_A_71_O	-0.667	11.225	4.697	0.231	12.047	4.52	1.23	98.27	42.47
419	2jsa-5	LYS_A_71_C	ASP_A_72_N	-0.667	11.225	4.697	-0.848	10.541	5.817	1.32	32.28	-104.82
420	2jsa-5	ASP_A_72_N	ASP_A_72_H	-0.848	10.541	5.817	-1.609	9.882	5.893	1.01	85.68	-139.11
421	2jsa-5	ASP_A_72_N	ASP_A_72_CA	-0.848	10.541	5.817	0.036	10.721	6.956	1.45	38.38	11.51
422	2jsa-5	ASP_A_72_CA	ASP_A_72_HA	0.036	10.721	6.956	0.736	11.528	6.739	1.09	101.48	49.06
423	2jsa-5	ASP_A_72_CA	ASP_A_72_C	0.036	10.721	6.956	0.804	9.423	7.211	1.53	80.40	-59.39
424	2jsa-5	ASP_A_72_C	ASP_A_72_O	0.804	9.423	7.211	1.983	9.452	7.559	1.23	73.56	1.41
425	2jsa-5	ASP_A_72_C	VAL_A_73_N	0.804	9.423	7.211	0.102	8.313	7.028	1.33	97.93	-122.31
426	2jsa-5	VAL_A_73_N	VAL_A_73_H	0.102	8.313	7.028	-0.865	8.363	6.741	1.01	106.51	177.04
427	2jsa-5	VAL_A_73_N	VAL_A_73_CA	0.102	8.313	7.028	0.704	7.007	7.235	1.45	81.81	-65.25
428	2jsa-5	VAL_A_73_CA	VAL_A_73_HA	0.704	7.007	7.235	0.766	6.822	8.308	1.09	10.31	-71.47
429	2jsa-5	VAL_A_73_CA	VAL_A_73_C	0.704	7.007	7.235	2.126	7.009	6.671	1.53	111.63	0.08
430	2jsa-5	VAL_A_73_C	VAL_A_73_O	2.126	7.009	6.671	3.082	6.719	7.389	1.23	54.29	-16.88
431	2jsa-5	VAL_A_73_C	CYS_A_74_N	2.126	7.009	6.671	2.222	7.339	5.392	1.32	164.96	73.78
432	2jsa-5	CYS_A_74_N	CYS_A_74_H	2.222	7.339	5.392	1.393	7.567	4.862	1.01	121.65	164.62
433	2jsa-5	CYS_A_74_N	CYS_A_74_CA	2.222	7.339	5.392	3.511	7.383	4.724	1.45	117.38	1.96
434	2jsa-5	CYS_A_74_CA	CYS_A_74_HA	3.511	7.383	4.724	4.111	6.544	5.079	1.09	71.01	-54.43
435	2jsa-5	CYS_A_74_CA	CYS_A_74_C	3.511	7.383	4.724	4.212	8.684	5.119	1.53	75.04	61.68
436	2jsa-5	CYS_A_74_C	CYS_A_74_O	4.212	8.684	5.119	4.358	9.589	4.3	1.23	131.78	80.84
437	2jsa-5	CYS_A_74_C	THR_A_75_N	4.212	8.684	5.119	4.627	8.736	6.377	1.33	18.39	7.14
438	2jsa-5	THR_A_75_N	THR_A_75_H	4.627	8.736	6.377	4.473	7.954	6.997	1.01	52.12	-101.14
439	2jsa-5	THR_A_75_N	THR_A_75_CA	4.627	8.736	6.377	5.31	9.911	6.891	1.45	69.28	59.83
440	2jsa-5	THR_A_75_CA	THR_A_75_HA	5.31	9.911	6.891	6.202	10.088	6.29	1.09	123.46	11.22
441	2jsa-5	THR_A_75_CA	THR_A_75_C	5.31	9.911	6.891	5.755	9.68	8.337	1.53	19.12	-27.43
442	2jsa-5	THR_A_75_C	THR_A_75_O	5.755	9.68	8.337	6.943	9.509	8.604	1.23	77.46	-8.19
443	2jsa-5	THR_A_75_C	LYS_A_76_N	5.755	9.68	8.337	4.777	9.682	9.231	1.33	47.57	179.88
444	2jsa-5	LYS_A_76_N	LYS_A_76_H	4.777	9.682	9.231	3.822	9.83	8.94	1.01	106.76	171.19
445	2jsa-5	LYS_A_76_N	LYS_A_76_CA	4.777	9.682	9.231	5.053	9.473	10.641	1.45	13.80	-37.13
446	2jsa-5	LYS_A_76_CA	LYS_A_76_HA	5.053	9.473	10.641	5.971	10.008	10.888	1.09	76.91	30.23
447	2jsa-5	LYS_A_76_CA	LYS_A_76_C	5.053	9.473	10.641	5.301	7.985	10.895	1.53	80.44	-80.54
448	2jsa-5	LYS_A_76_C	LYS_A_76_O	5.301	7.985	10.895	6.192	7.622	11.66	1.23	51.51	-22.17
449	2jsa-5	LYS_A_76_C	LEU_A_77_N	5.301	7.985	10.895	4.495	7.164	10.237	1.33	119.77	-134.47
450	2jsa-5	LEU_A_77_N	LEU_A_77_H	4.495	7.164	10.237	3.784	7.533	9.623	1.01	127.47	152.57
451	2jsa-5	LEU_A_77_N	LEU_A_77_CA	4.495	7.164	10.237	4.615	5.723	10.382	1.45	84.27	-85.24
452	2jsa-5	LEU_A_77_CA	LEU_A_77_HA	4.615	5.723	10.382	4.44	5.473	11.429	1.09	16.25	-124.99
453	2jsa-5	LEU_A_77_CA	LEU_A_77_C	4.615	5.723	10.382	6.043	5.298	10.035	1.53	103.11	-16.57
454	2jsa-5	LEU_A_77_C	LEU_A_77_O	6.043	5.298	10.035	6.464	4.192	10.371	1.23	74.15	-69.16
455	2jsa-5	LEU_A_77_C	ASN_A_78_N	6.043	5.298	10.035	6.749	6.198	9.367	1.32	120.28	51.89
456	2jsa-5	ASN_A_78_N	ASN_A_78_H	6.749	6.198	9.367	6.338	7.088	9.124	1.01	103.92	114.79
457	2jsa-5	ASN_A_78_N	ASN_A_78_CA	6.749	6.198	9.367	8.122	5.93	8.971	1.45	105.81	-11.04
458	2jsa-5	ASN_A_78_CA	ASN_A_78_HA	8.122	5.93	8.971	8.615	6.872	8.731	1.09	102.72	62.37
459	2jsa-5	ASN_A_78_CA	ASN_A_78_C	8.122	5.93	8.971	8.124	5.015	7.745	1.53	143.26	-89.87
460	2jsa-5	ASN_A_78_C	ASN_A_78_O	8.124	5.015	7.745	8.72	3.938	7.771	1.23	88.79	-61.04
461	2jsa-5	ASN_A_78_C	GLU_A_79_N	8.124	5.015	7.745	7.451	5.475	6.7	1.33	142.04	145.65
462	2jsa-5	GLU_A_79_N	GLU_A_79_H	7.451	5.475	6.7	6.985	6.37	6.749	1.01	87.22	117.50
463	2jsa-5	GLU_A_79_N	GLU_A_79_CA	7.451	5.475	6.7	7.369	4.711	5.468	1.45	148.05	-96.13
464	2jsa-5	GLU_A_79_CA	GLU_A_79_HA	7.369	4.711	5.468	7.73	3.703	5.672	1.09	79.21	-70.30
465	2jsa-5	GLU_A_79_CA	GLU_A_79_C	7.369	4.711	5.468	8.265	5.335	4.396	1.53	134.47	34.85
466	2jsa-5	GLU_A_79_C	GLU_A_79_O	8.265	5.335	4.396	9.313	4.784	4.06	1.23	105.84	-27.73
467	2jsa-5	GLU_A_79_C	CYS_A_80_N	8.265	5.335	4.396	7.82	6.475	3.888	1.33	112.54	111.32
468	2jsa-5	CYS_A_80_N	CYS_A_80_H	7.82	6.475	3.888	6.949	6.871	4.211	1.01	71.35	155.55
469	2jsa-5	CYS_A_80_N	CYS_A_80_CA	7.82	6.475	3.888	8.57	7.179	2.862	1.45	134.93	43.19
470	2jsa-5	CYS_A_80_CA	CYS_A_80_HA	8.57	7.179	2.862	8.639	6.535	1.985	1.09	143.55	-83.88
471	2jsa-5	CYS_A_80_CA	CYS_A_80_C	8.57	7.179	2.862	9.983	7.436	3.388	1.53	69.88	10.31
472	2jsa-5	CYS_A_80_C	CYS_A_80_O	9.983	7.436	3.388	10.964	7.183	2.691	1.23	124.53	-14.46
473	2jsa-5	CYS_A_80_C	PRO_A_81_N	9.983	7.436	3.388	10.043	7.948	4.647	1.36	22.27	83.32
474	2jsa-5	PRO_A_81_N	PRO_A_81_CA	10.043	7.948	4.647	11.32	8.241	5.275	1.45	64.39	12.92
475	2jsa-5	PRO_A_81_CA	PRO_A_81_HA	11.32	8.241	5.275	11.972	8.758	4.571	1.09	130.23	38.41
476	2jsa-5	PRO_A_81_CA	PRO_A_81_C	11.32	8.241	5.275	12.016	6.957	5.727	1.53	72.80	-61.54
477	2jsa-5	PRO_A_81_C	PRO_A_81_O	12.016	6.957	5.727	11.808	6.496	6.849	1.23	24.26	-114.28
1	2jsa-6	ARG_A_1_N	ARG_A_1_H	14.712	1.733	-2.113	15.435	2.427	-2.244	1.01	97.45	43.83
2	2jsa-6	ARG_A_1_N	ARG_A_1_CA	14.712	1.733	-2.113	13.475	2.133	-1.465	1.45	63.51	162.08
3	2jsa-6	ARG_A_1_CA	ARG_A_1_HA	13.475	2.133	-1.465	12.653	1.967	-2.161	1.09	129.69	-168.58
4	2jsa-6	ARG_A_1_CA	ARG_A_1_C	13.475	2.133	-1.465	13.524	3.618	-1.098	1.53	76.13	88.11
5	2jsa-6	ARG_A_1_C	ARG_A_1_O	13.524	3.618	-1.098	14.266	4.014	-0.201	1.23	43.16	28.09
6	2jsa-6	ARG_A_1_C	SER_A_2_N	13.524	3.618	-1.098	12.724	4.398	-1.81	1.32	122.51	135.73
7	2jsa-6	SER_A_2_N	SER_A_2_H	12.724	4.398	-1.81	12.139	4.003	-2.532	1.01	135.65	-145.97
8	2jsa-6	SER_A_2_N	SER_A_2_CA	12.724	4.398	-1.81	12.668	5.829	-1.571	1.45	80.53	92.24
9	2jsa-6	SER_A_2_CA	SER_A_2_HA	12.668	5.829	-1.571	12.331	5.991	-0.547	1.09	20.06	154.33
10	2jsa-6	SER_A_2_CA	SER_A_2_C	12.668	5.829	-1.571	11.665	6.481	-2.525	1.53	128.57	146.97
11	2jsa-6	SER_A_2_C	SER_A_2_O	11.665	6.481	-2.525	11.961	7.507	-3.135	1.23	119.74	73.91
12	2jsa-6	SER_A_2_C	ALA_A_3_N	11.665	6.481	-2.525	10.501	5.857	-2.625	1.32	94.33	-151.81
13	2jsa-6	ALA_A_3_N	ALA_A_3_H	10.501	5.857	-2.625	10.328	5.016	-2.094	1.01	58.27	-101.62
14	2jsa-6	ALA_A_3_N	ALA_A_3_CA	10.501	5.857	-2.625	9.453	6.363	-3.496	1.45	126.81	154.23
15	2jsa-6	ALA_A_3_CA	ALA_A_3_HA	9.453	6.363	-3.496	9.03	7.263	-3.049	1.09	65.80	115.17
16	2jsa-6	ALA_A_3_CA	ALA_A_3_C	9.453	6.363	-3.496	8.345	5.315	-3.616	1.53	94.50	-136.59
17	2jsa-6	ALA_A_3_C	ALA_A_3_O	8.345	5.315	-3.616	7.275	5.467	-3.027	1.23	61.41	171.91
18	2jsa-6	ALA_A_3_C	LEU_A_4_N	8.345	5.315	-3.616	8.638	4.275	-4.382	1.32	125.33	-74.27
19	2jsa-6	LEU_A_4_N	LEU_A_4_H	8.638	4.275	-4.382	9.538	4.216	-4.836	1.01	116.72	-3.75
20	2jsa-6	LEU_A_4_N	LEU_A_4_CA	8.638	4.275	-4.382	7.68	3.202	-4.586	1.45	98.07	-131.76
21	2jsa-6	LEU_A_4_CA	LEU_A_4_HA	7.68	3.202	-4.586	6.938	3.546	-5.306	1.09	131.36	155.13
22	2jsa-6	LEU_A_4_CA	LEU_A_4_C	7.68	3.202	-4.586	6.953	2.915	-3.27	1.53	30.71	-158.46
23	2jsa-6	LEU_A_4_C	LEU_A_4_O	6.953	2.915	-3.27	5.738	3.078	-3.18	1.23	85.80	172.36
24	2jsa-6	LEU_A_4_C	SER_A_5_N	6.953	2.915	-3.27	7.73	2.492	-2.283	1.33	41.87	-28.56
25	2jsa-6	SER_A_5_N	SER_A_5_H	7.73	2.492	-2.283	8.724	2.381	-2.429	1.01	98.31	-6.37
26	2jsa-6	SER_A_5_N	SER_A_5_CA	7.73	2.492	-2.283	7.176	2.181	-0.976	1.45	25.92	-150.69
27	2jsa-6	SER_A_5_CA	SER_A_5_HA	7.176	2.181	-0.976	6.705	1.2	-1.029	1.09	92.79	-115.65
28	2jsa-6	SER_A_5_CA	SER_A_5_C	7.176	2.181	-0.976	6.113	3.216	-0.599	1.53	75.74	135.76
29	2jsa-6	SER_A_5_C	SER_A_5_O	6.113	3.216	-0.599	4.966	2.862	-0.332	1.23	77.46	-162.85
30	2jsa-6	SER_A_5_C	CYS_A_6_N	6.113	3.216	-0.599	6.533	4.471	-0.589	1.32	89.57	71.50
31	2jsa-6	CYS_A_6_N	CYS_A_6_H	6.533	4.471	-0.589	7					

33	2jsa-6	CYS_A_6_CA	CYS_A_6_HA	5.632	5.559	-0.248	5.326	5.438	0.791	1.09	17.57	-158.42
34	2jsa-6	CYS_A_6_CA	CYS_A_6_C	5.632	5.559	-0.248	4.391	5.451	-1.137	1.53	125.51	-175.03
35	2jsa-6	CYS_A_6_C	CYS_A_6_O	4.391	5.451	-1.137	3.301	5.156	-0.654	1.23	66.84	-164.86
36	2jsa-6	CYS_A_6_C	GLN_A_7_N	4.391	5.451	-1.137	4.601	5.698	-2.423	1.33	165.85	49.63
37	2jsa-6	GLN_A_7_N	GLN_A_7_H	4.601	5.698	-2.423	5.526	5.938	-2.751	1.01	108.94	14.55
38	2jsa-6	GLN_A_7_N	GLN_A_7_CA	4.601	5.698	-2.423	3.514	5.631	-3.384	1.45	131.43	-176.47
39	2jsa-6	GLN_A_7_CA	GLN_A_7_HA	3.514	5.631	-3.384	2.926	6.544	-3.29	1.09	85.05	122.78
40	2jsa-6	GLN_A_7_CA	GLN_A_7_C	3.514	5.631	-3.384	2.605	4.44	-3.076	1.53	78.38	-127.35
41	2jsa-6	GLN_A_7_C	GLN_A_7_O	2.605	4.44	-3.076	1.401	4.606	-2.883	1.23	80.98	172.15
42	2jsa-6	GLN_A_7_C	MET_A_8_N	2.605	4.44	-3.076	3.215	3.265	-3.041	1.32	88.49	-62.56
43	2jsa-6	MET_A_8_N	MET_A_8_H	3.215	3.265	-3.041	4.209	3.203	-3.212	1.01	99.74	-3.57
44	2jsa-6	MET_A_8_N	MET_A_8_CA	3.215	3.265	-3.041	2.476	2.045	-2.76	1.45	78.86	-121.20
45	2jsa-6	MET_A_8_CA	MET_A_8_HA	2.476	2.045	-2.76	1.889	1.782	-3.639	1.09	143.80	-155.87
46	2jsa-6	MET_A_8_CA	MET_A_8_C	2.476	2.045	-2.76	1.532	2.238	-1.572	1.53	39.04	168.45
47	2jsa-6	MET_A_8_C	MET_A_8_O	1.532	2.238	-1.572	0.488	1.593	-1.493	1.23	86.32	-148.29
48	2jsa-6	MET_A_8_C	CYS_A_9_N	1.532	2.238	-1.572	1.933	3.129	-0.677	1.33	47.51	65.77
49	2jsa-6	CYS_A_9_N	CYS_A_9_H	1.933	3.129	-0.677	2.804	3.625	-0.807	1.01	97.39	29.66
50	2jsa-6	CYS_A_9_N	CYS_A_9_CA	1.933	3.129	-0.677	1.137	3.414	0.505	1.45	35.58	160.30
51	2jsa-6	CYS_A_9_CA	CYS_A_9_HA	1.137	3.414	0.505	0.897	2.469	0.993	1.09	63.41	-104.25
52	2jsa-6	CYS_A_9_CA	CYS_A_9_C	1.137	3.414	0.505	-0.168	4.076	0.055	1.53	107.09	153.10
53	2jsa-6	CYS_A_9_C	CYS_A_9_O	-0.168	4.076	0.055	-1.245	3.726	0.537	1.23	66.94	-162.00
54	2jsa-6	CYS_A_9_C	GLU_A_10_N	-0.168	4.076	0.055	-0.029	5.022	-0.863	1.33	133.83	81.64
55	2jsa-6	GLU_A_10_N	GLU_A_10_H	-0.029	5.022	-0.863	0.888	5.258	-1.215	1.01	110.39	14.43
56	2jsa-6	GLU_A_10_N	GLU_A_10_CA	-0.029	5.022	-0.863	-1.183	5.736	-1.382	1.45	110.93	148.25
57	2jsa-6	GLU_A_10_CA	GLU_A_10_HA	-1.183	5.736	-1.382	-1.755	6.113	-0.535	1.09	38.97	146.61
58	2jsa-6	GLU_A_10_CA	GLU_A_10_C	-1.183	5.736	-1.382	-2.077	4.788	-2.183	1.53	121.58	-133.32
59	2jsa-6	GLU_A_10_C	GLU_A_10_O	-2.077	4.788	-2.183	-3.185	5.154	-2.572	1.23	108.44	161.72
60	2jsa-6	GLU_A_10_C	LEU_A_11_N	-2.077	4.788	-2.183	-1.563	3.587	-2.405	1.33	99.64	-66.83
61	2jsa-6	LEU_A_11_N	LEU_A_11_H	-1.563	3.587	-2.405	-0.645	3.354	-2.054	1.01	69.67	-14.24
62	2jsa-6	LEU_A_11_N	LEU_A_11_CA	-1.563	3.587	-2.405	-2.302	2.584	-3.153	1.45	120.98	-126.38
63	2jsa-6	LEU_A_11_CA	LEU_A_11_HA	-2.302	2.584	-3.153	-2.998	3.1	-3.813	1.09	127.30	143.45
64	2jsa-6	LEU_A_11_CA	LEU_A_11_C	-2.302	2.584	-3.153	-3.124	1.734	-2.182	1.53	50.61	-134.04
65	2jsa-6	LEU_A_11_C	LEU_A_11_O	-3.124	1.734	-2.182	-4.329	1.564	-2.368	1.23	98.69	-171.97
66	2jsa-6	LEU_A_11_C	VAL_A_12_N	-3.124	1.734	-2.182	-2.441	1.223	-1.169	1.32	40.10	-36.80
67	2jsa-6	VAL_A_12_N	VAL_A_12_H	-2.441	1.223	-1.169	-1.451	1.405	-1.079	1.01	84.89	10.42
68	2jsa-6	VAL_A_12_N	VAL_A_12_CA	-2.441	1.223	-1.169	-3.093	0.394	-0.169	1.45	46.52	-128.18
69	2jsa-6	VAL_A_12_CA	VAL_A_12_HA	-3.093	0.394	-0.169	-3.6	-0.426	-0.678	1.09	117.83	-121.73
70	2jsa-6	VAL_A_12_CA	VAL_A_12_C	-3.093	0.394	-0.169	-4.149	1.225	0.565	1.53	61.36	141.80
71	2jsa-6	VAL_A_12_C	VAL_A_12_O	-4.149	1.225	0.565	-5.282	0.78	0.739	1.23	81.86	-158.56
72	2jsa-6	VAL_A_12_C	VAL_A_13_N	-4.149	1.225	0.565	-3.738	2.415	0.976	1.32	71.92	70.95
73	2jsa-6	VAL_A_13_N	VAL_A_13_H	-3.738	2.415	0.976	-2.79	2.715	0.799	1.01	100.09	17.56
74	2jsa-6	VAL_A_13_N	VAL_A_13_CA	-3.738	2.415	0.976	-4.634	3.311	1.687	1.45	60.70	135.00
75	2jsa-6	VAL_A_13_CA	VAL_A_13_HA	-4.634	3.311	1.687	-4.992	2.801	2.581	1.09	34.88	-125.07
76	2jsa-6	VAL_A_13_CA	VAL_A_13_C	-4.634	3.311	1.687	-5.842	3.625	0.803	1.53	125.31	165.43
77	2jsa-6	VAL_A_13_C	VAL_A_13_O	-5.842	3.625	0.803	-6.983	3.38	1.193	1.23	71.52	-167.88
78	2jsa-6	VAL_A_13_C	LYS_A_14_N	-5.842	3.625	0.803	-5.551	4.162	-0.373	1.33	152.55	61.55
79	2jsa-6	LYS_A_14_N	LYS_A_14_H	-5.551	4.162	-0.373	-4.589	4.336	-0.629	1.01	104.67	10.25
80	2jsa-6	LYS_A_14_N	LYS_A_14_CA	-5.551	4.162	-0.373	-6.6	4.512	-1.316	1.45	130.46	161.55
81	2jsa-6	LYS_A_14_CA	LYS_A_14_HA	-6.6	4.512	-1.316	-7.104	5.404	-0.944	1.09	70.04	119.47
82	2jsa-6	LYS_A_14_CA	LYS_A_14_C	-6.6	4.512	-1.316	-7.631	3.382	-1.368	1.53	91.95	-132.38
83	2jsa-6	LYS_A_14_C	LYS_A_14_O	-7.631	3.382	-1.368	-8.824	3.633	-1.528	1.23	97.48	168.12
84	2jsa-6	LYS_A_14_C	LYS_A_15_N	-7.631	3.382	-1.368	-7.132	2.163	-1.232	1.32	84.11	-67.74
85	2jsa-6	LYS_A_15_N	LYS_A_15_H	-7.132	2.163	-1.232	-6.138	2.031	-1.105	1.01	82.78	-7.56
86	2jsa-6	LYS_A_15_N	LYS_A_15_CA	-7.132	2.163	-1.232	-7.995	0.994	-1.262	1.45	91.18	-126.44
87	2jsa-6	LYS_A_15_CA	LYS_A_15_HA	-7.995	0.994	-1.262	-8.76	1.158	-2.02	1.09	134.09	167.90
88	2jsa-6	LYS_A_15_CA	LYS_A_15_C	-7.995	0.994	-1.262	-8.7	0.852	0.088	1.53	28.04	-168.61
89	2jsa-6	LYS_A_15_C	LYS_A_15_O	-8.7	0.852	0.088	-9.884	0.522	0.142	1.23	87.48	-164.43
90	2jsa-6	LYS_A_15_C	TYR_A_16_N	-8.7	0.852	0.088	-7.943	1.107	1.146	1.33	37.05	18.62
91	2jsa-6	TYR_A_16_N	TYR_A_16_H	-7.943	1.107	1.146	-6.975	1.371	1.027	1.01	96.76	15.26
92	2jsa-6	TYR_A_16_N	TYR_A_16_CA	-7.943	1.107	1.146	-8.482	1.012	2.492	1.45	22.13	-170.00
93	2jsa-6	TYR_A_16_CA	TYR_A_16_HA	-8.482	1.012	2.492	-9.068	0.1	2.6	1.09	84.31	-122.72
94	2jsa-6	TYR_A_16_CA	TYR_A_16_C	-8.482	1.012	2.492	-9.348	2.228	2.823	1.53	77.50	125.46
95	2jsa-6	TYR_A_16_C	TYR_A_16_O	-9.348	2.228	2.823	-10.571	2.121	2.904	1.23	86.23	-175.00
96	2jsa-6	TYR_A_16_C	GLU_A_17_N	-9.348	2.228	2.823	-8.681	3.358	3.006	1.32	82.06	59.45
97	2jsa-6	GLU_A_17_N	GLU_A_17_H	-8.681	3.358	3.006	-7.674	3.373	2.924	1.01	94.65	0.85
98	2jsa-6	GLU_A_17_N	GLU_A_17_CA	-8.681	3.358	3.006	-9.376	4.595	3.326	1.45	77.29	119.33
99	2jsa-6	GLU_A_17_CA	GLU_A_17_HA	-9.376	4.595	3.326	-9.646	4.566	4.382	1.09	14.42	-173.87
100	2jsa-6	GLU_A_17_CA	GLU_A_17_C	-9.376	4.595	3.326	-10.661	4.71	2.504	1.53	122.50	174.89
101	2jsa-6	GLU_A_17_C	GLU_A_17_O	-10.661	4.71	2.504	-11.678	5.192	2.999	1.23	66.26	154.64
102	2jsa-6	GLU_A_17_C	GLY_A_18_N	-10.661	4.71	2.504	-10.573	4.259	1.261	1.33	159.71	-78.96
103	2jsa-6	GLY_A_18_N	GLY_A_18_H	-10.573	4.259	1.261	-9.703	3.875	0.92	1.01	109.73	-23.82
104	2jsa-6	GLY_A_18_N	GLY_A_18_CA	-10.573	4.259	1.261	-11.716	4.305	0.365	1.45	128.07	177.70
105	2jsa-6	GLY_A_18_CA	GLY_A_18_C	-11.716	4.305	0.365	-12.088	2.904	-0.122	1.53	108.57	-104.87
106	2jsa-6	GLY_A_18_C	GLY_A_18_O	-12.088	2.904	-0.122	-12.307	2.696	-1.314	1.23	165.78	-136.48
107	2jsa-6	GLY_A_18_C	SER_A_19_N	-12.088	2.904	-0.122	-12.149	1.98	0.825	1.32	44.36	-93.78
108	2jsa-6	SER_A_19_N	SER_A_19_H	-12.149	1.98	0.825	-11.957	2.224	1.787	1.01	17.89	51.80
109	2jsa-6	SER_A_19_N	SER_A_19_CA	-12.149	1.98	0.825	-12.491	0.603	0.507	1.45	102.63	-103.95
110	2jsa-6	SER_A_19_CA	SER_A_19_HA	-12.491	0.603	0.507	-12.083	0.368	-0.476	1.09	154.41	-29.94
111	2jsa-6	SER_A_19_CA	SER_A_19_C	-12.491	0.603	0.507	-14.011	0.44	0.459	1.53	91.80	-173.88
112	2jsa-6	SER_A_19_C	SER_A_19_O	-14.011	0.44	0.459	-14.552	-0.089	-0.51	1.23	142.02	-135.64
113	2jsa-6	SER_A_19_C	ALA_A_20_N	-14.011	0.44	0.459	-14.657	0.904	1.519	1.33	36.88	144.31
114	2jsa-6	ALA_A_20_N	ALA_A_20_H	-14.657	0.904	1.519	-14.146	1.327	2.281	1.01	41.04	39.62
115	2jsa-6	ALA_A_20_N	ALA_A_20_CA	-14.657	0.904	1.519	-16.105	0.815	1.61	1.45	86.41	-176.48
116	2jsa-6	ALA_A_20_CA	ALA_A_20_HA	-16.105	0.815	1.61	-16.458	1.57	2.313	1.09	49.85	115.06
117	2jsa-6	ALA_A_20_CA	ALA_A_20_C	-16.105	0.815	1.61	-16.495	-0.564	2.145	1.53	69.53	-105.79
118	2jsa-6	ALA_A_20_C	ALA_A_20_O	-16.495	-0.564	2.145	-17.66	-0.808	2.455	1.23	75.40	-168.17
119	2jsa-6	ALA_A_20_C	ASP_A_21_N	-16.495	-0.564	2.145	-15.497	-1.432	2.237	1.33	86.02	-41.01
120	2jsa-6	ASP_A_21_N	ASP_A_21_H	-15.497	-1.432	2.237	-14.562	-1.164	1.963	1.01	105.73	15.99
121	2jsa-6	ASP_A_21_N	ASP_A_21_CA	-15.497	-1.432	2.237	-15.721	-2.78	2.73	1.45	70.16	-99.43
122	2jsa-6	ASP_A_21_CA	ASP_A_21_HA	-15.721	-2.78	2.73	-16.789	-2.928	2.891	1.09	81.51	-172.11
123	2jsa-6	ASP_A_21_CA	ASP_A_21_C	-15.721	-2.78	2.73	-14.966	-2.969	4.047	1.53	30.58	-14.05
124	2jsa-6	ASP_A_21_C	ASP_A_21_O	-14.								

126	2jsa-6	LYS_A_22_N	LYS_A_22_H	-14.058	-2.042	4.31	-13.904	-1.282	3.663	1.01	129.84	78.55
127	2jsa-6	LYS_A_22_N	LYS_A_22_CA	-14.058	-2.042	4.31	-13.266	-2.094	5.527	1.45	33.11	-3.76
128	2jsa-6	LYS_A_22_CA	LYS_A_22_HA	-13.266	-2.094	5.527	-12.429	-1.404	5.415	1.09	95.89	39.50
129	2jsa-6	LYS_A_22_CA	LYS_A_22_C	-13.266	-2.094	5.527	-12.689	-3.501	5.695	1.53	83.70	-67.70
130	2jsa-6	LYS_A_22_C	LYS_A_22_O	-12.689	-3.501	5.695	-13.075	-4.229	6.608	1.23	42.07	-117.93
131	2jsa-6	LYS_A_22_C	ASP_A_23_N	-12.689	-3.501	5.695	-11.776	-3.843	4.798	1.32	132.62	-20.54
132	2jsa-6	ASP_A_23_N	ASP_A_23_H	-11.776	-3.843	4.798	-11.508	-3.194	4.072	1.01	135.96	67.56
133	2jsa-6	ASP_A_23_N	ASP_A_23_CA	-11.776	-3.843	4.798	-11.143	-5.15	4.836	1.45	88.50	-64.16
134	2jsa-6	ASP_A_23_CA	ASP_A_23_HA	-11.143	-5.15	4.836	-11.09	-5.491	5.87	1.09	18.46	-81.17
135	2jsa-6	ASP_A_23_CA	ASP_A_23_C	-11.143	-5.15	4.836	-9.733	-5.046	4.25	1.53	112.51	4.22
136	2jsa-6	ASP_A_23_C	ASP_A_23_O	-9.733	-5.046	4.25	-9.568	-4.742	3.069	1.23	163.68	61.51
137	2jsa-6	ASP_A_23_C	ALA_A_24_N	-9.733	-5.046	4.25	-8.752	-5.304	5.103	1.33	49.94	-14.73
138	2jsa-6	ALA_A_24_N	ALA_A_24_H	-8.752	-5.304	5.103	-8.961	-5.547	6.061	1.01	18.50	-130.70
139	2jsa-6	ALA_A_24_N	ALA_A_24_CA	-8.752	-5.304	5.103	-7.362	-5.243	4.684	1.45	106.76	2.51
140	2jsa-6	ALA_A_24_CA	ALA_A_24_HA	-7.362	-5.243	4.684	-7.181	-4.279	4.208	1.09	115.89	79.37
141	2jsa-6	ALA_A_24_CA	ALA_A_24_C	-7.362	-5.243	4.684	-7.093	-6.347	3.66	1.53	132.02	-76.31
142	2jsa-6	ALA_A_24_C	ALA_A_24_O	-7.093	-6.347	3.66	-6.026	-6.385	3.048	1.23	119.82	-2.04
143	2jsa-6	ALA_A_24_C	ASN_A_25_N	-7.093	-6.347	3.66	-8.078	-7.22	3.505	1.33	96.72	-138.45
144	2jsa-6	ASN_A_25_N	ASN_A_25_H	-8.078	-7.22	3.505	-8.927	-7.128	4.043	1.01	57.29	173.82
145	2jsa-6	ASN_A_25_N	ASN_A_25_CA	-8.078	-7.22	3.505	-7.962	-8.322	2.565	1.45	130.31	-83.99
146	2jsa-6	ASN_A_25_CA	ASN_A_25_HA	-7.962	-8.322	2.565	-6.943	-8.71	2.595	1.09	88.42	-20.85
147	2jsa-6	ASN_A_25_CA	ASN_A_25_C	-7.962	-8.322	2.565	-8.286	-7.821	1.156	1.53	157.05	122.89
148	2jsa-6	ASN_A_25_C	ASN_A_25_O	-8.286	-7.821	1.156	-7.528	-8.061	0.219	1.23	139.68	-17.57
149	2jsa-6	ASN_A_25_C	VAL_A_26_N	-8.286	-7.821	1.156	-9.415	-7.135	1.051	1.33	94.54	148.72
150	2jsa-6	VAL_A_26_N	VAL_A_26_H	-9.415	-7.135	1.051	-9.99	-6.976	1.865	1.01	36.24	164.54
151	2jsa-6	VAL_A_26_N	VAL_A_26_CA	-9.415	-7.135	1.051	-9.849	-6.599	-0.226	1.45	151.63	129.00
152	2jsa-6	VAL_A_26_CA	VAL_A_26_HA	-9.849	-6.599	-0.226	-9.652	-7.345	-0.996	1.09	134.94	-75.21
153	2jsa-6	VAL_A_26_CA	VAL_A_26_C	-9.849	-6.599	-0.226	-9.03	-5.35	-0.556	1.53	102.46	56.75
154	2jsa-6	VAL_A_26_C	VAL_A_26_O	-9.03	-5.35	-0.556	-9.104	-4.83	-1.668	1.23	154.72	98.10
155	2jsa-6	VAL_A_26_C	ILE_A_27_N	-9.03	-5.35	-0.556	-8.267	-4.904	0.432	1.33	41.81	30.31
156	2jsa-6	ILE_A_27_N	ILE_A_27_H	-8.267	-4.904	0.432	-8.254	-5.383	1.321	1.01	28.32	-88.45
157	2jsa-6	ILE_A_27_N	ILE_A_27_CA	-8.267	-4.904	0.432	-7.436	-3.725	0.262	1.45	96.72	54.82
158	2jsa-6	ILE_A_27_CA	ILE_A_27_HA	-7.436	-3.725	0.262	-7.9	-3.091	-0.494	1.09	133.90	126.20
159	2jsa-6	ILE_A_27_CA	ILE_A_27_C	-7.436	-3.725	0.262	-6.062	-4.147	-0.264	1.53	110.10	-17.07
160	2jsa-6	ILE_A_27_C	ILE_A_27_O	-6.062	-4.147	-0.264	-5.711	-3.846	-1.405	1.23	157.94	40.61
161	2jsa-6	ILE_A_27_C	LYS_A_28_N	-6.062	-4.147	-0.264	-5.323	-4.838	0.591	1.32	49.80	-43.08
162	2jsa-6	LYS_A_28_N	LYS_A_28_H	-5.323	-4.838	0.591	-5.676	-5.05	1.513	1.01	24.07	-149.01
163	2jsa-6	LYS_A_28_N	LYS_A_28_CA	-5.323	-4.838	0.591	-3.996	-5.304	0.226	1.45	104.55	-19.35
164	2jsa-6	LYS_A_28_CA	LYS_A_28_HA	-3.996	-5.304	0.226	-3.334	-4.439	0.181	1.09	92.37	52.57
165	2jsa-6	LYS_A_28_CA	LYS_A_28_C	-3.996	-5.304	0.226	-4.045	-5.925	-1.171	1.53	155.97	-94.51
166	2jsa-6	LYS_A_28_C	LYS_A_28_O	-4.045	-5.925	-1.171	-3.163	-5.682	-1.994	1.23	131.97	15.40
167	2jsa-6	LYS_A_28_C	LYS_A_29_N	-4.045	-5.925	-1.171	-5.082	-6.717	-1.396	1.32	99.78	-142.63
168	2jsa-6	LYS_A_29_N	LYS_A_29_H	-5.082	-6.717	-1.396	-5.768	-6.874	-0.672	1.01	44.19	-167.11
169	2jsa-6	LYS_A_29_N	LYS_A_29_CA	-5.082	-6.717	-1.396	-5.258	-7.375	-2.68	1.45	152.06	-104.97
170	2jsa-6	LYS_A_29_CA	LYS_A_29_HA	-5.258	-7.375	-2.68	-4.334	-7.904	-2.917	1.09	102.55	-29.79
171	2jsa-6	LYS_A_29_CA	LYS_A_29_C	-5.258	-7.375	-2.68	-5.479	-6.318	-3.764	1.53	135.11	101.81
172	2jsa-6	LYS_A_29_C	LYS_A_29_O	-5.479	-6.318	-3.764	-4.777	-6.303	-4.773	1.23	145.17	1.22
173	2jsa-6	LYS_A_29_C	ASP_A_30_N	-5.479	-6.318	-3.764	-6.46	-5.461	-3.518	1.33	79.31	138.86
174	2jsa-6	ASP_A_30_N	ASP_A_30_H	-6.46	-5.461	-3.518	-6.998	-5.534	-2.666	1.01	32.51	-172.27
175	2jsa-6	ASP_A_30_N	ASP_A_30_CA	-6.46	-5.461	-3.518	-6.783	-4.404	-4.461	1.45	130.47	106.99
176	2jsa-6	ASP_A_30_CA	ASP_A_30_HA	-6.783	-4.404	-4.461	-7.295	-4.837	-5.32	1.09	142.02	-139.78
177	2jsa-6	ASP_A_30_CA	ASP_A_30_C	-6.783	-4.404	-4.461	-5.492	-3.72	-4.915	1.53	107.26	27.92
178	2jsa-6	ASP_A_30_C	ASP_A_30_O	-5.492	-3.72	-4.915	-5.218	-3.635	-6.111	1.23	166.51	17.23
179	2jsa-6	ASP_A_30_C	PHE_A_31_N	-5.492	-3.72	-4.915	-4.733	-3.249	-3.937	1.32	42.41	31.82
180	2jsa-6	PHE_A_31_N	PHE_A_31_H	-4.733	-3.249	-3.937	-5.02	-3.354	-2.975	1.01	17.62	-159.90
181	2jsa-6	PHE_A_31_N	PHE_A_31_CA	-4.733	-3.249	-3.937	-3.478	-2.575	-4.221	1.45	101.27	28.24
182	2jsa-6	PHE_A_31_CA	PHE_A_31_HA	-3.478	-2.575	-4.221	-3.67	-1.542	-4.512	1.09	105.48	100.53
183	2jsa-6	PHE_A_31_CA	PHE_A_31_C	-3.478	-2.575	-4.221	-2.712	-3.29	-5.337	1.53	136.80	-43.03
184	2jsa-6	PHE_A_31_C	PHE_A_31_O	-2.712	-3.29	-5.337	-2.307	-2.665	-6.315	1.23	142.71	57.06
185	2jsa-6	PHE_A_31_C	ASP_A_32_N	-2.712	-3.29	-5.337	-2.538	-4.59	-5.151	1.32	81.93	-82.38
186	2jsa-6	ASP_A_32_N	ASP_A_32_H	-2.538	-4.59	-5.151	-2.898	-5.038	-4.321	1.01	34.70	-128.78
187	2jsa-6	ASP_A_32_N	ASP_A_32_CA	-2.538	-4.59	-5.151	-1.828	-5.396	-6.129	1.45	132.32	-48.62
188	2jsa-6	ASP_A_32_CA	ASP_A_32_HA	-1.828	-5.396	-6.129	-0.806	-5.026	-6.221	1.09	94.84	19.90
189	2jsa-6	ASP_A_32_CA	ASP_A_32_C	-1.828	-5.396	-6.129	-2.541	-5.299	-7.479	1.53	151.94	172.25
190	2jsa-6	ASP_A_32_C	ASP_A_32_O	-2.541	-5.299	-7.479	-1.895	-5.252	-8.524	1.23	148.21	4.16
191	2jsa-6	ASP_A_32_C	ALA_A_33_N	-2.541	-5.299	-7.479	-3.864	-5.271	-7.412	1.32	87.10	178.79
192	2jsa-6	ALA_A_33_N	ALA_A_33_H	-3.864	-5.271	-7.412	-4.329	-5.314	-6.516	1.01	27.53	-174.72
193	2jsa-6	ALA_A_33_N	ALA_A_33_CA	-3.864	-5.271	-7.412	-4.672	-5.179	-8.616	1.45	145.96	173.50
194	2jsa-6	ALA_A_33_CA	ALA_A_33_HA	-4.672	-5.179	-8.616	-4.503	-6.07	-9.22	1.09	123.66	-79.26
195	2jsa-6	ALA_A_33_CA	ALA_A_33_C	-4.672	-5.179	-8.616	-4.237	-3.956	-9.426	1.53	121.96	70.42
196	2jsa-6	ALA_A_33_C	ALA_A_33_O	-4.237	-3.956	-9.426	-3.975	-4.062	-10.624	1.23	166.73	-22.03
197	2jsa-6	ALA_A_33_C	GLU_A_34_N	-4.237	-3.956	-9.426	-4.171	-2.824	-8.74	1.33	58.83	86.66
198	2jsa-6	GLU_A_34_N	GLU_A_34_H	-4.171	-2.824	-8.74	-4.398	-2.811	-7.756	1.01	13.01	176.72
199	2jsa-6	GLU_A_34_N	GLU_A_34_CA	-4.171	-2.824	-8.74	-3.772	-1.584	-9.382	1.45	116.24	72.16
200	2jsa-6	GLU_A_34_CA	GLU_A_34_HA	-3.772	-1.584	-9.382	-4.33	-1.491	-10.313	1.09	148.72	170.54
201	2jsa-6	GLU_A_34_CA	GLU_A_34_C	-3.772	-1.584	-9.382	-2.279	-1.616	-9.717	1.53	102.64	-1.23
202	2jsa-6	GLU_A_34_C	GLU_A_34_O	-2.279	-1.616	-9.717	-1.901	-1.567	-10.887	1.23	161.96	7.39
203	2jsa-6	GLU_A_34_C	CYS_A_35_N	-2.279	-1.616	-9.717	-1.472	-1.699	-8.671	1.32	37.80	-5.87
204	2jsa-6	CYS_A_35_N	CYS_A_35_H	-1.472	-1.699	-8.671	-1.853	-1.736	-7.736	1.01	22.26	-174.45
205	2jsa-6	CYS_A_35_N	CYS_A_35_CA	-1.472	-1.699	-8.671	-0.028	-1.739	-8.84	1.45	96.67	-1.59
206	2jsa-6	CYS_A_35_CA	CYS_A_35_HA	-0.028	-1.739	-8.84	0.323	-0.726	-9.039	1.09	100.52	70.89
207	2jsa-6	CYS_A_35_CA	CYS_A_35_C	-0.028	-1.739	-8.84	0.288	-2.611	-10.056	1.53	142.67	-70.08
208	2jsa-6	CYS_A_35_C	CYS_A_35_O	0.288	-2.611	-10.056	1.251	-2.351	-10.777	1.23	125.86	15.11
209	2jsa-6	CYS_A_35_C	LYS_A_36_N	0.288	-2.611	-10.056	-0.539	-3.628	-10.247	1.32	98.29	-129.12
210	2jsa-6	LYS_A_36_N	LYS_A_36_H	-0.539	-3.628	-10.247	-1.31	-3.782	-9.613	1.01	51.12	-168.70
211	2jsa-6	LYS_A_36_N	LYS_A_36_CA	-0.539	-3.628	-10.247	-0.359	-4.54	-11.364	1.45	140.23	-78.84
212	2jsa-6	LYS_A_36_CA	LYS_A_36_HA	-0.359	-4.54	-11.364	0.642	-4.967	-11.293	1.09	86.27	-23.10
213	2jsa-6	LYS_A_36_CA	LYS_A_36_C	-0.359	-4.54	-11.364	-0.438	-3.755	-12.676	1.53	148.98	95.75
214	2jsa-6	LYS_A_36_C	LYS_A_36_O	-0.438	-3.755	-12.676	0.586	-3.466	-13.293	1.23	120.11	15.76
215	2jsa-6	LYS_A_36_C	LYS_A_37_N	-0.438	-3.755	-12.676	-1.664	-3.431	-13.061	1.33	106.89	165.20
216	2jsa-6	LYS_A_37_N	LYS_A_37_H	-1.664	-3.431	-13.061	-2.46	-3.701	-12.502	1.01	56.37	-161.2

219	2jsa-6	LYS_A_37_CA	LYS_A_37_C	-1.89	-2.686	-14.287	-1.112	-1.37	-14.23	1.53	87.86	59.41
220	2jsa-6	LYS_A_37_C	LYS_A_37_O	-1.112	-1.37	-14.23	-0.735	-0.822	-15.264	1.23	147.25	55.47
221	2jsa-6	LYS_A_37_C	LEU_A_38_N	-1.112	-1.37	-14.23	-0.897	-0.9	-13.01	1.32	22.96	65.42
222	2jsa-6	LEU_A_38_N	LEU_A_38_H	-0.897	-0.9	-13.01	-1.237	-1.403	-12.203	1.01	36.96	-124.06
223	2jsa-6	LEU_A_38_N	LEU_A_38_CA	-0.897	-0.9	-13.01	-0.171	0.342	-12.804	1.45	81.85	59.69
224	2jsa-6	LEU_A_38_CA	LEU_A_38_HA	-0.171	0.342	-12.804	-0.616	1.103	-13.445	1.09	126.02	120.32
225	2jsa-6	LEU_A_38_CA	LEU_A_38_C	-0.171	0.342	-12.804	1.283	0.157	-13.243	1.53	106.67	-7.25
226	2jsa-6	LEU_A_38_C	LEU_A_38_O	1.283	0.157	-13.243	1.778	0.9	-14.089	1.23	133.46	56.33
227	2jsa-6	LEU_A_38_C	PHE_A_39_N	1.283	0.157	-13.243	1.925	-0.837	-12.648	1.32	63.31	-57.14
228	2jsa-6	PHE_A_39_N	PHE_A_39_H	1.925	-0.837	-12.648	1.454	-1.407	-11.961	1.01	47.10	-129.57
229	2jsa-6	PHE_A_39_N	PHE_A_39_CA	1.925	-0.837	-12.648	3.312	-1.129	-12.967	1.45	102.68	-11.89
230	2jsa-6	PHE_A_39_CA	PHE_A_39_HA	3.312	-1.129	-12.967	3.686	-0.403	-13.689	1.09	131.48	62.74
231	2jsa-6	PHE_A_39_CA	PHE_A_39_C	3.312	-1.129	-12.967	3.459	-2.542	-13.535	1.53	111.79	-84.06
232	2jsa-6	PHE_A_39_C	PHE_A_39_O	3.459	-2.542	-13.535	4.294	-3.317	-13.073	1.23	67.93	-42.87
233	2jsa-6	PHE_A_39_C	HIS_A_40_N	3.459	-2.542	-13.535	2.633	-2.835	-14.529	1.33	138.60	-160.47
234	2jsa-6	HIS_A_40_N	HIS_A_40_H	2.633	-2.835	-14.529	1.97	-2.148	-14.858	1.01	109.01	133.98
235	2jsa-6	HIS_A_40_N	HIS_A_40_CA	2.633	-2.835	-14.529	2.66	-4.141	-15.165	1.45	115.96	-88.82
236	2jsa-6	HIS_A_40_CA	HIS_A_40_HA	2.66	-4.141	-15.165	2.598	-4.897	-14.383	1.09	44.13	-94.69
237	2jsa-6	HIS_A_40_CA	HIS_A_40_C	2.66	-4.141	-15.165	3.992	-4.329	-15.894	1.53	118.45	-8.03
238	2jsa-6	HIS_A_40_C	HIS_A_40_O	3.992	-4.329	-15.894	4.603	-5.393	-15.811	1.23	86.13	-60.13
239	2jsa-6	HIS_A_40_C	THR_A_41_N	3.992	-4.329	-15.894	4.401	-3.28	-16.591	1.32	121.76	68.70
240	2jsa-6	THR_A_41_N	THR_A_41_H	4.401	-3.28	-16.591	3.847	-2.436	-16.613	1.01	91.25	123.28
241	2jsa-6	THR_A_41_N	THR_A_41_CA	4.401	-3.28	-16.591	5.649	-3.316	-17.335	1.45	120.79	-1.65
242	2jsa-6	THR_A_41_CA	THR_A_41_HA	5.649	-3.316	-17.335	5.651	-4.199	-17.974	1.09	125.89	-89.87
243	2jsa-6	THR_A_41_CA	THR_A_41_C	5.649	-3.316	-17.335	6.837	-3.426	-16.377	1.53	51.24	-5.29
244	2jsa-6	THR_A_41_C	THR_A_41_O	6.837	-3.426	-16.377	7.816	-4.11	-16.673	1.23	103.92	-34.94
245	2jsa-6	THR_A_41_C	ILE_A_42_N	6.837	-3.426	-16.377	6.712	-2.744	-15.248	1.32	31.56	100.39
246	2jsa-6	ILE_A_42_N	ILE_A_42_H	6.712	-2.744	-15.248	5.877	-2.204	-15.069	1.01	79.80	147.11
247	2jsa-6	ILE_A_42_N	ILE_A_42_CA	6.712	-2.744	-15.248	7.764	-2.756	-14.245	1.45	46.37	-0.65
248	2jsa-6	ILE_A_42_CA	ILE_A_42_HA	7.764	-2.756	-14.245	8.638	-2.257	-14.665	1.09	112.65	29.72
249	2jsa-6	ILE_A_42_CA	ILE_A_42_C	7.764	-2.756	-14.245	8.156	-4.204	-13.943	1.53	78.62	-74.85
250	2jsa-6	ILE_A_42_C	ILE_A_42_O	8.156	-4.204	-13.943	7.298	-5.084	-13.883	1.23	87.21	-134.27
251	2jsa-6	ILE_A_42_C	PRO_A_43_N	8.156	-4.204	-13.943	9.487	-4.411	-13.755	1.36	82.05	-8.84
252	2jsa-6	PRO_A_43_N	PRO_A_43_CA	9.487	-4.411	-13.755	10.004	-5.737	-13.459	1.45	78.25	-68.70
253	2jsa-6	PRO_A_43_CA	PRO_A_43_HA	10.004	-5.737	-13.459	9.547	-6.472	-14.121	1.09	127.41	-121.87
254	2jsa-6	PRO_A_43_CA	PRO_A_43_C	10.004	-5.737	-13.459	9.703	-6.133	-12.013	1.53	18.98	-127.24
255	2jsa-6	PRO_A_43_C	PRO_A_43_O	9.703	-6.133	-12.013	8.692	-6.779	-11.74	1.23	77.18	-147.42
256	2jsa-6	PRO_A_43_C	PHE_A_44_N	9.703	-6.133	-12.013	10.598	-5.728	-11.124	1.32	47.86	24.35
257	2jsa-6	PHE_A_44_N	PHE_A_44_H	10.598	-5.728	-11.124	11.406	-5.199	-11.42	1.01	107.04	33.21
258	2jsa-6	PHE_A_44_N	PHE_A_44_CA	10.598	-5.728	-11.124	10.441	-6.033	-9.711	1.45	13.65	-117.24
259	2jsa-6	PHE_A_44_CA	PHE_A_44_HA	10.441	-6.033	-9.711	10.268	-7.101	-9.58	1.09	83.10	-99.20
260	2jsa-6	PHE_A_44_CA	PHE_A_44_C	10.441	-6.033	-9.711	9.277	-5.244	-9.107	1.53	66.76	145.87
261	2jsa-6	PHE_A_44_C	PHE_A_44_O	9.277	-5.244	-9.107	8.979	-5.382	-7.921	1.23	15.48	-155.15
262	2jsa-6	PHE_A_44_C	GLY_A_45_N	9.277	-5.244	-9.107	8.651	-4.435	-9.949	1.32	129.46	127.73
263	2jsa-6	GLY_A_45_N	GLY_A_45_H	8.651	-4.435	-9.949	8.951	-4.373	-10.911	1.01	162.34	11.68
264	2jsa-6	GLY_A_45_N	GLY_A_45_CA	8.651	-4.435	-9.949	7.528	-3.624	-9.512	1.45	72.49	144.16
265	2jsa-6	GLY_A_45_CA	GLY_A_45_C	7.528	-3.624	-9.512	6.434	-4.493	-8.889	1.53	65.97	-141.54
266	2jsa-6	GLY_A_45_C	GLY_A_45_O	6.434	-4.493	-8.889	6.117	-4.348	-7.709	1.23	16.46	155.42
267	2jsa-6	GLY_A_45_C	THR_A_46_N	6.434	-4.493	-8.889	5.887	-5.379	-9.709	1.33	128.22	-121.69
268	2jsa-6	THR_A_46_N	THR_A_46_H	5.887	-5.379	-9.709	6.198	-5.444	-10.668	1.01	161.67	-11.81
269	2jsa-6	THR_A_46_N	THR_A_46_CA	5.887	-5.379	-9.709	4.835	-6.272	-9.252	1.45	71.68	-139.67
270	2jsa-6	THR_A_46_CA	THR_A_46_HA	4.835	-6.272	-9.252	4.006	-5.673	-8.876	1.09	69.81	144.15
271	2jsa-6	THR_A_46_CA	THR_A_46_C	4.835	-6.272	-9.252	5.341	-7.149	-8.104	1.53	41.41	-60.02
272	2jsa-6	THR_A_46_C	THR_A_46_O	5.341	-7.149	-8.104	4.574	-7.521	-7.218	1.23	43.89	-154.13
273	2jsa-6	THR_A_46_C	ARG_A_47_N	5.341	-7.149	-8.104	6.63	-7.454	-8.159	1.33	92.38	-13.31
274	2jsa-6	ARG_A_47_N	ARG_A_47_H	6.63	-7.454	-8.159	7.202	-7.114	-8.919	1.01	138.80	30.73
275	2jsa-6	ARG_A_47_N	ARG_A_47_CA	6.63	-7.454	-8.159	7.247	-8.279	-7.135	1.45	45.17	-53.21
276	2jsa-6	ARG_A_47_CA	ARG_A_47_HA	7.247	-8.279	-7.135	6.723	-9.234	-7.101	1.09	88.21	-118.75
277	2jsa-6	ARG_A_47_CA	ARG_A_47_C	7.247	-8.279	-7.135	7.136	-7.602	-5.768	1.53	26.65	99.31
278	2jsa-6	ARG_A_47_C	ARG_A_47_O	7.136	-7.602	-5.768	6.667	-8.211	-4.806	1.23	38.63	-127.60
279	2jsa-6	ARG_A_47_C	GLU_A_48_N	7.136	-7.602	-5.768	7.573	-6.352	-5.724	1.32	88.10	70.73
280	2jsa-6	GLU_A_48_N	GLU_A_48_H	7.573	-6.352	-5.724	7.945	-5.914	-6.555	1.01	145.34	49.66
281	2jsa-6	GLU_A_48_N	GLU_A_48_CA	7.573	-6.352	-5.724	7.528	-5.586	-4.49	1.45	31.87	93.36
282	2jsa-6	GLU_A_48_CA	GLU_A_48_HA	7.528	-5.586	-4.49	7.959	-6.197	-3.697	1.09	43.32	-54.80
283	2jsa-6	GLU_A_48_CA	GLU_A_48_C	7.528	-5.586	-4.49	6.08	-5.265	-4.118	1.53	75.92	167.50
284	2jsa-6	GLU_A_48_C	GLU_A_48_O	6.08	-5.265	-4.118	5.724	-5.26	-2.94	1.23	16.82	179.20
285	2jsa-6	GLU_A_48_C	CYS_A_49_N	6.08	-5.265	-4.118	5.282	-5.004	-5.143	1.32	140.68	161.89
286	2jsa-6	CYS_A_49_N	CYS_A_49_H	5.282	-5.004	-5.143	5.643	-5.026	-6.086	1.01	159.02	-3.49
287	2jsa-6	CYS_A_49_N	CYS_A_49_CA	5.282	-5.004	-5.143	3.88	-4.683	-4.938	1.45	81.89	167.10
288	2jsa-6	CYS_A_49_CA	CYS_A_49_HA	3.88	-4.683	-4.938	3.82	-3.796	-4.306	1.09	54.59	93.87
289	2jsa-6	CYS_A_49_CA	CYS_A_49_C	3.88	-4.683	-4.938	3.223	-5.852	-4.2	1.53	61.17	-119.34
290	2jsa-6	CYS_A_49_C	CYS_A_49_O	3.223	-5.852	-4.2	2.491	-5.647	-3.232	1.23	38.14	164.35
291	2jsa-6	CYS_A_49_C	ASP_A_50_N	3.223	-5.852	-4.2	3.506	-7.051	-4.685	1.32	111.49	-76.72
292	2jsa-6	ASP_A_50_N	ASP_A_50_H	3.506	-7.051	-4.685	4.116	-7.145	-5.485	1.01	142.35	-8.76
293	2jsa-6	ASP_A_50_N	ASP_A_50_CA	3.506	-7.051	-4.685	2.952	-8.252	-4.085	1.45	65.60	-114.76
294	2jsa-6	ASP_A_50_CA	ASP_A_50_HA	2.952	-8.252	-4.085	1.878	-8.12	-3.953	1.09	83.05	172.99
295	2jsa-6	ASP_A_50_CA	ASP_A_50_C	2.952	-8.252	-4.085	3.617	-8.492	-2.729	1.53	27.54	-19.84
296	2jsa-6	ASP_A_50_C	ASP_A_50_O	3.617	-8.492	-2.729	3.101	-9.246	-1.905	1.23	47.95	-124.39
297	2jsa-6	ASP_A_50_C	HIS_A_51_N	3.617	-8.492	-2.729	4.753	-7.838	-2.538	1.32	81.71	29.93
298	2jsa-6	HIS_A_51_N	HIS_A_51_H	4.753	-7.838	-2.538	5.12	-7.235	-3.261	1.01	135.69	58.67
299	2jsa-6	HIS_A_51_N	HIS_A_51_CA	4.753	-7.838	-2.538	5.495	-7.97	-1.296	1.45	31.25	-10.09
300	2jsa-6	HIS_A_51_CA	HIS_A_51_HA	5.495	-7.97	-1.296	5.133	-8.86	-0.781	1.09	61.81	-112.13
301	2jsa-6	HIS_A_51_CA	HIS_A_51_C	5.495	-7.97	-1.296	5.215	-6.763	-0.399	1.53	54.10	103.06
302	2jsa-6	HIS_A_51_C	HIS_A_51_O	5.215	-6.763	-0.399	5.855	-6.593	0.638	1.23	32.56	14.88
303	2jsa-6	HIS_A_51_C	TYR_A_52_N	5.215	-6.763	-0.399	4.259	-9.554	-0.832	1.33	109.07	139.76
304	2jsa-6	TYR_A_52_N	TYR_A_52_H	4.259	-5.954	-0.832	3.776	-6.154	-1.696	1.01	148.82	-157.51
305	2jsa-6	TYR_A_52_N	TYR_A_52_CA	4.259	-5.954	-0.832	3.887	-4.767	-0.081	1.45	58.88	107.40
306	2jsa-6	TYR_A_52_CA	TYR_A_52_HA	3.887	-4.767	-0.081	4.64	-4.549	0.677	1.09	45.96	16.15
307	2jsa-6	TYR_A_52_CA	TYR_A_52_C	3.887	-4.767	-0.081	2.519	-4.942	0.581	1.53	64.36	-172.71
308	2jsa-6	TYR_A_52_C	TYR_A_52_O	2.519	-4.942	0.581	2.289	-4.444	1.681	1.23	26.50	114.79
309	2jsa-6	TYR_A_52_C	VAL_A_53_N	2.519	-4.942	0.581	1.646	-5.654	-			

312	2jsa-6	VAL_A_53_CA	VAL_A_53_HA	0.307	-5.901	0.389	-0.136	-4.946	0.672	1.09	74.95	114.89
313	2jsa-6	VAL_A_53_CA	VAL_A_53_C	0.307	-5.901	0.389	0.394	-6.775	1.642	1.53	35.03	-84.32
314	2jsa-6	VAL_A_53_C	VAL_A_53_O	0.394	-6.775	1.642	-0.595	-6.945	2.354	1.23	54.64	-170.25
315	2jsa-6	VAL_A_53_C	ASN_A_54_N	0.394	-6.775	1.642	1.585	-7.305	1.873	1.32	79.95	-23.99
316	2jsa-6	ASN_A_54_N	ASN_A_54_H	1.585	-7.305	1.873	2.354	-7.121	1.245	1.01	128.46	13.46
317	2jsa-6	ASN_A_54_N	ASN_A_54_CA	1.585	-7.305	1.873	1.814	-8.157	3.028	1.45	37.37	-74.96
318	2jsa-6	ASN_A_54_CA	ASN_A_54_HA	1.814	-8.157	3.028	1.046	-7.959	3.775	1.09	46.71	165.54
319	2jsa-6	ASN_A_54_CA	ASN_A_54_C	1.814	-8.157	3.028	3.196	-7.857	3.612	1.53	67.56	12.25
320	2jsa-6	ASN_A_54_C	ASN_A_54_O	3.196	-7.857	3.612	4.069	-8.723	3.628	1.23	89.25	-44.77
321	2jsa-6	ASN_A_54_C	SER_A_55_N	3.196	-7.857	3.612	3.352	-6.627	4.077	1.32	69.44	82.77
322	2jsa-6	SER_A_55_N	SER_A_55_H	3.352	-6.627	4.077	2.59	-5.966	4.032	1.01	92.55	139.06
323	2jsa-6	SER_A_55_N	SER_A_55_CA	3.352	-6.627	4.077	4.613	-6.201	4.661	1.45	66.31	18.67
324	2jsa-6	SER_A_55_CA	SER_A_55_HA	4.613	-6.201	4.661	4.849	-6.869	5.489	1.09	40.55	-70.54
325	2jsa-6	SER_A_55_CA	SER_A_55_C	4.613	-6.201	4.661	4.485	-4.776	5.203	1.53	69.25	95.13
326	2jsa-6	SER_A_55_C	SER_A_55_O	4.485	-4.776	5.203	5.036	-4.456	6.254	1.23	31.23	30.15
327	2jsa-6	SER_A_55_C	LYS_A_56_N	4.485	-4.776	5.203	3.754	-3.958	4.459	1.33	124.14	131.79
328	2jsa-6	LYS_A_56_N	LYS_A_56_H	3.754	-3.958	4.459	3.33	-4.289	3.605	1.01	147.79	-142.02
329	2jsa-6	LYS_A_56_N	LYS_A_56_CA	3.754	-3.958	4.459	3.547	-2.575	4.852	1.45	74.30	98.51
330	2jsa-6	LYS_A_56_CA	LYS_A_56_HA	3.547	-2.575	4.852	3.805	-2.481	5.907	1.09	14.59	20.02
331	2jsa-6	LYS_A_56_CA	LYS_A_56_C	3.547	-2.575	4.852	2.065	-2.223	4.701	1.53	95.66	166.64
332	2jsa-6	LYS_A_56_C	LYS_A_56_O	2.065	-2.223	4.701	1.703	-1.048	4.666	1.23	91.63	-107.12
333	2jsa-6	LYS_A_56_C	VAL_A_57_N	2.065	-2.223	4.701	1.249	-3.263	4.618	1.32	93.59	-128.12
334	2jsa-6	VAL_A_57_N	VAL_A_57_H	1.249	-3.263	4.618	1.618	-4.203	4.655	1.01	87.90	-68.57
335	2jsa-6	VAL_A_57_N	VAL_A_57_CA	1.249	-3.263	4.618	-0.186	-3.079	4.473	1.45	95.72	172.69
336	2jsa-6	VAL_A_57_CA	VAL_A_57_HA	-0.186	-3.079	4.473	-0.37	-2.059	4.135	1.09	108.06	100.23
337	2jsa-6	VAL_A_57_CA	VAL_A_57_C	-0.186	-3.079	4.473	-0.858	-3.256	5.836	1.53	27.01	-165.24
338	2jsa-6	VAL_A_57_C	VAL_A_57_O	-0.858	-3.256	5.836	-1.949	-2.734	6.066	1.23	79.23	154.43
339	2jsa-6	VAL_A_57_C	ASP_A_58_N	-0.858	-3.256	5.836	-0.181	-3.994	6.704	1.33	49.08	-47.47
340	2jsa-6	ASP_A_58_N	ASP_A_58_H	-0.181	-3.994	6.704	0.711	-4.393	6.446	1.01	104.79	-24.10
341	2jsa-6	ASP_A_58_N	ASP_A_58_CA	-0.181	-3.994	6.704	-0.7	-4.246	8.037	1.45	23.40	-154.10
342	2jsa-6	ASP_A_58_CA	ASP_A_58_HA	-0.7	-4.246	8.037	-1.768	-4.452	7.971	1.09	93.47	-169.08
343	2jsa-6	ASP_A_58_CA	ASP_A_58_C	-0.7	-4.246	8.037	-0.46	-3.014	8.914	1.53	55.06	78.98
344	2jsa-6	ASP_A_58_C	ASP_A_58_O	-0.46	-3.014	8.914	-1.34	-2.606	9.671	1.23	52.03	155.13
345	2jsa-6	ASP_A_58_C	PRO_A_59_N	-0.46	-3.014	8.914	0.765	-2.442	8.778	1.36	95.74	25.03
346	2jsa-6	PRO_A_59_N	PRO_A_59_CA	0.765	-2.442	8.778	1.132	-1.265	9.548	1.45	58.01	72.68
347	2jsa-6	PRO_A_59_CA	PRO_A_59_HA	1.132	-1.265	9.548	0.832	-1.392	10.588	1.09	17.39	-157.06
348	2jsa-6	PRO_A_59_CA	PRO_A_59_C	1.132	-1.265	9.548	0.448	-0.013	8.996	1.53	111.15	118.65
349	2jsa-6	PRO_A_59_C	PRO_A_59_O	0.448	-0.013	8.996	-0.189	0.731	9.741	1.23	52.74	130.57
350	2jsa-6	PRO_A_59_C	ILE_A_60_N	0.448	-0.013	8.996	0.602	0.181	7.695	1.32	169.22	51.56
351	2jsa-6	ILE_A_60_N	ILE_A_60_H	0.602	0.181	7.695	1.138	-0.473	7.143	1.01	123.14	-50.66
352	2jsa-6	ILE_A_60_N	ILE_A_60_CA	0.602	0.181	7.695	0.007	1.331	7.034	1.45	117.04	117.36
353	2jsa-6	ILE_A_60_CA	ILE_A_60_HA	0.007	1.331	7.034	0.51	2.227	7.398	1.09	70.49	60.69
354	2jsa-6	ILE_A_60_CA	ILE_A_60_C	0.007	1.331	7.034	-1.468	1.432	7.427	1.53	75.11	176.08
355	2jsa-6	ILE_A_60_C	ILE_A_60_O	-1.468	1.432	7.427	-1.962	2.52	7.719	1.23	76.27	114.42
356	2jsa-6	ILE_A_60_C	ILE_A_61_N	-1.468	1.432	7.427	-2.129	0.284	7.421	1.32	90.26	-119.93
357	2jsa-6	ILE_A_61_N	ILE_A_61_H	-2.129	0.284	7.421	-1.657	-0.574	7.171	1.01	104.32	-61.18
358	2jsa-6	ILE_A_61_N	ILE_A_61_CA	-2.129	0.284	7.421	-3.538	0.231	7.773	1.45	75.98	-177.85
359	2jsa-6	ILE_A_61_CA	ILE_A_61_HA	-3.538	0.231	7.773	-4.042	1.059	7.274	1.09	117.24	121.33
360	2jsa-6	ILE_A_61_CA	ILE_A_61_C	-3.538	0.231	7.773	-3.69	0.436	9.282	1.53	9.60	126.56
361	2jsa-6	ILE_A_61_C	ILE_A_61_O	-3.69	0.436	9.282	-4.764	0.803	9.757	1.23	67.29	161.13
362	2jsa-6	ILE_A_61_C	HIS_A_62_N	-3.69	0.436	9.282	-2.599	0.191	9.994	1.33	57.51	-12.66
363	2jsa-6	HIS_A_62_N	HIS_A_62_H	-2.599	0.191	9.994	-1.749	-0.108	9.536	1.01	116.94	-19.38
364	2jsa-6	HIS_A_62_N	HIS_A_62_CA	-2.599	0.191	9.994	-2.598	0.344	11.438	1.45	6.05	89.63
365	2jsa-6	HIS_A_62_CA	HIS_A_62_HA	-2.598	0.344	11.438	-3.5	-0.127	11.827	1.09	69.08	-152.43
366	2jsa-6	HIS_A_62_CA	HIS_A_62_C	-2.598	0.344	11.438	-2.652	1.83	11.796	1.53	76.46	92.08
367	2jsa-6	HIS_A_62_C	HIS_A_62_O	-2.652	1.83	11.796	-3.049	2.192	12.904	1.23	25.87	137.64
368	2jsa-6	HIS_A_62_C	GLU_A_63_N	-2.652	1.83	11.796	-2.249	2.652	10.839	1.32	136.27	63.88
369	2jsa-6	GLU_A_63_N	GLU_A_63_H	-2.249	2.652	10.839	-1.936	2.285	9.952	1.01	151.46	-49.54
370	2jsa-6	GLU_A_63_N	GLU_A_63_CA	-2.249	2.652	10.839	-2.247	4.092	11.04	1.45	82.05	89.92
371	2jsa-6	GLU_A_63_CA	GLU_A_63_HA	-2.247	4.092	11.04	-2.01	4.286	12.086	1.09	16.32	39.30
372	2jsa-6	GLU_A_63_CA	GLU_A_63_C	-2.247	4.092	11.04	-3.632	4.671	10.745	1.53	101.12	157.31
373	2jsa-6	GLU_A_63_C	GLU_A_63_O	-3.632	4.671	10.745	-4.164	5.451	11.533	1.23	50.15	124.30
374	2jsa-6	GLU_A_63_C	LEU_A_64_N	-3.632	4.671	10.745	-4.177	4.266	9.606	1.33	149.20	-143.38
375	2jsa-6	LEU_A_64_N	LEU_A_64_H	-4.177	4.266	9.606	-3.682	3.622	9.006	1.01	126.45	-52.45
376	2jsa-6	LEU_A_64_N	LEU_A_64_CA	-4.177	4.266	9.606	-5.49	4.735	9.197	1.45	106.35	160.34
377	2jsa-6	LEU_A_64_CA	LEU_A_64_HA	-5.49	4.735	9.197	-5.495	5.823	9.264	1.09	86.48	90.26
378	2jsa-6	LEU_A_64_CA	LEU_A_64_C	-5.49	4.735	9.197	-6.543	4.204	10.172	1.53	50.42	-153.24
379	2jsa-6	LEU_A_64_C	LEU_A_64_O	-6.543	4.204	10.172	-7.52	4.89	10.469	1.23	76.03	144.93
380	2jsa-6	LEU_A_64_C	GLU_A_65_N	-6.543	4.204	10.172	-6.308	2.988	10.642	1.32	69.22	-79.06
381	2jsa-6	GLU_A_65_N	GLU_A_65_H	-6.308	2.988	10.642	-5.482	2.482	10.354	1.01	106.56	-31.49
382	2jsa-6	GLU_A_65_N	GLU_A_65_CA	-6.308	2.988	10.642	-7.224	2.358	11.576	1.45	49.97	-145.48
383	2jsa-6	GLU_A_65_CA	GLU_A_65_HA	-7.224	2.358	11.576	-8.24	2.549	11.232	1.09	108.41	169.35
384	2jsa-6	GLU_A_65_CA	GLU_A_65_C	-7.224	2.358	11.576	-7.065	2.969	12.97	1.53	24.37	75.41
385	2jsa-6	GLU_A_65_C	GLU_A_65_O	-7.065	2.969	12.97	-8.016	2.998	13.751	1.23	50.62	178.25
386	2jsa-6	GLU_A_65_C	GLY_A_66_N	-7.065	2.969	12.97	-5.858	3.443	13.24	1.32	78.24	21.44
387	2jsa-6	GLY_A_66_N	GLY_A_66_H	-5.858	3.443	13.24	-5.123	3.386	12.549	1.01	133.15	-4.43
388	2jsa-6	GLY_A_66_N	GLY_A_66_CA	-5.858	3.443	13.24	-5.562	4.052	14.525	1.45	27.79	64.08
389	2jsa-6	GLY_A_66_CA	GLY_A_66_C	-5.562	4.052	14.525	-6.125	5.472	14.601	1.53	87.15	111.63
390	2jsa-6	GLY_A_66_C	GLY_A_66_O	-6.125	5.472	14.601	-6.73	5.852	15.603	1.23	35.49	147.87
391	2jsa-6	GLY_A_66_C	GLY_A_67_N	-6.125	5.472	14.601	-5.907	6.219	13.528	1.33	144.05	73.73
392	2jsa-6	GLY_A_67_N	GLY_A_67_H	-5.907	6.219	13.528	-5.401	5.842	12.739	1.01	141.35	-36.69
393	2jsa-6	GLY_A_67_N	GLY_A_67_CA	-5.907	6.219	13.528	-6.386	7.589	13.461	1.45	92.64	109.27
394	2jsa-6	GLY_A_67_CA	GLY_A_67_C	-6.386	7.589	13.461	-5.53	8.422	12.504	1.53	128.70	44.22
395	2jsa-6	GLY_A_67_C	GLY_A_67_O	-5.53	8.422	12.504	-5.97	9.462	12.016	1.23	113.37	112.93
396	2jsa-6	GLY_A_67_C	THR_A_68_N	-5.53	8.422	12.504	-4.322	7.934	12.265	1.32	100.40	-22.00
397	2jsa-6	THR_A_68_N	THR_A_68_H	-4.322	7.934	12.265	-4.026	7.072	12.701	1.01	64.43	-71.05
398	2jsa-6	THR_A_68_N	THR_A_68_CA	-4.322	7.934	12.265	-3.399	8.62	11.376	1.45	127.71	36.62
399	2jsa-6	THR_A_68_CA	THR_A_68_HA	-3.399	8.62	11.376	-3.225	9.626	11.76	1.09	69.39	80.19
400	2jsa-6	THR_A_68_CA	THR_A_68_C	-3.399	8.62	11.376	-4.004	8.747	9.976	1.53	156.18	168.14
401	2jsa-6	THR_A_68_C	THR_A_68_O	-4.004	8.747	9.976	-4.745	7.87	9.534	1.23	111.06	-130.20
402	2jsa-6	THR_A_68_C	ALA_A_69_N	-4.004	8.747	9.976	-3.665	9.846				

405	2jsa-6	ALA_A_69_CA	ALA_A_69_HA	-4.165	10.099	7.977	-5.208	9.787	7.927	1.09	92.63	-163.35
406	2jsa-6	ALA_A_69_CA	ALA_A_69_C	-4.165	10.099	7.977	-3.362	9.269	6.973	1.53	131.00	-45.95
407	2jsa-6	ALA_A_69_C	ALA_A_69_O	-3.362	9.269	6.973	-2.323	8.707	7.316	1.23	73.81	-28.41
408	2jsa-6	ALA_A_69_C	PRO_A_70_N	-3.362	9.269	6.973	-3.889	9.215	5.721	1.36	157.07	-174.15
409	2jsa-6	PRO_A_70_N	PRO_A_70_CA	-3.889	9.215	5.721	-3.234	8.463	4.664	1.45	136.67	-48.94
410	2jsa-6	PRO_A_70_CA	PRO_A_70_HA	-3.234	8.463	4.664	-2.921	7.488	5.038	1.09	69.94	-72.20
411	2jsa-6	PRO_A_70_CA	PRO_A_70_C	-3.234	8.463	4.664	-1.997	9.204	4.15	1.53	109.62	30.92
412	2jsa-6	PRO_A_70_C	PRO_A_70_O	-1.997	9.204	4.15	-1.242	8.67	3.339	1.23	131.25	-35.27
413	2jsa-6	PRO_A_70_C	LYS_A_71_N	-1.997	9.204	4.15	-1.83	10.422	4.643	1.32	68.15	82.19
414	2jsa-6	LYS_A_71_N	LYS_A_71_H	-1.83	10.422	4.643	-2.492	10.798	5.307	1.01	48.91	150.40
415	2jsa-6	LYS_A_71_N	LYS_A_71_CA	-1.83	10.422	4.643	-0.698	11.241	4.243	1.45	105.98	35.89
416	2jsa-6	LYS_A_71_CA	LYS_A_71_HA	-0.698	11.241	4.243	-0.186	10.734	3.425	1.09	138.62	-44.72
417	2jsa-6	LYS_A_71_CA	LYS_A_71_C	-0.698	11.241	4.243	0.285	11.349	5.41	1.53	40.28	6.27
418	2jsa-6	LYS_A_71_C	LYS_A_71_O	0.285	11.349	5.41	1.341	11.968	5.283	1.23	95.92	30.38
419	2jsa-6	LYS_A_71_C	ASP_A_72_N	0.285	11.349	5.41	-0.097	10.738	6.523	1.33	32.92	-122.01
420	2jsa-6	ASP_A_72_N	ASP_A_72_H	-0.097	10.738	6.523	-0.979	10.248	6.558	1.01	88.01	-150.95
421	2jsa-6	ASP_A_72_H	ASP_A_72_CA	-0.097	10.738	6.523	0.738	10.759	7.712	1.45	35.09	1.44
422	2jsa-6	ASP_A_72_CA	ASP_A_72_HA	0.738	10.759	7.712	1.48	11.552	7.613	1.09	95.21	46.90
423	2jsa-6	ASP_A_72_CA	ASP_A_72_C	0.738	10.759	7.712	1.438	9.406	7.861	1.53	84.41	-62.64
424	2jsa-6	ASP_A_72_C	ASP_A_72_O	1.438	9.406	7.861	2.561	9.337	8.358	1.23	66.17	-3.52
425	2jsa-6	ASP_A_72_C	VAL_A_73_N	1.438	9.406	7.861	0.745	8.365	7.421	1.33	109.38	-123.65
426	2jsa-6	VAL_A_73_N	VAL_A_73_H	0.745	8.365	7.421	-0.173	8.497	7.023	1.01	113.23	171.82
427	2jsa-6	VAL_A_73_H	VAL_A_73_CA	0.745	8.365	7.421	1.287	7.019	7.5	1.45	86.88	-68.07
428	2jsa-6	VAL_A_73_CA	VAL_A_73_HA	1.287	7.019	7.5	1.474	6.784	8.548	1.09	15.99	-51.49
429	2jsa-6	VAL_A_73_HA	VAL_A_73_C	1.287	7.019	7.5	2.622	6.967	6.757	1.53	119.08	-2.23
430	2jsa-6	VAL_A_73_C	VAL_A_73_O	2.622	6.967	6.757	3.605	6.439	7.274	1.23	65.14	-28.24
431	2jsa-6	VAL_A_73_O	CYS_A_74_N	2.622	6.967	6.757	2.616	7.524	5.555	1.32	155.14	90.62
432	2jsa-6	CYS_A_74_N	CYS_A_74_H	2.616	7.524	5.555	1.772	7.943	5.193	1.01	111.02	153.60
433	2jsa-6	CYS_A_74_H	CYS_A_74_CA	2.616	7.524	5.555	3.816	7.547	4.734	1.45	124.37	1.10
434	2jsa-6	CYS_A_74_CA	CYS_A_74_HA	3.816	7.547	4.734	4.298	6.572	4.803	1.09	86.37	-63.69
435	2jsa-6	CYS_A_74_HA	CYS_A_74_C	3.816	7.547	4.734	4.767	8.602	5.304	1.53	68.13	47.97
436	2jsa-6	CYS_A_74_C	CYS_A_74_O	4.767	8.602	5.304	5.13	9.553	4.615	1.23	124.09	69.11
437	2jsa-6	CYS_A_74_O	THR_A_75_N	4.767	8.602	5.304	5.143	8.398	6.558	1.32	18.84	-28.48
438	2jsa-6	THR_A_75_N	THR_A_75_H	5.143	8.398	6.558	4.805	7.593	7.066	1.01	59.81	-112.78
439	2jsa-6	THR_A_75_H	THR_A_75_CA	5.143	8.398	6.558	6.044	9.319	7.229	1.45	62.49	45.63
440	2jsa-6	THR_A_75_CA	THR_A_75_HA	6.044	9.319	7.229	7.03	9.241	6.77	1.09	114.89	-4.52
441	2jsa-6	THR_A_75_HA	THR_A_75_C	6.044	9.319	7.229	6.183	8.949	8.706	1.53	14.98	-69.41
442	2jsa-6	THR_A_75_C	THR_A_75_O	6.183	8.949	8.706	7.242	9.143	9.302	1.23	61.03	10.38
443	2jsa-6	THR_A_75_O	LYS_A_76_N	6.183	8.949	8.706	5.098	8.423	9.256	1.33	65.48	-154.14
444	2jsa-6	LYS_A_76_N	LYS_A_76_H	5.098	8.423	9.256	4.261	8.293	8.706	1.01	123.00	-171.17
445	2jsa-6	LYS_A_76_H	LYS_A_76_CA	5.098	8.423	9.256	5.086	8.024	10.654	1.45	15.94	-91.72
446	2jsa-6	LYS_A_76_CA	LYS_A_76_HA	5.086	8.024	10.654	5.536	8.827	11.239	1.09	57.56	60.73
447	2jsa-6	LYS_A_76_HA	LYS_A_76_C	5.086	8.024	10.654	5.955	6.778	10.831	1.53	83.35	-55.11
448	2jsa-6	LYS_A_76_C	LYS_A_76_O	5.955	6.778	10.831	6.76	6.704	11.758	1.23	41.09	-5.25
449	2jsa-6	LYS_A_76_O	LEU_A_77_N	5.955	6.778	10.831	5.764	5.827	9.927	1.33	132.98	-101.36
450	2jsa-6	LEU_A_77_N	LEU_A_77_H	5.764	5.827	9.927	5.086	5.956	9.19	1.01	136.88	169.23
451	2jsa-6	LEU_A_77_H	LEU_A_77_CA	5.764	5.827	9.927	6.519	4.587	9.972	1.45	88.22	-58.66
452	2jsa-6	LEU_A_77_CA	LEU_A_77_HA	6.519	4.587	9.972	6.799	4.4	11.009	1.09	17.99	-33.74
453	2jsa-6	LEU_A_77_HA	LEU_A_77_C	6.519	4.587	9.972	7.809	4.752	9.164	1.53	121.85	7.29
454	2jsa-6	LEU_A_77_C	LEU_A_77_O	7.809	4.752	9.164	8.394	3.767	8.716	1.23	111.36	-59.29
455	2jsa-6	LEU_A_77_O	ASN_A_78_N	7.809	4.752	9.164	8.213	6.003	9.003	1.32	96.98	72.10
456	2jsa-6	ASN_A_78_N	ASN_A_78_H	8.213	6.003	9.003	7.682	6.764	9.401	1.01	66.79	124.91
457	2jsa-6	ASN_A_78_H	ASN_A_78_CA	8.213	6.003	9.003	9.422	6.309	8.256	1.45	120.92	14.20
458	2jsa-6	ASN_A_78_CA	ASN_A_78_HA	9.422	6.309	8.256	9.522	7.391	8.165	1.09	94.79	84.72
459	2jsa-6	ASN_A_78_HA	ASN_A_78_C	9.422	6.309	8.256	9.331	5.677	6.866	1.53	155.33	-98.19
460	2jsa-6	ASN_A_78_C	ASN_A_78_O	9.331	5.677	6.866	10.346	5.496	6.196	1.23	123.02	-10.11
461	2jsa-6	ASN_A_78_O	GLU_A_79_N	9.331	5.677	6.866	8.106	5.358	6.474	1.33	107.21	-165.40
462	2jsa-6	GLU_A_79_N	GLU_A_79_H	8.106	5.358	6.474	7.317	5.536	7.078	1.01	53.25	167.29
463	2jsa-6	GLU_A_79_H	GLU_A_79_CA	8.106	5.358	6.474	7.87	4.75	5.176	1.45	153.32	-111.21
464	2jsa-6	GLU_A_79_CA	GLU_A_79_HA	7.87	4.75	5.176	8.396	3.795	5.15	1.09	91.37	-61.15
465	2jsa-6	GLU_A_79_HA	GLU_A_79_C	7.87	4.75	5.176	8.432	5.638	4.064	1.53	136.62	57.67
466	2jsa-6	GLU_A_79_C	GLU_A_79_O	8.432	5.638	4.064	9.452	5.311	3.459	1.23	119.46	-17.78
467	2jsa-6	GLU_A_79_O	CYS_A_80_N	8.432	5.638	4.064	7.742	6.744	3.829	1.32	100.22	121.96
468	2jsa-6	CYS_A_80_N	CYS_A_80_H	7.742	6.744	3.829	6.912	6.95	4.367	1.01	57.83	166.06
469	2jsa-6	CYS_A_80_H	CYS_A_80_CA	7.742	6.744	3.829	8.16	7.682	2.8	1.45	135.06	65.98
470	2jsa-6	CYS_A_80_CA	CYS_A_80_HA	8.16	7.682	2.8	7.906	7.26	1.828	1.09	153.13	-121.04
471	2jsa-6	CYS_A_80_HA	CYS_A_80_C	8.16	7.682	2.8	9.679	7.839	2.88	1.53	87.00	5.90
472	2jsa-6	CYS_A_80_C	CYS_A_80_O	9.679	7.839	2.88	10.292	7.476	3.884	1.23	35.36	-30.63
473	2jsa-6	CYS_A_80_O	PRO_A_81_N	9.679	7.839	2.88	10.259	8.395	1.784	1.36	143.76	43.79
474	2jsa-6	PRO_A_81_N	PRO_A_81_CA	10.259	8.395	1.784	11.695	8.605	1.721	1.45	92.49	8.32
475	2jsa-6	PRO_A_81_CA	PRO_A_81_HA	11.695	8.605	1.721	12.218	7.717	2.077	1.09	70.94	-59.50
476	2jsa-6	PRO_A_81_HA	PRO_A_81_C	11.695	8.605	1.721	12.114	9.794	2.588	1.53	55.48	70.59
477	2jsa-6	PRO_A_81_C	PRO_A_81_O	12.114	9.794	2.588	13.246	9.85	3.065	1.23	67.18	2.83
1	2jsa-7	ARG_A_1_N	ARG_A_1_H	15.033	4.568	0.099	15.002	5.432	-0.423	1.01	121.12	92.05
2	2jsa-7	ARG_A_1_N	ARG_A_1_CA	15.033	4.568	0.099	13.793	3.844	0.318	1.45	81.33	-149.72
3	2jsa-7	ARG_A_1_CA	ARG_A_1_HA	13.793	3.844	0.318	13.886	2.858	-0.136	1.09	114.63	-84.61
4	2jsa-7	ARG_A_1_HA	ARG_A_1_C	13.793	3.844	0.318	12.624	4.584	-0.334	1.53	115.23	147.67
5	2jsa-7	ARG_A_1_C	ARG_A_1_O	12.624	4.584	-0.334	11.659	3.962	-0.775	1.23	111.01	-147.20
6	2jsa-7	ARG_A_1_O	SER_A_2_N	12.624	4.584	-0.334	12.748	5.903	-0.375	1.33	91.77	84.63
7	2jsa-7	SER_A_2_N	SER_A_2_H	12.748	5.903	-0.375	13.571	6.348	0.006	1.01	67.84	28.40
8	2jsa-7	SER_A_2_H	SER_A_2_CA	12.748	5.903	-0.375	11.714	6.735	-0.965	1.45	113.97	141.18
9	2jsa-7	SER_A_2_CA	SER_A_2_HA	11.714	6.735	-0.965	10.755	6.441	-0.54	1.09	67.04	-162.96
10	2jsa-7	SER_A_2_HA	SER_A_2_C	11.714	6.735	-0.965	11.668	6.516	-2.48	1.53	171.60	-101.86
11	2jsa-7	SER_A_2_C	SER_A_2_O	11.668	6.516	-2.48	12.527	7.011	-3.208	1.23	126.29	29.95
12	2jsa-7	SER_A_2_O	ALA_A_3_N	11.668	6.516	-2.48	10.656	5.776	-2.907	1.32	108.81	-143.82
13	2jsa-7	ALA_A_3_N	ALA_A_3_H	10.656	5.776	-2.907	9.987	5.402	-2.25	1.01	49.40	-150.79
14	2jsa-7	ALA_A_3_H	ALA_A_3_CA	10.656	5.776	-2.907	10.487	5.486	-4.322	1.45	166.66	-120.23
15	2jsa-7	ALA_A_3_CA	ALA_A_3_HA	10.487	5.486	-4.322	10.631	6.406	-4.888	1.09	121.29	81.10
16	2jsa-7	ALA_A_3_HA	ALA_A_3_C	10.487	5.486	-4.322	9.063	4.984	-4.568	1.53	99.25	-160.58
17	2jsa-7	ALA_A_3_C	ALA_A_3_O	9.063	4.984	-4.568	8.11	5.495	-3.981	1.23	61.51	151.80
18	2jsa-7	ALA_A_3_O	LEU_A_4_N	9.063	4.984	-4.568	8.962	3.988	-5.436	1.33	130.93	-95.79
19	2jsa-7	LEU_A_4_N</										

21	2jsa-7	LEU_A_4_CA	LEU_A_4_HA	7.671	3.411	-5.767	7.01	4.22	-6.078	1.09	106.58	129.25
22	2jsa-7	LEU_A_4_CA	LEU_A_4_C	7.671	3.411	-5.767	7.067	2.772	-4.515	1.53	35.08	-133.39
23	2jsa-7	LEU_A_4_C	LEU_A_4_O	7.067	2.772	-4.515	5.883	2.438	-4.494	1.23	89.02	-164.25
24	2jsa-7	LEU_A_4_C	SER_A_5_N	7.067	2.772	-4.515	7.907	2.623	-3.501	1.33	40.08	-10.06
25	2jsa-7	SER_A_5_N	SER_A_5_H	7.907	2.623	-3.501	8.868	2.923	-3.588	1.01	94.94	17.34
26	2jsa-7	SER_A_5_N	SER_A_5_CA	7.907	2.623	-3.501	7.471	2.03	-2.248	1.45	30.43	-126.32
27	2jsa-7	SER_A_5_CA	SER_A_5_HA	7.471	2.03	-2.248	6.985	1.08	-2.47	1.09	101.75	-117.09
28	2jsa-7	SER_A_5_CA	SER_A_5_C	7.471	2.03	-2.248	6.459	2.949	-1.559	1.53	63.25	137.76
29	2jsa-7	SER_A_5_C	SER_A_5_O	6.459	2.949	-1.559	5.395	2.499	-1.136	1.23	69.89	-157.07
30	2jsa-7	SER_A_5_C	CYS_A_6_N	6.459	2.949	-1.559	6.828	4.218	-1.467	1.32	86.02	73.79
31	2jsa-7	CYS_A_6_N	CYS_A_6_H	6.828	4.218	-1.467	7.719	4.517	-1.837	1.01	111.49	18.55
32	2jsa-7	CYS_A_6_N	CYS_A_6_CA	6.828	4.218	-1.467	5.966	5.204	-0.837	1.45	64.31	131.16
33	2jsa-7	CYS_A_6_CA	CYS_A_6_HA	5.966	5.204	-0.837	5.804	4.906	0.199	1.09	18.13	-118.53
34	2jsa-7	CYS_A_6_CA	CYS_A_6_C	5.966	5.204	-0.837	4.619	5.197	-1.562	1.53	118.29	-179.70
35	2jsa-7	CYS_A_6_C	CYS_A_6_O	4.619	5.197	-1.562	3.581	4.953	-0.948	1.23	60.07	-166.77
36	2jsa-7	CYS_A_6_C	GLN_A_7_N	4.619	5.197	-1.562	4.678	5.468	-2.857	1.32	167.91	77.72
37	2jsa-7	GLN_A_7_N	GLN_A_7_H	4.678	5.468	-2.857	5.567	5.66	-3.296	1.01	115.77	12.19
38	2jsa-7	GLN_A_7_N	GLN_A_7_CA	4.678	5.468	-2.857	3.474	5.497	-3.671	1.45	124.05	178.62
39	2jsa-7	GLN_A_7_CA	GLN_A_7_HA	3.474	5.497	-3.671	2.933	6.415	-3.441	1.09	77.82	120.51
40	2jsa-7	GLN_A_7_CA	GLN_A_7_C	3.474	5.497	-3.671	2.573	4.308	-3.329	1.53	77.09	-127.15
41	2jsa-7	GLN_A_7_C	GLN_A_7_O	2.573	4.308	-3.329	1.389	4.483	-3.049	1.23	76.83	171.59
42	2jsa-7	GLN_A_7_C	MET_A_8_N	2.573	4.308	-3.329	3.17	3.126	-3.362	1.32	91.43	-63.20
43	2jsa-7	MET_A_8_N	MET_A_8_H	3.17	3.126	-3.362	4.149	3.057	-3.601	1.01	103.69	-4.03
44	2jsa-7	MET_A_8_N	MET_A_8_CA	3.17	3.126	-3.362	2.436	1.909	-3.059	1.45	77.96	-121.10
45	2jsa-7	MET_A_8_CA	MET_A_8_HA	2.436	1.909	-3.059	1.761	1.693	-3.887	1.09	139.44	-162.26
46	2jsa-7	MET_A_8_CA	MET_A_8_C	2.436	1.909	-3.059	1.616	2.068	-1.778	1.53	33.11	169.03
47	2jsa-7	MET_A_8_C	MET_A_8_O	1.616	2.068	-1.778	0.528	1.506	-1.659	1.23	84.45	-152.68
48	2jsa-7	MET_A_8_C	CYS_A_9_N	1.616	2.068	-1.778	2.169	2.837	-0.851	1.33	45.62	54.28
49	2jsa-7	CYS_A_9_N	CYS_A_9_H	2.169	2.837	-0.851	3.067	3.269	-1.017	1.01	99.46	25.69
50	2jsa-7	CYS_A_9_N	CYS_A_9_CA	2.169	2.837	-0.851	1.502	3.077	0.417	1.45	29.21	160.21
51	2jsa-7	CYS_A_9_CA	CYS_A_9_HA	1.502	3.077	0.417	1.268	2.113	0.869	1.09	65.50	-103.64
52	2jsa-7	CYS_A_9_CA	CYS_A_9_C	1.502	3.077	0.417	0.191	3.816	0.138	1.53	100.50	150.59
53	2jsa-7	CYS_A_9_C	CYS_A_9_O	0.191	3.816	0.138	-0.821	3.559	0.788	1.23	58.10	-165.75
54	2jsa-7	CYS_A_9_C	GLU_A_10_N	0.191	3.816	0.138	0.254	4.722	-0.828	1.33	136.77	86.02
55	2jsa-7	GLU_A_10_N	GLU_A_10_H	0.254	4.722	-0.828	1.122	4.883	-1.319	1.01	119.08	10.51
56	2jsa-7	GLU_A_10_N	GLU_A_10_CA	0.254	4.722	-0.828	-0.915	5.499	-1.201	1.45	104.88	146.39
57	2jsa-7	GLU_A_10_CA	GLU_A_10_HA	-0.915	5.499	-1.201	-1.411	5.822	-0.286	1.09	32.90	146.93
58	2jsa-7	GLU_A_10_CA	GLU_A_10_C	-0.915	5.499	-1.201	-1.894	4.637	-2.0	1.53	121.49	-138.64
59	2jsa-7	GLU_A_10_C	GLU_A_10_O	-1.894	4.637	-2.0	-2.998	5.078	-2.317	1.23	104.93	158.23
60	2jsa-7	GLU_A_10_C	LEU_A_11_N	-1.894	4.637	-2.0	-1.455	3.425	-2.302	1.32	103.19	-70.09
61	2jsa-7	LEU_A_11_N	LEU_A_11_H	-1.455	3.425	-2.302	-0.535	3.129	-2.008	1.01	73.08	-17.84
62	2jsa-7	LEU_A_11_N	LEU_A_11_CA	-1.455	3.425	-2.302	-2.28	2.497	-3.058	1.45	121.33	-131.64
63	2jsa-7	LEU_A_11_CA	LEU_A_11_HA	-2.28	2.497	-3.058	-2.997	3.078	-3.637	1.09	122.10	140.98
64	2jsa-7	LEU_A_11_CA	LEU_A_11_C	-2.28	2.497	-3.058	-3.07	1.616	-2.088	1.53	50.66	-131.88
65	2jsa-7	LEU_A_11_C	LEU_A_11_O	-3.07	1.616	-2.088	-4.238	1.315	-2.327	1.23	101.21	-165.55
66	2jsa-7	LEU_A_11_C	VAL_A_12_N	-3.07	1.616	-2.088	-2.4	1.227	-1.012	1.33	35.75	-30.14
67	2jsa-7	VAL_A_12_N	VAL_A_12_H	-2.4	1.227	-1.012	-1.44	1.513	-0.879	1.01	82.44	16.59
68	2jsa-7	VAL_A_12_N	VAL_A_12_CA	-2.4	1.227	-1.012	-3.025	0.387	-0.005	1.45	46.12	-126.65
69	2jsa-7	VAL_A_12_CA	VAL_A_12_HA	-3.025	0.387	-0.005	-3.581	-0.402	-0.511	1.09	117.66	-125.17
70	2jsa-7	VAL_A_12_CA	VAL_A_12_C	-3.025	0.387	-0.005	-4.017	1.223	0.806	1.53	57.99	139.88
71	2jsa-7	VAL_A_12_C	VAL_A_12_O	-4.017	1.223	0.806	-5.153	0.804	1.026	1.23	79.70	-159.75
72	2jsa-7	VAL_A_12_C	VAL_A_13_N	-4.017	1.223	0.806	-3.553	2.39	1.228	1.32	71.43	68.32
73	2jsa-7	VAL_A_13_N	VAL_A_13_H	-3.553	2.39	1.228	-2.607	2.67	1.01	1.01	102.46	16.49
74	2jsa-7	VAL_A_13_N	VAL_A_13_CA	-3.553	2.39	1.228	-4.386	3.289	2.01	1.45	57.46	132.82
75	2jsa-7	VAL_A_13_CA	VAL_A_13_HA	-4.386	3.289	2.01	-4.778	2.739	2.866	1.09	38.27	-125.48
76	2jsa-7	VAL_A_13_CA	VAL_A_13_C	-4.386	3.289	2.01	-5.57	3.749	1.158	1.53	123.85	158.77
77	2jsa-7	VAL_A_13_C	VAL_A_13_O	-5.57	3.749	1.158	-6.724	3.519	1.516	1.23	73.08	-168.73
78	2jsa-7	VAL_A_13_C	LYS_A_14_N	-5.57	3.749	1.158	-5.244	4.393	0.047	1.32	146.99	63.15
79	2jsa-7	LYS_A_14_N	LYS_A_14_H	-5.244	4.393	0.047	-4.273	4.548	-0.184	1.01	103.22	9.07
80	2jsa-7	LYS_A_14_N	LYS_A_14_CA	-5.244	4.393	0.047	-6.266	4.888	-0.858	1.45	128.55	154.16
81	2jsa-7	LYS_A_14_CA	LYS_A_14_HA	-6.266	4.888	-0.858	-6.738	5.754	-0.393	1.09	64.76	118.59
82	2jsa-7	LYS_A_14_CA	LYS_A_14_C	-6.266	4.888	-0.858	-7.342	3.815	-1.043	1.53	96.94	-135.08
83	2jsa-7	LYS_A_14_C	LYS_A_14_O	-7.342	3.815	-1.043	-8.525	4.132	-1.16	1.23	95.46	165.00
84	2jsa-7	LYS_A_14_C	LYS_A_15_N	-7.342	3.815	-1.043	-6.893	2.569	-1.062	1.32	90.82	-70.18
85	2jsa-7	LYS_A_15_N	LYS_A_15_H	-6.893	2.569	-1.062	-5.905	2.383	-0.96	1.01	84.21	-10.66
86	2jsa-7	LYS_A_15_N	LYS_A_15_CA	-6.893	2.569	-1.062	-7.802	1.448	-1.229	1.45	96.60	-129.04
87	2jsa-7	LYS_A_15_CA	LYS_A_15_HA	-7.802	1.448	-1.229	-8.555	1.731	-1.965	1.09	132.46	159.40
88	2jsa-7	LYS_A_15_CA	LYS_A_15_C	-7.802	1.448	-1.229	-8.522	1.18	0.093	1.53	30.16	-159.58
89	2jsa-7	LYS_A_15_C	LYS_A_15_O	-8.522	1.18	0.093	-9.71	0.856	0.103	1.23	89.53	-164.74
90	2jsa-7	LYS_A_15_C	TYR_A_16_N	-8.522	1.18	0.093	-7.776	1.324	1.178	1.32	35.00	10.93
91	2jsa-7	TYR_A_16_N	TYR_A_16_H	-7.776	1.324	1.178	-6.805	1.592	1.096	1.01	94.65	15.43
92	2jsa-7	TYR_A_16_N	TYR_A_16_CA	-7.776	1.324	1.178	-8.329	1.101	2.503	1.45	24.23	-158.04
93	2jsa-7	TYR_A_16_CA	TYR_A_16_HA	-8.329	1.101	2.503	-8.922	0.187	2.516	1.09	89.32	-122.98
94	2jsa-7	TYR_A_16_CA	TYR_A_16_C	-8.329	1.101	2.503	-9.191	2.286	2.943	1.53	73.29	126.03
95	2jsa-7	TYR_A_16_C	TYR_A_16_O	-9.191	2.286	2.943	-10.417	2.187	2.979	1.23	88.32	-175.38
96	2jsa-7	TYR_A_16_C	GLU_A_17_N	-9.191	2.286	2.943	-8.516	3.38	3.267	1.33	75.85	58.33
97	2jsa-7	GLU_A_17_N	GLU_A_17_H	-8.516	3.38	3.267	-7.507	3.391	3.213	1.01	93.06	0.62
98	2jsa-7	GLU_A_17_N	GLU_A_17_CA	-8.516	3.38	3.267	-9.206	4.581	3.703	1.45	72.53	119.88
99	2jsa-7	GLU_A_17_CA	GLU_A_17_HA	-9.206	4.581	3.703	-9.529	4.429	4.733	1.09	19.12	-154.80
100	2jsa-7	GLU_A_17_CA	GLU_A_17_C	-9.206	4.581	3.703	-10.446	4.825	2.841	1.53	124.30	168.87
101	2jsa-7	GLU_A_17_C	GLU_A_17_O	-10.446	4.825	2.841	-11.436	5.383	3.313	1.23	67.45	150.59
102	2jsa-7	GLU_A_17_C	GLY_A_18_N	-10.446	4.825	2.841	-10.351	4.397	1.591	1.32	160.67	-77.49
103	2jsa-7	GLY_A_18_N	GLY_A_18_H	-10.351	4.397	1.591	-9.505	3.948	1.27	1.01	108.53	-27.96
104	2jsa-7	GLY_A_18_N	GLY_A_18_CA	-10.351	4.397	1.591	-11.453	4.562	0.658	1.45	129.94	171.48
105	2jsa-7	GLY_A_18_CA	GLY_A_18_C	-11.453	4.562	0.658	-11.927	3.208	0.125	1.53	110.38	-109.29
106	2jsa-7	GLY_A_18_C	GLY_A_18_O	-11.927	3.208	0.125	-12.236	3.076	-1.059	1.23	164.16	-156.87
107	2jsa-7	GLY_A_18_C	SER_A_19_N	-11.927	3.208	0.125	-11.972	2.237	1.025	1.32	47.20	-92.65
108	2jsa-7	SER_A_19_N	SER_A_19_H	-11.972	2.237	1.025	-11.706	2.418	1.983	1.01	18.56	34.23
109	2jsa-7	SER_A_19_N	SER_A_19_CA	-11.972	2.237	1.025	-12.403	0.898	0.66	1.45	104.55	-107.84
110	2jsa-7	SER_A_19_CA	SER_A_19_HA	-12.403	0.898	0.66	-11.984	0.659	-0.317	1.09	153.72	-29.70
111	2jsa-7	SER_A_19_CA	SER_A_19_C	-12.403	0.898	0.66	-13.93	0.849	0.566	1.53	93.52	-178.16
112	2jsa-7	SER_A_19_C	SER_A_19_O	-13.93	0.849	0.566	-14.479	0.45	-0			

114	2jsa-7	ALA_A_20_N	ALA_A_20_H	-14.572	1.258	1.649	-14.054	1.571	2.458	1.01	36.80	31.14
115	2jsa-7	ALA_A_20_N	ALA_A_20_CA	-14.572	1.258	1.649	-16.024	1.266	1.702	1.45	87.91	179.68
116	2jsa-7	ALA_A_20_CA	ALA_A_20_HA	-16.024	1.266	1.702	-16.343	1.968	2.473	1.09	45.00	114.44
117	2jsa-7	ALA_A_20_CA	ALA_A_20_C	-16.024	1.266	1.702	-16.523	-0.13	2.081	1.53	75.66	-109.67
118	2jsa-7	ALA_A_20_C	ALA_A_20_O	-16.523	-0.13	2.081	-17.716	-0.326	2.307	1.23	79.41	-170.67
119	2jsa-7	ALA_A_20_C	ASP_A_21_N	-16.523	-0.13	2.081	-15.585	-1.064	2.138	1.32	87.53	-44.88
120	2jsa-7	ASP_A_21_N	ASP_A_21_H	-15.585	-1.064	2.138	-14.622	-0.831	1.939	1.01	101.36	13.60
121	2jsa-7	ASP_A_21_N	ASP_A_21_CA	-15.585	-1.064	2.138	-15.914	-2.436	2.485	1.45	76.18	-103.48
122	2jsa-7	ASP_A_21_CA	ASP_A_21_HA	-15.914	-2.436	2.485	-16.997	-2.537	2.545	1.09	86.84	-174.67
123	2jsa-7	ASP_A_21_CA	ASP_A_21_C	-15.914	-2.436	2.485	-15.285	-2.78	3.837	1.53	27.94	-28.67
124	2jsa-7	ASP_A_21_C	ASP_A_21_O	-15.285	-2.78	3.837	-15.691	-3.742	4.488	1.23	58.06	-112.88
125	2jsa-7	ASP_A_21_C	LYS_A_22_N	-15.285	-2.78	3.837	-14.302	-1.977	4.217	1.32	73.33	39.24
126	2jsa-7	LYS_A_22_N	LYS_A_22_H	-14.302	-1.977	4.217	-14.019	-1.205	3.63	1.01	125.52	69.87
127	2jsa-7	LYS_A_22_N	LYS_A_22_CA	-14.302	-1.977	4.217	-13.612	-2.186	5.479	1.45	29.74	-16.85
128	2jsa-7	LYS_A_22_CA	LYS_A_22_HA	-13.612	-2.186	5.479	-12.747	-1.523	5.504	1.09	88.69	37.47
129	2jsa-7	LYS_A_22_CA	LYS_A_22_C	-13.612	-2.186	5.479	-13.096	-3.625	5.541	1.53	87.68	-70.27
130	2jsa-7	LYS_A_22_C	LYS_A_22_O	-13.096	-3.625	5.541	-13.52	-4.403	6.395	1.23	46.05	-118.59
131	2jsa-7	LYS_A_22_C	ASP_A_23_N	-13.096	-3.625	5.541	-12.189	-3.936	4.627	1.32	133.63	-18.93
132	2jsa-7	ASP_A_23_N	ASP_A_23_H	-12.189	-3.936	4.627	-11.887	-3.246	3.954	1.01	131.78	66.36
133	2jsa-7	ASP_A_23_N	ASP_A_23_CA	-12.189	-3.936	4.627	-11.611	-5.267	4.569	1.45	92.29	-66.53
134	2jsa-7	ASP_A_23_CA	ASP_A_23_HA	-11.611	-5.267	4.569	-11.635	-5.71	5.565	1.09	24.01	-93.10
135	2jsa-7	ASP_A_23_CA	ASP_A_23_C	-11.611	-5.267	4.569	-10.166	-5.17	4.077	1.53	108.76	3.84
136	2jsa-7	ASP_A_23_C	ASP_A_23_O	-10.166	-5.17	4.077	-9.924	-4.918	2.897	1.23	163.51	46.16
137	2jsa-7	ASP_A_23_C	ALA_A_24_N	-10.166	-5.17	4.077	-9.243	-5.375	5.005	1.32	45.53	-12.52
138	2jsa-7	ALA_A_24_N	ALA_A_24_H	-9.243	-5.375	5.005	-9.515	-5.577	5.956	1.01	19.61	-143.40
139	2jsa-7	ALA_A_24_N	ALA_A_24_CA	-9.243	-5.375	5.005	-7.828	-5.313	4.681	1.45	102.89	2.51
140	2jsa-7	ALA_A_24_CA	ALA_A_24_HA	-7.828	-5.313	4.681	-7.611	-4.339	4.242	1.09	113.75	77.44
141	2jsa-7	ALA_A_24_CA	ALA_A_24_C	-7.828	-5.313	4.681	-7.499	-6.395	3.649	1.53	132.38	-73.09
142	2jsa-7	ALA_A_24_C	ALA_A_24_O	-7.499	-6.395	3.649	-6.43	-6.371	3.041	1.23	119.62	1.29
143	2jsa-7	ALA_A_24_C	ASN_A_25_N	-7.499	-6.395	3.649	-8.436	-7.316	3.484	1.32	97.16	-135.49
144	2jsa-7	ASN_A_25_N	ASN_A_25_H	-8.436	-7.316	3.484	-9.291	-7.271	4.019	1.01	58.00	176.99
145	2jsa-7	ASN_A_25_N	ASN_A_25_CA	-8.436	-7.316	3.484	-8.259	-8.404	2.538	1.45	130.64	-80.76
146	2jsa-7	ASN_A_25_CA	ASN_A_25_HA	-8.259	-8.404	2.538	-7.23	-8.759	2.592	1.09	87.16	-19.03
147	2jsa-7	ASN_A_25_CA	ASN_A_25_C	-8.259	-8.404	2.538	-8.562	-7.898	1.125	1.53	157.34	120.91
148	2jsa-7	ASN_A_25_C	ASN_A_25_O	-8.562	-7.898	1.125	-7.89	-8.281	0.168	1.23	141.05	-29.68
149	2jsa-7	ASN_A_25_C	VAL_A_26_N	-8.562	-7.898	1.125	-9.573	-7.046	1.04	1.32	93.68	139.88
150	2jsa-7	VAL_A_26_N	VAL_A_26_H	-9.573	-7.046	1.04	-10.08	-6.775	1.87	1.01	34.71	151.87
151	2jsa-7	VAL_A_26_N	VAL_A_26_CA	-9.573	-7.046	1.04	-9.973	-6.485	-0.239	1.45	151.69	125.49
152	2jsa-7	VAL_A_26_CA	VAL_A_26_HA	-9.973	-6.485	-0.239	-9.754	-7.215	-1.019	1.09	135.66	-73.30
153	2jsa-7	VAL_A_26_CA	VAL_A_26_C	-9.973	-6.485	-0.239	-9.147	-5.228	-0.52	1.53	100.58	56.69
154	2jsa-7	VAL_A_26_C	VAL_A_26_O	-9.147	-5.228	-0.52	-9.217	-4.667	-1.612	1.23	152.63	97.11
155	2jsa-7	VAL_A_26_C	ILE_A_27_N	-9.147	-5.228	-0.52	-8.386	-4.822	0.485	1.32	40.64	28.08
156	2jsa-7	ILE_A_27_N	ILE_A_27_H	-8.386	-4.822	0.485	-8.378	-5.332	1.357	1.01	30.32	-89.10
157	2jsa-7	ILE_A_27_N	ILE_A_27_CA	-8.386	-4.822	0.485	-7.548	-3.642	0.359	1.45	94.98	54.62
158	2jsa-7	ILE_A_27_CA	ILE_A_27_HA	-7.548	-3.642	0.359	-7.986	-2.996	-0.402	1.09	134.28	124.14
159	2jsa-7	ILE_A_27_CA	ILE_A_27_C	-7.548	-3.642	0.359	-6.159	-4.057	-0.128	1.53	108.57	-16.63
160	2jsa-7	ILE_A_27_C	ILE_A_27_O	-6.159	-4.057	-0.128	-5.711	-3.616	-1.184	1.23	149.23	44.55
161	2jsa-7	ILE_A_27_C	LYS_A_28_N	-6.159	-4.057	-0.128	-5.515	-4.901	0.666	1.33	53.21	-52.66
162	2jsa-7	LYS_A_28_N	LYS_A_28_H	-5.515	-4.901	0.666	-5.944	-5.222	1.522	1.01	32.04	-143.19
163	2jsa-7	LYS_A_28_N	LYS_A_28_CA	-5.515	-4.901	0.666	-4.186	-5.381	0.328	1.45	103.45	-19.86
164	2jsa-7	LYS_A_28_CA	LYS_A_28_HA	-4.186	-5.381	0.328	-3.511	-4.525	0.312	1.09	90.84	51.74
165	2jsa-7	LYS_A_28_CA	LYS_A_28_C	-4.186	-5.381	0.328	-4.208	-5.982	-1.079	1.53	156.86	-92.10
166	2jsa-7	LYS_A_28_C	LYS_A_28_O	-4.208	-5.982	-1.079	-3.314	-5.722	-1.882	1.23	130.78	16.22
167	2jsa-7	LYS_A_28_C	LYS_A_29_N	-4.208	-5.982	-1.079	-5.239	-6.773	-1.334	1.32	101.10	-142.50
168	2jsa-7	LYS_A_29_N	LYS_A_29_H	-5.239	-6.773	-1.334	-5.938	-6.942	-0.625	1.01	45.41	-166.41
169	2jsa-7	LYS_A_29_N	LYS_A_29_CA	-5.239	-6.773	-1.334	-5.388	-7.412	-2.63	1.45	153.15	-103.13
170	2jsa-7	LYS_A_29_CA	LYS_A_29_HA	-5.388	-7.412	-2.63	-4.443	-7.895	-2.879	1.09	103.20	-27.07
171	2jsa-7	LYS_A_29_CA	LYS_A_29_C	-5.388	-7.412	-2.63	-5.659	-6.346	-3.693	1.53	134.02	104.26
172	2jsa-7	LYS_A_29_C	LYS_A_29_O	-5.659	-6.346	-3.693	-5.031	-6.345	-4.75	1.23	149.28	0.09
173	2jsa-7	LYS_A_29_C	ASP_A_30_N	-5.659	-6.346	-3.693	-6.593	-5.462	-3.374	1.32	76.07	136.58
174	2jsa-7	ASP_A_30_N	ASP_A_30_H	-6.593	-5.462	-3.374	-7.068	-5.523	-2.485	1.01	28.31	-172.68
175	2jsa-7	ASP_A_30_N	ASP_A_30_CA	-6.593	-5.462	-3.374	-6.954	-4.392	-4.287	1.45	128.96	108.64
176	2jsa-7	ASP_A_30_CA	ASP_A_30_HA	-6.954	-4.392	-4.287	-7.497	-4.814	-5.132	1.09	140.86	-142.15
177	2jsa-7	ASP_A_30_CA	ASP_A_30_C	-6.954	-4.392	-4.287	-5.684	-3.698	-4.781	1.53	108.85	28.65
178	2jsa-7	ASP_A_30_C	ASP_A_30_O	-5.684	-3.698	-4.781	-5.48	-3.552	-5.985	1.23	168.23	35.59
179	2jsa-7	ASP_A_30_C	PHE_A_31_N	-5.684	-3.698	-4.781	-4.862	-3.289	-3.825	1.33	43.84	26.45
180	2jsa-7	PHE_A_31_N	PHE_A_31_H	-4.862	-3.289	-3.825	-5.094	-3.443	-2.854	1.01	16.00	-146.42
181	2jsa-7	PHE_A_31_N	PHE_A_31_CA	-4.862	-3.289	-3.825	-3.616	-2.614	-4.147	1.45	102.80	28.45
182	2jsa-7	PHE_A_31_CA	PHE_A_31_HA	-3.616	-2.614	-4.147	-3.815	-1.576	-4.414	1.09	104.18	100.85
183	2jsa-7	PHE_A_31_CA	PHE_A_31_C	-3.616	-2.614	-4.147	-2.897	-3.313	-5.302	1.53	139.04	-44.19
184	2jsa-7	PHE_A_31_C	PHE_A_31_O	-2.897	-3.313	-5.302	-2.597	-2.689	-6.32	1.23	145.78	64.32
185	2jsa-7	PHE_A_31_C	ASP_A_32_N	-2.897	-3.313	-5.302	-2.64	-4.598	-5.106	1.33	81.49	-78.69
186	2jsa-7	ASP_A_32_N	ASP_A_32_H	-2.64	-4.598	-5.106	-2.914	-5.046	-4.243	1.01	31.32	-121.45
187	2jsa-7	ASP_A_32_N	ASP_A_32_CA	-2.64	-4.598	-5.106	-1.961	-5.388	-6.119	1.45	134.20	-49.32
188	2jsa-7	ASP_A_32_CA	ASP_A_32_HA	-1.961	-5.388	-6.119	-0.917	-5.079	-6.171	1.09	92.73	16.49
189	2jsa-7	ASP_A_32_CA	ASP_A_32_C	-1.961	-5.388	-6.119	-2.638	-5.164	-7.473	1.53	152.23	161.69
190	2jsa-7	ASP_A_32_C	ASP_A_32_O	-2.638	-5.164	-7.473	-1.967	-5.1	-8.502	1.23	146.77	5.45
191	2jsa-7	ASP_A_32_C	ALA_A_33_N	-2.638	-5.164	-7.473	-3.957	-5.05	-7.428	1.32	88.05	175.06
192	2jsa-7	ALA_A_33_N	ALA_A_33_H	-3.957	-5.05	-7.428	-4.443	-5.113	-6.545	1.01	29.03	-172.61
193	2jsa-7	ALA_A_33_N	ALA_A_33_CA	-3.957	-5.05	-7.428	-4.731	-4.835	-8.638	1.45	146.42	164.48
194	2jsa-7	ALA_A_33_CA	ALA_A_33_HA	-4.731	-4.835	-8.638	-4.674	-5.732	-9.254	1.09	124.42	-86.36
195	2jsa-7	ALA_A_33_CA	ALA_A_33_C	-4.731	-4.835	-8.638	-4.127	-3.669	-9.423	1.53	120.87	62.62
196	2jsa-7	ALA_A_33_C	ALA_A_33_O	-4.127	-3.669	-9.423	-3.761	-3.824	-10.588	1.23	161.16	-22.95
197	2jsa-7	ALA_A_33_C	GLU_A_34_N	-4.127	-3.669	-9.423	-4.042	-2.528	-8.756	1.32	59.76	85.74
198	2jsa-7	GLU_A_34_N	GLU_A_34_H	-4.042	-2.528	-8.756	-4.362	-2.473	-7.8	1.01	18.76	170.25
199	2jsa-7	GLU_A_34_N	GLU_A_34_CA	-4.042	-2.528	-8.756	-3.489	-1.337	-9.377	1.45	115.31	65.09
200	2jsa-7	GLU_A_34_CA	GLU_A_34_HA	-3.489	-1.337	-9.377	-3.943	-1.228	-10.362	1.09	154.64	166.50
201	2jsa-7	GLU_A_34_CA	GLU_A_34_C	-3.489	-1.337	-9.377	-1.977	-1.486	-9.559	1.53	96.83	-5.63
202	2jsa-7	GLU_A_34_C	GLU_A_34_O	-1.977	-1.486	-9.559	-1.466	-1.365	-10.671	1.23	154.72	13.32
203	2jsa-7	GLU_A_34_C	CYS_A_35_N	-1.977	-1.486	-9.559	-1.303	-1.747	-8.447	1.33	33.02	-21.17
204	2jsa-7	CYS_A_35_N	CYS_A_35_H	-1.303	-1.747	-8.447	-1.788	-1.834	-7.566	1.01		

207	2jsa-7	CYS_A_35_CA	CYS_A_35_C	0.14	-1.914	-8.47	0.515	-2.692	-9.733	1.53	145.64	-64.27
208	2jsa-7	CYS_A_35_C	CYS_A_35_O	0.515	-2.692	-9.733	1.595	-2.496	-10.289	1.23	116.86	10.29
209	2jsa-7	CYS_A_35_C	LYS_A_36_N	0.515	-2.692	-9.733	-0.399	-3.556	-10.151	1.33	108.38	-136.61
210	2jsa-7	LYS_A_36_N	LYS_A_36_H	-0.399	-3.556	-10.151	-1.266	-3.663	-9.645	1.01	59.92	-172.96
211	2jsa-7	LYS_A_36_N	LYS_A_36_CA	-0.399	-3.556	-10.151	-0.178	-4.364	-11.338	1.45	144.79	-74.70
212	2jsa-7	LYS_A_36_CA	LYS_A_36_HA	-0.178	-4.364	-11.338	0.816	-4.807	-11.265	1.09	86.16	-24.02
213	2jsa-7	LYS_A_36_CA	LYS_A_36_C	-0.178	-4.364	-11.338	-0.196	-3.461	-12.573	1.53	143.82	91.14
214	2jsa-7	LYS_A_36_C	LYS_A_36_O	-0.196	-3.461	-12.573	0.855	-3.132	-13.121	1.23	116.45	17.38
215	2jsa-7	LYS_A_36_C	LYS_A_37_N	-0.196	-3.461	-12.573	-1.402	-3.088	-12.977	1.33	107.75	162.81
216	2jsa-7	LYS_A_37_N	LYS_A_37_H	-1.402	-3.088	-12.977	-2.223	-3.398	-12.479	1.01	60.43	-159.31
217	2jsa-7	LYS_A_37_N	LYS_A_37_CA	-1.402	-3.088	-12.977	-1.57	-2.23	-14.138	1.45	143.02	101.08
218	2jsa-7	LYS_A_37_CA	LYS_A_37_HA	-1.57	-2.23	-14.138	-1.117	-2.729	-14.995	1.09	141.82	-47.77
219	2jsa-7	LYS_A_37_CA	LYS_A_37_C	-1.57	-2.23	-14.138	-0.815	-0.919	-13.912	1.53	81.50	60.06
220	2jsa-7	LYS_A_37_C	LYS_A_37_O	-0.815	-0.919	-13.912	-0.56	-0.175	-14.856	1.23	140.20	71.08
221	2jsa-7	LYS_A_37_C	LEU_A_38_N	-0.815	-0.919	-13.912	-0.479	-0.676	-12.653	1.33	18.23	35.87
222	2jsa-7	LEU_A_38_N	LEU_A_38_H	-0.479	-0.676	-12.653	-0.722	-1.333	-11.926	1.01	43.94	-110.30
223	2jsa-7	LEU_A_38_N	LEU_A_38_CA	-0.479	-0.676	-12.653	0.242	0.532	-12.29	1.45	75.53	59.17
224	2jsa-7	LEU_A_38_CA	LEU_A_38_HA	0.242	0.532	-12.29	-0.155	1.354	-12.886	1.09	123.14	115.78
225	2jsa-7	LEU_A_38_CA	LEU_A_38_C	0.242	0.532	-12.29	1.719	0.368	-12.652	1.53	103.69	-6.34
226	2jsa-7	LEU_A_38_C	LEU_A_38_O	1.719	0.368	-12.652	2.189	0.941	-13.634	1.23	142.96	50.64
227	2jsa-7	LEU_A_38_C	PHE_A_39_N	1.719	0.368	-12.652	2.411	-0.417	-11.839	1.33	52.16	-48.60
228	2jsa-7	PHE_A_39_N	PHE_A_39_H	2.411	-0.417	-11.839	1.959	-0.856	-11.05	1.01	38.61	-135.84
229	2jsa-7	PHE_A_39_N	PHE_A_39_CA	2.411	-0.417	-11.839	3.825	-0.664	-12.06	1.45	98.75	-9.91
230	2jsa-7	PHE_A_39_CA	PHE_A_39_HA	3.825	-0.664	-12.06	4.275	0.189	-12.568	1.09	117.78	62.19
231	2jsa-7	PHE_A_39_CA	PHE_A_39_C	3.825	-0.664	-12.06	4.037	-1.93	-12.894	1.53	123.01	-80.49
232	2jsa-7	PHE_A_39_C	PHE_A_39_O	4.037	-1.93	-12.894	5.039	-2.624	-12.73	1.23	82.34	-34.71
233	2jsa-7	PHE_A_39_C	HIS_A_40_N	4.037	-1.93	-12.894	3.076	-2.192	-13.768	1.33	131.27	-164.75
234	2jsa-7	HIS_A_40_N	HIS_A_40_H	3.076	-2.192	-13.768	2.279	-1.577	-13.847	1.01	94.49	142.34
235	2jsa-7	HIS_A_40_N	HIS_A_40_CA	3.076	-2.192	-13.768	3.146	-3.362	-14.626	1.45	126.21	-86.58
236	2jsa-7	HIS_A_40_CA	HIS_A_40_HA	3.146	-3.362	-14.626	3.037	-4.247	-13.998	1.09	54.84	-97.02
237	2jsa-7	HIS_A_40_CA	HIS_A_40_C	3.146	-3.362	-14.626	4.519	-3.428	-15.295	1.53	115.95	-2.75
238	2jsa-7	HIS_A_40_C	HIS_A_40_O	4.519	-3.428	-15.295	5.248	-4.406	-15.131	1.23	82.34	-53.30
239	2jsa-7	HIS_A_40_C	THR_A_41_N	4.519	-3.428	-15.295	4.832	-2.375	-16.036	1.33	124.00	73.45
240	2jsa-7	THR_A_41_N	THR_A_41_H	4.832	-2.375	-16.036	4.184	-1.606	-16.126	1.01	95.11	130.12
241	2jsa-7	THR_A_41_N	THR_A_41_CA	4.832	-2.375	-16.036	6.107	-2.301	-16.731	1.45	118.55	3.32
242	2jsa-7	THR_A_41_CA	THR_A_41_HA	6.107	-2.301	-16.731	6.423	-3.311	-16.993	1.09	103.91	-72.63
243	2jsa-7	THR_A_41_CA	THR_A_41_C	6.107	-2.301	-16.731	7.176	-1.694	-15.82	1.53	53.46	29.59
244	2jsa-7	THR_A_41_C	THR_A_41_O	7.176	-1.694	-15.82	7.604	-0.561	-16.028	1.23	99.74	69.31
245	2jsa-7	THR_A_41_C	ILE_A_42_N	7.176	-1.694	-15.82	7.577	-2.477	-14.829	1.33	41.60	-62.88
246	2jsa-7	ILE_A_42_N	ILE_A_42_H	7.577	-2.477	-14.829	7.183	-3.4	-14.718	1.01	83.69	-113.12
247	2jsa-7	ILE_A_42_N	ILE_A_42_CA	7.577	-2.477	-14.829	8.588	-2.031	-13.885	1.45	49.49	23.80
248	2jsa-7	ILE_A_42_CA	ILE_A_42_HA	8.588	-2.031	-13.885	9.277	-1.373	-14.414	1.09	119.04	43.68
249	2jsa-7	ILE_A_42_CA	ILE_A_42_C	8.588	-2.031	-13.885	9.386	-3.241	-13.392	1.53	71.22	-56.59
250	2jsa-7	ILE_A_42_C	ILE_A_42_O	9.386	-3.241	-13.392	8.824	-4.312	-13.173	1.23	79.74	-117.69
251	2jsa-7	ILE_A_42_C	PRO_A_43_N	9.386	-3.241	-13.392	10.718	-3.021	-13.227	1.36	83.03	9.38
252	2jsa-7	PRO_A_43_N	PRO_A_43_CA	10.718	-3.021	-13.227	11.599	-4.079	-12.763	1.45	71.38	-50.22
253	2jsa-7	PRO_A_43_CA	PRO_A_43_HA	11.599	-4.079	-12.763	11.381	-5.005	-13.294	1.09	119.17	-103.25
254	2jsa-7	PRO_A_43_CA	PRO_A_43_C	11.599	-4.079	-12.763	11.418	-4.326	-11.263	1.53	11.54	-126.23
255	2jsa-7	PRO_A_43_C	PRO_A_43_O	11.418	-4.326	-11.263	11.755	-3.471	-10.445	1.23	48.33	68.49
256	2jsa-7	PRO_A_43_C	PHE_A_44_N	11.418	-4.326	-11.263	10.886	-5.497	-10.948	1.32	76.24	-114.43
257	2jsa-7	PHE_A_44_N	PHE_A_44_H	10.886	-5.497	-10.948	10.633	-6.151	-11.674	1.01	135.99	-111.15
258	2jsa-7	PHE_A_44_N	PHE_A_44_CA	10.886	-5.497	-10.948	10.656	-5.867	-9.562	1.45	17.45	-121.87
259	2jsa-7	PHE_A_44_CA	PHE_A_44_HA	10.656	-5.867	-9.562	10.49	-6.942	-9.488	1.09	86.11	-98.78
260	2jsa-7	PHE_A_44_CA	PHE_A_44_C	10.656	-5.867	-9.562	9.452	-5.119	-8.988	1.53	67.95	148.15
261	2jsa-7	PHE_A_44_C	PHE_A_44_O	9.452	-5.119	-8.988	9.106	-5.294	-7.82	1.23	18.36	-153.17
262	2jsa-7	PHE_A_44_C	GLY_A_45_N	9.452	-5.119	-8.988	8.844	-4.301	-9.835	1.33	129.73	126.62
263	2jsa-7	GLY_A_45_N	GLY_A_45_H	8.844	-4.301	-9.835	9.183	-4.206	-10.782	1.01	159.61	15.65
264	2jsa-7	GLY_A_45_N	GLY_A_45_CA	8.844	-4.301	-9.835	7.685	-3.526	-9.426	1.45	73.65	146.23
265	2jsa-7	GLY_A_45_CA	GLY_A_45_C	7.685	-3.526	-9.426	6.569	-4.437	-8.913	1.53	70.40	-140.77
266	2jsa-7	GLY_A_45_C	GLY_A_45_O	6.569	-4.437	-8.913	6.19	-4.363	-7.745	1.23	18.29	168.95
267	2jsa-7	GLY_A_45_C	THR_A_46_N	6.569	-4.437	-8.913	6.074	-5.277	-9.811	1.33	132.65	-120.51
268	2jsa-7	THR_A_46_N	THR_A_46_H	6.074	-5.277	-9.811	6.435	-5.284	-10.754	1.01	159.05	-1.11
269	2jsa-7	THR_A_46_N	THR_A_46_CA	6.074	-5.277	-9.811	5.009	-6.202	-9.463	1.45	76.14	-139.02
270	2jsa-7	THR_A_46_CA	THR_A_46_HA	5.009	-6.202	-9.463	4.161	-5.632	-9.084	1.09	69.65	146.09
271	2jsa-7	THR_A_46_CA	THR_A_46_C	5.009	-6.202	-9.463	5.468	-7.153	-8.357	1.53	43.67	-64.24
272	2jsa-7	THR_A_46_C	THR_A_46_O	5.468	-7.153	-8.357	4.652	-7.659	-7.589	1.23	51.34	-148.20
273	2jsa-7	THR_A_46_C	ARG_A_47_N	5.468	-7.153	-8.357	6.775	-7.369	-8.311	1.33	88.01	-9.38
274	2jsa-7	ARG_A_47_N	ARG_A_47_H	6.775	-7.369	-8.311	7.388	-6.92	-8.976	1.01	131.19	36.22
275	2jsa-7	ARG_A_47_N	ARG_A_47_CA	6.775	-7.369	-8.311	7.354	-8.25	-7.312	1.45	46.54	-56.69
276	2jsa-7	ARG_A_47_CA	ARG_A_47_HA	7.354	-8.25	-7.312	6.821	-9.2	-7.342	1.09	91.58	-119.29
277	2jsa-7	ARG_A_47_CA	ARG_A_47_C	7.354	-8.25	-7.312	7.206	-7.64	-5.916	1.53	24.21	103.64
278	2jsa-7	ARG_A_47_C	ARG_A_47_O	7.206	-7.64	-5.916	6.841	-8.333	-4.968	1.23	39.56	-117.78
279	2jsa-7	ARG_A_47_C	GLU_A_48_N	7.206	-7.64	-5.916	7.497	-6.35	-5.835	1.32	86.49	77.29
280	2jsa-7	GLU_A_48_N	GLU_A_48_H	7.497	-6.35	-5.835	7.791	-5.842	-6.657	1.01	144.47	59.94
281	2jsa-7	GLU_A_48_N	GLU_A_48_CA	7.497	-6.35	-5.835	7.4	-5.639	-4.571	1.45	29.58	97.77
282	2jsa-7	GLU_A_48_CA	GLU_A_48_HA	7.4	-5.639	-4.571	7.859	-6.258	-3.799	1.09	44.95	-53.44
283	2jsa-7	GLU_A_48_CA	GLU_A_48_C	7.4	-5.639	-4.571	5.934	-5.415	-4.199	1.53	75.92	171.31
284	2jsa-7	GLU_A_48_C	GLU_A_48_O	5.934	-5.415	-4.199	5.579	-5.437	-3.021	1.23	16.80	-176.45
285	2jsa-7	GLU_A_48_C	CYS_A_49_N	5.934	-5.415	-4.199	5.121	-5.206	-5.223	1.32	140.66	165.58
286	2jsa-7	CYS_A_49_N	CYS_A_49_H	5.121	-5.206	-5.223	5.482	-5.203	-6.166	1.01	159.05	0.48
287	2jsa-7	CYS_A_49_N	CYS_A_49_CA	5.121	-5.206	-5.223	3.7	-4.978	-5.018	1.45	81.89	170.88
288	2jsa-7	CYS_A_49_CA	CYS_A_49_HA	3.7	-4.978	-5.018	3.577	-4.028	-4.497	1.09	61.46	97.38
289	2jsa-7	CYS_A_49_CA	CYS_A_49_C	3.7	-4.978	-5.018	3.16	-6.097	-4.125	1.53	54.29	-115.76
290	2jsa-7	CYS_A_49_C	CYS_A_49_O	3.16	-6.097	-4.125	2.422	-5.836	-3.175	1.23	39.49	160.52
291	2jsa-7	CYS_A_49_C	ASP_A_50_N	3.16	-6.097	-4.125	3.546	-7.319	-4.462	1.33	104.73	-72.47
292	2jsa-7	ASP_A_50_N	ASP_A_50_H	3.546	-7.319	-4.462	4.153	-7.46	-5.257	1.01	141.91	-13.08
293	2jsa-7	ASP_A_50_N	ASP_A_50_CA	3.546	-7.319	-4.462	3.109	-8.478	-3.702	1.45	58.47	-110.66
294	2jsa-7	ASP_A_50_CA	ASP_A_50_HA	3.109	-8.478	-3.702	2.046	-8.38	-3.483	1.09	78.41	174.73
295	2jsa-7	ASP_A_50_CA	ASP_A_50_C	3.109	-8.478	-3.702	3.903	-8.556	-2.397	1.53	31.44	-5.61
296	2jsa-7	ASP_A_50_C	ASP_A_50_O	3.903	-8.556	-2.397	3.435	-9.13	-1.414	1.23	36.99	-129.19
297	2jsa-7	ASP_A_50_C	HIS_A_51_N	3.903	-8.556							

300	2jsa-7	HIS_A_51_CA	HIS_A_51_HA	5.954	-7.966	-1.26	5.72	-8.849	-0.666	1.09	56.97	-104.84
301	2jsa-7	HIS_A_51_CA	HIS_A_51_C	5.954	-7.966	-1.26	5.656	-6.733	-0.405	1.53	56.02	103.59
302	2jsa-7	HIS_A_51_C	HIS_A_51_O	5.656	-6.733	-0.405	6.43	-6.388	0.486	1.23	43.56	24.02
303	2jsa-7	HIS_A_51_C	TYR_A_52_N	5.656	-6.733	-0.405	4.53	-6.102	-0.707	1.33	103.17	150.73
304	2jsa-7	TYR_A_52_N	TYR_A_52_H	4.53	-6.102	-0.707	3.941	-6.441	-1.454	1.01	137.71	-150.08
305	2jsa-7	TYR_A_52_N	TYR_A_52_CA	4.53	-6.102	-0.707	4.12	-4.914	0.024	1.45	59.82	109.04
306	2jsa-7	TYR_A_52_CA	TYR_A_52_HA	4.12	-4.914	0.024	4.891	-4.625	0.739	1.09	49.03	20.55
307	2jsa-7	TYR_A_52_CA	TYR_A_52_C	4.12	-4.914	0.024	2.797	-5.15	0.754	1.53	61.49	-169.89
308	2jsa-7	TYR_A_52_C	TYR_A_52_O	2.797	-5.15	0.754	2.642	-4.751	1.908	1.23	20.35	111.23
309	2jsa-7	TYR_A_52_C	VAL_A_53_N	2.797	-5.15	0.754	1.878	-5.798	0.054	1.32	121.90	-144.81
310	2jsa-7	VAL_A_53_N	VAL_A_53_H	1.878	-5.798	0.054	2.076	-6.097	-0.89	1.01	159.20	-56.49
311	2jsa-7	VAL_A_53_N	VAL_A_53_CA	1.878	-5.798	0.054	0.573	-6.092	0.622	1.45	66.99	-167.30
312	2jsa-7	VAL_A_53_CA	VAL_A_53_HA	0.573	-6.092	0.622	0.256	-5.236	1.218	1.09	56.86	110.32
313	2jsa-7	VAL_A_53_CA	VAL_A_53_C	0.573	-6.092	0.622	0.688	-7.302	1.553	1.53	52.55	-84.57
314	2jsa-7	VAL_A_53_C	VAL_A_53_O	0.688	-7.302	1.553	-0.047	-8.276	1.404	1.23	96.96	-127.04
315	2jsa-7	VAL_A_53_C	ASN_A_54_N	0.688	-7.302	1.553	1.616	-7.199	2.493	1.32	44.81	6.33
316	2jsa-7	ASN_A_54_N	ASN_A_54_H	1.616	-7.199	2.493	2.185	-6.367	2.557	1.01	86.37	55.63
317	2jsa-7	ASN_A_54_N	ASN_A_54_CA	1.616	-7.199	2.493	1.836	-8.272	3.447	1.45	48.94	-78.41
318	2jsa-7	ASN_A_54_CA	ASN_A_54_HA	1.836	-8.272	3.447	0.944	-8.391	4.062	1.09	55.65	-172.40
319	2jsa-7	ASN_A_54_CA	ASN_A_54_C	1.836	-8.272	3.447	3.035	-7.924	4.332	1.53	54.67	16.18
320	2jsa-7	ASN_A_54_C	ASN_A_54_O	3.035	-7.924	4.332	3.854	-8.787	4.642	1.23	75.40	-46.50
321	2jsa-7	ASN_A_54_C	SER_A_55_N	3.035	-7.924	4.332	3.1	-6.657	4.714	1.32	73.24	87.06
322	2jsa-7	SER_A_55_N	SER_A_55_H	3.1	-6.657	4.714	2.39	-6.001	4.422	1.01	106.81	137.26
323	2jsa-7	SER_A_55_N	SER_A_55_CA	3.1	-6.657	4.714	4.185	-6.184	5.557	1.45	54.54	23.55
324	2jsa-7	SER_A_55_CA	SER_A_55_HA	4.185	-6.184	5.557	4.121	-6.696	6.517	1.09	28.26	-97.13
325	2jsa-7	SER_A_55_CA	SER_A_55_C	4.185	-6.184	5.557	4.045	-4.679	5.794	1.53	81.09	95.31
326	2jsa-7	SER_A_55_C	SER_A_55_O	4.045	-4.679	5.794	4.292	-4.195	6.898	1.23	26.21	62.96
327	2jsa-7	SER_A_55_C	LYS_A_56_N	4.045	-4.679	5.794	3.649	-3.98	4.74	1.33	142.68	119.53
328	2jsa-7	LYS_A_56_N	LYS_A_56_H	3.649	-3.98	4.74	3.464	-4.444	3.863	1.01	150.34	-111.74
329	2jsa-7	LYS_A_56_N	LYS_A_56_CA	3.649	-3.98	4.74	3.473	-2.54	4.82	1.45	86.84	96.97
330	2jsa-7	LYS_A_56_CA	LYS_A_56_HA	3.473	-2.54	4.82	3.803	-2.214	5.807	1.09	25.17	44.65
331	2jsa-7	LYS_A_56_CA	LYS_A_56_C	3.473	-2.54	4.82	1.986	-2.204	4.692	1.53	94.80	167.27
332	2jsa-7	LYS_A_56_C	LYS_A_56_O	1.986	-2.204	4.692	1.602	-1.037	4.755	1.23	87.06	108.21
333	2jsa-7	LYS_A_56_C	VAL_A_57_N	1.986	-2.204	4.692	1.189	-3.248	4.515	1.33	97.67	-127.36
334	2jsa-7	VAL_A_57_N	VAL_A_57_H	1.189	-3.248	4.515	1.575	-4.18	4.472	1.01	92.44	-67.50
335	2jsa-7	VAL_A_57_N	VAL_A_57_CA	1.189	-3.248	4.515	-0.248	-3.079	4.379	1.45	95.37	173.29
336	2jsa-7	VAL_A_57_CA	VAL_A_57_HA	-0.248	-3.079	4.379	-0.449	-2.039	4.12	1.09	103.74	100.94
337	2jsa-7	VAL_A_57_CA	VAL_A_57_C	-0.248	-3.079	4.379	-0.921	-3.372	5.72	1.53	28.69	-156.47
338	2jsa-7	VAL_A_57_C	VAL_A_57_O	-0.921	-3.372	5.72	-2.028	-2.901	5.979	1.23	77.85	156.95
339	2jsa-7	VAL_A_57_C	ASP_A_58_N	-0.921	-3.372	5.72	-0.227	-4.15	6.537	1.32	51.92	-48.27
340	2jsa-7	ASP_A_58_N	ASP_A_58_H	-0.227	-4.15	6.537	0.677	-4.503	6.257	1.01	106.09	-21.33
341	2jsa-7	ASP_A_58_N	ASP_A_58_CA	-0.227	-4.15	6.537	-0.745	-4.513	7.846	1.45	25.79	-144.98
342	2jsa-7	ASP_A_58_CA	ASP_A_58_HA	-0.745	-4.513	7.846	-1.801	-4.764	7.754	1.09	94.84	-166.63
343	2jsa-7	ASP_A_58_CA	ASP_A_58_C	-0.745	-4.513	7.846	-0.572	-3.331	8.803	1.53	51.30	81.67
344	2jsa-7	ASP_A_58_C	ASP_A_58_O	-0.572	-3.331	8.803	-1.486	-2.999	9.556	1.23	52.25	160.04
345	2jsa-7	ASP_A_58_C	PRO_A_59_N	-0.572	-3.331	8.803	0.638	-2.714	8.741	1.36	92.61	27.02
346	2jsa-7	PRO_A_59_N	PRO_A_59_CA	0.638	-2.714	8.741	0.943	-1.577	9.593	1.45	54.10	74.98
347	2jsa-7	PRO_A_59_CA	PRO_A_59_HA	0.943	-1.577	9.593	0.617	-1.777	10.614	1.09	20.54	-148.47
348	2jsa-7	PRO_A_59_CA	PRO_A_59_C	0.943	-1.577	9.593	0.235	-0.315	9.097	1.53	108.92	119.29
349	2jsa-7	PRO_A_59_C	PRO_A_59_O	0.235	-0.315	9.097	-0.439	0.367	9.868	1.23	51.20	134.66
350	2jsa-7	PRO_A_59_C	ILE_A_60_N	0.235	-0.315	9.097	0.412	-0.042	7.813	1.32	165.78	57.04
351	2jsa-7	ILE_A_60_N	ILE_A_60_H	0.412	-0.042	7.813	0.979	-0.648	7.238	1.01	124.72	-46.90
352	2jsa-7	ILE_A_60_N	ILE_A_60_CA	0.412	-0.042	7.813	-0.201	1.126	7.205	1.45	114.75	117.69
353	2jsa-7	ILE_A_60_CA	ILE_A_60_HA	-0.201	1.126	7.205	0.283	2.013	7.615	1.09	67.91	61.38
354	2jsa-7	ILE_A_60_CA	ILE_A_60_C	-0.201	1.126	7.205	-1.68	1.182	7.594	1.53	75.27	177.83
355	2jsa-7	ILE_A_60_C	ILE_A_60_O	-1.68	1.182	7.594	-2.179	2.231	8.003	1.23	70.60	115.44
356	2jsa-7	ILE_A_60_C	ILE_A_61_N	-1.68	1.182	7.594	-2.339	0.042	7.454	1.32	96.07	-120.03
357	2jsa-7	ILE_A_61_N	ILE_A_61_H	-2.339	0.042	7.454	-1.864	-0.782	7.113	1.01	109.72	-60.04
358	2jsa-7	ILE_A_61_N	ILE_A_61_CA	-2.339	0.042	7.454	-3.751	-0.052	7.787	1.45	76.76	-176.19
359	2jsa-7	ILE_A_61_CA	ILE_A_61_HA	-3.751	-0.052	7.787	-4.267	0.78	7.307	1.09	116.12	121.81
360	2jsa-7	ILE_A_61_CA	ILE_A_61_C	-3.751	-0.052	7.787	-3.926	0.103	9.299	1.53	8.79	138.47
361	2jsa-7	ILE_A_61_C	ILE_A_61_O	-3.926	0.103	9.299	-4.996	0.489	9.768	1.23	67.59	160.16
362	2jsa-7	ILE_A_61_C	HIS_A_62_N	-3.926	0.103	9.299	-2.858	-0.204	10.021	1.33	56.99	-16.04
363	2jsa-7	HIS_A_62_N	HIS_A_62_H	-2.858	-0.204	10.021	-2.01	-0.514	9.568	1.01	116.64	-20.08
364	2jsa-7	HIS_A_62_N	HIS_A_62_CA	-2.858	-0.204	10.021	-2.879	-0.104	11.47	1.45	4.03	101.86
365	2jsa-7	HIS_A_62_CA	HIS_A_62_HA	-2.879	-0.104	11.47	-3.804	-0.558	11.825	1.09	70.99	-153.86
366	2jsa-7	HIS_A_62_CA	HIS_A_62_C	-2.879	-0.104	11.47	-2.891	1.37	11.882	1.53	74.38	90.47
367	2jsa-7	HIS_A_62_C	HIS_A_62_O	-2.891	1.37	11.882	-3.222	1.697	13.02	1.23	22.24	135.35
368	2jsa-7	HIS_A_62_C	GLU_A_63_N	-2.891	1.37	11.882	-2.525	2.219	10.934	1.32	135.72	66.68
369	2jsa-7	GLU_A_63_N	GLU_A_63_H	-2.525	2.219	10.934	-2.265	1.878	10.019	1.01	154.89	-52.68
370	2jsa-7	GLU_A_63_N	GLU_A_63_CA	-2.525	2.219	10.934	-2.489	3.65	11.183	1.45	80.13	88.56
371	2jsa-7	GLU_A_63_CA	GLU_A_63_HA	-2.489	3.65	11.183	-2.209	3.804	12.225	1.09	17.05	28.81
372	2jsa-7	GLU_A_63_CA	GLU_A_63_C	-2.489	3.65	11.183	-3.873	4.262	10.962	1.53	98.31	156.15
373	2jsa-7	GLU_A_63_C	GLU_A_63_O	-3.873	4.262	10.962	-4.383	4.98	11.82	1.23	45.75	125.39
374	2jsa-7	GLU_A_63_C	LEU_A_64_N	-3.873	4.262	10.962	-4.442	3.956	9.804	1.33	150.84	-151.73
375	2jsa-7	LEU_A_64_N	LEU_A_64_H	-4.442	3.956	9.804	-3.964	3.359	9.144	1.01	130.79	-51.32
376	2jsa-7	LEU_A_64_N	LEU_A_64_CA	-4.442	3.956	9.804	-5.758	4.468	9.459	1.45	103.73	158.74
377	2jsa-7	LEU_A_64_CA	LEU_A_64_HA	-5.758	4.468	9.459	-5.747	5.549	9.601	1.09	82.52	89.42
378	2jsa-7	LEU_A_64_CA	LEU_A_64_C	-5.758	4.468	9.459	-6.796	3.883	10.418	1.53	51.17	-150.60
379	2jsa-7	LEU_A_64_C	LEU_A_64_O	-6.796	3.883	10.418	-7.711	4.583	10.849	1.23	69.49	142.58
380	2jsa-7	LEU_A_64_C	GLU_A_65_N	-6.796	3.883	10.418	-6.619	2.606	10.724	1.33	76.65	-82.11
381	2jsa-7	GLU_A_65_N	GLU_A_65_H	-6.619	2.606	10.724	-5.842	2.092	10.332	1.01	112.82	-33.49
382	2jsa-7	GLU_A_65_N	GLU_A_65_CA	-6.619	2.606	10.724	-7.529	1.92	11.624	1.45	51.70	-142.99
383	2jsa-7	GLU_A_65_CA	GLU_A_65_HA	-7.529	1.92	11.624	-8.542	2.05	11.243	1.09	110.46	172.69
384	2jsa-7	GLU_A_65_CA	GLU_A_65_C	-7.529	1.92	11.624	-7.459	2.537	13.022	1.53	23.95	83.53
385	2jsa-7	GLU_A_65_C	GLU_A_65_O	-7.459	2.537	13.022	-8.475	2.652	13.705	1.23	56.26	173.54
386	2jsa-7	GLU_A_65_C	GLY_A_66_N	-7.459	2.537	13.022	-6.249	2.917	13.407	1.33	73.11	17.43
387	2jsa-7	GLY_A_66_N	GLY_A_66_H	-6.249	2.917	13.407	-5.456	2.791	12.794	1.01	127.36	-9.03
388	2jsa-7	GLY_A_66_N	GLY_A_66_CA	-6.249	2.917	13.407	-6.034	3.52	14.711	1.45	26.15	70.38
389	2jsa-7	GLY_A_66_CA	GLY_A_66_C	-6.034	3.52	14.711	-6.648	4.919	14.777	1.53	87.53	113.70
390	2jsa-7	GLY_A_66_C	GLY_A_66_O	-6.648	4.919	14.777	-7.462	5.202	15.655	1.23	44.47	

393	2jsa-7	GLY_A_67_N	GLY_A_67_CA	-6.236	5.757	13.837	-6.736	7.119	13.778	1.45	92.33	110.16
394	2jsa-7	GLY_A_67_C	GLY_A_67_O	-6.736	7.119	13.778	-5.728	8.045	13.095	1.53	116.52	42.57
395	2jsa-7	GLY_A_67_C	GLY_A_67_O	-5.728	8.045	13.095	-5.49	9.16	13.558	1.23	67.90	77.95
396	2jsa-7	GLY_A_67_C	THR_A_68_N	-5.728	8.045	13.095	-5.16	7.549	12.005	1.33	145.32	-41.13
397	2jsa-7	THR_A_68_N	THR_A_68_H	-5.16	7.549	12.005	-5.403	6.624	11.682	1.01	108.66	-104.72
398	2jsa-7	THR_A_68_N	THR_A_68_CA	-5.16	7.549	12.005	-4.183	8.317	11.254	1.45	121.15	38.17
399	2jsa-7	THR_A_68_CA	THR_A_68_HA	-4.183	8.317	11.254	-4.11	9.313	11.691	1.09	66.37	85.81
400	2jsa-7	THR_A_68_CA	THR_A_68_C	-4.183	8.317	11.254	-4.629	8.472	9.799	1.53	162.02	160.84
401	2jsa-7	THR_A_68_C	THR_A_68_O	-4.629	8.472	9.799	-5.161	7.534	9.206	1.23	118.81	-119.56
402	2jsa-7	THR_A_68_C	ALA_A_69_N	-4.629	8.472	9.799	-4.397	9.662	9.265	1.32	113.77	78.97
403	2jsa-7	ALA_A_69_N	ALA_A_69_H	-4.397	9.662	9.265	-3.956	10.388	9.812	1.01	57.22	58.72
404	2jsa-7	ALA_A_69_N	ALA_A_69_CA	-4.397	9.662	9.265	-4.769	9.951	7.891	1.45	161.08	142.16
405	2jsa-7	ALA_A_69_CA	ALA_A_69_HA	-4.769	9.951	7.891	-5.808	9.659	7.74	1.09	97.96	-164.30
406	2jsa-7	ALA_A_69_CA	ALA_A_69_C	-4.769	9.951	7.891	-3.892	9.127	6.946	1.53	128.14	-43.22
407	2jsa-7	ALA_A_69_C	ALA_A_69_O	-3.892	9.127	6.946	-2.852	8.61	7.35	1.23	70.82	-26.43
408	2jsa-7	ALA_A_69_C	PRO_A_70_N	-3.892	9.127	6.946	-4.356	9.028	5.671	1.36	159.59	-167.96
409	2jsa-7	PRO_A_70_N	PRO_A_70_CA	-4.356	9.028	5.671	-3.626	8.276	4.665	1.45	133.83	-45.85
410	2jsa-7	PRO_A_70_CA	PRO_A_70_HA	-3.626	8.276	4.665	-3.3	7.321	5.077	1.09	67.79	-71.15
411	2jsa-7	PRO_A_70_CA	PRO_A_70_C	-3.626	8.276	4.665	-2.392	9.047	4.193	1.53	107.97	32.00
412	2jsa-7	PRO_A_70_C	PRO_A_70_O	-2.392	9.047	4.193	-1.534	8.493	3.506	1.23	123.93	-32.85
413	2jsa-7	PRO_A_70_C	LYS_A_71_N	-2.392	9.047	4.193	-2.341	10.313	4.579	1.32	73.06	87.69
414	2jsa-7	LYS_A_71_N	LYS_A_71_H	-2.341	10.313	4.579	-3.082	10.703	5.143	1.01	56.04	152.24
415	2jsa-7	LYS_A_71_N	LYS_A_71_CA	-2.341	10.313	4.579	-1.226	11.166	4.204	1.45	104.96	37.42
416	2jsa-7	LYS_A_71_CA	LYS_A_71_HA	-1.226	11.166	4.204	-0.679	10.672	3.401	1.09	137.45	-42.09
417	2jsa-7	LYS_A_71_CA	LYS_A_71_C	-1.226	11.166	4.204	-0.275	11.309	5.394	1.53	38.94	8.55
418	2jsa-7	LYS_A_71_C	LYS_A_71_O	-0.275	11.309	5.394	0.764	11.959	5.289	1.23	94.90	32.03
419	2jsa-7	LYS_A_71_C	ASP_A_72_N	-0.275	11.309	5.394	-0.665	10.691	6.499	1.32	33.48	-122.25
420	2jsa-7	ASP_A_72_N	ASP_A_72_H	-0.665	10.691	6.499	-1.532	10.174	6.514	1.01	89.15	-149.19
421	2jsa-7	ASP_A_72_N	ASP_A_72_CA	-0.665	10.691	6.499	0.14	10.742	7.709	1.45	33.69	3.63
422	2jsa-7	ASP_A_72_CA	ASP_A_72_HA	0.14	10.742	7.709	0.855	11.561	7.628	1.09	94.26	48.88
423	2jsa-7	ASP_A_72_CA	ASP_A_72_C	0.14	10.742	7.709	0.885	9.416	7.875	1.53	83.77	-60.67
424	2jsa-7	ASP_A_72_C	ASP_A_72_O	0.885	9.416	7.875	2.032	9.396	8.319	1.23	68.84	-1.00
425	2jsa-7	ASP_A_72_C	VAL_A_73_N	0.885	9.416	7.875	0.203	8.341	7.51	1.32	106.00	-122.39
426	2jsa-7	VAL_A_73_N	VAL_A_73_H	0.203	8.341	7.51	-0.737	8.432	7.153	1.01	110.71	174.47
427	2jsa-7	VAL_A_73_N	VAL_A_73_CA	0.203	8.341	7.51	0.787	7.013	7.614	1.45	85.90	-66.26
428	2jsa-7	VAL_A_73_CA	VAL_A_73_HA	0.787	7.013	7.614	0.945	6.787	8.669	1.09	14.65	-55.04
429	2jsa-7	VAL_A_73_CA	VAL_A_73_C	0.787	7.013	7.614	2.15	7.005	6.917	1.53	117.08	-0.34
430	2jsa-7	VAL_A_73_C	VAL_A_73_O	2.15	7.005	6.917	3.158	6.642	7.523	1.23	60.51	-19.80
431	2jsa-7	VAL_A_73_C	CYS_A_74_N	2.15	7.005	6.917	2.138	7.409	5.656	1.32	162.23	91.70
432	2jsa-7	CYS_A_74_N	CYS_A_74_H	2.138	7.409	5.656	1.272	7.694	5.222	1.01	115.46	161.78
433	2jsa-7	CYS_A_74_N	CYS_A_74_CA	2.138	7.409	5.656	3.359	7.453	4.872	1.45	122.69	2.06
434	2jsa-7	CYS_A_74_CA	CYS_A_74_HA	3.359	7.453	4.872	3.957	6.575	5.119	1.09	76.91	-55.74
435	2jsa-7	CYS_A_74_CA	CYS_A_74_C	3.359	7.453	4.872	4.143	8.703	5.273	1.53	74.80	57.90
436	2jsa-7	CYS_A_74_C	CYS_A_74_O	4.143	8.703	5.273	4.31	9.62	4.469	1.23	130.78	79.68
437	2jsa-7	CYS_A_74_C	THR_A_75_N	4.143	8.703	5.273	4.604	8.701	6.515	1.32	20.36	-0.25
438	2jsa-7	THR_A_75_N	THR_A_75_H	4.604	8.701	6.515	4.43	7.912	7.121	1.01	53.13	-102.44
439	2jsa-7	THR_A_75_N	THR_A_75_CA	4.604	8.701	6.515	5.367	9.824	7.033	1.45	69.12	55.81
440	2jsa-7	THR_A_75_CA	THR_A_75_HA	5.367	9.824	7.033	6.122	10.103	6.298	1.09	132.40	20.28
441	2jsa-7	THR_A_75_CA	THR_A_75_C	5.367	9.824	7.033	6.089	9.429	8.322	1.53	32.56	-28.68
442	2jsa-7	THR_A_75_C	THR_A_75_O	6.089	9.429	8.322	7.318	9.465	8.386	1.23	87.02	1.68
443	2jsa-7	THR_A_75_C	LYS_A_76_N	6.089	9.429	8.322	5.297	9.06	9.317	1.32	41.29	-155.02
444	2jsa-7	LYS_A_76_N	LYS_A_76_H	5.297	9.06	9.317	4.295	9.054	9.194	1.01	97.00	-179.66
445	2jsa-7	LYS_A_76_N	LYS_A_76_CA	5.297	9.06	9.317	5.846	8.658	10.601	1.45	27.92	-36.21
446	2jsa-7	LYS_A_76_CA	LYS_A_76_HA	5.846	8.658	10.601	6.742	9.252	10.786	1.09	80.24	33.54
447	2jsa-7	LYS_A_76_CA	LYS_A_76_C	5.846	8.658	10.601	6.268	7.19	10.534	1.53	92.51	-73.96
448	2jsa-7	LYS_A_76_C	LYS_A_76_O	6.268	7.19	10.534	7.039	6.722	11.37	1.23	47.17	-31.26
449	2jsa-7	LYS_A_76_C	LEU_A_77_N	6.268	7.19	10.534	5.744	6.501	9.53	1.33	139.23	-127.25
450	2jsa-7	LEU_A_77_N	LEU_A_77_H	5.744	6.501	9.53	5.117	6.95	8.878	1.01	130.21	144.39
451	2jsa-7	LEU_A_77_N	LEU_A_77_CA	5.744	6.501	9.53	6.056	5.095	9.343	1.45	97.40	-77.49
452	2jsa-7	LEU_A_77_CA	LEU_A_77_HA	6.056	5.095	9.343	6.188	4.645	10.327	1.09	25.48	-73.65
453	2jsa-7	LEU_A_77_CA	LEU_A_77_C	6.056	5.095	9.343	7.383	4.968	8.591	1.53	119.43	-5.47
454	2jsa-7	LEU_A_77_C	LEU_A_77_O	7.383	4.968	8.591	7.898	3.865	8.417	1.23	98.13	-64.97
455	2jsa-7	LEU_A_77_C	ASN_A_78_N	7.383	4.968	8.591	7.899	6.112	8.167	1.32	108.67	65.72
456	2jsa-7	ASN_A_78_N	ASN_A_78_H	7.899	6.112	8.167	7.421	6.983	8.347	1.01	79.73	118.76
457	2jsa-7	ASN_A_78_N	ASN_A_78_CA	7.899	6.112	8.167	9.156	6.142	7.44	1.45	120.04	1.37
458	2jsa-7	ASN_A_78_CA	ASN_A_78_HA	9.156	6.142	7.44	9.478	7.177	7.327	1.09	95.95	72.72
459	2jsa-7	ASN_A_78_CA	ASN_A_78_C	9.156	6.142	7.44	8.958	5.506	6.062	1.53	154.20	-107.29
460	2jsa-7	ASN_A_78_C	ASN_A_78_O	8.958	5.506	6.062	9.892	4.944	5.494	1.23	117.52	-31.04
461	2jsa-7	ASN_A_78_C	GLU_A_79_N	8.958	5.506	6.062	7.734	5.616	5.565	1.33	112.02	174.86
462	2jsa-7	GLU_A_79_N	GLU_A_79_H	7.734	5.616	5.565	7.014	6.094	6.088	1.01	58.82	146.42
463	2jsa-7	GLU_A_79_N	GLU_A_79_CA	7.734	5.616	5.565	7.402	5.057	4.266	1.45	153.41	-120.71
464	2jsa-7	GLU_A_79_CA	GLU_A_79_HA	7.402	5.057	4.266	8.315	4.65	3.831	1.09	113.52	-24.03
465	2jsa-7	GLU_A_79_CA	GLU_A_79_C	7.402	5.057	4.266	6.872	6.152	3.337	1.53	127.37	115.83
466	2jsa-7	GLU_A_79_C	GLU_A_79_O	6.872	6.152	3.337	5.788	6.021	2.772	1.23	117.36	-173.11
467	2jsa-7	GLU_A_79_C	CYS_A_80_N	6.872	6.152	3.337	7.662	7.209	3.21	1.33	95.50	53.23
468	2jsa-7	CYS_A_80_N	CYS_A_80_H	7.662	7.209	3.21	8.541	7.25	3.706	1.01	60.59	2.67
469	2jsa-7	CYS_A_80_N	CYS_A_80_CA	7.662	7.209	3.21	7.286	8.326	2.36	1.45	125.80	108.60
470	2jsa-7	CYS_A_80_CA	CYS_A_80_HA	7.286	8.326	2.36	7.441	8.034	1.321	1.09	162.35	-62.04
471	2jsa-7	CYS_A_80_CA	CYS_A_80_C	7.286	8.326	2.36	8.211	9.503	2.678	1.53	78.01	51.84
472	2jsa-7	CYS_A_80_C	CYS_A_80_O	8.211	9.503	2.678	8.769	9.581	3.771	1.23	27.27	7.96
473	2jsa-7	CYS_A_80_C	PRO_A_81_N	8.211	9.503	2.678	8.347	10.413	1.677	1.36	137.41	81.50
474	2jsa-7	PRO_A_81_N	PRO_A_81_CA	8.347	10.413	1.677	9.194	11.583	1.839	1.45	83.60	54.10
475	2jsa-7	PRO_A_81_CA	PRO_A_81_HA	9.194	11.583	1.839	10.145	11.296	2.289	1.09	65.63	-16.79
476	2jsa-7	PRO_A_81_CA	PRO_A_81_C	9.194	11.583	1.839	8.527	12.623	2.74	1.53	53.90	122.67
477	2jsa-7	PRO_A_81_C	PRO_A_81_O	8.527	12.623	2.74	7.968	13.604	2.253	1.23	113.33	119.68
1	2jsa-8	ARG_A_1_N	ARG_A_1_H	15.458	8.607	-0.117	14.716	8.902	-0.735	1.01	127.74	158.32
2	2jsa-8	ARG_A_1_N	ARG_A_1_CA	15.458	8.607	-0.117	15.288	7.375	0.635	1.45	58.84	-97.86
3	2jsa-8	ARG_A_1_CA	ARG_A_1_HA	15.288	7.375	0.635	16.084	6.686	0.351	1.09	105.10	-40.88
4	2jsa-8	ARG_A_1_CA	ARG_A_1_C	15.288	7.375	0.635	13.936	6.737	0.31	1.53	102.26	-154.74
5	2jsa-8	ARG_A_1_C	ARG_A_1_O	13.936	6.737	0.31	12.941	7.005	0.982	1.23	56.89	164.93
6	2jsa-8	ARG_A_1_C	SER_A_2_N	13.936	6.737	0.31	13.944	5.905	-0.721	1.32	141.10	-89.45

9	2jsa-8	SER_A_2_CA	SER_A_2_HA	12.73	5.227	-1.143	13.006	4.251	-1.541	1.09	111.42	-74.21
10	2jsa-8	SER_A_2_CA	SER_A_2_C	12.73	5.227	-1.143	12.039	6.029	-2.247	1.53	136.20	130.75
11	2jsa-8	SER_A_2_C	SER_A_2_O	12.039	6.029	-2.247	12.687	6.789	-2.966	1.23	125.75	49.55
12	2jsa-8	SER_A_2_C	ALA_A_3_N	12.039	6.029	-2.247	10.732	5.833	-2.349	1.33	94.41	-171.47
13	2jsa-8	ALA_A_3_N	ALA_A_3_H	10.732	5.833	-2.349	10.265	5.191	-1.725	1.01	51.83	-126.03
14	2jsa-8	ALA_A_3_N	ALA_A_3_CA	10.732	5.833	-2.349	9.946	6.529	-3.353	1.45	133.72	138.48
15	2jsa-8	ALA_A_3_CA	ALA_A_3_HA	9.946	6.529	-3.353	9.704	7.524	-2.98	1.09	69.99	103.67
16	2jsa-8	ALA_A_3_CA	ALA_A_3_C	9.946	6.529	-3.353	8.64	5.77	-3.589	1.53	98.88	-149.84
17	2jsa-8	ALA_A_3_C	ALA_A_3_O	8.64	5.77	-3.589	7.561	6.273	-3.282	1.23	75.54	155.01
18	2jsa-8	ALA_A_3_C	LEU_A_4_N	8.64	5.77	-3.589	8.78	4.569	-4.131	1.33	114.14	-83.35
19	2jsa-8	LEU_A_4_N	LEU_A_4_H	8.78	4.569	-4.131	9.7	4.217	-4.356	1.01	102.87	-20.94
20	2jsa-8	LEU_A_4_N	LEU_A_4_CA	8.78	4.569	-4.131	7.624	3.735	-4.413	1.45	101.19	-144.19
21	2jsa-8	LEU_A_4_CA	LEU_A_4_HA	7.624	3.735	-4.413	6.914	4.326	-4.99	1.09	121.99	140.23
22	2jsa-8	LEU_A_4_CA	LEU_A_4_C	7.624	3.735	-4.413	6.948	3.349	-3.096	1.53	30.59	-150.27
23	2jsa-8	LEU_A_4_C	LEU_A_4_O	6.948	3.349	-3.096	5.761	3.026	-3.074	1.23	88.98	-164.78
24	2jsa-8	LEU_A_4_C	SER_A_5_N	6.948	3.349	-3.096	7.732	3.395	-2.029	1.32	36.35	3.36
25	2jsa-8	SER_A_5_N	SER_A_5_H	7.732	3.395	-2.029	8.7	3.67	-2.12	1.01	95.17	15.86
26	2jsa-8	SER_A_5_N	SER_A_5_CA	7.732	3.395	-2.029	7.223	3.054	-0.71	1.45	24.91	-146.18
27	2jsa-8	SER_A_5_CA	SER_A_5_HA	7.223	3.054	-0.71	6.881	2.019	-0.733	1.09	91.21	-108.29
28	2jsa-8	SER_A_5_CA	SER_A_5_C	7.223	3.054	-0.71	6.038	3.954	-0.358	1.53	76.69	142.78
29	2jsa-8	SER_A_5_C	SER_A_5_O	6.038	3.954	-0.358	5.099	3.518	0.306	1.23	57.33	-155.09
30	2jsa-8	SER_A_5_C	CYS_A_6_N	6.038	3.954	-0.358	6.121	5.194	-0.818	1.33	110.31	86.17
31	2jsa-8	CYS_A_6_N	CYS_A_6_H	6.121	5.194	-0.818	6.924	5.484	-1.358	1.01	122.31	19.86
32	2jsa-8	CYS_A_6_N	CYS_A_6_CA	6.121	5.194	-0.818	5.066	6.16	-0.559	1.45	79.74	137.52
33	2jsa-8	CYS_A_6_CA	CYS_A_6_HA	5.066	6.16	-0.559	4.758	6.061	0.482	1.09	17.26	-162.18
34	2jsa-8	CYS_A_6_CA	CYS_A_6_C	5.066	6.16	-0.559	3.873	5.82	-1.455	1.53	125.84	-164.09
35	2jsa-8	CYS_A_6_C	CYS_A_6_O	3.873	5.82	-1.455	2.819	5.417	-0.964	1.23	66.49	-159.08
36	2jsa-8	CYS_A_6_C	GLN_A_7_N	3.873	5.82	-1.455	4.078	5.994	-2.752	1.32	168.29	40.32
37	2jsa-8	GLN_A_7_N	GLN_A_7_H	4.078	5.994	-2.752	4.971	6.33	-3.085	1.01	109.24	20.62
38	2jsa-8	GLN_A_7_N	GLN_A_7_CA	4.078	5.994	-2.752	3.033	5.71	-3.719	1.45	131.76	-164.80
39	2jsa-8	GLN_A_7_CA	GLN_A_7_HA	3.033	5.71	-3.719	2.334	6.546	-3.714	1.09	89.74	129.90
40	2jsa-8	GLN_A_7_CA	GLN_A_7_C	3.033	5.71	-3.719	2.27	4.444	-3.322	1.53	74.97	-121.08
41	2jsa-8	GLN_A_7_C	GLN_A_7_O	2.27	4.444	-3.322	1.054	4.478	-3.146	1.23	81.77	178.40
42	2jsa-8	GLN_A_7_C	MET_A_8_N	2.27	4.444	-3.322	3.018	3.358	-3.194	1.32	84.46	-55.44
43	2jsa-8	MET_A_8_N	MET_A_8_H	3.018	3.358	-3.194	4.014	3.404	-3.357	1.01	99.28	2.64
44	2jsa-8	MET_A_8_N	MET_A_8_CA	3.018	3.358	-3.194	2.428	2.084	-2.82	1.45	75.08	-114.85
45	2jsa-8	MET_A_8_CA	MET_A_8_HA	2.428	2.084	-2.82	1.805	1.733	-3.642	1.09	138.98	-150.60
46	2jsa-8	MET_A_8_CA	MET_A_8_C	2.428	2.084	-2.82	1.563	2.226	-1.567	1.53	34.98	170.68
47	2jsa-8	MET_A_8_C	MET_A_8_O	1.563	2.226	-1.567	0.5	1.614	-1.469	1.23	85.43	-150.07
48	2jsa-8	MET_A_8_C	CYS_A_9_N	1.563	2.226	-1.567	2.05	3.037	-0.64	1.32	45.58	59.02
49	2jsa-8	CYS_A_9_N	CYS_A_9_H	2.05	3.037	-0.64	2.931	3.509	-0.789	1.01	98.48	28.18
50	2jsa-8	CYS_A_9_N	CYS_A_9_CA	2.05	3.037	-0.64	1.335	3.267	0.604	1.45	31.12	162.17
51	2jsa-8	CYS_A_9_CA	CYS_A_9_HA	1.335	3.267	0.604	1.086	2.3	1.041	1.09	66.36	-104.44
52	2jsa-8	CYS_A_9_CA	CYS_A_9_C	1.335	3.267	0.604	0.034	4.006	0.28	1.53	102.22	150.40
53	2jsa-8	CYS_A_9_C	CYS_A_9_O	0.034	4.006	0.28	-0.998	3.753	0.899	1.23	59.78	-166.23
54	2jsa-8	CYS_A_9_C	GLU_A_10_N	0.034	4.006	0.28	0.127	4.904	-0.69	1.33	137.05	84.09
55	2jsa-8	GLU_A_10_N	GLU_A_10_H	0.127	4.904	-0.69	1.01	5.06	-1.157	1.01	117.51	10.02
56	2jsa-8	GLU_A_10_N	GLU_A_10_CA	0.127	4.904	-0.69	-1.03	5.68	-1.103	1.45	106.51	146.15
57	2jsa-8	GLU_A_10_CA	GLU_A_10_HA	-1.03	5.68	-1.103	-1.55	6.013	-0.205	1.09	34.51	147.37
58	2jsa-8	GLU_A_10_CA	GLU_A_10_C	-1.03	5.68	-1.103	-1.988	4.811	-1.919	1.53	122.25	-137.79
59	2jsa-8	GLU_A_10_C	GLU_A_10_O	-1.988	4.811	-1.919	-3.073	5.257	-2.291	1.23	107.59	157.65
60	2jsa-8	GLU_A_10_C	LEU_A_11_N	-1.988	4.811	-1.919	-1.553	3.586	-2.175	1.32	101.14	-70.45
61	2jsa-8	LEU_A_11_N	LEU_A_11_H	-1.553	3.586	-2.175	-0.649	3.286	-1.837	1.01	70.46	-18.36
62	2jsa-8	LEU_A_11_N	LEU_A_11_CA	-1.553	3.586	-2.175	-2.359	2.65	-2.942	1.45	121.84	-130.73
63	2jsa-8	LEU_A_11_CA	LEU_A_11_HA	-2.359	2.65	-2.942	-3.047	3.226	-3.561	1.09	124.60	140.06
64	2jsa-8	LEU_A_11_CA	LEU_A_11_C	-2.359	2.65	-2.942	-3.195	1.8	-1.983	1.53	51.19	-134.52
65	2jsa-8	LEU_A_11_C	LEU_A_11_O	-3.195	1.8	-1.983	-4.4	1.642	-2.177	1.23	99.07	-172.53
66	2jsa-8	LEU_A_11_C	VAL_A_12_N	-3.195	1.8	-1.983	-2.523	1.274	-0.969	1.33	40.08	-38.05
67	2jsa-8	VAL_A_12_N	VAL_A_12_H	-2.523	1.274	-0.969	-1.532	1.446	-0.872	1.01	84.49	9.85
68	2jsa-8	VAL_A_12_N	VAL_A_12_CA	-2.523	1.274	-0.969	-3.189	0.444	0.02	1.45	47.10	-128.74
69	2jsa-8	VAL_A_12_CA	VAL_A_12_HA	-3.189	0.444	0.02	-3.718	-0.354	-0.5	1.09	118.51	-123.54
70	2jsa-8	VAL_A_12_CA	VAL_A_12_C	-3.189	0.444	0.02	-4.221	1.285	0.774	1.53	60.47	140.82
71	2jsa-8	VAL_A_12_C	VAL_A_12_O	-4.221	1.285	0.774	-5.347	0.843	0.99	1.23	79.88	-158.57
72	2jsa-8	VAL_A_12_C	VAL_A_13_N	-4.221	1.285	0.774	-3.797	2.482	1.154	1.33	73.34	70.49
73	2jsa-8	VAL_A_13_N	VAL_A_13_H	-3.797	2.482	1.154	-2.855	2.779	0.942	1.01	102.11	17.50
74	2jsa-8	VAL_A_13_N	VAL_A_13_CA	-3.797	2.482	1.154	-4.67	3.389	1.88	1.45	60.03	133.91
75	2jsa-8	VAL_A_13_CA	VAL_A_13_HA	-4.67	3.389	1.88	-5.064	2.864	2.75	1.09	37.03	-126.89
76	2jsa-8	VAL_A_13_CA	VAL_A_13_C	-4.67	3.389	1.88	-5.848	3.779	0.986	1.53	125.77	161.68
77	2jsa-8	VAL_A_13_C	VAL_A_13_O	-5.848	3.779	0.986	-7.005	3.553	1.342	1.23	73.20	-168.95
78	2jsa-8	VAL_A_13_C	LYS_A_14_N	-5.848	3.779	0.986	-5.516	4.359	-0.158	1.32	149.71	60.21
79	2jsa-8	LYS_A_14_N	LYS_A_14_H	-5.516	4.359	-0.158	-4.544	4.515	-0.386	1.01	103.04	9.12
80	2jsa-8	LYS_A_14_N	LYS_A_14_CA	-5.516	4.359	-0.158	-6.533	4.782	-1.105	1.45	130.69	157.42
81	2jsa-8	LYS_A_14_CA	LYS_A_14_HA	-6.533	4.782	-1.105	-7.025	5.666	-0.699	1.09	68.13	119.10
82	2jsa-8	LYS_A_14_CA	LYS_A_14_C	-6.533	4.782	-1.105	-7.589	3.683	-1.24	1.53	95.06	-133.86
83	2jsa-8	LYS_A_14_C	LYS_A_14_O	-7.589	3.683	-1.24	-8.764	3.971	-1.462	1.23	100.40	166.23
84	2jsa-8	LYS_A_14_C	LYS_A_15_N	-7.589	3.683	-1.24	-7.132	2.448	-1.098	1.32	83.85	-69.69
85	2jsa-8	LYS_A_15_N	LYS_A_15_H	-7.132	2.448	-1.098	-6.152	2.286	-0.914	1.01	79.51	-9.39
86	2jsa-8	LYS_A_15_N	LYS_A_15_CA	-7.132	2.448	-1.098	-8.022	1.305	-1.202	1.45	94.11	-127.91
87	2jsa-8	LYS_A_15_CA	LYS_A_15_HA	-8.022	1.305	-1.202	-8.771	1.529	-1.961	1.09	134.15	163.35
88	2jsa-8	LYS_A_15_CA	LYS_A_15_C	-8.022	1.305	-1.202	-8.752	1.111	0.129	1.53	29.57	-165.12
89	2jsa-8	LYS_A_15_C	LYS_A_15_O	-8.752	1.111	0.129	-9.942	0.799	0.149	1.23	89.07	-165.31
90	2jsa-8	LYS_A_15_C	TYR_A_16_N	-8.752	1.111	0.129	-8.009	1.304	1.209	1.33	35.40	14.56
91	2jsa-8	TYR_A_16_N	TYR_A_16_H	-8.009	1.304	1.209	-7.035	1.558	1.118	1.01	95.17	14.62
92	2jsa-8	TYR_A_16_N	TYR_A_16_CA	-8.009	1.304	1.209	-8.571	1.155	2.54	1.45	23.60	-165.15
93	2jsa-8	TYR_A_16_CA	TYR_A_16_HA	-8.571	1.155	2.54	-9.105	0.208	2.62	1.09	85.79	-119.42
94	2jsa-8	TYR_A_16_CA	TYR_A_16_C	-8.571	1.155	2.54	-9.514	2.313	2.871	1.53	77.50	129.16
95	2jsa-8	TYR_A_16_C	TYR_A_16_O	-9.514	2.313	2.871	-10.72	2.115	3.014	1.23	83.33	-170.68
96	2jsa-8	TYR_A_16_C	GLU_A_17_N	-9.514	2.313	2.871	-8.93	3.497	2.98	1.32	85.28	63.75
97	2jsa-8	GLU_A_17_N	GLU_A_17_H	-8.93	3.497	2.98	-7.932	3.586	2.847	1.01	97.56	5.10
98	2jsa-8	GLU_A_17_N	GLU_A_17_CA	-8.93	3.497	2.98	-9.704	4.688	3.291	1.45	77.65	123.02
99	2jsa-8	GLU_A_17_CA	GLU_A_17_HA	-9.704	4.688	3.291	-10.01	4.628	4.336	1.09	16.62	-168.91
100	2jsa-8	GLU_A_17_CA	GLU_A_17_C	-9.704	4.688	3.291	-10.963	4.743	2.424	1.53	124.53	177.50
101	2jsa-8	GLU_A_17_C	GLU_A_17_O	-10.963	4.743</							

102	2jsa-8	GLU_A_17_C	GLY_A_18_N	-10.963	4.743	2.424	-10.802	4.332	1.175	1.32	160.54	-68.61
103	2jsa-8	GLY_A_18_N	GLY_A_18_H	-10.802	4.332	1.175	-9.897	4.013	0.858	1.01	108.28	-19.42
104	2jsa-8	GLY_A_18_N	GLY_A_18_CA	-10.802	4.332	1.175	-11.912	4.33	0.238	1.45	130.17	-179.90
105	2jsa-8	GLY_A_18_CA	GLY_A_18_C	-11.912	4.33	0.238	-12.277	2.903	-0.178	1.53	105.77	-104.35
106	2jsa-8	GLY_A_18_C	GLY_A_18_O	-12.277	2.903	-0.178	-12.394	2.61	-1.366	1.23	165.13	-111.77
107	2jsa-8	GLY_A_18_C	SER_A_19_N	-12.277	2.903	-0.178	-12.445	2.054	0.826	1.33	40.76	-101.19
108	2jsa-8	SER_A_19_N	SER_A_19_H	-12.445	2.054	0.826	-12.332	2.365	1.781	1.01	19.11	70.03
109	2jsa-8	SER_A_19_N	SER_A_19_CA	-12.445	2.054	0.826	-12.794	0.664	0.578	1.45	99.82	-104.09
110	2jsa-8	SER_A_19_CA	SER_A_19_HA	-12.794	0.664	0.578	-12.62	0.45	-0.476	1.09	165.34	-50.89
111	2jsa-8	SER_A_19_CA	SER_A_19_C	-12.794	0.664	0.578	-14.275	0.434	0.888	1.53	78.31	-171.17
112	2jsa-8	SER_A_19_C	SER_A_19_O	-14.275	0.434	0.888	-14.974	-0.236	0.13	1.23	128.06	-136.21
113	2jsa-8	SER_A_19_C	ALA_A_20_N	-14.275	0.434	0.888	-14.708	1.001	2.005	1.33	32.57	127.37
114	2jsa-8	ALA_A_20_N	ALA_A_20_H	-14.708	1.001	2.005	-14.075	1.536	2.583	1.01	55.11	40.20
115	2jsa-8	ALA_A_20_N	ALA_A_20_CA	-14.708	1.001	2.005	-16.093	0.866	2.423	1.45	73.28	-174.43
116	2jsa-8	ALA_A_20_CA	ALA_A_20_HA	-16.093	0.866	2.423	-16.248	1.467	3.319	1.09	34.71	104.46
117	2jsa-8	ALA_A_20_CA	ALA_A_20_C	-16.093	0.866	2.423	-16.376	-0.598	2.767	1.53	77.01	-100.94
118	2jsa-8	ALA_A_20_C	ALA_A_20_O	-16.376	-0.598	2.767	-17.528	-0.982	2.963	1.23	80.83	-161.57
119	2jsa-8	ALA_A_20_C	ASP_A_21_N	-16.376	-0.598	2.767	-15.305	-1.375	2.83	1.32	87.27	-35.96
120	2jsa-8	ASP_A_21_N	ASP_A_21_H	-15.305	-1.375	2.83	-14.386	-0.992	2.657	1.01	99.86	22.62
121	2jsa-8	ASP_A_21_N	ASP_A_21_CA	-15.305	-1.375	2.83	-15.425	-2.788	3.147	1.45	77.40	-94.85
122	2jsa-8	ASP_A_21_CA	ASP_A_21_HA	-15.425	-2.788	3.147	-16.477	-3.033	3.292	1.09	82.35	-166.89
123	2jsa-8	ASP_A_21_CA	ASP_A_21_C	-15.425	-2.788	3.147	-14.639	-3.088	4.426	1.53	33.34	-20.89
124	2jsa-8	ASP_A_21_C	ASP_A_21_O	-14.639	-3.088	4.426	-14.757	-4.175	4.99	1.23	62.71	-96.20
125	2jsa-8	ASP_A_21_C	LYS_A_22_N	-14.639	-3.088	4.426	-13.856	-2.105	4.845	1.32	71.56	51.46
126	2jsa-8	LYS_A_22_N	LYS_A_22_H	-13.856	-2.105	4.845	-13.808	-1.238	4.33	1.01	120.67	86.83
127	2jsa-8	LYS_A_22_N	LYS_A_22_CA	-13.856	-2.105	4.845	-13.053	-2.25	6.047	1.45	34.17	-10.24
128	2jsa-8	LYS_A_22_CA	LYS_A_22_HA	-13.053	-2.25	6.047	-12.244	-1.52	6.003	1.09	92.31	42.06
129	2jsa-8	LYS_A_22_CA	LYS_A_22_C	-13.053	-2.25	6.047	-12.42	-3.643	6.067	1.53	89.25	-65.56
130	2jsa-8	LYS_A_22_C	LYS_A_22_O	-12.42	-3.643	6.067	-12.387	-4.299	7.108	1.23	32.25	-87.12
131	2jsa-8	LYS_A_22_C	ASP_A_23_N	-12.42	-3.643	6.067	-11.933	-4.054	4.906	1.32	151.24	-40.16
132	2jsa-8	ASP_A_23_N	ASP_A_23_H	-11.933	-4.054	4.906	-11.996	-3.462	4.09	1.01	143.89	96.07
133	2jsa-8	ASP_A_23_N	ASP_A_23_CA	-11.933	-4.054	4.906	-11.302	-5.356	4.777	1.45	95.09	-64.14
134	2jsa-8	ASP_A_23_CA	ASP_A_23_HA	-11.302	-5.356	4.777	-11.294	-5.845	5.751	1.09	26.66	-89.06
135	2jsa-8	ASP_A_23_CA	ASP_A_23_C	-11.302	-5.356	4.777	-9.869	-5.178	4.274	1.53	109.21	7.08
136	2jsa-8	ASP_A_23_C	ASP_A_23_O	-9.869	-5.178	4.274	-9.654	-4.71	3.156	1.23	155.27	65.33
137	2jsa-8	ASP_A_23_C	ALA_A_24_N	-9.869	-5.178	4.274	-8.926	-5.56	5.122	1.32	50.19	-22.05
138	2jsa-8	ALA_A_24_N	ALA_A_24_H	-8.926	-5.56	5.122	-9.176	-5.936	6.025	1.01	26.57	-123.62
139	2jsa-8	ALA_A_24_N	ALA_A_24_CA	-8.926	-5.56	5.122	-7.519	-5.447	4.777	1.45	103.73	4.59
140	2jsa-8	ALA_A_24_CA	ALA_A_24_HA	-7.519	-5.447	4.777	-7.345	-4.469	4.327	1.09	114.37	79.91
141	2jsa-8	ALA_A_24_CA	ALA_A_24_C	-7.519	-5.447	4.777	-7.163	-6.523	3.749	1.53	132.21	-71.69
142	2jsa-8	ALA_A_24_C	ALA_A_24_O	-7.163	-6.523	3.749	-6.032	-6.577	3.268	1.23	113.02	-2.73
143	2jsa-8	ALA_A_24_C	ASN_A_25_N	-7.163	-6.523	3.749	-8.149	-7.353	3.443	1.32	103.36	-139.91
144	2jsa-8	ASN_A_25_N	ASN_A_25_H	-8.149	-7.353	3.443	-9.054	-7.249	3.878	1.01	64.47	173.44
145	2jsa-8	ASN_A_25_N	ASN_A_25_CA	-8.149	-7.353	3.443	-7.954	-8.425	2.481	1.45	131.44	-79.69
146	2jsa-8	ASN_A_25_CA	ASN_A_25_HA	-7.954	-8.425	2.481	-6.917	-8.76	2.526	1.09	87.64	-17.90
147	2jsa-8	ASN_A_25_CA	ASN_A_25_C	-7.954	-8.425	2.481	-8.272	-7.908	1.077	1.53	156.62	121.60
148	2jsa-8	ASN_A_25_C	ASN_A_25_O	-8.272	-7.908	1.077	-7.513	-8.143	0.139	1.23	139.73	-17.20
149	2jsa-8	ASN_A_25_C	VAL_A_26_N	-8.272	-7.908	1.077	-9.396	-7.213	0.978	1.33	94.28	148.27
150	2jsa-8	VAL_A_26_N	VAL_A_26_H	-9.396	-7.213	0.978	-9.972	-7.058	1.793	1.01	36.20	164.94
151	2jsa-8	VAL_A_26_N	VAL_A_26_CA	-9.396	-7.213	0.978	-9.824	-6.661	-0.296	1.45	151.27	127.79
152	2jsa-8	VAL_A_26_CA	VAL_A_26_HA	-9.824	-6.661	-0.296	-9.524	-7.348	-1.087	1.09	136.54	-66.41
153	2jsa-8	VAL_A_26_CA	VAL_A_26_C	-9.824	-6.661	-0.296	-9.114	-5.326	-0.533	1.53	98.91	61.99
154	2jsa-8	VAL_A_26_C	VAL_A_26_O	-9.114	-5.326	-0.533	-9.225	-4.743	-1.61	1.23	151.14	100.78
155	2jsa-8	VAL_A_26_C	ILE_A_27_N	-9.114	-5.326	-0.533	-8.399	-4.883	0.49	1.32	39.43	31.78
156	2jsa-8	ILE_A_27_N	ILE_A_27_H	-8.399	-4.883	0.49	-8.35	-5.417	1.346	1.01	32.07	-84.76
157	2jsa-8	ILE_A_27_N	ILE_A_27_CA	-8.399	-4.883	0.49	-7.671	-3.628	0.407	1.45	93.27	59.88
158	2jsa-8	ILE_A_27_CA	ILE_A_27_HA	-7.671	-3.628	0.407	-8.175	-2.992	-0.321	1.09	131.90	128.40
159	2jsa-8	ILE_A_27_CA	ILE_A_27_C	-7.671	-3.628	0.407	-6.257	-3.898	-0.112	1.53	109.83	-10.81
160	2jsa-8	ILE_A_27_C	ILE_A_27_O	-6.257	-3.898	-0.112	-5.821	-3.283	-1.083	1.23	142.17	54.67
161	2jsa-8	ILE_A_27_C	LYS_A_28_N	-6.257	-3.898	-0.112	-5.58	-4.818	0.56	1.33	59.53	-53.65
162	2jsa-8	LYS_A_28_N	LYS_A_28_H	-5.58	-4.818	0.56	-6.002	-5.283	1.351	1.01	38.44	-132.22
163	2jsa-8	LYS_A_28_N	LYS_A_28_CA	-5.58	-4.818	0.56	-4.225	-5.177	0.179	1.45	105.21	-14.84
164	2jsa-8	LYS_A_28_CA	LYS_A_28_HA	-4.225	-5.177	0.179	-3.637	-4.261	0.122	1.09	93.00	57.30
165	2jsa-8	LYS_A_28_CA	LYS_A_28_C	-4.225	-5.177	0.179	-4.241	-5.807	-1.215	1.53	155.67	-91.45
166	2jsa-8	LYS_A_28_C	LYS_A_28_O	-4.241	-5.807	-1.215	-3.294	-5.647	-1.984	1.23	128.68	9.59
167	2jsa-8	LYS_A_28_C	LYS_A_29_N	-4.241	-5.807	-1.215	-5.327	-6.51	-1.499	1.32	102.38	-147.08
168	2jsa-8	LYS_A_29_N	LYS_A_29_H	-5.327	-6.51	-1.499	-6.067	-6.6	-0.818	1.01	47.59	-173.07
169	2jsa-8	LYS_A_29_N	LYS_A_29_CA	-5.327	-6.51	-1.499	-5.479	-7.164	-2.787	1.45	152.47	-103.08
170	2jsa-8	LYS_A_29_CA	LYS_A_29_HA	-5.479	-7.164	-2.787	-4.556	-7.702	-3.003	1.09	101.43	-30.24
171	2jsa-8	LYS_A_29_CA	LYS_A_29_C	-5.479	-7.164	-2.787	-5.664	-6.105	-3.874	1.53	135.32	99.91
172	2jsa-8	LYS_A_29_C	LYS_A_29_O	-5.664	-6.105	-3.874	-4.961	-6.117	-4.884	1.23	145.16	-0.98
173	2jsa-8	LYS_A_29_C	ASP_A_30_N	-5.664	-6.105	-3.874	-6.614	-5.213	-3.632	1.33	79.48	136.80
174	2jsa-8	ASP_A_30_N	ASP_A_30_H	-6.614	-5.213	-3.632	-7.154	-5.264	-2.78	1.01	32.48	-174.60
175	2jsa-8	ASP_A_30_N	ASP_A_30_CA	-6.614	-5.213	-3.632	-6.9	-4.149	-4.579	1.45	130.68	105.05
176	2jsa-8	ASP_A_30_CA	ASP_A_30_HA	-6.9	-4.149	-4.579	-7.382	-4.575	-5.459	1.09	143.83	-138.53
177	2jsa-8	ASP_A_30_CA	ASP_A_30_C	-6.9	-4.149	-4.579	-5.591	-3.466	-4.982	1.53	105.27	27.55
178	2jsa-8	ASP_A_30_C	ASP_A_30_O	-5.591	-3.466	-4.982	-5.327	-3.276	-6.168	1.23	164.66	35.74
179	2jsa-8	ASP_A_30_C	PHE_A_31_N	-5.591	-3.466	-4.982	-4.807	-3.117	-3.973	1.32	40.38	24.00
180	2jsa-8	PHE_A_31_N	PHE_A_31_H	-4.807	-3.117	-3.973	-5.088	-3.306	-3.021	1.01	19.58	-146.08
181	2jsa-8	PHE_A_31_N	PHE_A_31_CA	-4.807	-3.117	-3.973	-3.534	-2.459	-4.208	1.45	99.31	27.33
182	2jsa-8	PHE_A_31_CA	PHE_A_31_HA	-3.534	-2.459	-4.208	-3.701	-1.423	-4.503	1.09	105.70	99.16
183	2jsa-8	PHE_A_31_CA	PHE_A_31_C	-3.534	-2.459	-4.208	-2.736	-3.183	-5.295	1.53	135.25	-42.22
184	2jsa-8	PHE_A_31_C	PHE_A_31_O	-2.736	-3.183	-5.295	-2.334	-2.571	-6.285	1.23	143.51	56.70
185	2jsa-8	PHE_A_31_C	ASP_A_32_N	-2.736	-3.183	-5.295	-2.532	-4.473	-5.076	1.32	80.48	-81.01
186	2jsa-8	ASP_A_32_N	ASP_A_32_H	-2.532	-4.473	-5.076	-2.892	-4.91	-4.24	1.01	34.11	-129.48
187	2jsa-8	ASP_A_32_N	ASP_A_32_CA	-2.532	-4.473	-5.076	-1.789	-5.285	-6.025	1.45	130.77	-47.54
188	2jsa-8	ASP_A_32_CA	ASP_A_32_HA	-1.789	-5.285	-6.025	-0.76	-4.926	-6.073	1.09	92.52	19.23
189	2jsa-8	ASP_A_32_CA	ASP_A_32_C	-1.789	-5.285	-6.025	-2.443	-5.176	-7.404	1.53	154.32	170.54
190	2jsa-8	ASP_A_32_C	ASP_A_32_O	-2.443	-5.176	-7.404	-1.804	-5.442	-8.421	1.23	145.76	-22.60
191	2jsa-8	ASP_A_32_C	ALA_A_33_N	-2.443	-5.176	-7.404	-3.709	-4.785	-7.394	1.33	89.57	162.84
192	2jsa-8	ALA_A_33_N	ALA_A_33_H	-3.709	-4.785	-7.394	-4.172	-4.584	-6.519	1.01		

195	2jsa-8	ALA_A_33_CA	ALA_A_33_C	-4.456	-4.638	-8.631	-3.959	-3.399	-9.378	1.53	119.23	68.14
196	2jsa-8	ALA_A_33_C	ALA_A_33_O	-3.959	-3.399	-9.378	-3.541	-3.491	-10.531	1.23	159.63	-12.41
197	2jsa-8	ALA_A_33_C	GLU_A_34_N	-3.959	-3.399	-9.378	-4.021	-2.268	-8.69	1.33	58.73	93.14
198	2jsa-8	GLU_A_34_N	GLU_A_34_H	-4.021	-2.268	-8.69	-4.375	-2.267	-7.744	1.01	20.52	179.84
199	2jsa-8	GLU_A_34_N	GLU_A_34_CA	-4.021	-2.268	-8.69	-3.583	-1.012	-9.273	1.45	113.67	70.78
200	2jsa-8	GLU_A_34_CA	GLU_A_34_HA	-3.583	-1.012	-9.273	-3.824	-1.031	-10.336	1.09	167.19	-175.49
201	2jsa-8	GLU_A_34_CA	GLU_A_34_C	-3.583	-1.012	-9.273	-2.067	-0.86	-9.127	1.53	84.53	5.73
202	2jsa-8	GLU_A_34_C	GLU_A_34_O	-2.067	-0.86	-9.127	-1.533	0.239	-9.274	1.23	96.86	64.09
203	2jsa-8	GLU_A_34_C	CYS_A_35_N	-2.067	-0.86	-9.127	-1.417	-1.978	-8.84	1.32	77.49	-59.83
204	2jsa-8	CYS_A_35_N	CYS_A_35_H	-1.417	-1.978	-8.84	-1.921	-2.847	-8.734	1.01	83.98	-120.11
205	2jsa-8	CYS_A_35_N	CYS_A_35_CA	-1.417	-1.978	-8.84	0.027	-1.982	-8.673	1.45	83.40	-0.16
206	2jsa-8	CYS_A_35_CA	CYS_A_35_HA	0.027	-1.982	-8.673	0.393	-0.965	-8.82	1.09	97.74	70.21
207	2jsa-8	CYS_A_35_CA	CYS_A_35_C	0.027	-1.982	-8.673	0.633	-2.879	-9.754	1.53	134.96	-55.96
208	2jsa-8	CYS_A_35_C	CYS_A_35_O	0.633	-2.879	-9.754	1.649	-2.533	-10.355	1.23	119.25	18.81
209	2jsa-8	CYS_A_35_C	LYS_A_36_N	0.633	-2.879	-9.754	-0.016	-4.013	-9.969	1.32	99.34	-119.78
210	2jsa-8	LYS_A_36_N	LYS_A_36_H	-0.016	-4.013	-9.969	-0.846	-4.232	-9.437	1.01	58.21	-165.22
211	2jsa-8	LYS_A_36_N	LYS_A_36_CA	-0.016	-4.013	-9.969	0.446	-4.963	-10.968	1.45	133.40	-64.07
212	2jsa-8	LYS_A_36_CA	LYS_A_36_HA	0.446	-4.963	-10.968	1.493	-5.188	-10.761	1.09	79.06	-12.13
213	2jsa-8	LYS_A_36_CA	LYS_A_36_C	0.446	-4.963	-10.968	0.376	-4.316	-12.352	1.53	154.82	96.17
214	2jsa-8	LYS_A_36_C	LYS_A_36_O	0.376	-4.316	-12.352	1.381	-4.234	-13.055	1.23	124.88	4.66
215	2jsa-8	LYS_A_36_C	LYS_A_37_N	0.376	-4.316	-12.352	-0.823	-3.871	-12.701	1.33	105.26	159.64
216	2jsa-8	LYS_A_37_N	LYS_A_37_H	-0.823	-3.871	-12.701	-1.606	-3.971	-12.071	1.01	51.41	-172.72
217	2jsa-8	LYS_A_37_N	LYS_A_37_CA	-0.823	-3.871	-12.701	-1.038	-3.233	-13.989	1.45	152.40	108.62
218	2jsa-8	LYS_A_37_CA	LYS_A_37_HA	-1.038	-3.233	-13.989	-0.584	-3.86	-14.756	1.09	134.74	-54.09
219	2jsa-8	LYS_A_37_CA	LYS_A_37_C	-1.038	-3.233	-13.989	-0.321	-1.881	-14.01	1.53	90.79	62.06
220	2jsa-8	LYS_A_37_C	LYS_A_37_O	-0.321	-1.881	-14.01	0.169	-1.45	-15.053	1.23	147.97	41.33
221	2jsa-8	LYS_A_37_C	LEU_A_38_N	-0.321	-1.881	-14.01	-0.282	-1.25	-12.845	1.33	28.49	86.46
222	2jsa-8	LEU_A_38_N	LEU_A_38_H	-0.282	-1.25	-12.845	-0.705	-1.664	-12.027	1.01	35.89	-135.62
223	2jsa-8	LEU_A_38_N	LEU_A_38_CA	-0.282	-1.25	-12.845	0.367	0.044	-12.717	1.45	84.95	63.36
224	2jsa-8	LEU_A_38_CA	LEU_A_38_HA	0.367	0.044	-12.717	-0.102	0.729	-13.423	1.09	130.38	124.40
225	2jsa-8	LEU_A_38_CA	LEU_A_38_C	0.367	0.044	-12.717	1.84	-0.088	-13.107	1.53	104.77	-5.12
226	2jsa-8	LEU_A_38_C	LEU_A_38_O	1.84	-0.088	-13.107	2.315	0.613	-14.0	1.23	136.52	55.88
227	2jsa-8	LEU_A_38_C	PHE_A_39_N	1.84	-0.088	-13.107	2.524	-0.992	-12.421	1.33	58.82	-52.89
228	2jsa-8	PHE_A_39_N	PHE_A_39_H	2.524	-0.992	-12.421	2.069	-1.534	-11.7	1.01	44.47	-130.01
229	2jsa-8	PHE_A_39_N	PHE_A_39_CA	2.524	-0.992	-12.421	3.933	-1.225	-12.685	1.45	100.47	-9.39
230	2jsa-8	PHE_A_39_CA	PHE_A_39_HA	3.933	-1.225	-12.685	4.267	-0.585	-13.502	1.09	138.54	62.44
231	2jsa-8	PHE_A_39_CA	PHE_A_39_C	3.933	-1.225	-12.685	4.19	-2.69	-13.041	1.53	103.46	-80.05
232	2jsa-8	PHE_A_39_C	PHE_A_39_O	4.19	-2.69	-13.041	4.977	-3.365	-12.381	1.23	57.52	-40.62
233	2jsa-8	PHE_A_39_C	HIS_A_40_N	4.19	-2.69	-13.041	3.509	-3.139	-14.086	1.33	142.03	-146.60
234	2jsa-8	HIS_A_40_N	HIS_A_40_H	3.509	-3.139	-14.086	2.878	-2.527	-14.582	1.01	119.43	135.88
235	2jsa-8	HIS_A_40_N	HIS_A_40_CA	3.509	-3.139	-14.086	3.653	-4.513	-14.539	1.45	108.15	-84.02
236	2jsa-8	HIS_A_40_CA	HIS_A_40_HA	3.653	-4.513	-14.539	3.548	-5.166	-13.672	1.09	37.34	-99.13
237	2jsa-8	HIS_A_40_CA	HIS_A_40_C	3.653	-4.513	-14.539	5.055	-4.719	-15.114	1.53	112.09	-8.36
238	2jsa-8	HIS_A_40_C	HIS_A_40_O	5.055	-4.719	-15.114	5.815	-5.555	-14.625	1.23	66.60	-47.73
239	2jsa-8	HIS_A_40_C	THR_A_41_N	5.055	-4.719	-15.114	5.357	-3.943	-16.144	1.32	141.05	68.74
240	2jsa-8	THR_A_41_N	THR_A_41_H	5.357	-3.943	-16.144	4.684	-3.276	-16.493	1.01	110.22	135.26
241	2jsa-8	THR_A_41_N	THR_A_41_CA	5.357	-3.943	-16.144	6.655	-4.031	-16.792	1.45	116.48	-3.88
242	2jsa-8	THR_A_41_CA	THR_A_41_HA	6.655	-4.031	-16.792	6.745	-5.009	-17.265	1.09	115.72	-84.74
243	2jsa-8	THR_A_41_CA	THR_A_41_C	6.655	-4.031	-16.792	7.777	-3.902	-15.759	1.53	47.55	6.56
244	2jsa-8	THR_A_41_C	THR_A_41_O	7.777	-3.902	-15.759	8.767	-4.629	-15.82	1.23	92.84	-36.29
245	2jsa-8	THR_A_41_C	ILE_A_42_N	7.777	-3.902	-15.759	7.581	-2.974	-14.834	1.32	45.72	101.93
246	2jsa-8	ILE_A_42_N	ILE_A_42_H	7.581	-2.974	-14.834	6.74	-2.415	-14.844	1.01	90.57	146.39
247	2jsa-8	ILE_A_42_N	ILE_A_42_CA	7.581	-2.974	-14.834	8.564	-2.741	-13.789	1.45	44.03	13.33
248	2jsa-8	ILE_A_42_CA	ILE_A_42_HA	8.564	-2.741	-13.789	9.375	-2.149	-14.214	1.09	112.94	36.13
249	2jsa-8	ILE_A_42_CA	ILE_A_42_C	8.564	-2.741	-13.789	9.152	-4.08	-13.341	1.53	72.97	-66.29
250	2jsa-8	ILE_A_42_C	ILE_A_42_O	9.152	-4.08	-13.341	8.436	-5.076	-13.244	1.23	85.48	-125.71
251	2jsa-8	ILE_A_42_C	PRO_A_43_N	9.152	-4.08	-13.341	10.486	-4.061	-13.073	1.36	78.64	0.82
252	2jsa-8	PRO_A_43_N	PRO_A_43_CA	10.486	-4.061	-13.073	11.179	-5.262	-12.637	1.45	72.54	-60.01
253	2jsa-8	PRO_A_43_CA	PRO_A_43_HA	11.179	-5.262	-12.637	10.879	-6.11	-13.252	1.09	124.36	-109.48
254	2jsa-8	PRO_A_43_CA	PRO_A_43_C	11.179	-5.262	-12.637	10.853	-5.583	-11.177	1.53	17.40	-135.44
255	2jsa-8	PRO_A_43_C	PRO_A_43_O	10.853	-5.583	-11.177	10.515	-6.719	-10.847	1.23	74.44	-106.57
256	2jsa-8	PRO_A_43_C	PHE_A_44_N	10.853	-5.583	-11.177	10.969	-4.563	-10.34	1.32	50.81	83.51
257	2jsa-8	PHE_A_44_N	PHE_A_44_H	10.969	-4.563	-10.34	11.255	-3.656	-10.68	1.01	109.67	72.50
258	2jsa-8	PHE_A_44_N	PHE_A_44_CA	10.969	-4.563	-10.34	10.691	-4.722	-8.923	1.45	12.74	-150.23
259	2jsa-8	PHE_A_44_CA	PHE_A_44_HA	10.691	-4.722	-8.923	10.641	-5.782	-8.672	1.09	76.69	-92.70
260	2jsa-8	PHE_A_44_CA	PHE_A_44_C	10.691	-4.722	-8.923	9.376	-4.04	-8.541	1.53	75.54	152.59
261	2jsa-8	PHE_A_44_C	PHE_A_44_O	9.376	-4.04	-8.541	9.223	-3.564	-7.417	1.23	23.98	107.82
262	2jsa-8	PHE_A_44_C	GLY_A_45_N	9.376	-4.04	-8.541	8.46	-4.016	-9.498	1.32	136.24	178.50
263	2jsa-8	GLY_A_45_N	GLY_A_45_H	8.46	-4.016	-9.498	8.656	-4.428	-10.399	1.01	153.14	-64.56
264	2jsa-8	GLY_A_45_N	GLY_A_45_CA	8.46	-4.016	-9.498	7.163	-3.401	-9.277	1.45	81.25	154.63
265	2jsa-8	GLY_A_45_CA	GLY_A_45_C	7.163	-3.401	-9.277	6.175	-4.404	-8.676	1.53	66.88	-134.57
266	2jsa-8	GLY_A_45_C	GLY_A_45_O	6.175	-4.404	-8.676	5.879	-4.35	-7.483	1.23	14.16	169.66
267	2jsa-8	GLY_A_45_C	THR_A_46_N	6.175	-4.404	-8.676	5.694	-5.295	-9.53	1.32	130.15	-118.36
268	2jsa-8	THR_A_46_N	THR_A_46_H	5.694	-5.295	-9.53	5.983	-5.28	-10.498	1.01	163.36	2.97
269	2jsa-8	THR_A_46_N	THR_A_46_CA	5.694	-5.295	-9.53	4.747	-6.309	-9.098	1.45	72.71	-133.04
270	2jsa-8	THR_A_46_CA	THR_A_46_HA	4.747	-6.309	-9.098	3.852	-5.814	-8.72	1.09	69.72	151.05
271	2jsa-8	THR_A_46_CA	THR_A_46_C	4.747	-6.309	-9.098	5.339	-7.143	-7.961	1.53	41.97	-54.63
272	2jsa-8	THR_A_46_C	THR_A_46_O	5.339	-7.143	-7.961	4.619	-7.568	-7.058	1.23	42.80	-149.45
273	2jsa-8	THR_A_46_C	ARG_A_47_N	5.339	-7.143	-7.961	6.644	-7.351	-8.041	1.32	93.46	-9.06
274	2jsa-8	ARG_A_47_N	ARG_A_47_H	6.644	-7.351	-8.041	7.174	-6.971	-8.813	1.01	139.81	35.64
275	2jsa-8	ARG_A_47_N	ARG_A_47_CA	6.644	-7.351	-8.041	7.342	-8.126	-7.028	1.45	45.84	-47.99
276	2jsa-8	ARG_A_47_CA	ARG_A_47_HA	7.342	-8.126	-7.028	6.901	-9.122	-6.992	1.09	88.11	-113.88
277	2jsa-8	ARG_A_47_CA	ARG_A_47_C	7.342	-8.126	-7.028	7.191	-7.465	-5.656	1.53	26.30	102.87
278	2jsa-8	ARG_A_47_C	ARG_A_47_O	7.191	-7.465	-5.656	6.843	-8.128	-4.68	1.23	37.50	-117.69
279	2jsa-8	ARG_A_47_C	GLU_A_48_N	7.191	-7.465	-5.656	7.461	-6.169	-5.627	1.32	88.75	78.23
280	2jsa-8	GLU_A_48_N	GLU_A_48_H	7.461	-6.169	-5.627	7.742	-5.689	-6.47	1.01	146.58	59.65
281	2jsa-8	GLU_A_48_N	GLU_A_48_CA	7.461	-6.169	-5.627	7.36	-5.412	-4.392	1.45	31.73	97.60
282	2jsa-8	GLU_A_48_CA	GLU_A_48_HA	7.36	-5.412	-4.392	7.886	-5.965	-3.614	1.09	44.45	-46.43
283	2jsa-8	GLU_A_48_CA	GLU_A_48_C	7.36	-5.412	-4.392	5.895	-5.27	-3.974	1.53	74.15	174.46
284	2jsa-8	GLU_A_48_C	GLU_A_48_O	5.895	-5.27	-3.974	5.577	-5.316	-2.787	1.23	15.15	-171.77
285	2jsa-8	GLU_A_48_C	CYS_A_49_N	5.895	-5.							

288	2jsa-8	CYS_A_49_CA	CYS_A_49_HA	3.619	-4.948	-4.726	3.458	-3.997	-4.218	1.09	62.23	99.61
289	2jsa-8	CYS_A_49_CA	CYS_A_49_C	3.619	-4.948	-4.726	3.172	-6.079	-3.797	1.53	52.62	-111.57
290	2jsa-8	CYS_A_49_C	CYS_A_49_O	3.172	-6.079	-3.797	2.754	-5.831	-2.668	1.23	23.29	149.32
291	2jsa-8	CYS_A_49_C	ASP_A_50_N	3.172	-6.079	-3.797	3.274	-7.298	-4.308	1.33	112.67	-85.22
292	2jsa-8	ASP_A_50_N	ASP_A_50_H	3.274	-7.298	-4.308	3.625	-7.429	-5.246	1.01	158.23	-20.47
293	2jsa-8	ASP_A_50_N	ASP_A_50_CA	3.274	-7.298	-4.308	2.886	-8.467	-3.538	1.45	57.99	-108.36
294	2jsa-8	ASP_A_50_CA	ASP_A_50_HA	2.886	-8.467	-3.538	1.814	-8.428	-3.348	1.09	79.96	177.92
295	2jsa-8	ASP_A_50_CA	ASP_A_50_C	2.886	-8.467	-3.538	3.648	-8.476	-2.212	1.53	29.89	-0.68
296	2jsa-8	ASP_A_50_C	ASP_A_50_O	3.648	-8.476	-2.212	3.168	-9.019	-1.218	1.23	36.10	-131.48
297	2jsa-8	ASP_A_50_C	HIS_A_51_N	3.648	-8.476	-2.212	4.825	-7.867	-2.238	1.33	91.12	27.36
298	2jsa-8	HIS_A_51_N	HIS_A_51_H	4.825	-7.867	-2.238	5.159	-7.441	-3.091	1.01	147.60	51.90
299	2jsa-8	HIS_A_51_N	HIS_A_51_CA	4.825	-7.867	-2.238	5.658	-7.798	-1.05	1.45	35.13	4.74
300	2jsa-8	HIS_A_51_CA	HIS_A_51_HA	5.658	-7.798	-1.05	5.453	-8.679	-0.443	1.09	56.14	-103.10
301	2jsa-8	HIS_A_51_CA	HIS_A_51_C	5.658	-7.798	-1.05	5.281	-6.563	-0.229	1.53	57.55	106.98
302	2jsa-8	HIS_A_51_C	HIS_A_51_O	5.281	-6.563	-0.229	5.973	-6.212	0.726	1.23	39.09	26.90
303	2jsa-8	HIS_A_51_C	TYR_A_52_N	5.281	-6.563	-0.229	4.184	-5.938	-0.631	1.33	107.66	150.33
304	2jsa-8	TYR_A_52_N	TYR_A_52_H	4.184	-5.938	-0.631	3.665	-6.282	-1.426	1.01	141.93	-146.46
305	2jsa-8	TYR_A_52_N	TYR_A_52_CA	4.184	-5.938	-0.631	3.706	-4.75	0.056	1.45	61.79	111.92
306	2jsa-8	TYR_A_52_CA	TYR_A_52_HA	3.706	-4.75	0.056	4.434	-4.426	0.801	1.09	46.93	23.99
307	2jsa-8	TYR_A_52_CA	TYR_A_52_C	3.706	-4.75	0.056	2.356	-5.01	0.727	1.53	63.98	-169.10
308	2jsa-8	TYR_A_52_C	TYR_A_52_O	2.356	-5.01	0.727	2.168	-4.68	1.897	1.23	17.98	119.67
309	2jsa-8	TYR_A_52_C	VAL_A_53_N	2.356	-5.01	0.727	1.453	-5.6	-0.042	1.32	125.49	-146.84
310	2jsa-8	VAL_A_53_N	VAL_A_53_H	1.453	-5.6	-0.042	1.679	-5.844	-0.995	1.01	160.76	-47.19
311	2jsa-8	VAL_A_53_N	VAL_A_53_CA	1.453	-5.6	-0.042	0.126	-5.908	0.463	1.45	69.66	-166.93
312	2jsa-8	VAL_A_53_CA	VAL_A_53_C	0.126	-5.908	0.463	-0.363	-4.974	0.739	1.09	75.33	117.63
313	2jsa-8	VAL_A_53_C	VAL_A_53_O	0.126	-5.908	0.463	0.253	-6.769	1.722	1.53	34.66	-81.61
314	2jsa-8	VAL_A_53_C	VAL_A_53_O	0.253	-6.769	1.722	-0.663	-6.813	2.543	1.23	48.16	-177.25
315	2jsa-8	VAL_A_53_C	ASN_A_54_N	0.253	-6.769	1.722	1.394	-7.431	1.836	1.32	85.06	-30.12
316	2jsa-8	ASN_A_54_N	ASN_A_54_H	1.394	-7.431	1.836	2.104	-7.347	1.122	1.01	134.96	6.75
317	2jsa-8	ASN_A_54_N	ASN_A_54_C	1.394	-7.431	1.836	1.652	-8.287	2.981	1.45	37.98	-73.23
318	2jsa-8	ASN_A_54_C	ASN_A_54_HA	1.652	-8.287	2.981	0.919	-8.073	3.759	1.09	44.46	163.72
319	2jsa-8	ASN_A_54_C	ASN_A_54_O	1.652	-8.287	2.981	3.063	-8.017	3.508	1.53	69.86	10.83
320	2jsa-8	ASN_A_54_C	ASN_A_54_O	3.063	-8.017	3.508	3.891	-8.924	3.571	1.23	87.06	-47.61
321	2jsa-8	ASN_A_54_C	SER_A_55_N	3.063	-8.017	3.508	3.294	-6.764	3.872	1.33	74.06	79.55
322	2jsa-8	SER_A_55_N	SER_A_55_H	3.294	-6.764	3.872	2.566	-6.069	3.793	1.01	94.49	136.33
323	2jsa-8	SER_A_55_N	SER_A_55_CA	3.294	-6.764	3.872	4.59	-6.362	4.391	1.45	69.07	17.23
324	2jsa-8	SER_A_55_CA	SER_A_55_HA	4.59	-6.362	4.391	4.843	-7.018	5.224	1.09	40.17	-68.91
325	2jsa-8	SER_A_55_CA	SER_A_55_C	4.59	-6.362	4.391	4.526	-4.921	4.903	1.53	70.46	92.54
326	2jsa-8	SER_A_55_C	SER_A_55_O	4.526	-4.921	4.903	5.079	-4.608	5.956	1.23	31.11	29.51
327	2jsa-8	SER_A_55_C	LYS_A_56_N	4.526	-4.921	4.903	3.846	-4.084	4.133	1.33	125.53	129.09
328	2jsa-8	LYS_A_56_N	LYS_A_56_H	3.846	-4.084	4.133	3.418	-4.412	3.279	1.01	147.73	-142.54
329	2jsa-8	LYS_A_56_N	LYS_A_56_CA	3.846	-4.084	4.133	3.701	-2.684	4.496	1.45	75.54	95.91
330	2jsa-8	LYS_A_56_CA	LYS_A_56_HA	3.701	-2.684	4.496	4.104	-2.552	5.5	1.09	22.90	18.14
331	2jsa-8	LYS_A_56_CA	LYS_A_56_C	3.701	-2.684	4.496	2.215	-2.324	4.541	1.53	88.31	166.38
332	2jsa-8	LYS_A_56_C	LYS_A_56_O	2.215	-2.324	4.541	1.858	-1.146	4.545	1.23	89.81	106.86
333	2jsa-8	LYS_A_56_C	VAL_A_57_N	2.215	-2.324	4.541	1.389	-3.359	4.573	1.32	88.62	-128.59
334	2jsa-8	VAL_A_57_N	VAL_A_57_H	1.389	-3.359	4.573	1.754	-4.301	4.567	1.01	90.34	-68.82
335	2jsa-8	VAL_A_57_N	VAL_A_57_CA	1.389	-3.359	4.573	-0.05	-3.166	4.617	1.45	88.26	172.36
336	2jsa-8	VAL_A_57_CA	VAL_A_57_HA	-0.05	-3.166	4.617	-0.273	-2.159	4.264	1.09	108.89	102.49
337	2jsa-8	VAL_A_57_CA	VAL_A_57_C	-0.05	-3.166	4.617	-0.533	-3.279	6.064	1.53	18.92	-166.83
338	2jsa-8	VAL_A_57_C	VAL_A_57_O	-0.533	-3.279	6.064	-1.312	-2.449	6.53	1.23	67.74	133.18
339	2jsa-8	VAL_A_57_C	ASP_A_58_N	-0.533	-3.279	6.064	-0.047	-4.312	6.737	1.33	59.48	-64.80
340	2jsa-8	ASP_A_58_N	ASP_A_58_H	-0.047	-4.312	6.737	0.592	-4.955	6.291	1.01	116.20	-45.18
341	2jsa-8	ASP_A_58_N	ASP_A_58_CA	-0.047	-4.312	6.737	-0.418	-4.544	8.122	1.45	17.53	-147.98
342	2jsa-8	ASP_A_58_CA	ASP_A_58_HA	-0.418	-4.544	8.122	-1.468	-4.833	8.166	1.09	87.69	-164.61
343	2jsa-8	ASP_A_58_CA	ASP_A_58_C	-0.418	-4.544	8.122	-0.198	-3.261	8.927	1.53	58.27	80.27
344	2jsa-8	ASP_A_58_C	ASP_A_58_O	-0.198	-3.261	8.927	-1.05	-2.87	9.723	1.23	49.66	155.35
345	2jsa-8	ASP_A_58_C	PRO_A_59_N	-0.198	-3.261	8.927	0.979	-2.625	8.684	1.36	100.29	28.38
346	2jsa-8	PRO_A_59_N	PRO_A_59_CA	0.979	-2.625	8.684	1.322	-1.394	9.375	1.45	61.60	74.43
347	2jsa-8	PRO_A_59_CA	PRO_A_59_HA	1.322	-1.394	9.375	1.1	-1.489	10.438	1.09	12.80	-156.83
348	2jsa-8	PRO_A_59_CA	PRO_A_59_C	1.322	-1.394	9.375	0.526	-0.212	8.817	1.53	111.38	123.96
349	2jsa-8	PRO_A_59_C	PRO_A_59_O	0.526	-0.212	8.817	-0.175	0.475	9.558	1.23	52.95	135.58
350	2jsa-8	PRO_A_59_C	ILE_A_60_N	0.526	-0.212	8.817	0.664	-0.01	7.514	1.33	169.37	55.66
351	2jsa-8	ILE_A_60_N	ILE_A_60_H	0.664	-0.01	7.514	1.258	-0.615	6.965	1.01	122.92	-45.53
352	2jsa-8	ILE_A_60_N	ILE_A_60_CA	0.664	-0.01	7.514	-0.032	1.078	6.849	1.45	117.24	122.61
353	2jsa-8	ILE_A_60_CA	ILE_A_60_HA	-0.032	1.078	6.849	0.434	2.015	7.157	1.09	73.60	63.56
354	2jsa-8	ILE_A_60_CA	ILE_A_60_C	-0.032	1.078	6.849	-1.488	1.107	7.315	1.53	72.26	178.86
355	2jsa-8	ILE_A_60_C	ILE_A_60_O	-1.488	1.107	7.315	-1.952	2.111	7.854	1.23	64.02	114.80
356	2jsa-8	ILE_A_60_C	ILE_A_61_N	-1.488	1.107	7.315	-2.172	-0.006	7.091	1.33	99.73	-121.57
357	2jsa-8	ILE_A_61_N	ILE_A_61_H	-2.172	-0.006	7.091	-1.727	-0.794	6.643	1.01	116.34	-60.55
358	2jsa-8	ILE_A_61_N	ILE_A_61_CA	-2.172	-0.006	7.091	-3.566	-0.121	7.482	1.45	74.38	-175.28
359	2jsa-8	ILE_A_61_CA	ILE_A_61_HA	-3.566	-0.121	7.482	-4.124	0.667	6.976	1.09	117.66	125.30
360	2jsa-8	ILE_A_61_CA	ILE_A_61_C	-3.566	-0.121	7.482	-3.69	0.115	8.988	1.53	10.04	117.72
361	2jsa-8	ILE_A_61_C	ILE_A_61_O	-3.69	0.115	8.988	-4.758	0.48	9.478	1.23	66.53	161.13
362	2jsa-8	ILE_A_61_C	HIS_A_62_N	-3.69	0.115	8.988	-2.582	-0.102	9.682	1.33	58.42	-11.08
363	2jsa-8	HIS_A_62_N	HIS_A_62_H	-2.582	-0.102	9.682	-1.738	-0.4	9.214	1.01	117.60	-19.45
364	2jsa-8	HIS_A_62_N	HIS_A_62_CA	-2.582	-0.102	9.682	-2.554	0.082	11.123	1.45	7.36	81.35
365	2jsa-8	HIS_A_62_CA	HIS_A_62_HA	-2.554	0.082	11.123	-3.379	-0.487	11.552	1.09	66.83	-145.41
366	2jsa-8	HIS_A_62_CA	HIS_A_62_C	-2.554	0.082	11.123	-2.777	1.558	11.456	1.53	77.42	98.59
367	2jsa-8	HIS_A_62_C	HIS_A_62_O	-2.777	1.558	11.456	-3.656	1.893	12.249	1.23	49.87	159.14
368	2jsa-8	HIS_A_62_C	GLU_A_63_N	-2.777	1.558	11.456	-1.968	2.402	10.834	1.32	118.01	46.21
369	2jsa-8	GLU_A_63_N	GLU_A_63_H	-1.968	2.402	10.834	-1.267	2.056	10.194	1.01	129.31	-26.27
370	2jsa-8	GLU_A_63_N	GLU_A_63_CA	-1.968	2.402	10.834	-2.067	3.835	11.054	1.45	81.29	93.95
371	2jsa-8	GLU_A_63_CA	GLU_A_63_HA	-2.067	3.835	11.054	-1.824	4.034	12.098	1.09	16.74	39.32
372	2jsa-8	GLU_A_63_CA	GLU_A_63_C	-2.067	3.835	11.054	-3.496	4.314	10.794	1.53	99.79	161.47
373	2jsa-8	GLU_A_63_C	GLU_A_63_O	-3.496	4.314	10.794	-4.078	5.017	11.619	1.23	47.89	129.62
374	2jsa-8	GLU_A_63_C	LEU_A_64_N	-3.496	4.314	10.794	-4.02	3.916	9.644	1.32	150.22	-142.78
375	2jsa-8	LEU_A_64_N	LEU_A_64_H	-4.02	3.916	9.644	-3.482	3.339	9.013	1.01	128.65	-47.00
376	2jsa-8	LEU_A_64_N	LEU_A_64_CA	-4.02	3.916	9.644	-5.37	4.297	9.265	1.45	105.12	164.24
377	2jsa-8	LEU_A_64_CA	LEU_A_64_HA	-5.37	4.297	9.265	-5.428	5.386	9.27	1.09	89.74	93.05
378	2jsa-8	LEU_A_64_CA	LEU_A_64_C	-5.37	4.297	9.265	-6.355	3.774	10.312	1.53	46.81	-152.03
379	2jsa-8</											

381	2jsa-8	GLU_A_65_N	GLU_A_65_H	-6.097	2.554	10.763	-5.298	2.042	10.417	1.01	110.03	-32.65
382	2jsa-8	GLU_A_65_N	GLU_A_65_CA	-6.097	2.554	10.763	-6.95	1.929	11.76	1.45	46.69	-143.77
383	2jsa-8	GLU_A_65_CA	GLU_A_65_HA	-6.95	1.929	11.76	-7.949	1.832	11.337	1.09	112.85	-174.45
384	2jsa-8	GLU_A_65_CA	GLU_A_65_C	-6.95	1.929	11.76	-7.039	2.81	13.009	1.53	35.33	95.77
385	2jsa-8	GLU_A_65_C	GLU_A_65_O	-7.039	2.81	13.009	-8.131	3.19	13.427	1.23	70.12	160.81
386	2jsa-8	GLU_A_65_C	GLY_A_66_N	-7.039	2.81	13.009	-5.876	3.109	13.568	1.32	65.04	14.42
387	2jsa-8	GLY_A_66_N	GLY_A_66_H	-5.876	3.109	13.568	-5.015	2.761	13.169	1.01	113.25	-22.01
388	2jsa-8	GLY_A_66_N	GLY_A_66_CA	-5.876	3.109	13.568	-5.809	3.938	14.76	1.45	34.90	85.38
389	2jsa-8	GLY_A_66_CA	GLY_A_66_C	-5.809	3.938	14.76	-6.505	5.281	14.533	1.53	98.53	117.40
390	2jsa-8	GLY_A_66_C	GLY_A_66_O	-6.505	5.281	14.533	-7.275	5.736	15.377	1.23	46.66	149.42
391	2jsa-8	GLY_A_66_C	GLY_A_67_N	-6.505	5.281	14.533	-6.209	5.879	13.387	1.33	149.79	63.67
392	2jsa-8	GLY_A_67_N	GLY_A_67_H	-6.209	5.879	13.387	-5.566	5.447	12.739	1.01	129.91	-33.90
393	2jsa-8	GLY_A_67_N	GLY_A_67_CA	-6.209	5.879	13.387	-6.797	7.161	13.039	1.45	103.86	114.64
394	2jsa-8	GLY_A_67_CA	GLY_A_67_C	-6.797	7.161	13.039	-5.743	8.108	12.463	1.53	112.12	41.94
395	2jsa-8	GLY_A_67_C	GLY_A_67_O	-5.743	8.108	12.463	-5.688	9.28	12.831	1.23	72.59	87.31
396	2jsa-8	GLY_A_67_C	THR_A_68_N	-5.743	8.108	12.463	-4.931	7.564	11.568	1.33	132.48	-33.82
397	2jsa-8	THR_A_68_N	THR_A_68_H	-4.931	7.564	11.568	-5.033	6.592	11.313	1.01	104.62	-95.99
398	2jsa-8	THR_A_68_N	THR_A_68_CA	-4.931	7.564	11.568	-3.882	8.347	10.936	1.45	115.77	36.74
399	2jsa-8	THR_A_68_CA	THR_A_68_HA	-3.882	8.347	10.936	-3.84	9.326	11.413	1.09	64.04	87.54
400	2jsa-8	THR_A_68_CA	THR_A_68_C	-3.882	8.347	10.936	-4.193	8.559	9.454	1.53	165.75	145.72
401	2jsa-8	THR_A_68_C	THR_A_68_O	-4.193	8.559	9.454	-4.64	7.637	8.772	1.23	123.65	-115.86
402	2jsa-8	THR_A_68_C	ALA_A_69_N	-4.193	8.559	9.454	-3.946	9.778	8.998	1.32	110.13	78.55
403	2jsa-8	ALA_A_69_N	ALA_A_69_H	-3.946	9.778	8.998	-3.579	10.487	9.617	1.01	52.21	62.63
404	2jsa-8	ALA_A_69_N	ALA_A_69_CA	-3.946	9.778	8.998	-4.195	10.123	7.609	1.45	162.97	125.82
405	2jsa-8	ALA_A_69_CA	ALA_A_69_HA	-4.195	10.123	7.609	-5.257	9.994	7.401	1.09	101.00	-173.07
406	2jsa-8	ALA_A_69_CA	ALA_A_69_C	-4.195	10.123	7.609	-3.405	9.175	6.703	1.53	126.29	-50.19
407	2jsa-8	ALA_A_69_C	ALA_A_69_O	-3.405	9.175	6.703	-2.464	8.524	7.152	1.23	68.57	-34.68
408	2jsa-8	ALA_A_69_C	PRO_A_70_N	-3.405	9.175	6.703	-3.829	9.127	5.412	1.36	161.71	-173.54
409	2jsa-8	PRO_A_70_N	PRO_A_70_CA	-3.829	9.127	5.412	-3.172	8.27	4.44	1.45	131.99	-52.53
410	2jsa-8	PRO_A_70_CA	PRO_A_70_HA	-3.172	8.27	4.44	-2.997	7.284	4.87	1.09	66.76	-79.94
411	2jsa-8	PRO_A_70_CA	PRO_A_70_C	-3.172	8.27	4.44	-1.825	8.858	4.013	1.53	106.20	23.58
412	2jsa-8	PRO_A_70_C	PRO_A_70_O	-1.825	8.858	4.013	-1.024	8.181	3.37	1.23	121.51	-40.20
413	2jsa-8	PRO_A_70_C	LYS_A_71_N	-1.825	8.858	4.013	-1.618	10.112	4.387	1.32	73.60	80.63
414	2jsa-8	LYS_A_71_N	LYS_A_71_H	-1.618	10.112	4.387	-2.322	10.609	4.914	1.01	58.55	144.78
415	2jsa-8	LYS_A_71_N	LYS_A_71_CA	-1.618	10.112	4.387	-0.382	10.799	4.051	1.45	103.37	29.07
416	2jsa-8	LYS_A_71_CA	LYS_A_71_HA	-0.382	10.799	4.051	0.107	10.243	3.251	1.09	137.21	-48.67
417	2jsa-8	LYS_A_71_CA	LYS_A_71_C	-0.382	10.799	4.051	0.551	10.784	5.263	1.53	37.59	-0.92
418	2jsa-8	LYS_A_71_C	LYS_A_71_O	0.551	10.784	5.263	1.761	10.952	5.121	1.23	96.63	7.90
419	2jsa-8	LYS_A_71_C	ASP_A_72_N	0.551	10.784	5.263	-0.047	10.581	6.427	1.32	28.48	-161.25
420	2jsa-8	ASP_A_72_N	ASP_A_72_H	-0.047	10.581	6.427	-1.047	10.451	6.469	1.01	87.62	-172.59
421	2jsa-8	ASP_A_72_N	ASP_A_72_CA	-0.047	10.581	6.427	0.715	10.542	7.663	1.45	31.69	-2.93
422	2jsa-8	ASP_A_72_CA	ASP_A_72_HA	0.715	10.542	7.663	1.475	11.323	7.637	1.09	91.37	45.78
423	2jsa-8	ASP_A_72_CA	ASP_A_72_C	0.715	10.542	7.663	1.382	9.172	7.804	1.53	84.71	-64.04
424	2jsa-8	ASP_A_72_C	ASP_A_72_O	1.382	9.172	7.804	2.439	9.053	8.419	1.23	59.96	-6.42
425	2jsa-8	ASP_A_72_C	VAL_A_73_N	1.382	9.172	7.804	0.735	8.173	7.223	1.32	116.02	-122.93
426	2jsa-8	VAL_A_73_N	VAL_A_73_H	0.735	8.173	7.223	-0.131	8.345	6.734	1.01	118.98	168.77
427	2jsa-8	VAL_A_73_N	VAL_A_73_CA	0.735	8.173	7.223	1.251	6.816	7.275	1.45	87.95	-69.18
428	2jsa-8	VAL_A_73_CA	VAL_A_73_HA	1.251	6.816	7.275	1.48	6.574	8.313	1.09	17.80	-46.58
429	2jsa-8	VAL_A_73_CA	VAL_A_73_C	1.251	6.816	7.275	2.551	6.738	6.471	1.53	121.69	-3.43
430	2jsa-8	VAL_A_73_C	VAL_A_73_O	2.551	6.738	6.471	3.549	6.199	6.948	1.23	67.19	-28.37
431	2jsa-8	VAL_A_73_C	CYS_A_74_N	2.551	6.738	6.471	2.498	7.284	5.265	1.32	155.54	95.54
432	2jsa-8	CYS_A_74_N	CYS_A_74_H	2.498	7.284	5.265	1.644	7.711	4.937	1.01	108.96	153.43
433	2jsa-8	CYS_A_74_N	CYS_A_74_CA	2.498	7.284	5.265	3.658	7.284	4.391	1.45	127.00	0.00
434	2jsa-8	CYS_A_74_CA	CYS_A_74_HA	3.658	7.284	4.391	4.128	6.302	4.445	1.09	87.16	-64.42
435	2jsa-8	CYS_A_74_CA	CYS_A_74_C	3.658	7.284	4.391	4.65	8.326	4.909	1.53	70.20	46.41
436	2jsa-8	CYS_A_74_C	CYS_A_74_O	4.65	8.326	4.909	4.96	9.293	4.214	1.23	124.39	72.23
437	2jsa-8	CYS_A_74_C	THR_A_75_N	4.65	8.326	4.909	5.121	8.096	6.126	1.33	23.30	-26.03
438	2jsa-8	THR_A_75_N	THR_A_75_H	5.121	8.096	6.126	4.822	7.28	6.641	1.01	59.35	-110.12
439	2jsa-8	THR_A_75_N	THR_A_75_CA	5.121	8.096	6.126	6.072	9.003	6.745	1.45	64.78	43.64
440	2jsa-8	THR_A_75_CA	THR_A_75_HA	6.072	9.003	6.745	6.976	9.033	6.136	1.09	123.95	1.90
441	2jsa-8	THR_A_75_CA	THR_A_75_C	6.072	9.003	6.745	6.459	8.501	8.138	1.53	24.47	-52.37
442	2jsa-8	THR_A_75_C	THR_A_75_O	6.459	8.501	8.138	7.641	8.388	8.455	1.23	75.05	-5.46
443	2jsa-8	THR_A_75_C	LYS_A_76_N	6.459	8.501	8.138	5.437	8.214	8.933	1.33	53.17	-164.31
444	2jsa-8	LYS_A_76_N	LYS_A_76_H	5.437	8.214	8.933	4.489	8.332	8.606	1.01	108.90	172.90
445	2jsa-8	LYS_A_76_N	LYS_A_76_CA	5.437	8.214	8.933	5.655	7.727	10.285	1.45	21.54	-65.88
446	2jsa-8	LYS_A_76_CA	LYS_A_76_HA	5.655	7.727	10.285	6.253	8.467	10.818	1.09	60.74	51.06
447	2jsa-8	LYS_A_76_CA	LYS_A_76_C	5.655	7.727	10.285	6.463	6.429	10.231	1.53	92.02	-58.10
448	2jsa-8	LYS_A_76_C	LYS_A_76_O	6.463	6.429	10.231	7.408	6.249	10.997	1.23	51.47	-10.78
449	2jsa-8	LYS_A_76_C	LEU_A_77_N	6.463	6.429	10.231	6.062	5.558	9.316	1.33	133.66	-114.72
450	2jsa-8	LEU_A_77_N	LEU_A_77_H	6.062	5.558	9.316	5.278	5.773	8.718	1.01	126.34	164.66
451	2jsa-8	LEU_A_77_N	LEU_A_77_CA	6.062	5.558	9.316	6.737	4.281	9.152	1.45	96.48	-62.14
452	2jsa-8	LEU_A_77_CA	LEU_A_77_HA	6.737	4.281	9.152	7.25	4.047	10.086	1.09	31.12	-24.52
453	2jsa-8	LEU_A_77_CA	LEU_A_77_C	6.737	4.281	9.152	7.799	4.409	8.058	1.53	135.64	6.87
454	2jsa-8	LEU_A_77_C	LEU_A_77_O	7.799	4.409	8.058	8.046	3.46	7.314	1.23	127.19	-75.41
455	2jsa-8	LEU_A_77_C	ASN_A_78_N	7.799	4.409	8.058	8.4	5.588	7.994	1.32	92.77	62.99
456	2jsa-8	ASN_A_78_N	ASN_A_78_H	8.4	5.588	7.994	8.148	6.323	8.639	1.01	50.30	108.92
457	2jsa-8	ASN_A_78_N	ASN_A_78_CA	8.4	5.588	7.994	9.429	5.85	7.004	1.45	132.99	14.28
458	2jsa-8	ASN_A_78_CA	ASN_A_78_HA	9.429	5.85	7.004	9.556	6.928	6.899	1.09	95.53	83.28
459	2jsa-8	ASN_A_78_CA	ASN_A_78_C	9.429	5.85	7.004	9.009	5.243	5.664	1.53	151.15	-124.68
460	2jsa-8	ASN_A_78_C	ASN_A_78_O	9.009	5.243	5.664	9.852	4.786	4.894	1.23	128.76	-28.46
461	2jsa-8	ASN_A_78_C	GLU_A_79_N	9.009	5.243	5.664	7.706	5.258	5.426	1.32	100.35	179.34
462	2jsa-8	GLU_A_79_N	GLU_A_79_H	7.706	5.258	5.426	7.07	5.651	6.105	1.01	47.75	148.29
463	2jsa-8	GLU_A_79_N	GLU_A_79_CA	7.706	5.258	5.426	7.164	4.715	4.193	1.45	148.11	-134.95
464	2jsa-8	GLU_A_79_CA	GLU_A_79_HA	7.164	4.715	4.193	7.736	3.823	3.938	1.09	103.53	-57.33
465	2jsa-8	GLU_A_79_CA	GLU_A_79_C	7.164	4.715	4.193	7.317	5.726	3.054	1.53	138.08	81.39
466	2jsa-8	GLU_A_79_C	GLU_A_79_O	7.317	5.726	3.054	6.82	5.505	1.951	1.23	153.75	-156.03
467	2jsa-8	GLU_A_79_C	CYS_A_80_N	7.317	5.726	3.054	8.007	6.815	3.361	1.33	76.61	57.64
468	2jsa-8	CYS_A_80_N	CYS_A_80_H	8.007	6.815	3.361	8.388	6.931	4.289	1.01	23.23	16.93
469	2jsa-8	CYS_A_80_N	CYS_A_80_CA	8.007	6.815	3.361	8.232	7.86	2.379	1.45	132.57	77.85
470	2jsa-8	CYS_A_80_CA	CYS_A_80_HA	8.232	7.86	2.379	8.547	7.391	1.447	1.09	148.78	-56.11
471	2jsa-8	CYS_A_80_CA	CYS_A_80_C	8.232	7.86	2.379	9.366	8.756	2.88			

474	2jsa-8	PRO_A_81_N	PRO_A_81_CA	10.274	9.118	1.935	11.406	9.967	2.27	1.45	76.68	36.87
475	2jsa-8	PRO_A_81_CA	PRO_A_81_HA	11.406	9.967	2.27	11.867	9.627	3.197	1.09	31.71	-36.41
476	2jsa-8	PRO_A_81_CA	PRO_A_81_C	11.406	9.967	2.27	10.965	11.42	2.452	1.53	83.17	106.88
477	2jsa-8	PRO_A_81_C	PRO_A_81_O	10.965	11.42	2.452	11.775	12.338	2.333	1.23	95.55	48.58
1	2jsa-9	ARG_A_1_N	ARG_A_1_H	13.527	0.363	-3.759	14.347	0.948	-3.834	1.01	94.26	35.50
2	2jsa-9	ARG_A_1_N	ARG_A_1_CA	13.527	0.363	-3.759	12.492	0.736	-2.81	1.45	49.22	160.18
3	2jsa-9	ARG_A_1_CA	ARG_A_1_HA	12.492	0.736	-2.81	11.567	0.907	-3.36	1.09	120.31	169.53
4	2jsa-9	ARG_A_1_CA	ARG_A_1_C	12.492	0.736	-2.81	12.882	2.023	-2.079	1.53	61.47	73.14
5	2jsa-9	ARG_A_1_C	ARG_A_1_O	12.882	2.023	-2.079	13.427	1.974	-0.976	1.23	26.39	-5.14
6	2jsa-9	ARG_A_1_C	SER_A_2_N	12.882	2.023	-2.079	12.587	3.144	-2.721	1.33	118.98	104.74
7	2jsa-9	SER_A_2_N	SER_A_2_H	12.587	3.144	-2.721	12.137	3.109	-3.625	1.01	153.47	-175.55
8	2jsa-9	SER_A_2_N	SER_A_2_CA	12.587	3.144	-2.721	12.9	4.441	-2.145	1.45	66.65	76.43
9	2jsa-9	SER_A_2_CA	SER_A_2_HA	12.9	4.441	-2.145	12.545	4.452	-1.114	1.09	19.01	178.23
10	2jsa-9	SER_A_2_CA	SER_A_2_C	12.9	4.441	-2.145	12.181	5.545	-2.923	1.53	120.56	123.07
11	2jsa-9	SER_A_2_C	SER_A_2_O	12.181	5.545	-2.923	12.77	6.584	-3.22	1.23	103.96	60.45
12	2jsa-9	SER_A_2_C	ALA_A_3_N	12.181	5.545	-2.923	10.919	5.283	-3.231	1.33	103.44	-168.27
13	2jsa-9	ALA_A_3_N	ALA_A_3_H	10.919	5.283	-3.231	10.499	4.407	-2.955	1.01	74.14	-115.62
14	2jsa-9	ALA_A_3_N	ALA_A_3_CA	10.919	5.283	-3.231	10.116	6.243	-3.969	1.45	120.53	129.91
15	2jsa-9	ALA_A_3_CA	ALA_A_3_HA	10.116	6.243	-3.969	9.883	7.082	-3.314	1.09	53.05	105.52
16	2jsa-9	ALA_A_3_CA	ALA_A_3_C	10.116	6.243	-3.969	8.803	5.581	-4.395	1.53	106.16	-153.24
17	2jsa-9	ALA_A_3_C	ALA_A_3_O	8.803	5.581	-4.395	7.728	5.98	-3.949	1.23	68.75	159.64
18	2jsa-9	ALA_A_3_C	LEU_A_4_N	8.803	5.581	-4.395	8.934	4.579	-5.252	1.32	130.30	-82.55
19	2jsa-9	LEU_A_4_N	LEU_A_4_H	8.934	4.579	-5.252	9.85	4.303	-5.576	1.01	108.71	-16.77
20	2jsa-9	LEU_A_4_N	LEU_A_4_CA	8.934	4.579	-5.252	7.772	3.858	-5.743	1.45	109.75	-148.18
21	2jsa-9	LEU_A_4_CA	LEU_A_4_HA	7.772	3.858	-5.743	7.1	4.579	-6.208	1.09	115.26	132.99
22	2jsa-9	LEU_A_4_CA	LEU_A_4_C	7.772	3.858	-5.743	7.032	3.227	-4.561	1.53	39.45	-139.55
23	2jsa-9	LEU_A_4_C	LEU_A_4_O	7.032	3.227	-4.561	5.845	2.918	-4.661	1.23	94.66	-165.41
24	2jsa-9	LEU_A_4_C	SER_A_5_N	7.032	3.227	-4.561	7.763	3.056	-3.47	1.32	34.53	-13.17
25	2jsa-9	SER_A_5_N	SER_A_5_H	7.763	3.056	-3.47	8.734	3.335	-3.459	1.01	89.38	16.03
26	2jsa-9	SER_A_5_N	SER_A_5_CA	7.763	3.056	-3.47	7.19	2.468	-2.271	1.45	34.40	-134.26
27	2jsa-9	SER_A_5_CA	SER_A_5_HA	7.19	2.468	-2.271	6.656	1.562	-2.556	1.09	105.16	-120.52
28	2jsa-9	SER_A_5_CA	SER_A_5_C	7.19	2.468	-2.271	6.198	3.442	-1.633	1.53	65.35	135.52
29	2jsa-9	SER_A_5_C	SER_A_5_O	6.198	3.442	-1.633	5.173	3.026	-1.094	1.23	64.02	-157.91
30	2jsa-9	SER_A_5_C	CYS_A_6_N	6.198	3.442	-1.633	6.537	4.721	-1.715	1.33	93.55	75.16
31	2jsa-9	CYS_A_6_N	CYS_A_6_H	6.537	4.721	-1.715	7.395	4.992	-2.174	1.01	117.03	17.53
32	2jsa-9	CYS_A_6_N	CYS_A_6_CA	6.537	4.721	-1.715	5.688	5.756	-1.152	1.45	67.19	129.36
33	2jsa-9	CYS_A_6_CA	CYS_A_6_HA	5.688	5.756	-1.152	5.559	5.553	-0.089	1.09	12.75	-122.43
34	2jsa-9	CYS_A_6_CA	CYS_A_6_C	5.688	5.756	-1.152	4.32	5.679	-1.832	1.53	116.39	-176.78
35	2jsa-9	CYS_A_6_C	CYS_A_6_O	4.32	5.679	-1.832	3.301	5.502	-1.167	1.23	57.26	-170.15
36	2jsa-9	CYS_A_6_C	GLN_A_7_N	4.32	5.679	-1.832	4.341	5.816	-3.15	1.33	174.00	81.29
37	2jsa-9	GLN_A_7_N	GLN_A_7_H	4.341	5.816	-3.15	5.217	5.959	-3.632	1.01	118.50	9.27
38	2jsa-9	GLN_A_7_N	GLN_A_7_CA	4.341	5.816	-3.15	3.115	5.765	-3.928	1.45	122.38	-177.62
39	2jsa-9	GLN_A_7_CA	GLN_A_7_HA	3.115	5.765	-3.928	2.558	6.683	-3.74	1.09	80.07	121.25
40	2jsa-9	GLN_A_7_CA	GLN_A_7_C	3.115	5.765	-3.928	2.255	4.579	-3.484	1.53	73.14	-125.95
41	2jsa-9	GLN_A_7_C	GLN_A_7_O	2.255	4.579	-3.484	1.067	4.739	-3.207	1.23	76.99	172.33
42	2jsa-9	GLN_A_7_C	MET_A_8_N	2.255	4.579	-3.484	2.888	3.416	-3.431	1.33	87.71	-61.44
43	2jsa-9	MET_A_8_N	MET_A_8_H	2.888	3.416	-3.431	3.867	3.358	-3.675	1.01	103.97	-3.39
44	2jsa-9	MET_A_8_N	MET_A_8_CA	2.888	3.416	-3.431	2.196	2.205	-3.025	1.45	73.77	-119.74
45	2jsa-9	MET_A_8_CA	MET_A_8_HA	2.196	2.205	-3.025	1.526	1.899	-3.828	1.09	137.47	-155.45
46	2jsa-9	MET_A_8_CA	MET_A_8_C	2.196	2.205	-3.025	1.375	2.442	-1.756	1.53	33.96	163.90
47	2jsa-9	MET_A_8_C	MET_A_8_O	1.375	2.442	-1.756	0.267	1.925	-1.625	1.23	83.88	-154.99
48	2jsa-9	MET_A_8_C	CYS_A_9_N	1.375	2.442	-1.756	1.95	3.223	-0.855	1.32	47.11	53.64
49	2jsa-9	CYS_A_9_N	CYS_A_9_H	1.95	3.223	-0.855	2.865	3.614	-1.031	1.01	100.03	23.14
50	2jsa-9	CYS_A_9_N	CYS_A_9_CA	1.95	3.223	-0.855	1.285	3.536	0.4	1.45	30.35	154.79
51	2jsa-9	CYS_A_9_CA	CYS_A_9_HA	1.285	3.536	0.4	1.075	2.601	0.919	1.09	61.56	-102.66
52	2jsa-9	CYS_A_9_CA	CYS_A_9_C	1.285	3.536	0.4	-0.043	4.224	0.08	1.53	102.08	152.61
53	2jsa-9	CYS_A_9_C	CYS_A_9_O	-0.043	4.224	0.08	-1.035	4.023	0.781	1.23	55.29	-168.55
54	2jsa-9	CYS_A_9_C	GLU_A_10_N	-0.043	4.224	0.08	-0.02	5.022	-0.977	1.32	142.94	88.35
55	2jsa-9	GLU_A_10_N	GLU_A_10_H	-0.02	5.022	-0.977	0.832	5.14	-1.507	1.01	121.64	7.89
56	2jsa-9	GLU_A_10_N	GLU_A_10_CA	-0.02	5.022	-0.977	-1.211	5.742	-1.398	1.45	106.83	148.85
57	2jsa-9	GLU_A_10_CA	GLU_A_10_HA	-1.211	5.742	-1.398	-1.726	6.093	-0.504	1.09	34.88	145.72
58	2jsa-9	GLU_A_10_CA	GLU_A_10_C	-1.211	5.742	-1.398	-2.154	4.809	-2.159	1.53	119.84	-135.31
59	2jsa-9	GLU_A_10_C	GLU_A_10_O	-2.154	4.809	-2.159	-3.275	5.191	-2.493	1.23	105.75	161.18
60	2jsa-9	GLU_A_10_C	LEU_A_11_N	-2.154	4.809	-2.159	-1.664	3.604	-2.414	1.33	101.09	-67.87
61	2jsa-9	LEU_A_11_N	LEU_A_11_H	-1.664	3.604	-2.414	-0.732	3.359	-2.11	1.01	72.49	-14.73
62	2jsa-9	LEU_A_11_N	LEU_A_11_CA	-1.664	3.604	-2.414	-2.449	2.614	-3.132	1.45	119.61	-128.41
63	2jsa-9	LEU_A_11_CA	LEU_A_11_HA	-2.449	2.614	-3.132	-3.148	3.143	-3.78	1.09	126.47	142.88
64	2jsa-9	LEU_A_11_CA	LEU_A_11_C	-2.449	2.614	-3.132	-3.269	1.797	-2.132	1.53	49.18	-135.11
65	2jsa-9	LEU_A_11_C	LEU_A_11_O	-3.269	1.797	-2.132	-4.471	1.61	-2.315	1.23	98.56	-171.16
66	2jsa-9	LEU_A_11_C	VAL_A_12_N	-3.269	1.797	-2.132	-2.586	1.333	-1.095	1.33	38.53	-34.19
67	2jsa-9	VAL_A_12_N	VAL_A_12_H	-2.586	1.333	-1.095	-1.598	1.527	-1.008	1.01	85.06	11.11
68	2jsa-9	VAL_A_12_N	VAL_A_12_CA	-2.586	1.333	-1.095	-3.236	0.54	-0.065	1.45	44.87	-129.34
69	2jsa-9	VAL_A_12_CA	VAL_A_12_HA	-3.236	0.54	-0.065	-3.744	-0.297	-0.544	1.09	116.07	-121.25
70	2jsa-9	VAL_A_12_CA	VAL_A_12_C	-3.236	0.54	-0.065	-4.29	1.395	0.642	1.53	62.48	140.95
71	2jsa-9	VAL_A_12_C	VAL_A_12_O	-4.29	1.395	0.642	-5.445	0.987	0.765	1.23	84.27	-160.54
72	2jsa-9	VAL_A_12_C	VAL_A_13_N	-4.29	1.395	0.642	-3.856	2.565	1.086	1.32	70.41	69.65
73	2jsa-9	VAL_A_13_N	VAL_A_13_H	-3.856	2.565	1.086	-2.892	2.836	0.949	1.01	97.79	15.70
74	2jsa-9	VAL_A_13_N	VAL_A_13_CA	-3.856	2.565	1.086	-4.749	3.481	1.776	1.45	61.66	134.27
75	2jsa-9	VAL_A_13_CA	VAL_A_13_HA	-4.749	3.481	1.776	-5.136	2.981	2.664	1.09	35.45	-127.74
76	2jsa-9	VAL_A_13_CA	VAL_A_13_C	-4.749	3.481	1.776	-5.932	3.818	0.866	1.53	126.49	164.10
77	2jsa-9	VAL_A_13_C	VAL_A_13_O	-5.932	3.818	0.866	-7.083	3.584	1.227	1.23	72.92	-168.51
78	2jsa-9	VAL_A_13_C	LYS_A_14_N	-5.932	3.818	0.866	-5.605	4.362	-0.298	1.33	151.40	58.99
79	2jsa-9	LYS_A_14_N	LYS_A_14_H	-5.605	4.362	-0.298	-4.635	4.526	-0.529	1.01	103.21	9.60
80	2jsa-9	LYS_A_14_N	LYS_A_14_CA	-5.605	4.362	-0.298	-6.627	4.733	-1.262	1.45	131.56	160.05
81	2jsa-9	LYS_A_14_CA	LYS_A_14_HA	-6.627	4.733	-1.262	-7.139	5.619	-0.887	1.09	69.87	120.02
82	2jsa-9	LYS_A_14_CA	LYS_A_14_C	-6.627	4.733	-1.262	-7.658	3.609	-1.365	1.53	93.86	-132.53
83	2jsa-9	LYS_A_14_C	LYS_A_14_O	-7.658	3.609	-1.365	-8.839	3.864	-1.598	1.23	100.92	167.82
84	2jsa-9	LYS_A_14_C	LYS_A_15_N	-7.658	3.609	-1.365	-7.176	2.388	-1.185	1.32	82.19	-68.46
85	2jsa-9	LYS_A_15_N	LYS_A_15_H	-7.176	2.388	-1.185	-6.193	2.252	-0.996	1.01	79.22	-7.88
86	2jsa-9	LYS_A_15_N	LYS_A_15_CA	-7.176	2.388	-1.185	-8.042	1.223	-1.254	1.45	92.72	-126.63
87	2jsa-9	LYS_A_15_CA	LYS_A_15_HA	-8.042	1.223	-1.254	-8.766	1.388	-2.052	1.09	137.06	167.16
88	2jsa-9	LYS_A_15_CA	LYS_A_15_C	-8.042	1.223	-1.254	-8.818	1.091	0.058	1.53	30.96	-170.35
89	2jsa-9	LYS_A_15_C	LYS_A									

90	2jsa-9	LYS_A_15_C	TYR_A_16_N	-8.818	1.091	0.058	-8.109	1.324	1.153	1.33	34.28	18.19
91	2jsa-9	TYR_A_16_N	TYR_A_16_H	-8.109	1.324	1.153	-7.131	1.567	1.084	1.01	93.92	13.95
92	2jsa-9	TYR_A_16_N	TYR_A_16_CA	-8.109	1.324	1.153	-8.717	1.235	2.47	1.45	25.01	-171.67
93	2jsa-9	TYR_A_16_CA	TYR_A_16_HA	-8.717	1.235	2.47	-9.296	0.316	2.557	1.09	85.42	-122.21
94	2jsa-9	TYR_A_16_CA	TYR_A_16_C	-8.717	1.235	2.47	-9.616	2.444	2.742	1.53	79.77	126.63
95	2jsa-9	TYR_A_16_C	TYR_A_16_O	-9.616	2.444	2.742	-10.833	2.305	2.852	1.23	84.87	-173.48
96	2jsa-9	TYR_A_16_C	GLU_A_17_N	-9.616	2.444	2.742	-8.981	3.603	2.843	1.33	85.63	61.28
97	2jsa-9	GLU_A_17_N	GLU_A_17_H	-8.981	3.603	2.843	-7.977	3.643	2.741	1.01	95.80	2.28
98	2jsa-9	GLU_A_17_N	GLU_A_17_CA	-8.981	3.603	2.843	-9.708	4.835	3.1	1.45	79.82	120.54
99	2jsa-9	GLU_A_17_CA	GLU_A_17_HA	-9.708	4.835	3.1	-9.959	4.864	4.16	1.09	13.41	173.41
100	2jsa-9	GLU_A_17_CA	GLU_A_17_C	-9.708	4.835	3.1	-11.009	4.86	2.296	1.53	121.71	178.90
101	2jsa-9	GLU_A_17_C	GLU_A_17_O	-11.009	4.86	2.296	-12.049	5.274	2.807	1.23	65.46	158.29
102	2jsa-9	GLU_A_17_C	GLY_A_18_N	-11.009	4.86	2.296	-10.91	4.413	1.053	1.32	159.78	-77.51
103	2jsa-9	GLY_A_18_N	GLY_A_18_H	-10.91	4.413	1.053	-10.021	4.088	0.699	1.01	110.51	-20.08
104	2jsa-9	GLY_A_18_N	GLY_A_18_CA	-10.91	4.413	1.053	-12.066	4.38	0.175	1.45	127.21	-178.36
105	2jsa-9	GLY_A_18_CA	GLY_A_18_C	-12.066	4.38	0.175	-12.418	2.942	-0.215	1.53	104.76	-103.75
106	2jsa-9	GLY_A_18_C	GLY_A_18_O	-12.418	2.942	-0.215	-12.722	2.666	-1.374	1.23	160.49	-137.76
107	2jsa-9	GLY_A_18_C	SER_A_19_N	-12.418	2.942	-0.215	-12.364	2.065	0.777	1.33	41.53	-86.48
108	2jsa-9	SER_A_19_N	SER_A_19_H	-12.364	2.065	0.777	-12.106	2.363	1.707	1.01	22.97	49.11
109	2jsa-9	SER_A_19_N	SER_A_19_CA	-12.364	2.065	0.777	-12.673	0.662	0.552	1.45	98.90	-102.42
110	2jsa-9	SER_A_19_CA	SER_A_19_HA	-12.673	0.662	0.552	-12.156	0.339	-0.351	1.09	145.98	-32.00
111	2jsa-9	SER_A_19_CA	SER_A_19_C	-12.673	0.662	0.552	-14.179	0.485	0.346	1.53	97.74	-173.30
112	2jsa-9	SER_A_19_C	SER_A_19_O	-14.179	0.485	0.346	-14.606	-0.134	-0.628	1.23	142.33	-124.60
113	2jsa-9	SER_A_19_C	ALA_A_20_N	-14.179	0.485	0.346	-14.941	1.039	1.277	1.32	45.34	143.98
114	2jsa-9	ALA_A_20_N	ALA_A_20_H	-14.941	1.039	1.277	-14.52	1.533	2.051	1.01	39.98	49.56
115	2jsa-9	ALA_A_20_N	ALA_A_20_CA	-14.941	1.039	1.277	-16.389	0.949	1.209	1.45	92.68	-176.44
116	2jsa-9	ALA_A_20_CA	ALA_A_20_HA	-16.389	0.949	1.209	-16.818	1.774	1.778	1.09	58.54	117.47
117	2jsa-9	ALA_A_20_CA	ALA_A_20_C	-16.389	0.949	1.209	-16.845	-0.366	1.844	1.53	65.48	-109.12
118	2jsa-9	ALA_A_20_C	ALA_A_20_O	-16.845	-0.366	1.844	-18.031	-0.55	2.115	1.23	77.28	-171.18
119	2jsa-9	ALA_A_20_C	ASP_A_21_N	-16.845	-0.366	1.844	-15.879	-1.247	2.062	1.33	80.53	-42.37
120	2jsa-9	ASP_A_21_N	ASP_A_21_H	-15.879	-1.247	2.062	-14.925	-1.029	1.812	1.01	104.33	12.87
121	2jsa-9	ASP_A_21_N	ASP_A_21_CA	-15.879	-1.247	2.062	-16.167	-2.539	2.661	1.45	65.65	-102.57
122	2jsa-9	ASP_A_21_CA	ASP_A_21_HA	-16.167	-2.539	2.661	-17.244	-2.639	2.791	1.09	83.15	-174.70
123	2jsa-9	ASP_A_21_CA	ASP_A_21_C	-16.167	-2.539	2.661	-15.468	-2.634	4.018	1.53	27.47	-7.74
124	2jsa-9	ASP_A_21_C	ASP_A_21_O	-15.468	-2.634	4.018	-15.94	-3.331	4.916	1.23	43.15	-124.11
125	2jsa-9	ASP_A_21_C	LYS_A_22_N	-15.468	-2.634	4.018	-14.354	-1.924	4.126	1.33	85.33	32.51
126	2jsa-9	LYS_A_22_N	LYS_A_22_H	-14.354	-1.924	4.126	-14.023	-1.374	3.346	1.01	140.55	58.96
127	2jsa-9	LYS_A_22_N	LYS_A_22_CA	-14.354	-1.924	4.126	-13.586	-1.92	5.36	1.45	31.90	0.30
128	2jsa-9	LYS_A_22_CA	LYS_A_22_HA	-13.586	-1.92	5.36	-12.749	-1.232	5.235	1.09	96.58	39.42
129	2jsa-9	LYS_A_22_CA	LYS_A_22_C	-13.586	-1.92	5.36	-13.008	-3.316	5.599	1.53	81.01	-67.51
130	2jsa-9	LYS_A_22_C	LYS_A_22_O	-13.008	-3.316	5.599	-13.332	-3.963	6.594	1.23	36.03	-116.60
131	2jsa-9	LYS_A_22_C	ASP_A_23_N	-13.008	-3.316	5.599	-12.163	-3.739	4.672	1.32	134.45	-26.59
132	2jsa-9	ASP_A_23_N	ASP_A_23_H	-12.163	-3.739	4.672	-11.943	-3.153	3.879	1.01	141.72	69.42
133	2jsa-9	ASP_A_23_N	ASP_A_23_CA	-12.163	-3.739	4.672	-11.536	-5.046	4.77	1.45	86.13	-64.37
134	2jsa-9	ASP_A_23_CA	ASP_A_23_HA	-11.536	-5.046	4.77	-11.521	-5.356	5.815	1.09	16.54	-87.23
135	2jsa-9	ASP_A_23_CA	ASP_A_23_C	-11.536	-5.046	4.77	-10.106	-4.964	4.233	1.53	110.55	3.28
136	2jsa-9	ASP_A_23_C	ASP_A_23_O	-10.106	-4.964	4.233	-9.898	-4.702	3.049	1.23	164.22	51.55
137	2jsa-9	ASP_A_23_C	ALA_A_24_N	-10.106	-4.964	4.233	-9.157	-5.192	5.129	1.32	47.45	-13.51
138	2jsa-9	ALA_A_24_N	ALA_A_24_H	-9.157	-5.192	5.129	-9.401	-5.4	6.087	1.01	18.50	-139.55
139	2jsa-9	ALA_A_24_N	ALA_A_24_CA	-9.157	-5.192	5.129	-7.753	-5.148	4.76	1.45	104.72	1.80
140	2jsa-9	ALA_A_24_CA	ALA_A_24_HA	-7.753	-5.148	4.76	-7.541	-4.181	4.303	1.09	114.78	77.63
141	2jsa-9	ALA_A_24_CA	ALA_A_24_C	-7.753	-5.148	4.76	-7.464	-6.243	3.731	1.53	132.26	-75.22
142	2jsa-9	ALA_A_24_C	ALA_A_24_O	-7.464	-6.243	3.731	-6.391	-6.269	3.132	1.23	119.17	-1.39
143	2jsa-9	ALA_A_24_C	ASN_A_25_N	-7.464	-6.243	3.731	-8.442	-7.121	3.56	1.33	97.41	-138.08
144	2jsa-9	ASN_A_25_N	ASN_A_25_H	-8.442	-7.121	3.56	-9.298	-7.038	4.089	1.01	58.40	174.46
145	2jsa-9	ASN_A_25_N	ASN_A_25_CA	-8.442	-7.121	3.56	-8.307	-8.216	2.614	1.45	130.61	-82.97
146	2jsa-9	ASN_A_25_CA	ASN_A_25_HA	-8.307	-8.216	2.614	-7.293	-8.613	2.67	1.09	87.06	-21.38
147	2jsa-9	ASN_A_25_CA	ASN_A_25_C	-8.307	-8.216	2.614	-8.587	-7.701	1.201	1.53	157.47	118.53
148	2jsa-9	ASN_A_25_C	ASN_A_25_O	-8.587	-7.701	1.201	-7.882	-8.054	0.256	1.23	140.16	-26.60
149	2jsa-9	ASN_A_25_C	VAL_A_26_N	-8.587	-7.701	1.201	-9.617	-6.874	1.099	1.32	94.42	141.24
150	2jsa-9	VAL_A_26_N	VAL_A_26_H	-9.617	-6.874	1.099	-10.152	-6.626	1.919	1.01	35.72	155.13
151	2jsa-9	VAL_A_26_N	VAL_A_26_CA	-9.617	-6.874	1.099	-9.999	-6.307	-0.183	1.45	151.93	123.97
152	2jsa-9	VAL_A_26_CA	VAL_A_26_HA	-9.999	-6.307	-0.183	-9.801	-7.046	-0.959	1.09	135.41	-75.00
153	2jsa-9	VAL_A_26_CA	VAL_A_26_C	-9.999	-6.307	-0.183	-9.136	-5.076	-0.469	1.53	100.77	54.97
154	2jsa-9	VAL_A_26_C	VAL_A_26_O	-9.136	-5.076	-0.469	-9.187	-4.518	-1.563	1.23	152.88	95.22
155	2jsa-9	VAL_A_26_C	ILE_A_27_N	-9.136	-5.076	-0.469	-8.363	-4.689	0.535	1.32	40.73	26.59
156	2jsa-9	ILE_A_27_N	ILE_A_27_H	-8.363	-4.689	0.535	-8.371	-5.197	1.408	1.01	30.20	-90.90
157	2jsa-9	ILE_A_27_N	ILE_A_27_CA	-8.363	-4.689	0.535	-7.49	-3.535	0.406	1.45	95.09	52.89
158	2jsa-9	ILE_A_27_CA	ILE_A_27_HA	-7.49	-3.535	0.406	-7.909	-2.878	-0.356	1.09	134.36	122.53
159	2jsa-9	ILE_A_27_CA	ILE_A_27_C	-7.49	-3.535	0.406	-6.115	-3.993	-0.082	1.53	108.61	-18.42
160	2jsa-9	ILE_A_27_C	ILE_A_27_O	-6.115	-3.993	-0.082	-5.697	-3.646	-1.186	1.23	153.80	39.70
161	2jsa-9	ILE_A_27_C	LYS_A_28_N	-6.115	-3.993	-0.082	-5.449	-4.765	0.764	1.32	50.32	-49.22
162	2jsa-9	LYS_A_28_N	LYS_A_28_H	-5.449	-4.765	0.764	-5.854	-5.01	1.656	1.01	27.95	-148.83
163	2jsa-9	LYS_A_28_N	LYS_A_28_CA	-5.449	-4.765	0.764	-4.129	-5.274	0.433	1.45	103.17	-21.09
164	2jsa-9	LYS_A_28_CA	LYS_A_28_HA	-4.129	-5.274	0.433	-3.441	-4.429	0.393	1.09	92.10	50.85
165	2jsa-9	LYS_A_28_CA	LYS_A_28_C	-4.129	-5.274	0.433	-4.167	-5.91	-0.959	1.53	155.41	-93.42
166	2jsa-9	LYS_A_28_C	LYS_A_28_O	-4.167	-5.91	-0.959	-3.234	-5.749	-1.744	1.23	129.66	9.79
167	2jsa-9	LYS_A_28_C	LYS_A_29_N	-4.167	-5.91	-0.959	-5.255	-6.618	-1.221	1.32	101.41	-146.95
168	2jsa-9	LYS_A_29_N	LYS_A_29_H	-5.255	-6.618	-1.221	-5.983	-6.707	-0.527	1.01	46.58	-173.03
169	2jsa-9	LYS_A_29_N	LYS_A_29_CA	-5.255	-6.618	-1.221	-5.427	-7.279	-2.504	1.45	151.97	-104.59
170	2jsa-9	LYS_A_29_CA	LYS_A_29_HA	-5.427	-7.279	-2.504	-4.504	-7.812	-2.735	1.09	102.23	-30.00
171	2jsa-9	LYS_A_29_CA	LYS_A_29_C	-5.427	-7.279	-2.504	-5.639	-6.224	-3.592	1.53	135.32	101.36
172	2jsa-9	LYS_A_29_C	LYS_A_29_O	-5.639	-6.224	-3.592	-4.899	-6.182	-4.573	1.23	142.93	3.25
173	2jsa-9	LYS_A_29_C	ASP_A_30_N	-5.639	-6.224	-3.592	-6.654	-5.397	-3.38	1.33	80.80	140.83
174	2jsa-9	ASP_A_30_N	ASP_A_30_H	-6.654	-5.397	-3.38	-7.222	-5.49	-2.55	1.01	34.74	-170.70
175	2jsa-9	ASP_A_30_N	ASP_A_30_CA	-6.654	-5.397	-3.38	-6.972	-4.345	-4.33	1.45	130.84	106.82
176	2jsa-9	ASP_A_30_CA	ASP_A_30_HA	-6.972	-4.345	-4.33	-7.497	-4.78	-5.18	1.09	141.27	-140.36
177	2jsa-9	ASP_A_30_CA	ASP_A_30_C	-6.972	-4.345	-4.33	-5.676	-3.681	-4.804	1.53	108.03	27.13
178	2jsa-9	ASP_A_30_C	ASP_A_30_O	-5.676	-3.681	-4.804	-5.426	-3.585	-6.004	1.23	167.42	21.01
179	2jsa-9	ASP_A_30_C	PHE_A_31_N	-5.676	-3.681	-4.804	-4.887	-3.241	-3.834	1.33	42.96	29.15
180	2jsa-9	PHE_A_31_N	PHE_A_31_H	-4.887	-3.241	-3.834	-5.156	-3.355				

183	2jsa-9	PHE_A_31_CA	PHE_A_31_C	-3.624	-2.589	-4.137	-2.877	-3.33	-5.248	1.53	136.56	-44.77
184	2jsa-9	PHE_A_31_C	PHE_A_31_O	-2.877	-3.33	-5.248	-2.652	-2.779	-6.323	1.23	151.03	67.79
185	2jsa-9	PHE_A_31_C	ASP_A_32_N	-2.877	-3.33	-5.248	-2.513	-4.568	-4.947	1.33	76.87	-73.62
186	2jsa-9	ASP_A_32_N	ASP_A_32_H	-2.513	-4.568	-4.947	-2.73	-4.957	-4.04	1.01	26.16	-119.15
187	2jsa-9	ASP_A_32_N	ASP_A_32_CA	-2.513	-4.568	-4.947	-1.796	-5.39	-5.908	1.45	131.38	-48.90
188	2jsa-9	ASP_A_32_CA	ASP_A_32_HA	-1.796	-5.39	-5.908	-0.759	-5.055	-5.959	1.09	92.68	17.90
189	2jsa-9	ASP_A_32_CA	ASP_A_32_C	-1.796	-5.39	-5.908	-2.454	-5.255	-7.281	1.53	153.93	168.41
190	2jsa-9	ASP_A_32_C	ASP_A_32_O	-2.454	-5.255	-7.281	-1.773	-5.28	-8.306	1.23	146.38	-2.10
191	2jsa-9	ASP_A_32_C	ALA_A_33_N	-2.454	-5.255	-7.281	-3.772	-5.114	-7.259	1.33	89.05	173.89
192	2jsa-9	ALA_A_33_N	ALA_A_33_H	-3.772	-5.114	-7.259	-4.267	-5.102	-6.379	1.01	29.36	178.61
193	2jsa-9	ALA_A_33_N	ALA_A_33_CA	-3.772	-5.114	-7.259	-4.53	-4.975	-8.491	1.45	147.97	169.61
194	2jsa-9	ALA_A_33_CA	ALA_A_33_HA	-4.53	-4.975	-8.491	-4.346	-5.849	-9.116	1.09	124.98	-78.11
195	2jsa-9	ALA_A_33_CA	ALA_A_33_C	-4.53	-4.975	-8.491	-4.05	-3.732	-9.243	1.53	119.44	68.89
196	2jsa-9	ALA_A_33_C	ALA_A_33_O	-4.05	-3.732	-9.243	-3.625	-3.824	-10.393	1.23	159.29	-12.21
197	2jsa-9	ALA_A_33_C	GLU_A_34_N	-4.05	-3.732	-9.243	-4.135	-2.599	-8.562	1.32	59.06	94.29
198	2jsa-9	GLU_A_34_N	GLU_A_34_H	-4.135	-2.599	-8.562	-4.495	-2.598	-7.618	1.01	20.87	179.84
199	2jsa-9	GLU_A_34_N	GLU_A_34_CA	-4.135	-2.599	-8.562	-3.714	-1.339	-9.151	1.45	113.91	71.52
200	2jsa-9	GLU_A_34_CA	GLU_A_34_HA	-3.714	-1.339	-9.151	-3.874	-1.399	-10.227	1.09	170.98	-159.44
201	2jsa-9	GLU_A_34_CA	GLU_A_34_C	-3.714	-1.339	-9.151	-2.224	-1.107	-8.9	1.53	80.55	8.85
202	2jsa-9	GLU_A_34_C	GLU_A_34_O	-2.224	-1.107	-8.9	-1.769	0.035	-8.847	1.23	87.53	68.28
203	2jsa-9	GLU_A_34_C	CYS_A_35_N	-2.224	-1.107	-8.9	-1.502	-2.209	-8.753	1.33	83.63	-56.77
204	2jsa-9	CYS_A_35_N	CYS_A_35_H	-1.502	-2.209	-8.753	-1.942	-3.116	-8.81	1.01	93.24	-115.88
205	2jsa-9	CYS_A_35_N	CYS_A_35_CA	-1.502	-2.209	-8.753	-0.072	-2.141	-8.509	1.45	80.33	2.72
206	2jsa-9	CYS_A_35_CA	CYS_A_35_HA	-0.072	-2.141	-8.509	0.232	-1.094	-8.539	1.09	91.58	73.81
207	2jsa-9	CYS_A_35_CA	CYS_A_35_C	-0.072	-2.141	-8.509	0.644	-2.888	-9.636	1.53	137.44	-46.21
208	2jsa-9	CYS_A_35_C	CYS_A_35_O	0.644	-2.888	-9.636	1.498	-2.321	-10.316	1.23	123.56	33.58
209	2jsa-9	CYS_A_35_C	LYS_A_36_N	0.644	-2.888	-9.636	0.27	-4.148	-9.798	1.32	97.03	-106.53
210	2jsa-9	LYS_A_36_N	LYS_A_36_H	0.27	-4.148	-9.798	-0.439	-4.549	-9.201	1.01	53.76	-150.51
211	2jsa-9	LYS_A_36_N	LYS_A_36_CA	0.27	-4.148	-9.798	0.866	-4.978	-10.831	1.45	135.31	-54.32
212	2jsa-9	LYS_A_36_CA	LYS_A_36_HA	0.866	-4.978	-10.831	1.95	-4.909	-10.736	1.09	85.00	3.64
213	2jsa-9	LYS_A_36_CA	LYS_A_36_C	0.866	-4.978	-10.831	0.484	-4.427	-12.206	1.53	154.01	124.73
214	2jsa-9	LYS_A_36_C	LYS_A_36_O	0.484	-4.427	-12.206	1.291	-4.448	-13.134	1.23	138.98	-1.49
215	2jsa-9	LYS_A_36_C	LYS_A_37_N	0.484	-4.427	-12.206	-0.748	-3.946	-12.294	1.33	93.81	158.67
216	2jsa-9	LYS_A_37_N	LYS_A_37_H	-0.748	-3.946	-12.294	-1.358	-3.961	-11.489	1.01	37.16	-178.59
217	2jsa-9	LYS_A_37_N	LYS_A_37_CA	-0.748	-3.946	-12.294	-1.247	-3.39	-13.54	1.45	149.05	131.91
218	2jsa-9	LYS_A_37_CA	LYS_A_37_HA	-1.247	-3.39	-13.54	-0.902	-4.025	-14.356	1.09	138.47	-61.48
219	2jsa-9	LYS_A_37_CA	LYS_A_37_C	-1.247	-3.39	-13.54	-0.647	-1.998	-13.749	1.53	97.85	66.68
220	2jsa-9	LYS_A_37_C	LYS_A_37_O	-0.647	-1.998	-13.749	-0.241	-1.654	-14.858	1.23	154.37	40.27
221	2jsa-9	LYS_A_37_C	LEU_A_38_N	-0.647	-1.998	-13.749	-0.61	-1.235	-12.666	1.33	35.20	87.22
222	2jsa-9	LEU_A_38_N	LEU_A_38_H	-0.61	-1.235	-12.666	-0.962	-1.583	-11.786	1.01	29.36	-135.33
223	2jsa-9	LEU_A_38_N	LEU_A_38_CA	-0.61	-1.235	-12.666	-0.066	0.111	-12.718	1.45	92.05	67.99
224	2jsa-9	LEU_A_38_CA	LEU_A_38_HA	-0.066	0.111	-12.718	-0.486	0.612	-13.59	1.09	143.14	129.97
225	2jsa-9	LEU_A_38_CA	LEU_A_38_C	-0.066	0.111	-12.718	1.45	0.037	-12.91	1.53	97.21	-2.79
226	2jsa-9	LEU_A_38_C	LEU_A_38_O	1.45	0.037	-12.91	1.984	0.577	-13.877	1.23	141.86	45.32
227	2jsa-9	LEU_A_38_C	PHE_A_39_N	1.45	0.037	-12.91	2.101	-0.636	-11.972	1.33	44.95	-45.95
228	2jsa-9	PHE_A_39_N	PHE_A_39_H	2.101	-0.636	-11.972	1.597	-1.054	-11.203	1.01	40.41	-140.33
229	2jsa-9	PHE_A_39_N	PHE_A_39_CA	2.101	-0.636	-11.972	3.545	-0.788	-12.026	1.45	92.13	-6.01
230	2jsa-9	PHE_A_39_CA	PHE_A_39_HA	3.545	-0.788	-12.026	3.996	0.107	-12.454	1.09	113.13	63.26
231	2jsa-9	PHE_A_39_CA	PHE_A_39_C	3.545	-0.788	-12.026	3.937	-2.01	-12.859	1.53	122.99	-72.21
232	2jsa-9	PHE_A_39_C	PHE_A_39_O	3.937	-2.01	-12.859	5.015	-2.574	-12.672	1.23	81.26	-27.62
233	2jsa-9	PHE_A_39_C	HIS_A_40_N	3.937	-2.01	-12.859	3.041	-2.384	-13.761	1.33	132.89	-157.34
234	2jsa-9	HIS_A_40_N	HIS_A_40_H	3.041	-2.384	-13.761	2.175	-1.874	-13.86	1.01	95.63	149.51
235	2jsa-9	HIS_A_40_N	HIS_A_40_CA	3.041	-2.384	-13.761	3.281	-3.528	-14.622	1.45	126.37	-78.15
236	2jsa-9	HIS_A_40_CA	HIS_A_40_HA	3.281	-3.528	-14.622	3.425	-4.402	-13.987	1.09	54.36	-80.64
237	2jsa-9	HIS_A_40_CA	HIS_A_40_C	3.281	-3.528	-14.622	4.568	-3.311	-15.421	1.53	121.47	9.57
238	2jsa-9	HIS_A_40_C	HIS_A_40_O	4.568	-3.311	-15.421	5.144	-4.26	-15.948	1.23	115.39	-58.74
239	2jsa-9	HIS_A_40_C	THR_A_41_N	4.568	-3.311	-15.421	4.981	-2.054	-15.483	1.32	92.68	71.81
240	2jsa-9	THR_A_41_N	THR_A_41_H	4.981	-2.054	-15.483	4.457	-1.323	-15.023	1.01	62.91	125.63
241	2jsa-9	THR_A_41_N	THR_A_41_CA	4.981	-2.054	-15.483	6.189	-1.698	-16.208	1.45	119.93	16.42
242	2jsa-9	THR_A_41_CA	THR_A_41_HA	6.189	-1.698	-16.208	6.333	-2.412	-17.019	1.09	138.07	-78.60
243	2jsa-9	THR_A_41_CA	THR_A_41_C	6.189	-1.698	-16.208	7.408	-1.78	-15.287	1.53	52.99	-3.85
244	2jsa-9	THR_A_41_C	THR_A_41_O	7.408	-1.78	-15.287	8.365	-2.496	-15.579	1.23	103.73	-36.80
245	2jsa-9	THR_A_41_C	ILE_A_42_N	7.408	-1.78	-15.287	7.333	-1.038	-14.191	1.33	34.23	95.77
246	2jsa-9	ILE_A_42_N	ILE_A_42_H	7.333	-1.038	-14.191	6.514	-0.474	-14.013	1.01	79.85	145.45
247	2jsa-9	ILE_A_42_N	ILE_A_42_CA	7.333	-1.038	-14.191	8.417	-1.018	-13.225	1.45	48.30	1.06
248	2jsa-9	ILE_A_42_CA	ILE_A_42_HA	8.417	-1.018	-13.225	9.125	-0.245	-13.527	1.09	106.07	47.51
249	2jsa-9	ILE_A_42_CA	ILE_A_42_C	8.417	-1.018	-13.225	9.151	-2.36	-13.261	1.53	91.35	-61.32
250	2jsa-9	ILE_A_42_C	ILE_A_42_O	9.151	-2.36	-13.261	8.523	-3.412	-13.374	1.23	95.27	-120.84
251	2jsa-9	ILE_A_42_C	PRO_A_43_N	9.151	-2.36	-13.261	10.505	-2.277	-13.159	1.36	85.70	3.51
252	2jsa-9	PRO_A_43_N	PRO_A_43_CA	10.505	-2.277	-13.159	11.331	-3.473	-13.179	1.45	90.79	-55.37
253	2jsa-9	PRO_A_43_CA	PRO_A_43_HA	11.331	-3.473	-13.179	11.002	-4.141	-13.974	1.09	136.87	-116.22
254	2jsa-9	PRO_A_43_CA	PRO_A_43_C	11.331	-3.473	-13.179	11.242	-4.222	-11.847	1.53	29.52	-96.78
255	2jsa-9	PRO_A_43_C	PRO_A_43_O	11.242	-4.222	-11.847	11.864	-3.825	-10.864	1.23	36.89	32.55
256	2jsa-9	PRO_A_43_C	PHE_A_44_N	11.242	-4.222	-11.847	10.463	-5.294	-11.86	1.33	90.56	-126.01
257	2jsa-9	PHE_A_44_N	PHE_A_44_H	10.463	-5.294	-11.86	9.982	-5.563	-12.706	1.01	146.92	-150.78
258	2jsa-9	PHE_A_44_N	PHE_A_44_CA	10.463	-5.294	-11.86	10.285	-6.103	-10.665	1.45	34.73	-102.41
259	2jsa-9	PHE_A_44_CA	PHE_A_44_HA	10.285	-6.103	-10.665	9.876	-7.076	-10.935	1.09	104.35	-112.80
260	2jsa-9	PHE_A_44_CA	PHE_A_44_C	10.285	-6.103	-10.665	9.353	-5.411	-9.669	1.53	49.37	143.41
261	2jsa-9	PHE_A_44_C	PHE_A_44_O	9.353	-5.411	-9.669	9.045	-5.964	-8.615	1.23	30.99	-119.12
262	2jsa-9	PHE_A_44_C	GLY_A_45_N	9.353	-5.411	-9.669	8.93	-4.211	-10.038	1.32	106.17	109.42
263	2jsa-9	GLY_A_45_N	GLY_A_45_H	8.93	-4.211	-10.038	9.225	-3.817	-10.92	1.01	150.84	53.18
264	2jsa-9	GLY_A_45_N	GLY_A_45_CA	8.93	-4.211	-10.038	8.039	-3.438	-9.189	1.45	54.26	139.06
265	2jsa-9	GLY_A_45_CA	GLY_A_45_C	8.039	-3.438	-9.189	6.903	-4.309	-8.65	1.53	69.37	-142.52
266	2jsa-9	GLY_A_45_C	GLY_A_45_O	6.903	-4.309	-8.65	6.546	-4.213	-7.475	1.23	17.46	164.95
267	2jsa-9	GLY_A_45_C	THR_A_46_N	6.903	-4.309	-8.65	6.366	-5.139	-9.532	1.32	131.74	-122.90
268	2jsa-9	THR_A_46_N	THR_A_46_H	6.366	-5.139	-9.532	6.711	-5.165	-10.481	1.01	159.97	-4.31
269	2jsa-9	THR_A_46_N	THR_A_46_CA	6.366	-5.139	-9.532	5.277	-6.026	-9.159	1.45	75.13	-140.84
270	2jsa-9	THR_A_46_CA	THR_A_46_HA	5.277	-6.026	-9.159	4.398	-5.424	-8.931	1.09	77.92	145.59
271	2jsa-9	THR_A_46_CA	THR_A_46_C	5.277	-6.026	-9.159	5.643	-6.82	-7.903	1.53	34.84	-65.25
272	2jsa-9	THR_A_46_C	THR_A_46_O	5.643	-6.82	-7.903	4.848	-6.913	-6.97	1.23	40.63	-173.33
273	2jsa-9	THR_A_46_C	ARG_A_47_N	5.643	-6.82	-7.90						

276	2jsa-9	ARG_A_47_CA	ARG_A_47_HA	7.329	-8.156	-6.796	6.726	-9.061	-6.723	1.09	86.16	-123.68
277	2jsa-9	ARG_A_47_CA	ARG_A_47_C	7.329	-8.156	-6.796	7.191	-7.358	-5.496	1.53	31.92	99.81
278	2jsa-9	ARG_A_47_C	ARG_A_47_O	7.191	-7.358	-5.496	6.847	-7.916	-4.455	1.23	32.20	-121.65
279	2jsa-9	ARG_A_47_C	GLU_A_48_N	7.191	-7.358	-5.496	7.466	-6.067	-5.6	1.32	94.51	77.97
280	2jsa-9	GLU_A_48_N	GLU_A_48_H	7.466	-6.067	-5.6	7.743	-5.676	-6.489	1.01	151.68	54.68
281	2jsa-9	GLU_A_48_N	GLU_A_48_CA	7.466	-6.067	-5.6	7.376	-5.188	-4.447	1.45	37.46	95.85
282	2jsa-9	GLU_A_48_CA	GLU_A_48_HA	7.376	-5.188	-4.447	7.863	-5.683	-3.607	1.09	39.58	-45.47
283	2jsa-9	GLU_A_48_CA	GLU_A_48_C	7.376	-5.188	-4.447	5.911	-4.943	-4.078	1.53	76.05	170.51
284	2jsa-9	GLU_A_48_C	GLU_A_48_O	5.911	-4.943	-4.078	5.576	-4.826	-2.901	1.23	16.78	160.75
285	2jsa-9	GLU_A_48_C	CYS_A_49_N	5.911	-4.943	-4.078	5.079	-4.872	-5.107	1.33	140.94	175.12
286	2jsa-9	CYS_A_49_N	CYS_A_49_H	5.079	-4.872	-5.107	5.426	-4.977	-6.05	1.01	158.97	-16.84
287	2jsa-9	CYS_A_49_N	CYS_A_49_CA	5.079	-4.872	-5.107	3.658	-4.644	-4.906	1.45	82.05	170.88
288	2jsa-9	CYS_A_49_CA	CYS_A_49_HA	3.658	-4.644	-4.906	3.531	-3.674	-4.425	1.09	63.82	97.46
289	2jsa-9	CYS_A_49_CA	CYS_A_49_C	3.658	-4.644	-4.906	3.126	-5.726	-3.965	1.53	52.03	-116.18
290	2jsa-9	CYS_A_49_C	CYS_A_49_O	3.126	-5.726	-3.965	2.58	-5.419	-2.906	1.23	30.60	150.65
291	2jsa-9	CYS_A_49_C	ASP_A_50_N	3.126	-5.726	-3.965	3.304	-6.97	-4.385	1.32	108.48	-81.86
292	2jsa-9	ASP_A_50_N	ASP_A_50_H	3.304	-6.97	-4.385	3.762	-7.149	-5.268	1.01	150.89	-21.35
293	2jsa-9	ASP_A_50_N	ASP_A_50_CA	3.304	-6.97	-4.385	2.848	-8.1	-3.592	1.45	56.94	-111.98
294	2jsa-9	ASP_A_50_CA	ASP_A_50_HA	2.848	-8.1	-3.592	1.77	-8.024	-3.45	1.09	82.51	175.97
295	2jsa-9	ASP_A_50_CA	ASP_A_50_C	2.848	-8.1	-3.592	3.554	-8.083	-2.235	1.53	27.49	1.38
296	2jsa-9	ASP_A_50_C	ASP_A_50_O	3.554	-8.083	-2.235	3.014	-8.568	-1.243	1.23	36.19	-138.07
297	2jsa-9	ASP_A_50_C	HIS_A_51_N	3.554	-8.083	-2.235	4.754	-7.52	-2.234	1.33	89.96	25.13
298	2jsa-9	HIS_A_51_N	HIS_A_51_H	4.754	-7.52	-2.234	5.139	-7.142	-3.088	1.01	147.72	44.47
299	2jsa-9	HIS_A_51_N	HIS_A_51_CA	4.754	-7.52	-2.234	5.54	-7.433	-1.015	1.45	32.97	6.32
300	2jsa-9	HIS_A_51_CA	HIS_A_51_HA	5.54	-7.433	-1.015	5.364	-8.339	-0.435	1.09	57.85	-100.99
301	2jsa-9	HIS_A_51_CA	HIS_A_51_C	5.54	-7.433	-1.015	5.064	-6.242	-0.181	1.53	56.97	111.78
302	2jsa-9	HIS_A_51_C	HIS_A_51_O	5.064	-6.242	-0.181	5.588	-5.99	0.903	1.23	28.21	25.68
303	2jsa-9	HIS_A_51_C	TYR_A_52_N	5.064	-6.242	-0.181	4.076	-5.54	-0.718	1.33	113.90	144.61
304	2jsa-9	TYR_A_52_N	TYR_A_52_H	4.076	-5.54	-0.718	3.695	-5.804	-1.615	1.01	152.67	-145.28
305	2jsa-9	TYR_A_52_N	TYR_A_52_CA	4.076	-5.54	-0.718	3.523	-4.383	-0.037	1.45	62.03	115.55
306	2jsa-9	TYR_A_52_CA	TYR_A_52_HA	3.523	-4.383	-0.037	4.228	-4.01	0.706	1.09	47.03	27.88
307	2jsa-9	TYR_A_52_CA	TYR_A_52_C	3.523	-4.383	-0.037	2.193	-4.725	0.636	1.53	63.89	-165.58
308	2jsa-9	TYR_A_52_C	TYR_A_52_O	2.193	-4.725	0.636	1.838	-4.134	1.654	1.23	34.11	120.99
309	2jsa-9	TYR_A_52_C	VAL_A_53_N	2.193	-4.725	0.636	1.493	-5.679	0.039	1.33	116.77	-126.27
310	2jsa-9	VAL_A_53_N	VAL_A_53_H	1.493	-5.679	0.039	1.847	-6.122	-0.797	1.01	145.85	-51.37
311	2jsa-9	VAL_A_53_N	VAL_A_53_CA	1.493	-5.679	0.039	0.209	-6.108	0.568	1.45	68.66	-161.52
312	2jsa-9	VAL_A_53_CA	VAL_A_53_HA	0.209	-6.108	0.568	-0.235	-5.274	1.112	1.09	60.07	118.03
313	2jsa-9	VAL_A_53_CA	VAL_A_53_C	0.209	-6.108	0.568	0.427	-7.257	1.555	1.53	49.84	-79.26
314	2jsa-9	VAL_A_53_C	VAL_A_53_O	0.427	-7.257	1.555	-0.395	-8.167	1.644	1.23	85.85	-132.09
315	2jsa-9	VAL_A_53_C	ASN_A_54_N	0.427	-7.257	1.555	1.538	-7.175	2.272	1.32	57.23	4.22
316	2jsa-9	ASN_A_54_N	ASN_A_54_H	1.538	-7.175	2.272	2.168	-6.396	2.147	1.01	97.11	51.04
317	2jsa-9	ASN_A_54_N	ASN_A_54_CA	1.538	-7.175	2.272	1.874	-8.196	3.249	1.45	47.73	-71.78
318	2jsa-9	ASN_A_54_CA	ASN_A_54_HA	1.874	-8.196	3.249	1.078	-8.256	3.991	1.09	47.09	-175.69
319	2jsa-9	ASN_A_54_CA	ASN_A_54_C	1.874	-8.196	3.249	3.193	-7.829	3.932	1.53	63.49	15.55
320	2jsa-9	ASN_A_54_C	ASN_A_54_O	3.193	-7.829	3.932	4.08	-8.67	4.073	1.23	83.42	-43.48
321	2jsa-9	ASN_A_54_C	SER_A_55_N	3.193	-7.829	3.932	3.282	-6.571	4.339	1.33	72.11	85.95
322	2jsa-9	SER_A_55_N	SER_A_55_H	3.282	-6.571	4.339	2.513	-5.933	4.191	1.01	98.43	140.32
323	2jsa-9	SER_A_55_N	SER_A_55_CA	3.282	-6.571	4.339	4.477	-6.081	5.004	1.45	62.76	22.30
324	2jsa-9	SER_A_55_CA	SER_A_55_HA	4.477	-6.081	5.004	4.513	-6.513	6.004	1.09	23.44	-85.24
325	2jsa-9	SER_A_55_CA	SER_A_55_C	4.477	-6.081	5.004	4.419	-4.558	5.13	1.53	85.27	92.18
326	2jsa-9	SER_A_55_C	SER_A_55_O	4.419	-4.558	5.13	4.953	-3.99	6.082	1.23	39.31	46.77
327	2jsa-9	SER_A_55_C	LYS_A_56_N	4.419	-4.558	5.13	3.765	-3.939	4.158	1.33	137.19	136.57
328	2jsa-9	LYS_A_56_N	LYS_A_56_H	3.765	-3.939	4.158	3.35	-4.47	3.406	1.01	138.13	-128.01
329	2jsa-9	LYS_A_56_N	LYS_A_56_CA	3.765	-3.939	4.158	3.63	-2.493	4.149	1.45	90.36	95.33
330	2jsa-9	LYS_A_56_CA	LYS_A_56_HA	3.63	-2.493	4.149	4.136	-2.101	5.032	1.09	35.94	37.77
331	2jsa-9	LYS_A_56_CA	LYS_A_56_C	3.63	-2.493	4.149	2.15	-2.122	4.259	1.53	85.88	165.93
332	2jsa-9	LYS_A_56_C	LYS_A_56_O	2.15	-2.122	4.259	1.807	-0.946	4.371	1.23	84.78	106.26
333	2jsa-9	LYS_A_56_C	VAL_A_57_N	2.15	-2.122	4.259	1.312	-3.148	4.223	1.33	91.56	-129.24
334	2jsa-9	VAL_A_57_N	VAL_A_57_H	1.312	-3.148	4.223	1.665	-4.089	4.129	1.01	95.34	-69.44
335	2jsa-9	VAL_A_57_N	VAL_A_57_CA	1.312	-3.148	4.223	-0.124	-2.946	4.317	1.45	86.29	171.99
336	2jsa-9	VAL_A_57_CA	VAL_A_57_HA	-0.124	-2.946	4.317	-0.343	-1.911	4.053	1.09	104.01	101.95
337	2jsa-9	VAL_A_57_CA	VAL_A_57_C	-0.124	-2.946	4.317	-0.573	-3.172	5.761	1.53	19.19	-153.28
338	2jsa-9	VAL_A_57_C	VAL_A_57_O	-0.573	-3.172	5.761	-1.312	-2.363	6.32	1.23	62.97	132.41
339	2jsa-9	VAL_A_57_C	ASP_A_58_N	-0.573	-3.172	5.761	-0.108	-4.277	6.326	1.33	64.77	-67.18
340	2jsa-9	ASP_A_58_N	ASP_A_58_H	-0.108	-4.277	6.326	0.497	-4.898	5.807	1.01	120.91	-45.75
341	2jsa-9	ASP_A_58_N	ASP_A_58_CA	-0.108	-4.277	6.326	-0.453	-4.621	7.694	1.45	19.60	-135.08
342	2jsa-9	ASP_A_58_CA	ASP_A_58_HA	-0.453	-4.621	7.694	-1.512	-4.871	7.742	1.09	87.47	-166.72
343	2jsa-9	ASP_A_58_CA	ASP_A_58_C	-0.453	-4.621	7.694	-0.158	-3.427	8.605	1.53	53.47	76.12
344	2jsa-9	ASP_A_58_C	ASP_A_58_O	-0.158	-3.427	8.605	-0.962	-3.09	9.473	1.23	45.12	157.26
345	2jsa-9	ASP_A_58_C	PRO_A_59_N	-0.158	-3.427	8.605	1.028	-2.803	8.37	1.36	99.95	27.75
346	2jsa-9	PRO_A_59_N	PRO_A_59_CA	1.028	-2.803	8.37	1.438	-1.655	9.159	1.45	57.09	70.35
347	2jsa-9	PRO_A_59_CA	PRO_A_59_HA	1.438	-1.655	9.159	1.257	-1.845	10.217	1.09	13.93	-133.61
348	2jsa-9	PRO_A_59_CA	PRO_A_59_C	1.438	-1.655	9.159	0.66	-0.402	8.751	1.53	105.46	121.84
349	2jsa-9	PRO_A_59_C	PRO_A_59_O	0.66	-0.402	8.751	0.02	0.235	9.585	1.23	47.27	135.13
350	2jsa-9	PRO_A_59_C	ILE_A_60_N	0.66	-0.402	8.751	0.741	-0.087	7.465	1.33	165.81	75.58
351	2jsa-9	ILE_A_60_N	ILE_A_60_H	0.741	-0.087	7.465	1.286	-0.658	6.835	1.01	128.59	-46.33
352	2jsa-9	ILE_A_60_N	ILE_A_60_CA	0.741	-0.087	7.465	0.052	1.077	6.936	1.45	111.36	120.62
353	2jsa-9	ILE_A_60_CA	ILE_A_60_HA	0.052	1.077	6.936	0.567	1.967	7.298	1.09	70.61	59.94
354	2jsa-9	ILE_A_60_CA	ILE_A_60_C	0.052	1.077	6.936	-1.377	1.111	7.483	1.53	69.06	178.64
355	2jsa-9	ILE_A_60_C	ILE_A_60_O	-1.377	1.111	7.483	-1.774	2.077	8.134	1.23	58.06	112.34
356	2jsa-9	ILE_A_60_C	ILE_A_61_N	-1.377	1.111	7.483	-2.112	0.046	7.198	1.33	102.42	-124.61
357	2jsa-9	ILE_A_61_N	ILE_A_61_H	-2.112	0.046	7.198	-1.72	-0.712	6.657	1.01	122.37	-62.65
358	2jsa-9	ILE_A_61_N	ILE_A_61_CA	-2.112	0.046	7.198	-3.487	-0.059	7.653	1.45	71.74	-175.63
359	2jsa-9	ILE_A_61_CA	ILE_A_61_HA	-3.487	-0.059	7.653	-4.034	0.803	7.271	1.09	110.51	122.40
360	2jsa-9	ILE_A_61_CA	ILE_A_61_C	-3.487	-0.059	7.653	-3.522	0.009	9.181	1.53	2.87	117.24
361	2jsa-9	ILE_A_61_C	ILE_A_61_O	-3.522	0.009	9.181	-4.548	0.348	9.768	1.23	61.49	161.72
362	2jsa-9	ILE_A_61_C	HIS_A_62_N	-3.522	0.009	9.181	-2.386	-0.318	9.782	1.33	63.05	-16.06
363	2jsa-9	HIS_A_62_N	HIS_A_62_H	-2.386	-0.318	9.782	-1.58	-0.586	9.236	1.01	122.73	-18.39
364	2jsa-9	HIS_A_62_N	HIS_A_62_CA	-2.386	-0.318	9.782	-2.274	-0.299	11.23	1.45	4.49	9.63
365	2jsa-9	HIS_A_62_CA	HIS_A_62_HA	-2.274	-0.299	11.23	-3.094	-0.889	11.639	1.09	67.96	-144.26
366	2jsa-9	HIS_A_62_CA	HIS_A_62_C	-2.274	-0.299	11.23	-2.428	1.136	11.738	1.53	70.61	96.13
367	2jsa-9	HIS_A_62_C	HIS_A_62_O	-2.428	1.136							

369	2jsa-9	GLU_A_63_N	GLU_A_63_H	-2.003	2.074	10.903	-1.613	1.818	10.007	1.01	152.50	-33.28
370	2jsa-9	GLU_A_63_N	GLU_A_63_CA	-2.003	2.074	10.903	-2.087	3.481	11.253	1.45	76.05	93.42
371	2jsa-9	GLU_A_63_CA	GLU_A_63_HA	-2.087	3.481	11.253	-1.916	3.572	12.326	1.09	10.23	28.02
372	2jsa-9	GLU_A_63_CA	GLU_A_63_C	-2.087	3.481	11.253	-3.483	4.024	10.94	1.53	101.80	158.75
373	2jsa-9	GLU_A_63_C	GLU_A_63_O	-3.483	4.024	10.94	-4.169	4.531	11.826	1.23	43.91	143.53
374	2jsa-9	GLU_A_63_C	LEU_A_64_N	-3.483	4.024	10.94	-3.863	3.898	9.677	1.32	162.41	-161.66
375	2jsa-9	LEU_A_64_N	LEU_A_64_H	-3.863	3.898	9.677	-3.247	3.47	9.001	1.01	132.03	-34.79
376	2jsa-9	LEU_A_64_N	LEU_A_64_CA	-3.863	3.898	9.677	-5.164	4.369	9.237	1.45	107.64	160.10
377	2jsa-9	LEU_A_64_CA	LEU_A_64_HA	-5.164	4.369	9.237	-5.181	5.455	9.336	1.09	84.79	90.90
378	2jsa-9	LEU_A_64_CA	LEU_A_64_C	-5.164	4.369	9.237	-6.246	3.801	10.157	1.53	53.03	-152.30
379	2jsa-9	LEU_A_64_C	LEU_A_64_O	-6.246	3.801	10.157	-7.133	4.529	10.602	1.23	68.80	140.62
380	2jsa-9	LEU_A_64_C	GLU_A_65_N	-6.246	3.801	10.157	-6.138	2.506	10.415	1.32	78.77	-85.23
381	2jsa-9	GLU_A_65_N	GLU_A_65_H	-6.138	2.506	10.415	-5.382	1.969	10.014	1.01	113.39	-35.39
382	2jsa-9	GLU_A_65_N	GLU_A_65_CA	-6.138	2.506	10.415	-7.096	1.833	11.275	1.45	53.70	-144.91
383	2jsa-9	GLU_A_65_CA	GLU_A_65_HA	-7.096	1.833	11.275	-8.091	1.989	10.859	1.09	112.44	171.09
384	2jsa-9	GLU_A_65_CA	GLU_A_65_C	-7.096	1.833	11.275	-7.063	2.436	12.681	1.53	23.24	86.87
385	2jsa-9	GLU_A_65_C	GLU_A_65_O	-7.063	2.436	12.681	-8.102	2.575	13.325	1.23	58.44	172.38
386	2jsa-9	GLU_A_65_C	GLY_A_66_N	-7.063	2.436	12.681	-5.859	2.775	13.117	1.32	70.78	15.73
387	2jsa-9	GLY_A_66_N	GLY_A_66_H	-5.859	2.775	13.117	-5.047	2.63	12.533	1.01	125.30	-10.12
388	2jsa-9	GLY_A_66_N	GLY_A_66_CA	-5.859	2.775	13.117	-5.676	3.359	14.434	1.45	24.92	72.60
389	2jsa-9	GLY_A_66_CA	GLY_A_66_C	-5.676	3.359	14.434	-6.346	4.732	14.523	1.53	86.67	116.01
390	2jsa-9	GLY_A_66_C	GLY_A_66_O	-6.346	4.732	14.523	-6.744	5.164	15.604	1.23	28.52	132.65
391	2jsa-9	GLY_A_66_C	GLY_A_67_N	-6.346	4.732	14.523	-6.451	5.379	13.372	1.32	150.34	99.22
392	2jsa-9	GLY_A_67_N	GLY_A_67_H	-6.451	5.379	13.372	-6.101	4.963	12.521	1.01	147.43	-49.92
393	2jsa-9	GLY_A_67_N	GLY_A_67_CA	-6.451	5.379	13.372	-7.067	6.694	13.305	1.45	92.64	115.10
394	2jsa-9	GLY_A_67_CA	GLY_A_67_C	-7.067	6.694	13.305	-6.156	7.69	12.583	1.53	118.14	47.55
395	2jsa-9	GLY_A_67_C	GLY_A_67_O	-6.156	7.69	12.583	-6.523	8.849	12.994	1.23	98.84	107.57
396	2jsa-9	GLY_A_67_C	THR_A_68_N	-6.156	7.69	12.583	-4.986	7.201	12.199	1.32	106.85	-22.68
397	2jsa-9	THR_A_68_N	THR_A_68_H	-4.986	7.201	12.199	-4.75	6.237	12.388	1.01	79.22	-76.24
398	2jsa-9	THR_A_68_N	THR_A_68_CA	-4.986	7.201	12.199	-4.02	8.033	11.501	1.45	118.70	40.74
399	2jsa-9	THR_A_68_CA	THR_A_68_HA	-4.02	8.033	11.501	-3.92	8.977	12.036	1.09	60.60	83.95
400	2jsa-9	THR_A_68_CA	THR_A_68_C	-4.02	8.033	11.501	-4.508	8.344	10.085	1.53	157.77	147.49
401	2jsa-9	THR_A_68_C	THR_A_68_O	-4.508	8.344	10.085	-5.339	7.621	9.538	1.23	116.41	-138.98
402	2jsa-9	THR_A_68_C	ALA_A_69_N	-4.508	8.344	10.085	-3.97	9.42	9.531	1.32	114.73	63.43
403	2jsa-9	ALA_A_69_N	ALA_A_69_H	-3.97	9.42	9.531	-3.29	9.968	10.04	1.01	59.77	38.86
404	2jsa-9	ALA_A_69_N	ALA_A_69_CA	-3.97	9.42	9.531	-4.341	9.837	8.189	1.45	157.42	131.66
405	2jsa-9	ALA_A_69_CA	ALA_A_69_HA	-4.341	9.837	8.189	-5.382	9.568	8.014	1.09	99.24	-165.51
406	2jsa-9	ALA_A_69_CA	ALA_A_69_C	-4.341	9.837	8.189	-3.471	9.094	7.172	1.53	131.63	-40.50
407	2jsa-9	ALA_A_69_C	ALA_A_69_O	-3.471	9.094	7.172	-2.44	8.526	7.529	1.23	73.13	-28.85
408	2jsa-9	ALA_A_69_C	PRO_A_70_N	-3.471	9.094	7.172	-3.93	9.123	5.893	1.36	160.22	176.38
409	2jsa-9	PRO_A_70_N	PRO_A_70_CA	-3.93	9.123	5.893	-3.206	8.461	4.821	1.45	137.54	-42.44
410	2jsa-9	PRO_A_70_CA	PRO_A_70_HA	-3.206	8.461	4.821	-2.894	7.467	5.141	1.09	72.93	-72.57
411	2jsa-9	PRO_A_70_CA	PRO_A_70_C	-3.206	8.461	4.821	-1.96	9.256	4.428	1.53	104.89	32.54
412	2jsa-9	PRO_A_70_C	PRO_A_70_O	-1.96	9.256	4.428	-1.207	8.843	3.547	1.23	135.73	-28.74
413	2jsa-9	PRO_A_70_C	LYS_A_71_N	-1.96	9.256	4.428	-1.779	10.383	5.102	1.33	59.44	80.88
414	2jsa-9	LYS_A_71_N	LYS_A_71_H	-1.779	10.383	5.102	-2.438	10.661	5.815	1.01	45.09	157.13
415	2jsa-9	LYS_A_71_N	LYS_A_71_CA	-1.779	10.383	5.102	-0.637	11.24	4.834	1.45	100.63	36.89
416	2jsa-9	LYS_A_71_CA	LYS_A_71_HA	-0.637	11.24	4.834	-0.107	10.836	3.971	1.09	142.32	-37.32
417	2jsa-9	LYS_A_71_CA	LYS_A_71_C	-0.637	11.24	4.834	0.319	11.197	6.028	1.53	38.71	-2.58
418	2jsa-9	LYS_A_71_C	LYS_A_71_O	0.319	11.197	6.028	1.426	11.728	5.961	1.23	93.12	25.63
419	2jsa-9	LYS_A_71_C	ASP_A_72_N	0.319	11.197	6.028	-0.144	10.559	7.093	1.33	36.51	-125.97
420	2jsa-9	ASP_A_72_N	ASP_A_72_H	-0.144	10.559	7.093	-1.065	10.146	7.078	1.01	90.85	-155.85
421	2jsa-9	ASP_A_72_N	ASP_A_72_CA	-0.144	10.559	7.093	0.655	10.439	8.301	1.45	33.78	-8.54
422	2jsa-9	ASP_A_72_CA	ASP_A_72_HA	0.655	10.439	8.301	1.422	11.214	8.299	1.09	90.11	45.30
423	2jsa-9	ASP_A_72_CA	ASP_A_72_C	0.655	10.439	8.301	1.312	9.057	8.338	1.53	88.61	-64.57
424	2jsa-9	ASP_A_72_C	ASP_A_72_O	1.312	9.057	8.338	2.43	8.91	8.83	1.23	66.43	-7.49
425	2jsa-9	ASP_A_72_C	VAL_A_73_N	1.312	9.057	8.338	0.59	8.08	7.811	1.32	113.45	-126.46
426	2jsa-9	VAL_A_73_N	VAL_A_73_H	0.59	8.08	7.811	-0.322	8.274	7.424	1.01	112.54	167.99
427	2jsa-9	VAL_A_73_N	VAL_A_73_CA	0.59	8.08	7.811	1.088	6.715	7.777	1.45	91.34	-69.96
428	2jsa-9	VAL_A_73_CA	VAL_A_73_HA	1.088	6.715	7.777	1.3	6.4	8.799	1.09	20.38	-56.06
429	2jsa-9	VAL_A_73_CA	VAL_A_73_C	1.088	6.715	7.777	2.397	6.675	6.987	1.53	121.10	-1.75
430	2jsa-9	VAL_A_73_C	VAL_A_73_O	2.397	6.675	6.987	3.405	6.165	7.474	1.23	66.68	-26.84
431	2jsa-9	VAL_A_73_C	CYS_A_74_N	2.397	6.675	6.987	2.339	7.217	5.78	1.32	155.70	96.11
432	2jsa-9	CYS_A_74_N	CYS_A_74_H	2.339	7.217	5.78	1.476	7.619	5.444	1.01	109.44	155.02
433	2jsa-9	CYS_A_74_N	CYS_A_74_CA	2.339	7.217	5.78	3.508	7.248	4.917	1.45	126.43	1.52
434	2jsa-9	CYS_A_74_CA	CYS_A_74_HA	3.508	7.248	4.917	4.028	6.294	5.009	1.09	85.16	-61.41
435	2jsa-9	CYS_A_74_CA	CYS_A_74_C	3.508	7.248	4.917	4.438	8.36	5.088	1.53	71.29	50.09
436	2jsa-9	CYS_A_74_C	CYS_A_74_O	4.438	8.36	5.408	4.585	9.389	4.748	1.23	122.41	81.87
437	2jsa-9	CYS_A_74_C	THR_A_75_N	4.438	8.36	5.408	5.042	8.116	6.562	1.33	29.44	-22.00
438	2jsa-9	THR_A_75_N	THR_A_75_H	5.042	8.116	6.562	4.875	7.248	7.05	1.01	61.10	-100.89
439	2jsa-9	THR_A_75_N	THR_A_75_CA	5.042	8.116	6.562	5.953	9.084	7.149	1.45	66.17	46.74
440	2jsa-9	THR_A_75_CA	THR_A_75_HA	5.953	9.084	7.149	6.834	9.167	6.512	1.09	125.75	5.38
441	2jsa-9	THR_A_75_CA	THR_A_75_C	5.953	9.084	7.149	6.414	8.613	8.53	1.53	25.51	-45.61
442	2jsa-9	THR_A_75_C	THR_A_75_O	6.414	8.613	8.53	7.582	8.761	8.882	1.23	73.35	7.22
443	2jsa-9	THR_A_75_C	LYS_A_76_N	6.414	8.613	8.53	5.471	8.054	9.274	1.32	55.84	-149.34
444	2jsa-9	LYS_A_76_N	LYS_A_76_H	5.471	8.054	9.274	4.53	7.964	8.919	1.01	110.58	-174.54
445	2jsa-9	LYS_A_76_N	LYS_A_76_CA	5.471	8.054	9.274	5.764	7.561	10.608	1.45	23.26	-59.28
446	2jsa-9	LYS_A_76_CA	LYS_A_76_HA	5.764	7.561	10.608	6.413	8.286	11.101	1.09	63.13	48.17
447	2jsa-9	LYS_A_76_CA	LYS_A_76_C	5.764	7.561	10.608	6.536	6.243	10.501	1.53	94.01	-59.64
448	2jsa-9	LYS_A_76_C	LYS_A_76_O	6.536	6.243	10.501	7.54	6.051	11.186	1.23	56.17	-10.83
449	2jsa-9	LYS_A_76_C	LEU_A_77_N	6.536	6.243	10.501	6.037	5.371	9.64	1.32	130.60	-119.78
450	2jsa-9	LEU_A_77_N	LEU_A_77_H	6.037	5.371	9.64	5.206	5.596	9.112	1.01	121.52	164.85
451	2jsa-9	LEU_A_77_N	LEU_A_77_CA	6.037	5.371	9.64	6.667	4.077	9.434	1.45	98.15	-64.04
452	2jsa-9	LEU_A_77_CA	LEU_A_77_HA	6.667	4.077	9.434	7.153	3.786	10.366	1.09	31.29	-30.91
453	2jsa-9	LEU_A_77_CA	LEU_A_77_C	6.667	4.077	9.434	7.753	4.208	8.365	1.53	134.34	6.88
454	2jsa-9	LEU_A_77_C	LEU_A_77_O	7.753	4.208	8.365	8.196	3.209	7.799	1.23	117.38	-66.09
455	2jsa-9	LEU_A_77_C	ASN_A_78_N	7.753	4.208	8.365	8.152	5.447	8.12	1.32	100.66	72.15
456	2jsa-9	ASN_A_78_N	ASN_A_78_H	8.152	5.447	8.12	7.744	6.221	8.624	1.01	60.06	117.80
457	2jsa-9	ASN_A_78_N	ASN_A_78_CA	8.152	5.447	8.12	9.179	5.721	7.129	1.45	132.99	14.94
458	2jsa-9	ASN_A_78_CA	ASN_A_78_HA	9.179	5.721	7.129	9.227	6.796	6.953	1.09	99.29	87.44
459	2jsa-9	ASN_A_78_CA	ASN_A_78_C	9.179	5.721	7						

462	2jsa-9	GLU_A_79_N	GLU_A_79_H	7.546	5.007	5.507	6.877	5.472	6.104	1.01	53.77	145.20
463	2jsa-9	GLU_A_79_N	GLU_A_79_CA	7.546	5.007	5.507	7.071	4.356	4.297	1.45	146.34	-126.12
464	2jsa-9	GLU_A_79_CA	GLU_A_79_HA	7.071	4.356	4.297	7.914	3.838	3.84	1.09	114.79	-31.57
465	2jsa-9	GLU_A_79_CA	GLU_A_79_C	7.071	4.356	4.297	6.55	5.398	3.304	1.53	130.44	116.57
466	2jsa-9	GLU_A_79_C	GLU_A_79_O	6.55	5.398	3.304	5.358	5.434	3.005	1.23	104.08	178.27
467	2jsa-9	GLU_A_79_C	CYS_A_80_N	6.55	5.398	3.304	7.471	6.219	2.82	1.33	111.42	41.71
468	2jsa-9	CYS_A_80_N	CYS_A_80_H	7.471	6.219	2.82	8.435	6.13	3.11	1.01	73.32	-5.27
469	2jsa-9	CYS_A_80_N	CYS_A_80_CA	7.471	6.219	2.82	7.121	7.258	1.867	1.45	131.00	108.62
470	2jsa-9	CYS_A_80_CA	CYS_A_80_HA	7.121	7.258	1.867	6.747	6.78	0.962	1.09	146.15	-128.04
471	2jsa-9	CYS_A_80_CA	CYS_A_80_C	7.121	7.258	1.867	8.39	8.036	1.516	1.53	103.27	31.51
472	2jsa-9	CYS_A_80_C	CYS_A_80_O	8.39	8.036	1.516	8.484	9.232	1.791	1.23	77.09	85.51
473	2jsa-9	CYS_A_80_C	PRO_A_81_N	8.39	8.036	1.516	9.359	7.309	0.899	1.36	116.99	-36.88
474	2jsa-9	PRO_A_81_N	PRO_A_81_CA	9.359	7.309	0.899	10.618	7.919	0.509	1.45	105.58	25.85
475	2jsa-9	PRO_A_81_CA	PRO_A_81_HA	10.618	7.919	0.509	11.0	8.539	1.321	1.09	41.89	58.36
476	2jsa-9	PRO_A_81_CA	PRO_A_81_C	10.618	7.919	0.509	10.441	8.798	-0.731	1.53	144.13	101.39
477	2jsa-9	PRO_A_81_C	PRO_A_81_O	10.441	8.798	-0.731	9.569	9.665	-0.762	1.23	91.44	135.16
1	2jsa-10	ARG_A_1_N	ARG_A_1_H	16.471	2.049	0.959	17.049	2.625	0.364	1.01	126.10	44.90
2	2jsa-10	ARG_A_1_N	ARG_A_1_CA	16.471	2.049	0.959	15.098	2.458	1.199	1.45	80.49	163.41
3	2jsa-10	ARG_A_1_CA	ARG_A_1_HA	15.098	2.458	1.199	14.437	1.672	0.834	1.09	109.57	-130.06
4	2jsa-10	ARG_A_1_CA	ARG_A_1_C	15.098	2.458	1.199	14.79	3.756	0.449	1.53	119.34	103.35
5	2jsa-10	ARG_A_1_C	ARG_A_1_O	14.79	3.756	0.449	15.627	4.255	-0.304	1.23	127.69	30.80
6	2jsa-10	ARG_A_1_C	SER_A_2_N	14.79	3.756	0.449	13.59	4.266	0.68	1.32	79.95	156.97
7	2jsa-10	SER_A_2_N	SER_A_2_H	13.59	4.266	0.68	12.954	3.802	1.313	1.01	51.20	-143.89
8	2jsa-10	SER_A_2_N	SER_A_2_CA	13.59	4.266	0.68	13.162	5.496	0.036	1.45	116.31	109.19
9	2jsa-10	SER_A_2_CA	SER_A_2_HA	13.162	5.496	0.036	12.179	5.762	0.425	1.09	69.09	164.86
10	2jsa-10	SER_A_2_CA	SER_A_2_C	13.162	5.496	0.036	13.051	5.283	-1.475	1.53	170.97	-117.53
11	2jsa-10	SER_A_2_C	SER_A_2_O	13.051	5.283	-1.475	14.061	5.26	-2.178	1.23	124.83	-1.30
12	2jsa-10	SER_A_2_C	ALA_A_3_N	13.051	5.283	-1.475	11.816	5.134	-1.93	1.32	110.09	-173.12
13	2jsa-10	ALA_A_3_N	ALA_A_3_H	11.816	5.134	-1.93	11.033	5.164	-1.293	1.01	50.89	177.81
14	2jsa-10	ALA_A_3_N	ALA_A_3_CA	11.816	5.134	-1.93	11.56	4.924	-3.346	1.45	166.84	-140.64
15	2jsa-10	ALA_A_3_CA	ALA_A_3_HA	11.56	4.924	-3.346	12.114	5.669	-3.917	1.09	121.59	53.36
16	2jsa-10	ALA_A_3_CA	ALA_A_3_C	11.56	4.924	-3.346	10.067	5.114	-3.622	1.53	100.39	172.75
17	2jsa-10	ALA_A_3_C	ALA_A_3_O	10.067	5.114	-3.622	9.386	5.843	-2.903	1.23	54.22	133.05
18	2jsa-10	ALA_A_3_C	LEU_A_4_N	10.067	5.114	-3.622	9.602	4.445	-4.668	1.33	142.08	-124.80
19	2jsa-10	LEU_A_4_N	LEU_A_4_H	9.602	4.445	-4.668	10.22	3.864	-5.216	1.01	122.86	-43.23
20	2jsa-10	LEU_A_4_N	LEU_A_4_CA	9.602	4.445	-4.668	8.203	4.531	-5.049	1.45	105.21	176.48
21	2jsa-10	LEU_A_4_CA	LEU_A_4_HA	8.203	4.531	-5.049	7.929	5.585	-5.092	1.09	92.26	104.57
22	2jsa-10	LEU_A_4_CA	LEU_A_4_C	8.203	4.531	-5.049	7.344	3.87	-3.969	1.53	45.10	-142.42
23	2jsa-10	LEU_A_4_C	LEU_A_4_O	7.344	3.87	-3.969	6.119	3.981	-3.992	1.23	91.07	174.82
24	2jsa-10	LEU_A_4_C	SER_A_5_N	7.344	3.87	-3.969	8.02	3.197	-3.049	1.33	46.04	-44.87
25	2jsa-10	SER_A_5_N	SER_A_5_H	8.02	3.197	-3.049	9.028	3.148	-3.092	1.01	92.44	-2.78
26	2jsa-10	SER_A_5_N	SER_A_5_CA	8.02	3.197	-3.049	7.333	2.519	-1.963	1.45	41.63	-135.38
27	2jsa-10	SER_A_5_CA	SER_A_5_HA	7.333	2.519	-1.963	6.852	1.629	-2.367	1.09	111.77	-118.39
28	2jsa-10	SER_A_5_CA	SER_A_5_C	7.333	2.519	-1.963	6.257	3.433	-1.373	1.53	67.32	139.65
29	2jsa-10	SER_A_5_C	SER_A_5_O	6.257	3.433	-1.373	5.212	2.961	-0.928	1.23	68.79	-155.69
30	2jsa-10	SER_A_5_C	CYS_A_6_N	6.257	3.433	-1.373	6.551	4.725	-1.386	1.33	90.56	77.18
31	2jsa-10	CYS_A_6_N	CYS_A_6_H	6.551	4.725	-1.386	7.431	5.043	-1.768	1.01	112.21	19.87
32	2jsa-10	CYS_A_6_N	CYS_A_6_CA	6.551	4.725	-1.386	5.623	5.709	-0.857	1.45	68.64	133.32
33	2jsa-10	CYS_A_6_CA	CYS_A_6_HA	5.623	5.709	-0.857	5.452	5.487	0.197	1.09	14.89	-127.61
34	2jsa-10	CYS_A_6_CA	CYS_A_6_C	5.623	5.709	-0.857	4.295	5.569	-1.606	1.53	119.29	-173.98
35	2jsa-10	CYS_A_6_C	CYS_A_6_O	4.295	5.569	-1.606	3.279	5.211	-1.014	1.23	61.21	-160.59
36	2jsa-10	CYS_A_6_C	GLN_A_7_N	4.295	5.569	-1.606	4.348	5.861	-2.898	1.33	167.06	79.71
37	2jsa-10	GLN_A_7_N	GLN_A_7_H	4.348	5.861	-2.898	5.219	6.152	-3.318	1.01	114.58	18.47
38	2jsa-10	GLN_A_7_N	GLN_A_7_CA	4.348	5.861	-2.898	3.164	5.772	-3.734	1.45	125.15	-175.70
39	2jsa-10	GLN_A_7_CA	GLN_A_7_HA	3.164	5.772	-3.734	2.558	6.66	-3.555	1.09	80.55	124.31
40	2jsa-10	GLN_A_7_CA	GLN_A_7_C	3.164	5.772	-3.734	2.337	4.542	-3.355	1.53	75.66	-123.92
41	2jsa-10	GLN_A_7_C	GLN_A_7_O	2.337	4.542	-3.355	1.142	4.652	-3.087	1.23	77.41	174.74
42	2jsa-10	GLN_A_7_C	MET_A_8_N	2.337	4.542	-3.355	3.007	3.399	-3.344	1.32	89.52	-59.62
43	2jsa-10	MET_A_8_N	MET_A_8_H	3.007	3.399	-3.344	3.99	3.383	-3.576	1.01	103.28	-0.93
44	2jsa-10	MET_A_8_N	MET_A_8_CA	3.007	3.399	-3.344	2.349	2.149	-3.002	1.45	76.39	-117.76
45	2jsa-10	MET_A_8_CA	MET_A_8_HA	2.349	2.149	-3.002	1.726	1.841	-3.841	1.09	140.36	-153.69
46	2jsa-10	MET_A_8_CA	MET_A_8_C	2.349	2.149	-3.002	1.467	2.316	-1.763	1.53	35.92	169.28
47	2jsa-10	MET_A_8_C	MET_A_8_O	1.467	2.316	-1.763	0.395	1.717	-1.674	1.23	85.85	-150.80
48	2jsa-10	MET_A_8_C	CYS_A_9_N	1.467	2.316	-1.763	1.948	3.132	-0.838	1.32	45.68	59.48
49	2jsa-10	CYS_A_9_N	CYS_A_9_H	1.948	3.132	-0.838	2.836	3.592	-0.979	1.01	98.03	27.38
50	2jsa-10	CYS_A_9_N	CYS_A_9_CA	1.948	3.132	-0.838	1.217	3.386	0.393	1.45	32.16	160.84
51	2jsa-10	CYS_A_9_CA	CYS_A_9_HA	1.217	3.386	0.393	1.005	2.429	0.87	1.09	64.05	-102.49
52	2jsa-10	CYS_A_9_CA	CYS_A_9_C	1.217	3.386	0.393	-0.111	4.055	0.032	1.53	103.65	153.26
53	2jsa-10	CYS_A_9_C	CYS_A_9_O	-0.111	4.055	0.032	-1.15	3.731	0.06	1.23	62.19	-162.68
54	2jsa-10	CYS_A_9_C	GLU_A_10_N	-0.111	4.055	0.032	-0.035	4.977	-0.917	1.33	135.73	85.29
55	2jsa-10	GLU_A_10_N	GLU_A_10_H	-0.035	4.977	-0.917	0.854	5.192	-1.346	1.01	115.13	13.60
56	2jsa-10	GLU_A_10_N	GLU_A_10_CA	-0.035	4.977	-0.917	-1.217	5.694	-1.36	1.45	107.77	148.76
57	2jsa-10	GLU_A_10_CA	GLU_A_10_HA	-1.217	5.694	-1.36	-1.745	6.053	-0.476	1.09	35.84	145.79
58	2jsa-10	GLU_A_10_CA	GLU_A_10_C	-1.217	5.694	-1.36	-2.149	4.757	-2.13	1.53	120.23	-134.85
59	2jsa-10	GLU_A_10_C	GLU_A_10_O	-2.149	4.757	-2.13	-3.261	5.141	-2.492	1.23	107.10	160.95
60	2jsa-10	GLU_A_10_C	LEU_A_11_N	-2.149	4.757	-2.13	-1.663	3.547	-2.359	1.32	99.96	-68.12
61	2jsa-10	LEU_A_11_N	LEU_A_11_H	-1.663	3.547	-2.359	-0.739	3.3	-2.032	1.01	71.12	-14.97
62	2jsa-10	LEU_A_11_N	LEU_A_11_CA	-1.663	3.547	-2.359	-2.438	2.552	-3.079	1.45	119.72	-127.91
63	2jsa-10	LEU_A_11_CA	LEU_A_11_HA	-2.438	2.552	-3.079	-3.177	3.075	-3.685	1.09	123.80	144.71
64	2jsa-10	LEU_A_11_CA	LEU_A_11_C	-2.438	2.552	-3.079	-3.194	1.677	-2.077	1.53	49.09	-130.83
65	2jsa-10	LEU_A_11_C	LEU_A_11_O	-3.194	1.677	-2.077	-4.349	1.319	-2.307	1.23	100.77	-162.78
66	2jsa-10	LEU_A_11_C	VAL_A_12_N	-3.194	1.677	-2.077	-2.512	1.358	-0.987	1.32	34.63	-25.07
67	2jsa-10	VAL_A_12_N	VAL_A_12_H	-2.512	1.358	-0.987	-1.565	1.688	-0.864	1.01	83.01	-19.21
68	2jsa-10	VAL_A_12_N	VAL_A_12_CA	-2.512	1.358	-0.987	-3.104	0.532	0.051	1.45	44.39	-125.63
69	2jsa-10	VAL_A_12_CA	VAL_A_12_HA	-3.104	0.532	0.051	-3.639	-0.289	-0.426	1.09	115.96	-123.09
70	2jsa-10	VAL_A_12_CA	VAL_A_12_C	-3.104	0.532	0.051	-4.117	1.363	0.842	1.53	58.88	140.64
71	2jsa-10	VAL_A_12_C	VAL_A_12_O	-4.117	1.363	0.842	-5.209	0.887	1.152	1.23	75.41	-156.45
72	2jsa-10	VAL_A_12_C	VAL_A_13_N	-4.117	1.363	0.842	-3.719	2.589	1.147	1.32	76.69	72.01
73	2jsa-10	VAL_A_13_N	VAL_A_13_H	-3.719	2.589	1.147	-2.807	2.914	0.859	1.01	106.57	19.61
74	2jsa-10	VAL_A_13_N	VAL_A_13_CA	-3.719	2.589	1.147	-4.577	3.49	1.897	1.45	58.92	133.60
75	2jsa-10	VAL_A_13_CA	VAL_A_13_HA	-4.577	3.49	1.897	-4.911	2.977	2.799	1.09	34.16	-123.07
76	2jsa-10	VAL_A_13_CA	VAL_A_13_C	-4.577	3.49	1.897	-5.81					

78	2jsa-10	VAL_A_13_C	LYS_A_14_N	-5.811	3.828	1.058	-5.556	4.43	-0.096	1.33	150.47	67.04
79	2jsa-10	LYS_A_14_N	LYS_A_14_H	-5.556	4.43	-0.096	-4.603	4.633	-0.364	1.01	105.38	12.02
80	2jsa-10	LYS_A_14_N	LYS_A_14_CA	-5.556	4.43	-0.096	-6.632	4.809	-0.995	1.45	128.24	160.60
81	2jsa-10	LYS_A_14_CA	LYS_A_14_HA	-6.632	4.809	-0.995	-7.164	5.65	-0.549	1.09	65.86	122.32
82	2jsa-10	LYS_A_14_CA	LYS_A_14_C	-6.632	4.809	-0.995	-7.62	3.648	-1.121	1.53	94.72	-130.40
83	2jsa-10	LYS_A_14_C	LYS_A_14_O	-7.62	3.648	-1.121	-8.817	3.864	-1.297	1.23	98.23	169.77
84	2jsa-10	LYS_A_14_C	LYS_A_15_N	-7.62	3.648	-1.121	-7.081	2.441	-1.024	1.33	85.80	-65.94
85	2jsa-10	LYS_A_15_N	LYS_A_15_H	-7.081	2.441	-1.024	-6.087	2.338	-0.878	1.01	81.69	-5.92
86	2jsa-10	LYS_A_15_N	LYS_A_15_CA	-7.081	2.441	-1.024	-7.9	1.246	-1.124	1.45	93.95	-124.43
87	2jsa-10	LYS_A_15_CA	LYS_A_15_HA	-7.9	1.246	-1.124	-8.682	1.434	-1.859	1.09	132.42	166.48
88	2jsa-10	LYS_A_15_CA	LYS_A_15_C	-7.9	1.246	-1.124	-8.58	0.983	0.221	1.53	28.46	-158.86
89	2jsa-10	LYS_A_15_C	LYS_A_15_O	-8.58	0.983	0.221	-9.714	0.51	0.266	1.23	87.90	-157.36
90	2jsa-10	LYS_A_15_C	TYR_A_16_N	-8.58	0.983	0.221	-7.858	1.304	1.285	1.33	36.60	23.97
91	2jsa-10	TYR_A_16_N	TYR_A_16_H	-7.858	1.304	1.285	-6.931	1.689	1.173	1.01	96.37	22.55
92	2jsa-10	TYR_A_16_N	TYR_A_16_CA	-7.858	1.304	1.285	-8.377	1.11	2.629	1.45	22.40	-159.50
93	2jsa-10	TYR_A_16_CA	TYR_A_16_HA	-8.377	1.11	2.629	-8.866	0.139	2.708	1.09	85.84	-116.73
94	2jsa-10	TYR_A_16_CA	TYR_A_16_C	-8.377	1.11	2.629	-9.362	2.22	3.002	1.53	75.89	131.59
95	2jsa-10	TYR_A_16_C	TYR_A_16_O	-9.362	2.22	3.002	-10.562	1.977	3.116	1.23	84.68	-168.55
96	2jsa-10	TYR_A_16_C	GLU_A_17_N	-9.362	2.22	3.002	-8.817	3.414	3.18	1.32	82.28	65.47
97	2jsa-10	GLU_A_17_N	GLU_A_17_H	-8.817	3.414	3.18	-7.821	3.541	3.067	1.01	96.42	7.27
98	2jsa-10	GLU_A_17_N	GLU_A_17_CA	-8.817	3.414	3.18	-9.632	4.562	3.539	1.45	75.69	125.37
99	2jsa-10	GLU_A_17_CA	GLU_A_17_HA	-9.632	4.562	3.539	-10.154	4.328	4.467	1.09	31.65	-155.85
100	2jsa-10	GLU_A_17_CA	GLU_A_17_C	-9.632	4.562	3.539	-10.677	4.831	2.453	1.53	135.18	165.56
101	2jsa-10	GLU_A_17_C	GLU_A_17_O	-10.677	4.831	2.453	-11.653	5.542	2.688	1.23	78.99	143.93
102	2jsa-10	GLU_A_17_C	GLY_A_18_N	-10.677	4.831	2.453	-10.437	4.247	1.288	1.33	151.54	-67.66
103	2jsa-10	GLY_A_18_N	GLY_A_18_H	-10.437	4.247	1.288	-9.614	3.674	1.167	1.01	96.88	-34.85
104	2jsa-10	GLY_A_18_N	GLY_A_18_CA	-10.437	4.247	1.288	-11.344	4.415	0.165	1.45	140.60	169.51
105	2jsa-10	GLY_A_18_CA	GLY_A_18_C	-11.344	4.415	0.165	-11.871	3.063	-0.319	1.53	108.45	-111.30
106	2jsa-10	GLY_A_18_C	GLY_A_18_O	-11.871	3.063	-0.319	-12.163	2.894	-1.503	1.23	164.10	-149.94
107	2jsa-10	GLY_A_18_C	SER_A_19_N	-11.871	3.063	-0.319	-11.979	2.134	0.621	1.33	44.86	-96.63
108	2jsa-10	SER_A_19_N	SER_A_19_H	-11.979	2.134	0.621	-11.722	2.343	1.575	1.01	19.15	39.12
109	2jsa-10	SER_A_19_N	SER_A_19_CA	-11.979	2.134	0.621	-12.467	0.802	0.304	1.45	102.60	-110.12
110	2jsa-10	SER_A_19_CA	SER_A_19_HA	-12.467	0.802	0.304	-12.102	0.531	-0.687	1.09	155.36	-36.59
111	2jsa-10	SER_A_19_CA	SER_A_19_C	-12.467	0.802	0.304	-13.996	0.798	0.281	1.53	90.86	-179.85
112	2jsa-10	SER_A_19_C	SER_A_19_O	-13.996	0.798	0.281	-14.605	0.389	-0.707	1.23	143.41	-146.11
113	2jsa-10	SER_A_19_C	ALA_A_20_N	-13.996	0.798	0.281	-14.574	1.256	1.381	1.32	33.84	141.61
114	2jsa-10	ALA_A_20_N	ALA_A_20_H	-14.574	1.256	1.381	-14.01	1.575	2.156	1.01	39.90	29.49
115	2jsa-10	ALA_A_20_N	ALA_A_20_CA	-14.574	1.256	1.381	-16.022	1.309	1.5	1.45	85.30	177.90
116	2jsa-10	ALA_A_20_CA	ALA_A_20_HA	-16.022	1.309	1.5	-16.285	2.053	2.252	1.09	46.38	109.47
117	2jsa-10	ALA_A_20_CA	ALA_A_20_C	-16.022	1.309	1.5	-16.542	-0.053	1.964	1.53	72.35	-110.90
118	2jsa-10	ALA_A_20_C	ALA_A_20_O	-16.542	-0.053	1.964	-17.727	-0.202	2.257	1.23	76.22	-172.83
119	2jsa-10	ALA_A_20_C	ASP_A_21_N	-16.542	-0.053	1.964	-15.629	-1.012	2.018	1.33	87.66	-46.41
120	2jsa-10	ASP_A_21_N	ASP_A_21_H	-15.629	-1.012	2.018	-14.671	-0.818	1.762	1.01	104.68	11.45
121	2jsa-10	ASP_A_21_N	ASP_A_21_CA	-15.629	-1.012	2.018	-15.98	-2.357	2.443	1.45	73.00	-104.63
122	2jsa-10	ASP_A_21_CA	ASP_A_21_HA	-15.98	-2.357	2.443	-17.065	-2.44	2.502	1.09	86.90	-175.63
123	2jsa-10	ASP_A_21_CA	ASP_A_21_C	-15.98	-2.357	2.443	-15.362	-2.631	3.815	1.53	26.23	-23.91
124	2jsa-10	ASP_A_21_C	ASP_A_21_O	-15.362	-2.631	3.815	-15.828	-3.504	4.546	1.23	53.55	-118.09
125	2jsa-10	ASP_A_21_C	LYS_A_22_N	-15.362	-2.631	3.815	-14.323	-1.87	4.124	1.32	76.51	36.22
126	2jsa-10	LYS_A_22_N	LYS_A_22_H	-14.323	-1.87	4.124	-13.993	-1.171	3.474	1.01	130.06	64.73
127	2jsa-10	LYS_A_22_N	LYS_A_22_CA	-14.323	-1.87	4.124	-13.637	-2.021	5.396	1.45	28.91	-12.41
128	2jsa-10	LYS_A_22_CA	LYS_A_22_HA	-13.637	-2.021	5.396	-12.776	-1.352	5.396	1.09	90.00	37.85
129	2jsa-10	LYS_A_22_CA	LYS_A_22_C	-13.637	-2.021	5.396	-13.112	-3.452	5.522	1.53	85.27	-69.85
130	2jsa-10	LYS_A_22_C	LYS_A_22_O	-13.112	-3.452	5.522	-13.557	-4.207	6.385	1.23	45.44	-120.52
131	2jsa-10	LYS_A_22_C	ASP_A_23_N	-13.112	-3.452	5.522	-12.173	-3.784	4.647	1.33	131.30	-19.47
132	2jsa-10	ASP_A_23_N	ASP_A_23_H	-12.173	-3.784	4.647	-11.854	-3.112	3.963	1.01	132.60	64.61
133	2jsa-10	ASP_A_23_N	ASP_A_23_CA	-12.173	-3.784	4.647	-11.584	-5.112	4.649	1.45	89.92	-66.08
134	2jsa-10	ASP_A_23_CA	ASP_A_23_HA	-11.584	-5.112	4.649	-11.612	-5.512	5.663	1.09	21.58	-94.00
135	2jsa-10	ASP_A_23_CA	ASP_A_23_C	-11.584	-5.112	4.649	-10.135	-5.022	4.165	1.53	108.44	3.55
136	2jsa-10	ASP_A_23_C	ASP_A_23_O	-10.135	-5.022	4.165	-9.885	-4.777	2.986	1.23	163.46	44.42
137	2jsa-10	ASP_A_23_C	ALA_A_24_N	-10.135	-5.022	4.165	-9.218	-5.228	5.1	1.33	45.15	-12.66
138	2jsa-10	ALA_A_24_N	ALA_A_24_H	-9.218	-5.228	5.1	-9.496	-5.425	6.051	1.01	19.71	-144.68
139	2jsa-10	ALA_A_24_N	ALA_A_24_CA	-9.218	-5.228	5.1	-7.802	-5.174	4.783	1.45	102.61	2.18
140	2jsa-10	ALA_A_24_CA	ALA_A_24_HA	-7.802	-5.174	4.783	-7.575	-4.196	4.358	1.09	112.94	76.93
141	2jsa-10	ALA_A_24_CA	ALA_A_24_C	-7.802	-5.174	4.783	-7.475	-6.244	3.739	1.53	133.02	-73.01
142	2jsa-10	ALA_A_24_C	ALA_A_24_O	-7.475	-6.244	3.739	-6.395	-6.234	3.152	1.23	118.52	0.53
143	2jsa-10	ALA_A_24_C	ASN_A_25_N	-7.475	-6.244	3.739	-8.43	-7.141	3.54	1.33	98.64	-136.79
144	2jsa-10	ASN_A_25_N	ASN_A_25_H	-8.43	-7.141	3.54	-9.294	-7.087	4.059	1.01	59.06	176.42
145	2jsa-10	ASN_A_25_N	ASN_A_25_CA	-8.43	-7.141	3.54	-8.258	-8.216	2.577	1.45	131.49	-80.91
146	2jsa-10	ASN_A_25_CA	ASN_A_25_HA	-8.258	-8.216	2.577	-7.246	-8.613	2.663	1.09	85.48	-21.42
147	2jsa-10	ASN_A_25_CA	ASN_A_25_C	-8.258	-8.216	2.577	-8.484	-7.67	1.166	1.53	157.28	112.49
148	2jsa-10	ASN_A_25_C	ASN_A_25_O	-8.484	-7.67	1.166	-7.619	-7.798	0.301	1.23	134.69	-8.42
149	2jsa-10	ASN_A_25_C	VAL_A_26_N	-8.484	-7.67	1.166	-9.652	-7.074	0.976	1.32	98.24	152.97
150	2jsa-10	VAL_A_26_N	VAL_A_26_H	-9.652	-7.074	0.976	-10.316	-7.005	1.734	1.01	41.37	174.07
151	2jsa-10	VAL_A_26_N	VAL_A_26_CA	-9.652	-7.074	0.976	-10.004	-6.51	-0.316	1.45	152.77	121.97
152	2jsa-10	VAL_A_26_CA	VAL_A_26_HA	-10.004	-6.51	-0.316	-9.739	-7.23	-1.09	1.09	135.25	-69.79
153	2jsa-10	VAL_A_26_CA	VAL_A_26_C	-10.004	-6.51	-0.316	-9.187	-5.237	-0.55	1.53	98.79	57.31
154	2jsa-10	VAL_A_26_C	VAL_A_26_O	-9.187	-5.237	-0.55	-9.255	-4.641	-1.624	1.23	150.82	96.51
155	2jsa-10	VAL_A_26_C	ILE_A_27_N	-9.187	-5.237	-0.55	-8.433	-4.859	0.472	1.33	39.53	26.63
156	2jsa-10	ILE_A_27_N	ILE_A_27_H	-8.433	-4.859	0.472	-8.425	-5.398	1.326	1.01	32.26	-89.15
157	2jsa-10	ILE_A_27_N	ILE_A_27_CA	-8.433	-4.859	0.472	-7.603	-3.669	0.39	1.45	93.23	55.11
158	2jsa-10	ILE_A_27_CA	ILE_A_27_HA	-7.603	-3.669	0.39	-8.073	-2.977	-0.308	1.09	129.84	124.18
159	2jsa-10	ILE_A_27_CA	ILE_A_27_C	-7.603	-3.669	0.39	-6.234	-4.045	-0.18	1.53	111.88	-15.36
160	2jsa-10	ILE_A_27_C	ILE_A_27_O	-6.234	-4.045	-0.18	-5.888	-3.643	-1.289	1.23	154.44	49.28
161	2jsa-10	ILE_A_27_C	LYS_A_28_N	-6.234	-4.045	-0.18	-5.493	-4.811	0.606	1.32	53.59	-45.95
162	2jsa-10	LYS_A_28_N	LYS_A_28_H	-5.493	-4.811	0.606	-5.842	-5.104	1.507	1.01	26.83	-139.99
163	2jsa-10	LYS_A_28_N	LYS_A_28_CA	-5.493	-4.811	0.606	-4.168	-5.246	0.193	1.45	106.50	-18.18
164	2jsa-10	LYS_A_28_CA	LYS_A_28_HA	-4.168	-5.246	0.193	-3.53	-4.365	0.122	1.09	93.73	54.09
165	2jsa-10	LYS_A_28_CA	LYS_A_28_C	-4.168	-5.246	0.193	-4.253	-5.873	-1.2	1.53	155.57	-97.72
166	2jsa-10	LYS_A_28_C	LYS_A_28_O	-4.253	-5.873	-1.2	-3.354	-5.694	-2.02	1.23	131.81	11.26
167	2jsa-10	LYS_A_28_C	LYS_A_29_N	-4.253	-5.873	-1.2	-5.341	-6.594	-1.424	1.32	99.74	-146.47
168	2jsa-10											

171	2jsa-10	LYS_A_29_CA	LYS_A_29_C	-5.555	-7.249	-2.704	-5.762	-6.187	-3.786	1.53	135.00	101.03
172	2jsa-10	LYS_A_29_C	LYS_A_29_O	-5.762	-6.187	-3.786	-5.145	-6.25	-4.849	1.23	149.74	-5.83
173	2jsa-10	LYS_A_29_C	ASP_A_30_N	-5.762	-6.187	-3.786	-6.633	-5.236	-3.478	1.33	76.57	132.49
174	2jsa-10	ASP_A_30_N	ASP_A_30_H	-6.633	-5.236	-3.478	-7.105	-5.248	-2.585	1.01	27.87	-178.54
175	2jsa-10	ASP_A_30_N	ASP_A_30_CA	-6.633	-5.236	-3.478	-6.928	-4.162	-4.411	1.45	129.95	105.36
176	2jsa-10	ASP_A_30_CA	ASP_A_30_HA	-6.928	-4.162	-4.411	-7.494	-4.565	-5.25	1.09	140.37	-144.55
177	2jsa-10	ASP_A_30_CA	ASP_A_30_C	-6.928	-4.162	-4.411	-5.618	-3.553	-4.914	1.53	109.20	24.93
178	2jsa-10	ASP_A_30_C	ASP_A_30_O	-5.618	-3.553	-4.914	-5.399	-3.455	-6.121	1.23	168.76	24.11
179	2jsa-10	ASP_A_30_C	PHE_A_31_N	-5.618	-3.553	-4.914	-4.782	-3.162	-3.964	1.32	44.17	25.07
180	2jsa-10	PHE_A_31_N	PHE_A_31_H	-4.782	-3.162	-3.964	-5.028	-3.275	-2.991	1.01	15.55	-155.33
181	2jsa-10	PHE_A_31_N	PHE_A_31_CA	-4.782	-3.162	-3.964	-3.499	-2.565	-4.296	1.45	103.20	24.95
182	2jsa-10	PHE_A_31_CA	PHE_A_31_HA	-3.499	-2.565	-4.296	-3.639	-1.525	-4.591	1.09	105.70	97.67
183	2jsa-10	PHE_A_31_CA	PHE_A_31_C	-3.499	-2.565	-4.296	-2.814	-3.333	-5.427	1.53	137.70	-48.27
184	2jsa-10	PHE_A_31_C	PHE_A_31_O	-2.814	-3.333	-5.427	-2.502	-2.763	-6.471	1.23	148.10	61.31
185	2jsa-10	PHE_A_31_C	ASP_A_32_N	-2.814	-3.333	-5.427	-2.598	-4.618	-5.181	1.33	79.31	-80.46
186	2jsa-10	ASP_A_32_N	ASP_A_32_H	-2.598	-4.618	-5.181	-2.88	-5.022	-4.299	1.01	29.19	-124.92
187	2jsa-10	ASP_A_32_N	ASP_A_32_CA	-2.598	-4.618	-5.181	-1.954	-5.47	-6.166	1.45	132.68	-52.92
188	2jsa-10	ASP_A_32_CA	ASP_A_32_HA	-1.954	-5.47	-6.166	-0.897	-5.21	-6.226	1.09	93.16	13.82
189	2jsa-10	ASP_A_32_CA	ASP_A_32_C	-1.954	-5.47	-6.166	-2.62	-5.261	-7.529	1.53	152.88	162.58
190	2jsa-10	ASP_A_32_C	ASP_A_32_O	-2.62	-5.261	-7.529	-1.981	-5.425	-8.567	1.23	147.56	-14.39
191	2jsa-10	ASP_A_32_C	ALA_A_33_N	-2.62	-5.261	-7.529	-3.895	-4.903	-7.48	1.33	87.88	164.32
192	2jsa-10	ALA_A_33_N	ALA_A_33_H	-3.895	-4.903	-7.48	-4.357	-4.788	-6.589	1.01	28.12	166.02
193	2jsa-10	ALA_A_33_N	ALA_A_33_CA	-3.895	-4.903	-7.48	-4.654	-4.67	-8.696	1.45	146.86	162.93
194	2jsa-10	ALA_A_33_CA	ALA_A_33_HA	-4.654	-4.67	-8.696	-4.527	-5.527	-9.357	1.09	127.34	-81.57
195	2jsa-10	ALA_A_33_CA	ALA_A_33_C	-4.654	-4.67	-8.696	-4.107	-3.428	-9.403	1.53	117.52	66.23
196	2jsa-10	ALA_A_33_C	ALA_A_33_O	-4.107	-3.428	-9.403	-3.631	-3.512	-10.534	1.23	156.86	-10.01
197	2jsa-10	ALA_A_33_C	GLU_A_34_N	-4.107	-3.428	-9.403	-4.195	-2.303	-8.707	1.33	58.33	94.47
198	2jsa-10	GLU_A_34_N	GLU_A_34_H	-4.195	-2.303	-8.707	-4.599	-2.308	-7.781	1.01	23.57	-179.29
199	2jsa-10	GLU_A_34_N	GLU_A_34_CA	-4.195	-2.303	-8.707	-3.714	-1.046	-9.254	1.45	112.12	69.06
200	2jsa-10	GLU_A_34_CA	GLU_A_34_HA	-3.714	-1.046	-9.254	-3.9	-1.052	-10.328	1.09	170.17	-178.15
201	2jsa-10	GLU_A_34_CA	GLU_A_34_C	-3.714	-1.046	-9.254	-2.207	-0.91	-9.029	1.53	81.54	5.16
202	2jsa-10	GLU_A_34_C	GLU_A_34_O	-2.207	-0.91	-9.029	-1.681	0.2	-8.978	1.23	87.62	64.64
203	2jsa-10	GLU_A_34_C	CYS_A_35_N	-2.207	-0.91	-9.029	-1.554	-2.057	-8.901	1.33	84.46	-60.35
204	2jsa-10	CYS_A_35_N	CYS_A_35_H	-1.554	-2.057	-8.901	-2.051	-2.934	-8.954	1.01	93.01	-119.54
205	2jsa-10	CYS_A_35_N	CYS_A_35_CA	-1.554	-2.057	-8.901	-0.118	-2.08	-8.684	1.45	81.41	-0.92
206	2jsa-10	CYS_A_35_CA	CYS_A_35_HA	-0.118	-2.08	-8.684	0.258	-1.06	-8.764	1.09	94.21	69.76
207	2jsa-10	CYS_A_35_CA	CYS_A_35_C	-0.118	-2.08	-8.684	0.522	-2.922	-9.788	1.53	136.23	-52.76
208	2jsa-10	CYS_A_35_C	CYS_A_35_O	0.522	-2.922	-9.788	1.506	-2.507	-10.399	1.23	119.78	22.87
209	2jsa-10	CYS_A_35_C	LYS_A_36_N	0.522	-2.922	-9.788	-0.061	-4.091	-10.011	1.33	99.69	-116.51
210	2jsa-10	LYS_A_36_N	LYS_A_36_H	-0.061	-4.091	-10.011	-0.867	-4.368	-9.469	1.01	57.55	-161.03
211	2jsa-10	LYS_A_36_N	LYS_A_36_CA	-0.061	-4.091	-10.011	0.44	-4.995	-11.031	1.45	134.62	-61.00
212	2jsa-10	LYS_A_36_CA	LYS_A_36_HA	0.44	-4.995	-11.031	1.504	-5.152	-10.85	1.09	80.45	-8.39
213	2jsa-10	LYS_A_36_CA	LYS_A_36_C	0.44	-4.995	-11.031	0.294	-4.338	-12.405	1.53	153.90	102.53
214	2jsa-10	LYS_A_36_C	LYS_A_36_O	0.294	-4.338	-12.405	1.165	-4.482	-13.262	1.23	134.15	-9.39
215	2jsa-10	LYS_A_36_C	LYS_A_37_N	0.294	-4.338	-12.405	-0.815	-3.631	-12.572	1.33	97.24	147.48
216	2jsa-10	LYS_A_37_N	LYS_A_37_H	-0.815	-3.631	-12.572	-1.488	-3.556	-11.823	1.01	42.12	173.64
217	2jsa-10	LYS_A_37_N	LYS_A_37_CA	-0.815	-3.631	-12.572	-1.085	-2.952	-13.827	1.45	149.79	111.68
218	2jsa-10	LYS_A_37_CA	LYS_A_37_HA	-1.085	-2.952	-13.827	-0.649	-3.544	-14.631	1.09	137.56	-53.63
219	2jsa-10	LYS_A_37_CA	LYS_A_37_C	-1.085	-2.952	-13.827	-0.391	-1.588	-13.826	1.53	89.96	63.03
220	2jsa-10	LYS_A_37_C	LYS_A_37_O	-0.391	-1.588	-13.826	0.104	-1.139	-14.858	1.23	147.07	42.21
221	2jsa-10	LYS_A_37_C	LEU_A_38_N	-0.391	-1.588	-13.826	-0.376	-0.97	-12.655	1.32	27.83	88.61
222	2jsa-10	LEU_A_38_N	LEU_A_38_H	-0.376	-0.97	-12.655	-0.803	-1.4	-11.847	1.01	36.87	-134.80
223	2jsa-10	LEU_A_38_N	LEU_A_38_CA	-0.376	-0.97	-12.655	0.251	0.333	-12.505	1.45	84.08	64.30
224	2jsa-10	LEU_A_38_CA	LEU_A_38_HA	0.251	0.333	-12.505	-0.142	0.988	-13.282	1.09	135.49	120.96
225	2jsa-10	LEU_A_38_CA	LEU_A_38_C	0.251	0.333	-12.505	1.758	0.199	-12.73	1.53	98.46	-5.08
226	2jsa-10	LEU_A_38_C	LEU_A_38_O	1.758	0.199	-12.73	2.294	0.731	-13.7	1.23	142.10	44.79
227	2jsa-10	LEU_A_38_C	PHE_A_39_N	1.758	0.199	-12.73	2.399	-0.516	-11.816	1.33	46.41	-48.12
228	2jsa-10	PHE_A_39_N	PHE_A_39_H	2.399	-0.516	-11.816	1.894	-0.925	-11.043	1.01	40.05	-141.00
229	2jsa-10	PHE_A_39_N	PHE_A_39_CA	2.399	-0.516	-11.816	3.834	-0.727	-11.903	1.45	93.43	-8.36
230	2jsa-10	PHE_A_39_CA	PHE_A_39_HA	3.834	-0.727	-11.903	4.31	0.144	-12.355	1.09	114.48	61.34
231	2jsa-10	PHE_A_39_CA	PHE_A_39_C	3.834	-0.727	-11.903	4.156	-1.975	-12.727	1.53	122.59	-75.53
232	2jsa-10	PHE_A_39_C	PHE_A_39_O	4.156	-1.975	-12.727	5.192	-2.605	-12.526	1.23	80.59	-31.30
233	2jsa-10	PHE_A_39_C	HIS_A_40_N	4.156	-1.975	-12.727	3.248	-2.292	-13.639	1.33	133.48	-160.75
234	2jsa-10	HIS_A_40_N	HIS_A_40_H	3.248	-2.292	-13.639	2.419	-1.726	-13.749	1.01	96.25	145.68
235	2jsa-10	HIS_A_40_N	HIS_A_40_CA	3.248	-2.292	-13.639	3.422	-3.453	-14.495	1.45	126.10	-81.48
236	2jsa-10	HIS_A_40_CA	HIS_A_40_HA	3.422	-3.453	-14.495	3.451	-4.338	-13.859	1.09	54.31	-88.12
237	2jsa-10	HIS_A_40_CA	HIS_A_40_C	3.422	-3.453	-14.495	4.763	-3.356	-15.226	1.53	118.53	4.14
238	2jsa-10	HIS_A_40_C	HIS_A_40_O	4.763	-3.356	-15.226	5.557	-4.294	-15.204	1.23	88.97	-49.75
239	2jsa-10	HIS_A_40_C	THR_A_41_N	4.763	-3.356	-15.226	4.974	-2.21	-15.857	1.33	118.44	79.57
240	2jsa-10	THR_A_41_N	THR_A_41_H	4.974	-2.21	-15.857	4.277	-1.48	-15.832	1.01	88.58	133.68
241	2jsa-10	THR_A_41_N	THR_A_41_CA	4.974	-2.21	-15.857	6.205	-1.977	-16.594	1.45	120.47	10.72
242	2jsa-10	THR_A_41_CA	THR_A_41_HA	6.205	-1.977	-16.594	6.264	-2.694	-17.413	1.09	138.70	-85.30
243	2jsa-10	THR_A_41_CA	THR_A_41_C	6.205	-1.977	-16.594	7.418	-2.196	-15.688	1.53	53.68	-10.23
244	2jsa-10	THR_A_41_C	THR_A_41_O	7.418	-2.196	-15.688	8.374	-2.866	-16.076	1.23	108.38	-35.02
245	2jsa-10	THR_A_41_C	ILE_A_42_N	7.418	-2.196	-15.688	7.34	-1.617	-14.498	1.33	26.15	97.67
246	2jsa-10	ILE_A_42_N	ILE_A_42_H	7.34	-1.617	-14.498	6.523	-1.08	-14.246	1.01	75.55	146.68
247	2jsa-10	ILE_A_42_N	ILE_A_42_CA	7.34	-1.617	-14.498	8.42	-1.741	-13.534	1.45	48.43	-6.55
248	2jsa-10	ILE_A_42_CA	ILE_A_42_HA	8.42	-1.741	-13.534	9.25	-1.121	-13.875	1.09	108.22	36.76
249	2jsa-10	ILE_A_42_CA	ILE_A_42_C	8.42	-1.741	-13.534	8.906	-3.192	-13.502	1.53	88.80	-71.48
250	2jsa-10	ILE_A_42_C	ILE_A_42_O	8.906	-3.192	-13.502	8.108	-4.12	-13.62	1.23	95.51	-130.69
251	2jsa-10	ILE_A_42_C	PRO_A_43_N	8.906	-3.192	-13.502	10.247	-3.344	-13.339	1.36	83.11	-6.47
252	2jsa-10	PRO_A_43_N	PRO_A_43_CA	10.247	-3.344	-13.339	10.85	-4.666	-13.291	1.45	88.11	-65.48
253	2jsa-10	PRO_A_43_CA	PRO_A_43_HA	10.85	-4.666	-13.291	10.442	-5.291	-14.085	1.09	136.77	-123.14
254	2jsa-10	PRO_A_43_CA	PRO_A_43_C	10.85	-4.666	-13.291	10.574	-5.345	-11.948	1.53	28.62	-112.12
255	2jsa-10	PRO_A_43_C	PRO_A_43_O	10.574	-5.345	-11.948	10.073	-4.668	-11.907	1.23	88.09	-114.04
256	2jsa-10	PRO_A_43_C	PHE_A_44_N	10.574	-5.345	-11.948	10.913	-4.636	-10.882	1.32	36.40	64.45
257	2jsa-10	PHE_A_44_N	PHE_A_44_H	10.913	-4.636	-10.882	11.321	-3.718	-10.99	1.01	96.14	66.04
258	2jsa-10	PHE_A_44_N	PHE_A_44_CA	10.913	-4.636	-10.882	10.708	-5.157	-9.54	1.45	22.65	-111.48
259	2jsa-10	PHE_A_44_CA	PHE_A_44_HA	10.708	-5.157	-9.54	10.515	-6.229	-9.584	1.09	92.31	-100.21
260	2jsa-10	PHE_A_44_CA	PHE_A_44_C	10.708	-5.157	-9.54	9.539	-4.451	-8.85	1.53	63.1	

264	2jsa-10	GLY_A_45_N	GLY_A_45_CA	8.558	-4.074	-9.657	7.384	-3.392	-9.14	1.45	69.15	149.85
265	2jsa-10	GLY_A_45_CA	GLY_A_45_C	7.384	-3.392	-9.14	6.341	-4.396	-8.645	1.53	71.12	-136.09
266	2jsa-10	GLY_A_45_C	GLY_A_45_O	6.341	-4.396	-8.645	5.909	-4.33	-7.495	1.23	20.81	171.31
267	2jsa-10	GLY_A_45_C	THR_A_46_N	6.341	-4.396	-8.645	5.967	-5.302	-9.536	1.32	132.27	-112.43
268	2jsa-10	THR_A_46_N	THR_A_46_H	5.967	-5.302	-9.536	6.366	-5.297	-10.464	1.01	156.73	0.72
269	2jsa-10	THR_A_46_N	THR_A_46_CA	5.967	-5.302	-9.536	4.983	-6.317	-9.204	1.45	76.78	-134.11
270	2jsa-10	THR_A_46_CA	THR_A_46_HA	4.983	-6.317	-9.204	4.06	-5.824	-8.9	1.09	73.80	151.89
271	2jsa-10	THR_A_46_CA	THR_A_46_C	4.983	-6.317	-9.204	5.471	-7.169	-8.03	1.53	39.91	-60.20
272	2jsa-10	THR_A_46_C	THR_A_46_O	5.471	-7.169	-8.03	4.698	-7.493	-7.131	1.23	42.99	-157.26
273	2jsa-10	THR_A_46_C	ARG_A_47_N	5.471	-7.169	-8.03	6.751	-7.507	-8.078	1.32	92.08	-14.79
274	2jsa-10	ARG_A_47_N	ARG_A_47_H	6.751	-7.507	-8.078	7.329	-7.205	-8.85	1.01	139.81	27.59
275	2jsa-10	ARG_A_47_N	ARG_A_47_CA	6.751	-7.507	-8.078	7.351	-8.315	-7.031	1.45	43.87	-53.40
276	2jsa-10	ARG_A_47_CA	ARG_A_47_HA	7.351	-8.315	-7.031	6.815	-9.263	-6.978	1.09	87.21	-119.48
277	2jsa-10	ARG_A_47_CA	ARG_A_47_C	7.351	-8.315	-7.031	7.239	-7.603	-5.681	1.53	28.10	98.94
278	2jsa-10	ARG_A_47_C	ARG_A_47_O	7.239	-7.603	-5.681	6.923	-8.227	-4.67	1.23	34.68	-116.86
279	2jsa-10	ARG_A_47_C	GLU_A_48_N	7.239	-7.603	-5.681	7.502	-6.305	-5.709	1.32	91.21	78.55
280	2jsa-10	GLU_A_48_N	GLU_A_48_H	7.502	-6.305	-5.709	7.754	-5.856	-6.578	1.01	149.35	60.70
281	2jsa-10	GLU_A_48_N	GLU_A_48_CA	7.502	-6.305	-5.709	7.435	-5.501	-4.501	1.45	33.74	94.76
282	2jsa-10	GLU_A_48_CA	GLU_A_48_HA	7.435	-5.501	-4.501	7.937	-6.048	-3.703	1.09	42.93	-47.46
283	2jsa-10	GLU_A_48_CA	GLU_A_48_C	7.435	-5.501	-4.501	5.977	-5.281	-4.091	1.53	74.46	171.42
284	2jsa-10	GLU_A_48_C	GLU_A_48_O	5.977	-5.281	-4.091	5.68	-5.114	-2.91	1.23	16.09	150.65
285	2jsa-10	GLU_A_48_C	CYS_A_49_N	5.977	-5.281	-4.091	5.107	-5.286	-5.09	1.32	138.95	-179.67
286	2jsa-10	CYS_A_49_N	CYS_A_49_H	5.107	-5.286	-5.09	5.424	-5.428	-6.038	1.01	159.88	-24.13
287	2jsa-10	CYS_A_49_N	CYS_A_49_CA	5.107	-5.286	-5.09	3.689	-5.09	-4.849	1.45	80.44	172.13
288	2jsa-10	CYS_A_49_CA	CYS_A_49_HA	3.689	-5.09	-4.849	3.549	-4.097	-4.422	1.09	66.94	98.03
289	2jsa-10	CYS_A_49_CA	CYS_A_49_C	3.689	-5.09	-4.849	3.227	-6.129	-3.825	1.53	48.00	-113.97
290	2jsa-10	CYS_A_49_C	CYS_A_49_O	3.227	-6.129	-3.825	2.85	-5.78	-2.707	1.23	24.68	137.21
291	2jsa-10	CYS_A_49_C	ASP_A_50_N	3.227	-6.129	-3.825	3.273	-7.386	-4.243	1.33	108.38	-87.90
292	2jsa-10	ASP_A_50_N	ASP_A_50_H	3.273	-7.386	-4.243	3.596	-7.601	-5.176	1.01	157.42	-33.65
293	2jsa-10	ASP_A_50_N	ASP_A_50_CA	3.273	-7.386	-4.243	2.863	-8.477	-3.377	1.45	53.39	-110.60
294	2jsa-10	ASP_A_50_CA	ASP_A_50_HA	2.863	-8.477	-3.377	1.805	-8.365	-3.139	1.09	77.39	173.96
295	2jsa-10	ASP_A_50_CA	ASP_A_50_C	2.863	-8.477	-3.377	3.692	-8.441	-2.091	1.53	32.83	2.49
296	2jsa-10	ASP_A_50_C	ASP_A_50_O	3.692	-8.441	-2.091	3.242	-8.907	-1.045	1.23	31.77	-134.00
297	2jsa-10	ASP_A_50_C	HIS_A_51_N	3.692	-8.441	-2.091	4.887	-7.881	-2.211	1.33	95.20	25.11
298	2jsa-10	HIS_A_51_N	HIS_A_51_H	4.887	-7.881	-2.211	5.192	-7.517	-3.103	1.01	151.97	50.04
299	2jsa-10	HIS_A_51_N	HIS_A_51_CA	4.887	-7.881	-2.211	5.782	-7.778	-1.071	1.45	38.32	6.56
300	2jsa-10	HIS_A_51_CA	HIS_A_51_HA	5.782	-7.778	-1.071	5.647	-8.667	-0.454	1.09	55.54	-98.63
301	2jsa-10	HIS_A_51_CA	HIS_A_51_C	5.782	-7.778	-1.071	5.402	-6.559	-0.229	1.53	56.60	107.31
302	2jsa-10	HIS_A_51_C	HIS_A_51_O	5.402	-6.559	-0.229	6.036	-6.28	0.788	1.23	34.26	23.75
303	2jsa-10	HIS_A_51_C	TYR_A_52_N	5.402	-6.559	-0.229	4.367	-5.865	-0.682	1.33	109.98	146.16
304	2jsa-10	TYR_A_52_N	TYR_A_52_H	4.367	-5.865	-0.682	3.893	-6.153	-1.526	1.01	146.69	-148.72
305	2jsa-10	TYR_A_52_N	TYR_A_52_CA	4.367	-5.865	-0.682	3.895	-4.683	0.016	1.45	61.26	111.77
306	2jsa-10	TYR_A_52_CA	TYR_A_52_HA	3.895	-4.683	0.016	4.599	-4.402	0.8	1.09	44.03	21.76
307	2jsa-10	TYR_A_52_CA	TYR_A_52_C	3.895	-4.683	0.016	2.509	-4.922	0.622	1.53	66.69	-170.22
308	2jsa-10	TYR_A_52_C	TYR_A_52_O	2.509	-4.922	0.622	2.285	-4.638	1.798	1.23	17.10	128.26
309	2jsa-10	TYR_A_52_C	VAL_A_53_N	2.509	-4.922	0.622	1.617	-5.439	-0.208	1.32	128.84	-149.90
310	2jsa-10	VAL_A_53_N	VAL_A_53_H	1.617	-5.439	-0.208	1.872	-5.646	-1.163	1.01	161.02	-39.07
311	2jsa-10	VAL_A_53_N	VAL_A_53_CA	1.617	-5.439	-0.208	0.26	-5.719	0.23	1.45	72.46	-168.34
312	2jsa-10	VAL_A_53_CA	VAL_A_53_HA	0.26	-5.719	0.23	-0.222	-4.774	0.482	1.09	76.64	117.02
313	2jsa-10	VAL_A_53_CA	VAL_A_53_C	0.26	-5.719	0.23	0.305	-6.581	1.493	1.53	34.35	-87.01
314	2jsa-10	VAL_A_53_C	VAL_A_53_O	0.305	-6.581	1.493	-0.662	-6.626	2.252	1.23	51.90	-177.34
315	2jsa-10	VAL_A_53_C	ASN_A_54_N	0.305	-6.581	1.493	1.436	-7.245	1.679	1.32	81.93	-30.42
316	2jsa-10	ASN_A_54_N	ASN_A_54_H	1.436	-7.245	1.679	2.19	-7.161	1.012	1.01	131.32	6.36
317	2jsa-10	ASN_A_54_N	ASN_A_54_CA	1.436	-7.245	1.679	1.62	-8.103	2.837	1.45	37.15	-77.90
318	2jsa-10	ASN_A_54_CA	ASN_A_54_HA	1.62	-8.103	2.837	0.875	-7.849	3.591	1.09	46.23	161.17
319	2jsa-10	ASN_A_54_CA	ASN_A_54_C	1.62	-8.103	2.837	3.025	-7.892	3.405	1.53	68.21	8.54
320	2jsa-10	ASN_A_54_C	ASN_A_54_O	3.025	-7.892	3.405	3.881	-8.769	3.292	1.23	95.27	-45.69
321	2jsa-10	ASN_A_54_C	SER_A_55_N	3.025	-7.892	3.405	3.219	-6.727	4.002	1.32	63.18	80.55
322	2jsa-10	SER_A_55_N	SER_A_55_H	3.219	-6.727	4.002	2.469	-6.053	4.058	1.01	86.82	138.06
323	2jsa-10	SER_A_55_N	SER_A_55_CA	3.219	-6.727	4.002	4.506	-6.391	4.589	1.45	66.19	14.63
324	2jsa-10	SER_A_55_CA	SER_A_55_HA	4.506	-6.391	4.589	4.647	-7.003	5.48	1.09	35.18	-77.03
325	2jsa-10	SER_A_55_CA	SER_A_55_C	4.506	-6.391	4.589	4.525	-4.917	4.998	1.53	74.49	89.26
326	2jsa-10	SER_A_55_C	SER_A_55_O	4.525	-4.917	4.998	5.163	-4.552	5.985	1.23	36.68	29.77
327	2jsa-10	SER_A_55_C	LYS_A_56_N	4.525	-4.917	4.998	3.82	-4.11	4.22	1.32	125.98	131.14
328	2jsa-10	LYS_A_56_N	LYS_A_56_H	3.82	-4.11	4.22	3.321	-4.48	3.424	1.01	142.03	-143.44
329	2jsa-10	LYS_A_56_N	LYS_A_56_CA	3.82	-4.11	4.22	3.748	-2.684	4.49	1.45	79.29	92.89
330	2jsa-10	LYS_A_56_CA	LYS_A_56_HA	3.748	-2.684	4.49	4.175	-2.505	5.477	1.09	25.13	22.74
331	2jsa-10	LYS_A_56_CA	LYS_A_56_C	3.748	-2.684	4.49	2.282	-2.25	4.531	1.53	88.46	163.51
332	2jsa-10	LYS_A_56_C	LYS_A_56_O	2.282	-2.25	4.531	1.985	-1.066	4.68	1.23	83.04	104.08
333	2jsa-10	LYS_A_56_C	VAL_A_57_N	2.282	-2.25	4.531	1.403	-3.233	4.398	1.33	95.76	-131.80
334	2jsa-10	VAL_A_57_N	VAL_A_57_H	1.403	-3.233	4.398	1.719	-4.185	4.28	1.01	96.71	-71.64
335	2jsa-10	VAL_A_57_N	VAL_A_57_CA	1.403	-3.233	4.398	-0.026	-2.967	4.418	1.45	89.21	169.46
336	2jsa-10	VAL_A_57_CA	VAL_A_57_HA	-0.026	-2.967	4.418	-0.183	-1.914	4.185	1.09	102.34	98.48
337	2jsa-10	VAL_A_57_CA	VAL_A_57_C	-0.026	-2.967	4.418	-0.569	-3.229	5.824	1.53	23.21	-154.24
338	2jsa-10	VAL_A_57_C	VAL_A_57_O	-0.569	-3.229	5.824	-1.36	-2.443	6.344	1.23	65.00	135.18
339	2jsa-10	VAL_A_57_C	ASP_A_58_N	-0.569	-3.229	5.824	-0.121	-4.335	6.401	1.33	64.19	-67.95
340	2jsa-10	ASP_A_58_N	ASP_A_58_H	-0.121	-4.335	6.401	0.53	-4.936	5.915	1.01	118.75	-42.71
341	2jsa-10	ASP_A_58_N	ASP_A_58_CA	-0.121	-4.335	6.401	-0.552	-4.708	7.737	1.45	23.11	-139.13
342	2jsa-10	ASP_A_58_CA	ASP_A_58_HA	-0.552	-4.708	7.737	-1.618	-4.931	7.718	1.09	91.00	-168.18
343	2jsa-10	ASP_A_58_CA	ASP_A_58_C	-0.552	-4.708	7.737	-0.281	-3.55	8.698	1.53	51.06	76.83
344	2jsa-10	ASP_A_58_C	ASP_A_58_O	-0.281	-3.55	8.698	-1.129	-3.213	9.524	1.23	47.85	158.33
345	2jsa-10	ASP_A_58_C	PRO_A_59_N	-0.281	-3.55	8.698	0.934	-2.957	8.557	1.36	95.95	26.02
346	2jsa-10	PRO_A_59_N	PRO_A_59_CA	0.934	-2.957	8.557	1.327	-1.843	9.404	1.45	54.36	70.57
347	2jsa-10	PRO_A_59_CA	PRO_A_59_HA	1.327	-1.843	9.404	1.073	-2.056	10.443	1.09	17.70	-140.02
348	2jsa-10	PRO_A_59_CA	PRO_A_59_C	1.327	-1.843	9.404	0.613	-0.557	8.984	1.53	105.94	119.04
349	2jsa-10	PRO_A_59_C	PRO_A_59_O	0.613	-0.557	8.984	-0.083	0.061	9.788	1.23	49.18	138.40
350	2jsa-10	PRO_A_59_C	ILE_A_60_N	0.613	-0.557	8.984	0.81	-0.193	7.725	1.33	161.80	61.58
351	2jsa-10	ILE_A_60_N	ILE_A_60_H	0.81	-0.193	7.725	1.395	-0.751	7.119	1.01	126.85	-43.65
352	2jsa-10	ILE_A_60_N	ILE_A_60_CA	0.81	-0.193	7.725	0.192	1.009	7.19	1.45	111.60	117.21
353	2jsa-10	ILE_A_60_CA	ILE_A_60_HA	0.192	1.009	7.19	0.688	1.871	7.637	1.09	65.80	60.08
354	2jsa-10	ILE_A_60_CA	ILE_A_60_C	0.192	1.009	7.19	-1.279	1.051	7.607	1.53</		

357	2jsa-10	ILE_A_61_N	ILE_A_61_H	-1.981	-0.029	7.294	-1.539	-0.802	6.817	1.01	118.18	-60.24
358	2jsa-10	ILE_A_61_N	ILE_A_61_CA	-1.981	-0.029	7.294	-3.392	-0.127	7.628	1.45	76.71	-176.03
359	2jsa-10	ILE_A_61_CA	ILE_A_61_HA	-3.392	-0.127	7.628	-3.901	0.736	7.199	1.09	113.18	120.53
360	2jsa-10	ILE_A_61_CA	ILE_A_61_C	-3.392	-0.127	7.628	-3.556	-0.056	9.148	1.53	6.71	156.59
361	2jsa-10	ILE_A_61_C	ILE_A_61_O	-3.556	-0.056	9.148	-4.62	0.313	9.644	1.23	66.23	160.87
362	2jsa-10	ILE_A_61_C	HIS_A_62_N	-3.556	-0.056	9.148	-2.489	-0.416	9.845	1.32	58.24	-18.64
363	2jsa-10	HIS_A_62_N	HIS_A_62_H	-2.489	-0.416	9.845	-1.647	-0.71	9.37	1.01	118.04	-19.25
364	2jsa-10	HIS_A_62_N	HIS_A_62_CA	-2.489	-0.416	9.845	-2.501	-0.398	11.298	1.45	0.85	123.69
365	2jsa-10	HIS_A_62_CA	HIS_A_62_HA	-2.501	-0.398	11.298	-3.362	-0.974	11.635	1.09	71.98	-146.22
366	2jsa-10	HIS_A_62_CA	HIS_A_62_C	-2.501	-0.398	11.298	-2.676	1.041	11.791	1.53	71.22	96.93
367	2jsa-10	HIS_A_62_C	HIS_A_62_O	-2.676	1.041	11.791	-3.49	1.303	12.674	1.23	44.08	162.16
368	2jsa-10	HIS_A_62_C	GLU_A_63_N	-2.676	1.041	11.791	-1.896	1.933	11.199	1.32	116.55	48.83
369	2jsa-10	GLU_A_63_N	GLU_A_63_H	-1.896	1.933	11.199	-1.248	1.645	10.479	1.01	135.44	-23.96
370	2jsa-10	GLU_A_63_N	GLU_A_63_CA	-1.896	1.933	11.199	-1.954	3.338	11.568	1.45	75.30	92.36
371	2jsa-10	GLU_A_63_CA	GLU_A_63_HA	-1.954	3.338	11.568	-1.744	3.416	12.635	1.09	11.86	20.38
372	2jsa-10	GLU_A_63_CA	GLU_A_63_C	-1.954	3.338	11.568	-3.355	3.897	11.311	1.53	99.67	158.25
373	2jsa-10	GLU_A_63_C	GLU_A_63_O	-3.355	3.897	11.311	-3.963	4.49	12.2	1.23	43.69	135.72
374	2jsa-10	GLU_A_63_C	LEU_A_64_N	-3.355	3.897	11.311	-3.826	3.687	10.09	1.33	157.10	-155.97
375	2jsa-10	LEU_A_64_N	LEU_A_64_H	-3.826	3.687	10.09	-3.27	3.19	9.408	1.01	132.44	-41.79
376	2jsa-10	LEU_A_64_N	LEU_A_64_CA	-3.826	3.687	10.09	-5.144	4.164	9.706	1.45	105.32	160.10
377	2jsa-10	LEU_A_64_CA	LEU_A_64_HA	-5.144	4.164	9.706	-5.16	5.247	9.829	1.09	83.52	90.85
378	2jsa-10	LEU_A_64_CA	LEU_A_64_C	-5.144	4.164	9.706	-6.191	3.572	10.651	1.53	51.84	-150.52
379	2jsa-10	LEU_A_64_C	LEU_A_64_O	-6.191	3.572	10.651	-7.174	4.231	10.986	1.23	74.19	146.16
380	2jsa-10	LEU_A_64_C	GLU_A_65_N	-6.191	3.572	10.651	-5.946	2.334	11.054	1.32	72.29	-78.81
381	2jsa-10	GLU_A_65_N	GLU_A_65_H	-5.946	2.334	11.054	-5.117	1.851	10.738	1.01	108.23	-30.23
382	2jsa-10	GLU_A_65_N	GLU_A_65_CA	-5.946	2.334	11.054	-6.855	1.646	11.954	1.45	51.71	-142.88
383	2jsa-10	GLU_A_65_CA	GLU_A_65_HA	-6.855	1.646	11.954	-7.854	1.688	11.521	1.09	113.42	177.59
384	2jsa-10	GLU_A_65_CA	GLU_A_65_C	-6.855	1.646	11.954	-6.891	2.349	13.312	1.53	27.40	92.93
385	2jsa-10	GLU_A_65_C	GLU_A_65_O	-6.891	2.349	13.312	-7.875	2.245	14.044	1.23	53.51	-173.97
386	2jsa-10	GLU_A_65_C	GLY_A_66_N	-6.891	2.349	13.312	-5.806	3.048	13.61	1.32	77.00	32.79
387	2jsa-10	GLY_A_66_N	GLY_A_66_H	-5.806	3.048	13.61	-5.033	3.088	12.961	1.01	129.98	2.96
388	2jsa-10	GLY_A_66_N	GLY_A_66_CA	-5.806	3.048	13.61	-5.7	3.768	14.867	1.45	30.07	81.62
389	2jsa-10	GLY_A_66_CA	GLY_A_66_C	-5.7	3.768	14.867	-6.346	5.152	14.763	1.53	93.90	115.02
390	2jsa-10	GLY_A_66_C	GLY_A_66_O	-6.346	5.152	14.763	-6.76	5.725	15.77	1.23	35.07	125.85
391	2jsa-10	GLY_A_66_C	GLY_A_67_N	-6.346	5.152	14.763	-6.413	5.648	13.537	1.32	157.79	97.69
392	2jsa-10	GLY_A_67_N	GLY_A_67_H	-6.413	5.648	13.537	-6.053	5.12	12.755	1.01	140.74	-55.71
393	2jsa-10	GLY_A_67_N	GLY_A_67_CA	-6.413	5.648	13.537	-7.001	6.953	13.288	1.45	99.87	114.26
394	2jsa-10	GLY_A_67_CA	GLY_A_67_C	-7.001	6.953	13.288	-6.028	7.857	12.53	1.53	119.71	42.89
395	2jsa-10	GLY_A_67_C	GLY_A_67_O	-6.028	7.857	12.53	-6.331	9.02	12.266	1.23	102.39	104.60
396	2jsa-10	GLY_A_67_C	THR_A_68_N	-6.028	7.857	12.53	-4.877	7.29	12.2	1.32	104.42	-26.23
397	2jsa-10	THR_A_68_N	THR_A_68_H	-4.877	7.29	12.2	-4.694	6.328	12.449	1.01	75.73	-79.23
398	2jsa-10	THR_A_68_N	THR_A_68_CA	-4.877	7.29	12.2	-3.856	8.031	11.477	1.45	119.82	35.97
399	2jsa-10	THR_A_68_CA	THR_A_68_HA	-3.856	8.031	11.477	-3.721	9.001	11.957	1.09	63.89	82.08
400	2jsa-10	THR_A_68_CA	THR_A_68_C	-3.856	8.031	11.477	-4.299	8.277	10.033	1.53	160.66	150.96
401	2jsa-10	THR_A_68_C	THR_A_68_O	-4.299	8.277	10.033	-4.905	7.408	9.409	1.23	120.50	-124.89
402	2jsa-10	THR_A_68_C	ALA_A_69_N	-4.299	8.277	10.033	-3.979	9.467	9.545	1.33	111.60	74.95
403	2jsa-10	ALA_A_69_N	ALA_A_69_H	-3.979	9.467	9.545	-3.479	10.134	10.116	1.01	55.59	53.14
404	2jsa-10	ALA_A_69_N	ALA_A_69_CA	-3.979	9.467	9.545	-4.337	9.839	8.187	1.45	159.18	133.90
405	2jsa-10	ALA_A_69_CA	ALA_A_69_HA	-4.337	9.839	8.187	-5.394	9.624	8.031	1.09	98.23	-168.50
406	2jsa-10	ALA_A_69_CA	ALA_A_69_C	-4.337	9.839	8.187	-3.521	9.0	7.201	1.53	130.11	-45.80
407	2jsa-10	ALA_A_69_C	ALA_A_69_O	-3.521	9.0	7.201	-2.517	8.397	7.577	1.23	72.20	-30.99
408	2jsa-10	ALA_A_69_C	PRO_A_70_N	-3.521	9.0	7.201	-3.996	8.986	5.927	1.36	159.54	-178.31
409	2jsa-10	PRO_A_70_N	PRO_A_70_CA	-3.996	8.986	5.927	-3.323	8.231	4.885	1.45	135.85	-48.29
410	2jsa-10	PRO_A_70_CA	PRO_A_70_HA	-3.323	8.231	4.885	-3.06	7.24	5.254	1.09	70.21	-75.14
411	2jsa-10	PRO_A_70_CA	PRO_A_70_C	-3.323	8.231	4.885	-2.042	8.936	4.436	1.53	107.07	28.83
412	2jsa-10	PRO_A_70_C	PRO_A_70_O	-2.042	8.936	4.436	-1.15	8.309	3.868	1.23	117.52	-35.10
413	2jsa-10	PRO_A_70_C	LYS_A_71_N	-2.042	8.936	4.436	-1.993	10.232	4.708	1.33	78.16	87.83
414	2jsa-10	LYS_A_71_N	LYS_A_71_H	-1.993	10.232	4.708	-2.765	10.683	5.178	1.01	62.27	149.71
415	2jsa-10	LYS_A_71_N	LYS_A_71_CA	-1.993	10.232	4.708	-0.835	11.031	4.34	1.45	104.66	34.61
416	2jsa-10	LYS_A_71_CA	LYS_A_71_HA	-0.835	11.031	4.34	-0.295	10.502	3.554	1.09	136.12	-44.41
417	2jsa-10	LYS_A_71_CA	LYS_A_71_C	-0.835	11.031	4.34	0.1	11.152	5.545	1.53	38.04	7.37
418	2jsa-10	LYS_A_71_C	LYS_A_71_O	0.1	11.152	5.545	1.118	11.838	5.477	1.23	93.17	33.97
419	2jsa-10	LYS_A_71_C	ASP_A_72_N	0.1	11.152	5.545	-0.281	10.476	6.619	1.32	35.85	-119.41
420	2jsa-10	ASP_A_72_N	ASP_A_72_H	-0.281	10.476	6.619	-1.132	9.933	6.604	1.01	90.85	-147.46
421	2jsa-10	ASP_A_72_N	ASP_A_72_CA	-0.281	10.476	6.619	0.511	10.5	7.837	1.45	33.05	1.74
422	2jsa-10	ASP_A_72_CA	ASP_A_72_HA	0.511	10.5	7.837	1.236	11.312	7.775	1.09	93.26	48.24
423	2jsa-10	ASP_A_72_CA	ASP_A_72_C	0.511	10.5	7.837	1.239	9.163	7.993	1.53	84.15	-61.43
424	2jsa-10	ASP_A_72_C	ASP_A_72_O	1.239	9.163	7.993	2.342	9.113	8.535	1.23	63.85	-2.60
425	2jsa-10	ASP_A_72_C	VAL_A_73_N	1.239	9.163	7.993	0.593	8.114	7.509	1.32	111.45	-121.63
426	2jsa-10	VAL_A_73_N	VAL_A_73_H	0.593	8.114	7.509	-0.312	8.23	7.077	1.01	115.34	172.70
427	2jsa-10	VAL_A_73_N	VAL_A_73_CA	0.593	8.114	7.509	1.165	6.78	7.587	1.45	86.92	-66.79
428	2jsa-10	VAL_A_73_CA	VAL_A_73_HA	1.165	6.78	7.587	1.419	6.574	8.627	1.09	17.46	-39.04
429	2jsa-10	VAL_A_73_CA	VAL_A_73_C	1.165	6.78	7.587	2.456	6.735	6.766	1.53	122.44	-2.00
430	2jsa-10	VAL_A_73_C	VAL_A_73_O	2.456	6.735	6.766	3.453	6.162	7.201	1.23	69.28	-29.89
431	2jsa-10	VAL_A_73_C	CYS_A_74_N	2.456	6.735	6.766	2.393	7.346	5.592	1.32	152.38	95.89
432	2jsa-10	CYS_A_74_N	CYS_A_74_H	2.393	7.346	5.592	1.539	7.797	5.298	1.01	106.93	152.16
433	2jsa-10	CYS_A_74_N	CYS_A_74_CA	2.393	7.346	5.592	3.545	7.382	4.705	1.45	127.58	1.79
434	2jsa-10	CYS_A_74_CA	CYS_A_74_HA	3.545	7.382	4.705	4.07	6.43	4.784	1.09	85.84	-61.12
435	2jsa-10	CYS_A_74_CA	CYS_A_74_C	3.545	7.382	4.705	4.482	8.495	5.18	1.53	71.92	49.91
436	2jsa-10	CYS_A_74_C	CYS_A_74_O	4.482	8.495	5.18	4.665	9.494	4.487	1.23	124.31	79.62
437	2jsa-10	CYS_A_74_C	THR_A_75_N	4.482	8.495	5.18	5.049	8.284	6.358	1.32	27.18	-20.41
438	2jsa-10	THR_A_75_N	THR_A_75_H	5.049	8.284	6.358	4.852	7.438	6.874	1.01	59.29	-103.11
439	2jsa-10	THR_A_75_N	THR_A_75_CA	5.049	8.284	6.358	5.963	9.256	6.933	1.45	66.69	46.76
440	2jsa-10	THR_A_75_CA	THR_A_75_HA	5.963	9.256	6.933	6.867	9.29	6.324	1.09	123.95	2.15
441	2jsa-10	THR_A_75_CA	THR_A_75_C	5.963	9.256	6.933	6.365	8.839	8.349	1.53	22.25	-46.05
442	2jsa-10	THR_A_75_C	THR_A_75_O	6.365	8.839	8.349	7.516	8.478	8.591	1.23	78.66	-17.41
443	2jsa-10	THR_A_75_C	LYS_A_76_N	6.365	8.839	8.349	5.394	8.899	9.248	1.32	47.26	176.46
444	2jsa-10	LYS_A_76_N	LYS_A_76_H	5.394	8.899	9.248	4.47	9.203	8.978	1.01	105.51	161.79
445	2jsa-10	LYS_A_76_N	LYS_A_76_CA	5.394	8.899	9.248	5.632	8.532	10.633	1.45	17.53	-57.04
446	2jsa-10	LYS_A_76_CA	LYS_A_76_HA	5.632	8.532	10.633	6.44	9.158	11.014	1.09	69.56	37.77</

450	2jsa-10	LEU_A_77_N	LEU_A_77_H	5.533	6.266	9.815	4.846	6.622	9.166	1.01	129.99	152.61
451	2jsa-10	LEU_A_77_N	LEU_A_77_CA	5.533	6.266	9.815	5.882	4.857	9.761	1.45	92.13	-76.09
452	2jsa-10	LEU_A_77_CA	LEU_A_77_HA	5.882	4.857	9.761	5.878	4.469	10.78	1.09	20.85	-90.59
453	2jsa-10	LEU_A_77_CA	LEU_A_77_C	5.882	4.857	9.761	7.302	4.709	9.212	1.53	111.03	-5.95
454	2jsa-10	LEU_A_77_C	LEU_A_77_O	7.302	4.709	9.212	7.85	3.608	9.189	1.23	91.07	-63.54
455	2jsa-10	LEU_A_77_C	ASN_A_78_N	7.302	4.709	9.212	7.858	5.833	8.785	1.32	108.80	63.68
456	2jsa-10	ASN_A_78_N	ASN_A_78_H	7.858	5.833	8.785	7.349	6.704	8.836	1.01	87.11	120.30
457	2jsa-10	ASN_A_78_N	ASN_A_78_CA	7.858	5.833	8.785	9.203	5.842	8.238	1.45	112.13	0.38
458	2jsa-10	ASN_A_78_CA	ASN_A_78_HA	9.203	5.842	8.238	9.528	6.875	8.108	1.09	96.85	72.54
459	2jsa-10	ASN_A_78_CA	ASN_A_78_C	9.203	5.842	8.238	9.207	5.122	6.888	1.53	151.93	-89.68
460	2jsa-10	ASN_A_78_C	ASN_A_78_O	9.207	5.122	6.888	10.214	4.534	6.497	1.23	108.54	-30.28
461	2jsa-10	ASN_A_78_C	GLU_A_79_N	9.207	5.122	6.888	8.068	5.191	6.215	1.32	120.53	176.53
462	2jsa-10	GLU_A_79_N	GLU_A_79_H	8.068	5.191	6.215	7.28	5.693	6.599	1.01	67.66	147.50
463	2jsa-10	GLU_A_79_N	GLU_A_79_CA	8.068	5.191	6.215	7.926	4.553	4.918	1.45	153.25	-102.55
464	2jsa-10	GLU_A_79_CA	GLU_A_79_HA	7.926	4.553	4.918	8.651	3.741	4.86	1.09	93.05	-48.24
465	2jsa-10	GLU_A_79_CA	GLU_A_79_C	7.926	4.553	4.918	8.231	5.551	3.799	1.53	137.00	73.01
466	2jsa-10	GLU_A_79_C	GLU_A_79_O	8.231	5.551	3.799	9.366	5.635	3.33	1.23	112.40	4.23
467	2jsa-10	GLU_A_79_C	CYS_A_80_N	8.231	5.551	3.799	7.2	6.283	3.404	1.32	107.35	144.63
468	2jsa-10	CYS_A_80_N	CYS_A_80_H	7.2	6.283	3.404	6.296	6.162	3.836	1.01	64.66	-172.38
469	2jsa-10	CYS_A_80_N	CYS_A_80_CA	7.2	6.283	3.404	7.344	7.271	2.349	1.45	136.58	81.71
470	2jsa-10	CYS_A_80_CA	CYS_A_80_HA	7.344	7.271	2.349	7.765	6.778	1.473	1.09	143.50	-49.50
471	2jsa-10	CYS_A_80_CA	CYS_A_80_C	7.344	7.271	2.349	8.328	8.342	2.825	1.53	71.88	47.42
472	2jsa-10	CYS_A_80_C	CYS_A_80_O	8.328	8.342	2.825	8.295	8.75	3.985	1.23	19.44	94.62
473	2jsa-10	CYS_A_80_C	PRO_A_81_N	8.328	8.342	2.825	9.205	8.779	1.881	1.36	133.93	26.49
474	2jsa-10	PRO_A_81_N	PRO_A_81_CA	9.205	8.779	1.881	10.197	9.793	2.193	1.45	77.60	45.63
475	2jsa-10	PRO_A_81_CA	PRO_A_81_HA	10.197	9.793	2.193	10.673	9.569	3.148	1.09	28.85	-25.20
476	2jsa-10	PRO_A_81_CA	PRO_A_81_C	10.197	9.793	2.193	9.554	11.178	2.284	1.53	86.59	114.90
477	2jsa-10	PRO_A_81_C	PRO_A_81_O	9.554	11.178	2.284	9.673	11.855	3.304	1.23	33.98	80.03
1	2jsa-11	ARG_A_1_N	ARG_A_1_H	13.063	-0.16	-2.146	14.039	0.095	-2.083	1.01	86.43	14.64
2	2jsa-11	ARG_A_1_N	ARG_A_1_CA	13.063	-0.16	-2.146	12.061	0.852	-1.859	1.45	78.61	134.72
3	2jsa-11	ARG_A_1_CA	ARG_A_1_HA	12.061	0.852	-1.859	11.449	0.993	-2.75	1.09	144.82	167.03
4	2jsa-11	ARG_A_1_CA	ARG_A_1_C	12.061	0.852	-1.859	12.734	2.179	-1.501	1.53	76.47	63.11
5	2jsa-11	ARG_A_1_C	ARG_A_1_O	12.734	2.179	-1.501	12.977	2.46	-0.329	1.23	17.59	49.15
6	2jsa-11	ARG_A_1_C	SER_A_2_N	12.734	2.179	-1.501	13.017	2.959	-2.534	1.32	141.23	70.06
7	2jsa-11	SER_A_2_N	SER_A_2_H	13.017	2.959	-2.534	12.789	2.664	-3.472	1.01	158.32	-127.70
8	2jsa-11	SER_A_2_N	SER_A_2_CA	13.017	2.959	-2.534	13.657	4.25	-2.343	1.45	82.45	63.63
9	2jsa-11	SER_A_2_CA	SER_A_2_HA	13.657	4.25	-2.343	13.836	4.389	-1.277	1.09	12.00	37.83
10	2jsa-11	SER_A_2_CA	SER_A_2_C	13.657	4.25	-2.343	12.737	5.369	-2.836	1.53	108.79	129.43
11	2jsa-11	SER_A_2_C	SER_A_2_O	12.737	5.369	-2.836	13.205	6.442	-3.209	1.23	107.67	66.44
12	2jsa-11	SER_A_2_C	ALA_A_3_N	12.737	5.369	-2.836	11.445	5.078	-2.82	1.32	89.31	-167.31
13	2jsa-11	ALA_A_3_N	ALA_A_3_H	11.445	5.078	-2.82	11.132	4.173	-2.501	1.01	71.58	-109.08
14	2jsa-11	ALA_A_3_N	ALA_A_3_CA	11.445	5.078	-2.82	10.454	6.046	-3.259	1.45	107.58	135.67
15	2jsa-11	ALA_A_3_CA	ALA_A_3_HA	10.454	6.046	-3.259	10.283	6.762	-2.455	1.09	42.48	103.43
16	2jsa-11	ALA_A_3_CA	ALA_A_3_C	10.454	6.046	-3.259	9.138	5.324	-3.552	1.53	101.05	-151.25
17	2jsa-11	ALA_A_3_C	ALA_A_3_O	9.138	5.324	-3.552	8.081	5.733	-3.073	1.23	67.09	158.85
18	2jsa-11	ALA_A_3_C	LEU_A_4_N	9.138	5.324	-3.552	9.243	4.263	-4.339	1.33	126.43	-84.35
19	2jsa-11	LEU_A_4_N	LEU_A_4_H	9.243	4.263	-4.339	10.145	3.984	-4.698	1.01	110.82	-17.19
20	2jsa-11	LEU_A_4_N	LEU_A_4_CA	9.243	4.263	-4.339	8.073	3.481	-4.702	1.45	104.46	-146.24
21	2jsa-11	LEU_A_4_CA	LEU_A_4_HA	8.073	3.481	-4.702	7.49	4.06	-5.418	1.09	131.07	135.20
22	2jsa-11	LEU_A_4_CA	LEU_A_4_C	8.073	3.481	-4.702	7.205	3.265	-3.462	1.53	35.80	-166.03
23	2jsa-11	LEU_A_4_C	LEU_A_4_O	7.205	3.265	-3.462	6.027	3.618	-3.455	1.23	89.67	163.32
24	2jsa-11	LEU_A_4_C	SER_A_5_N	7.205	3.265	-3.462	7.82	2.686	-2.441	1.33	39.60	-43.27
25	2jsa-11	SER_A_5_N	SER_A_5_H	7.82	2.686	-2.441	8.793	2.423	-2.516	1.01	94.26	-15.13
26	2jsa-11	SER_A_5_N	SER_A_5_CA	7.82	2.686	-2.441	7.118	2.418	-1.198	1.45	31.15	-159.10
27	2jsa-11	SER_A_5_CA	SER_A_5_HA	7.118	2.418	-1.198	6.538	1.504	-1.323	1.09	96.59	-122.40
28	2jsa-11	SER_A_5_CA	SER_A_5_C	7.118	2.418	-1.198	6.16	3.569	-0.88	1.53	78.01	129.77
29	2jsa-11	SER_A_5_C	SER_A_5_O	6.16	3.569	-0.88	5.057	3.343	-0.383	1.23	66.18	-168.42
30	2jsa-11	SER_A_5_C	CYS_A_6_N	6.16	3.569	-0.88	6.615	4.776	-1.18	1.32	103.09	69.35
31	2jsa-11	CYS_A_6_N	CYS_A_6_H	6.615	4.776	-1.18	7.533	4.887	-1.587	1.01	113.76	6.89
32	2jsa-11	CYS_A_6_N	CYS_A_6_CA	6.615	4.776	-1.18	5.811	5.961	-0.933	1.45	80.21	124.16
33	2jsa-11	CYS_A_6_CA	CYS_A_6_HA	5.811	5.961	-0.933	5.641	6.042	0.141	1.09	9.94	154.52
34	2jsa-11	CYS_A_6_CA	CYS_A_6_C	5.811	5.961	-0.933	4.461	5.78	-1.627	1.53	117.00	-127.36
35	2jsa-11	CYS_A_6_C	CYS_A_6_O	4.461	5.78	-1.627	3.443	5.574	-0.968	1.23	57.61	-168.56
36	2jsa-11	CYS_A_6_C	GLN_A_7_N	4.461	5.78	-1.627	4.495	5.862	-2.949	1.32	176.16	67.48
37	2jsa-11	GLN_A_7_N	GLN_A_7_H	4.495	5.862	-2.949	5.369	6.034	-3.425	1.01	118.12	11.13
38	2jsa-11	GLN_A_7_N	GLN_A_7_CA	4.495	5.862	-2.949	3.286	5.709	-3.74	1.45	122.99	-172.79
39	2jsa-11	GLN_A_7_CA	GLN_A_7_HA	3.286	5.709	-3.74	2.68	6.605	-3.605	1.09	82.89	124.07
40	2jsa-11	GLN_A_7_CA	GLN_A_7_C	3.286	5.709	-3.74	2.48	4.505	-3.249	1.53	71.28	-123.80
41	2jsa-11	GLN_A_7_C	GLN_A_7_O	2.48	4.505	-3.249	1.283	4.619	-2.987	1.23	77.71	174.56
42	2jsa-11	GLN_A_7_C	MET_A_8_N	2.48	4.505	-3.249	3.167	3.378	-3.141	1.32	85.32	-58.63
43	2jsa-11	MET_A_8_N	MET_A_8_H	3.167	3.378	-3.141	4.149	3.357	-3.376	1.01	103.46	-1.23
44	2jsa-11	MET_A_8_N	MET_A_8_CA	3.167	3.378	-3.141	2.53	2.154	-2.687	1.45	71.79	-117.49
45	2jsa-11	MET_A_8_CA	MET_A_8_HA	2.53	2.154	-2.687	1.898	1.772	-3.488	1.09	137.33	-148.85
46	2jsa-11	MET_A_8_CA	MET_A_8_C	2.53	2.154	-2.687	1.666	2.411	-1.452	1.53	36.13	163.43
47	2jsa-11	MET_A_8_C	MET_A_8_O	1.666	2.411	-1.452	0.527	1.952	-1.38	1.23	86.64	-158.05
48	2jsa-11	MET_A_8_C	CYS_A_9_N	1.666	2.411	-1.452	2.239	3.144	-0.51	1.32	44.64	51.98
49	2jsa-11	CYS_A_9_N	CYS_A_9_H	2.239	3.144	-0.51	3.18	3.49	-0.637	1.01	97.22	20.19
50	2jsa-11	CYS_A_9_N	CYS_A_9_CA	2.239	3.144	-0.51	1.536	3.468	0.72	1.45	32.18	155.26
51	2jsa-11	CYS_A_9_CA	CYS_A_9_HA	1.536	3.468	0.72	1.279	2.536	1.224	1.09	62.47	-105.42
52	2jsa-11	CYS_A_9_CA	CYS_A_9_C	1.536	3.468	0.72	0.242	4.199	0.354	1.53	103.83	150.54
53	2jsa-11	CYS_A_9_C	CYS_A_9_O	0.242	4.199	0.354	-0.764	4.071	1.05	1.23	55.54	-172.75
54	2jsa-11	CYS_A_9_C	GLU_A_10_N	0.242	4.199	0.354	0.31	4.947	-0.737	1.32	145.46	84.81
55	2jsa-11	GLU_A_10_N	GLU_A_10_H	0.31	4.947	-0.737	1.172	5.004	-1.261	1.01	121.24	3.78
56	2jsa-11	GLU_A_10_N	GLU_A_10_CA	0.31	4.947	-0.737	-0.843	5.697	-1.203	1.45	108.72	146.96
57	2jsa-11	GLU_A_10_CA	GLU_A_10_HA	-0.843	5.697	-1.203	-1.39	6.052	-0.329	1.09	36.73	147.02
58	2jsa-11	GLU_A_10_CA	GLU_A_10_C	-0.843	5.697	-1.203	-1.771	4.793	-2.016	1.53	122.11	-135.75
59	2jsa-11	GLU_A_10_C	GLU_A_10_O	-1.771	4.793	-2.016	-2.838	5.223	-2.453	1.23	110.80	158.05
60	2jsa-11	GLU_A_10_C	LEU_A_11_N	-1.771	4.793	-2.016	-1.332	3.556	-2.196	1.32	97.81	-70.46
61	2jsa-11	LEU_A_11_N	LEU_A_11_H	-1.332	3.556	-2.196	-0.444	3.27	-1.808	1.01	67.42	-17.85
62	2jsa-11	LEU_A_11_N	LEU_A_11_CA	-1.332	3.556	-2.196	-2.11	2.587	-2.949	1.45	121.21	-128.76
63	2jsa-11	LEU_A_11_CA	LEU_A_11_HA	-2.11	2.587	-2.949	-2.775	3.134	-3.617	1.09	127.80	140.56
64	2jsa-11	LEU_A_11_CA	LEU_A_11_C	-2.11	2.587	-2.949						

66	2jsa-11	LEU_A_11_C	VAL_A_12_N	-2.981	1.778	-1.985	-2.367	1.369	-0.885	1.32	33.85	-33.67
67	2jsa-11	VAL_A_12_N	VAL_A_12_H	-2.367	1.369	-0.885	-1.395	1.595	-0.731	1.01	81.23	13.09
68	2jsa-11	VAL_A_12_N	VAL_A_12_CA	-2.367	1.369	-0.885	-3.072	0.59	0.12	1.45	46.27	-132.15
69	2jsa-11	VAL_A_12_CA	VAL_A_12_HA	-3.072	0.59	0.12	-3.553	-0.254	-0.373	1.09	116.91	-119.68
70	2jsa-11	VAL_A_12_CA	VAL_A_12_C	-3.072	0.59	0.12	-4.163	1.456	0.755	1.53	65.49	141.56
71	2jsa-11	VAL_A_12_C	VAL_A_12_O	-4.163	1.456	0.755	-5.249	0.966	1.059	1.23	75.69	-155.72
72	2jsa-11	VAL_A_12_C	VAL_A_13_N	-4.163	1.456	0.755	-3.835	2.727	0.937	1.33	82.11	75.53
73	2jsa-11	VAL_A_13_N	VAL_A_13_H	-3.835	2.727	0.937	-2.922	3.061	0.664	1.01	105.69	20.09
74	2jsa-11	VAL_A_13_N	VAL_A_13_CA	-3.835	2.727	0.937	-4.774	3.663	1.53	1.45	65.90	135.09
75	2jsa-11	VAL_A_13_CA	VAL_A_13_HA	-4.774	3.663	1.53	-5.167	3.223	2.446	1.09	32.78	-131.77
76	2jsa-11	VAL_A_13_CA	VAL_A_13_C	-4.774	3.663	1.53	-5.944	3.884	0.57	1.53	128.88	169.30
77	2jsa-11	VAL_A_13_C	VAL_A_13_O	-5.944	3.884	0.57	-7.095	3.628	0.919	1.23	73.51	-167.46
78	2jsa-11	VAL_A_13_C	LYS_A_14_N	-5.944	3.884	0.57	-5.608	4.357	-0.622	1.33	154.05	54.61
79	2jsa-11	LYS_A_14_N	LYS_A_14_H	-5.608	4.357	-0.622	-4.64	4.544	-0.841	1.01	102.52	10.93
80	2jsa-11	LYS_A_14_N	LYS_A_14_CA	-5.608	4.357	-0.622	-6.617	4.616	-1.635	1.45	134.20	165.60
81	2jsa-11	LYS_A_14_CA	LYS_A_14_HA	-6.617	4.616	-1.635	-7.204	5.477	-1.315	1.09	72.93	124.28
82	2jsa-11	LYS_A_14_CA	LYS_A_14_C	-6.617	4.616	-1.635	-7.562	3.415	-1.726	1.53	93.41	-128.20
83	2jsa-11	LYS_A_14_C	LYS_A_14_O	-7.562	3.415	-1.726	-8.745	3.573	-2.021	1.23	103.88	172.39
84	2jsa-11	LYS_A_14_C	LYS_A_15_N	-7.562	3.415	-1.726	-7.004	2.242	-1.466	1.32	78.68	-64.56
85	2jsa-11	LYS_A_15_N	LYS_A_15_H	-7.004	2.242	-1.466	-6.023	2.187	-1.229	1.01	76.44	-3.21
86	2jsa-11	LYS_A_15_N	LYS_A_15_CA	-7.004	2.242	-1.466	-7.781	1.016	-1.514	1.45	91.89	-122.37
87	2jsa-11	LYS_A_15_CA	LYS_A_15_HA	-7.781	1.016	-1.514	-8.513	1.112	-2.316	1.09	137.37	172.53
88	2jsa-11	LYS_A_15_CA	LYS_A_15_C	-7.781	1.016	-1.514	-8.549	0.852	-0.201	1.53	30.88	-167.95
89	2jsa-11	LYS_A_15_C	LYS_A_15_O	-8.549	0.852	-0.201	-9.708	0.438	-0.203	1.23	90.09	-160.34
90	2jsa-11	LYS_A_15_C	TYR_A_16_N	-8.549	0.852	-0.201	-7.872	1.183	0.888	1.32	34.68	26.06
91	2jsa-11	TYR_A_16_N	TYR_A_16_H	-7.872	1.183	0.888	-6.92	1.514	0.814	1.01	94.20	19.17
92	2jsa-11	TYR_A_16_N	TYR_A_16_CA	-7.872	1.183	0.888	-8.475	1.078	2.205	1.45	24.93	-170.12
93	2jsa-11	TYR_A_16_CA	TYR_A_16_HA	-8.475	1.078	2.205	-8.973	0.115	2.316	1.09	84.15	-117.35
94	2jsa-11	TYR_A_16_CA	TYR_A_16_C	-8.475	1.078	2.205	-9.476	2.21	2.443	1.53	81.05	131.49
95	2jsa-11	TYR_A_16_C	TYR_A_16_O	-9.476	2.21	2.443	-10.681	1.973	2.518	1.23	86.51	-168.87
96	2jsa-11	TYR_A_16_C	GLU_A_17_N	-9.476	2.21	2.443	-8.94	3.416	2.555	1.32	85.15	66.04
97	2jsa-11	GLU_A_17_N	GLU_A_17_H	-8.94	3.416	2.555	-7.939	3.537	2.484	1.01	94.03	6.89
98	2jsa-11	GLU_A_17_N	GLU_A_17_CA	-8.94	3.416	2.555	-9.772	4.587	2.781	1.45	81.06	125.39
99	2jsa-11	GLU_A_17_CA	GLU_A_17_HA	-9.772	4.587	2.781	-10.106	4.568	3.819	1.09	17.86	-176.74
100	2jsa-11	GLU_A_17_CA	GLU_A_17_C	-9.772	4.587	2.781	-11.006	4.544	1.879	1.53	126.15	-178.00
101	2jsa-11	GLU_A_17_C	GLU_A_17_O	-11.006	4.544	1.879	-12.113	4.846	2.321	1.23	68.93	164.74
102	2jsa-11	GLU_A_17_C	GLY_A_18_N	-11.006	4.544	1.879	-10.773	4.167	0.63	1.33	160.46	-58.28
103	2jsa-11	GLY_A_18_N	GLY_A_18_H	-10.773	4.167	0.63	-9.835	3.934	0.336	1.01	106.92	-13.95
104	2jsa-11	GLY_A_18_N	GLY_A_18_CA	-10.773	4.167	0.63	-11.853	4.081	-0.339	1.45	131.81	-175.45
105	2jsa-11	GLY_A_18_CA	GLY_A_18_C	-11.853	4.081	-0.339	-12.065	2.637	-0.796	1.53	107.39	-98.35
106	2jsa-11	GLY_A_18_C	GLY_A_18_O	-12.065	2.637	-0.796	-12.184	2.371	-1.992	1.23	166.31	-114.10
107	2jsa-11	GLY_A_18_C	SER_A_19_N	-12.065	2.637	-0.796	-12.107	1.741	0.179	1.32	42.61	-92.68
108	2jsa-11	SER_A_19_N	SER_A_19_H	-12.107	1.741	0.179	-12.003	2.031	1.141	1.01	17.76	70.27
109	2jsa-11	SER_A_19_N	SER_A_19_CA	-12.107	1.741	0.179	-12.303	0.33	-0.109	1.45	101.43	-97.91
110	2jsa-11	SER_A_19_CA	SER_A_19_HA	-12.303	0.33	-0.109	-11.761	0.09	-1.024	1.09	147.06	-23.88
111	2jsa-11	SER_A_19_CA	SER_A_19_C	-12.303	0.33	-0.109	-13.789	0.042	-0.329	1.53	98.27	-169.03
112	2jsa-11	SER_A_19_C	SER_A_19_O	-13.789	0.042	-0.329	-14.164	-0.588	-1.318	1.23	143.45	-120.76
113	2jsa-11	SER_A_19_C	ALA_A_20_N	-13.789	0.042	-0.329	-14.596	0.518	0.608	1.33	45.00	149.47
114	2jsa-11	ALA_A_20_N	ALA_A_20_H	-14.596	0.518	0.608	-14.218	1.027	1.394	1.01	38.89	53.40
115	2jsa-11	ALA_A_20_N	ALA_A_20_CA	-14.596	0.518	0.608	-16.034	0.32	0.529	1.45	93.12	-172.16
116	2jsa-11	ALA_A_20_CA	ALA_A_20_HA	-16.034	0.32	0.529	-16.527	1.092	1.119	1.09	57.21	122.56
117	2jsa-11	ALA_A_20_CA	ALA_A_20_C	-16.034	0.32	0.529	-16.389	-1.044	1.123	1.53	67.15	-104.59
118	2jsa-11	ALA_A_20_C	ALA_A_20_O	-16.389	-1.044	1.123	-16.97	-1.889	0.443	1.23	123.55	-124.51
119	2jsa-11	ALA_A_20_C	ASP_A_21_N	-16.389	-1.044	1.123	-16.026	-1.218	2.385	1.32	17.69	-25.61
120	2jsa-11	ASP_A_21_N	ASP_A_21_H	-16.026	-1.218	2.385	-15.55	-0.479	2.884	1.01	60.42	57.21
121	2jsa-11	ASP_A_21_N	ASP_A_21_CA	-16.026	-1.218	2.385	-16.299	-2.465	3.078	1.45	61.50	-102.35
122	2jsa-11	ASP_A_21_CA	ASP_A_21_HA	-16.299	-2.465	3.078	-17.351	-2.491	3.362	1.09	74.90	-178.58
123	2jsa-11	ASP_A_21_CA	ASP_A_21_C	-16.299	-2.465	3.078	-15.421	-2.552	4.328	1.53	35.22	-5.66
124	2jsa-11	ASP_A_21_C	ASP_A_21_O	-15.421	-2.552	4.328	-15.791	-3.199	5.307	1.23	37.28	-119.76
125	2jsa-11	ASP_A_21_C	LYS_A_22_N	-15.421	-2.552	4.328	-14.275	-1.892	4.254	1.32	93.20	29.94
126	2jsa-11	LYS_A_22_N	LYS_A_22_H	-14.275	-1.892	4.254	-14.035	-1.381	3.417	1.01	146.00	64.84
127	2jsa-11	LYS_A_22_N	LYS_A_22_CA	-14.275	-1.892	4.254	-13.342	-1.887	5.367	1.45	39.97	0.31
128	2jsa-11	LYS_A_22_CA	LYS_A_22_HA	-13.342	-1.887	5.367	-12.5	-1.248	5.099	1.09	104.23	37.20
129	2jsa-11	LYS_A_22_CA	LYS_A_22_C	-13.342	-1.887	5.367	-12.8	-3.302	5.581	1.53	81.96	-69.04
130	2jsa-11	LYS_A_22_C	LYS_A_22_O	-12.8	-3.302	5.581	-13.019	-3.902	6.632	1.23	31.29	-110.05
131	2jsa-11	LYS_A_22_C	ASP_A_23_N	-12.8	-3.302	5.581	-12.105	-3.795	4.566	1.33	139.99	-35.35
132	2jsa-11	ASP_A_23_N	ASP_A_23_H	-12.105	-3.795	4.566	-11.965	-3.245	3.73	1.01	145.83	75.72
133	2jsa-11	ASP_A_23_N	ASP_A_23_CA	-12.105	-3.795	4.566	-11.532	-5.129	4.629	1.45	87.52	-66.75
134	2jsa-11	ASP_A_23_CA	ASP_A_23_HA	-11.532	-5.129	4.629	-11.541	-5.472	5.664	1.09	18.34	-91.50
135	2jsa-11	ASP_A_23_CA	ASP_A_23_C	-11.532	-5.129	4.629	-10.094	-5.086	4.109	1.53	109.87	1.71
136	2jsa-11	ASP_A_23_C	ASP_A_23_O	-10.094	-5.086	4.109	-9.868	-5.031	2.901	1.23	169.10	13.68
137	2jsa-11	ASP_A_23_C	ALA_A_24_N	-10.094	-5.086	4.109	-9.158	-5.112	5.047	1.33	44.95	-1.59
138	2jsa-11	ALA_A_24_N	ALA_A_24_H	-9.158	-5.112	5.047	-9.416	-5.156	6.023	1.01	15.01	-170.32
139	2jsa-11	ALA_A_24_N	ALA_A_24_CA	-9.158	-5.112	5.047	-7.748	-5.077	4.698	1.45	103.90	1.42
140	2jsa-11	ALA_A_24_CA	ALA_A_24_HA	-7.748	-5.077	4.698	-7.521	-4.11	4.25	1.09	114.28	76.79
141	2jsa-11	ALA_A_24_CA	ALA_A_24_C	-7.748	-5.077	4.698	-7.455	-6.169	3.667	1.53	132.36	-74.98
142	2jsa-11	ALA_A_24_C	ALA_A_24_O	-7.455	-6.169	3.667	-6.432	-6.124	2.984	1.23	123.70	2.52
143	2jsa-11	ALA_A_24_C	ASN_A_25_N	-7.455	-6.169	3.667	-8.371	-7.124	3.587	1.33	93.46	-133.81
144	2jsa-11	ASN_A_25_N	ASN_A_25_H	-8.371	-7.124	3.587	-9.188	-7.096	4.18	1.01	54.04	178.04
145	2jsa-11	ASN_A_25_N	ASN_A_25_CA	-8.371	-7.124	3.587	-8.223	-8.225	2.651	1.45	130.12	-82.34
146	2jsa-11	ASN_A_25_CA	ASN_A_25_HA	-8.223	-8.225	2.651	-7.213	-8.627	2.731	1.09	85.79	-21.70
147	2jsa-11	ASN_A_25_CA	ASN_A_25_C	-8.223	-8.225	2.651	-8.469	-7.717	1.229	1.53	158.35	115.84
148	2jsa-11	ASN_A_25_C	ASN_A_25_O	-8.469	-7.717	1.229	-7.629	-7.892	0.348	1.23	135.76	-11.77
149	2jsa-11	ASN_A_25_C	VAL_A_26_N	-8.469	-7.717	1.229	-9.628	-7.098	1.049	1.33	97.80	151.89
150	2jsa-11	VAL_A_26_N	VAL_A_26_H	-9.628	-7.098	1.049	-10.272	-6.99	1.819	1.01	40.30	170.48
151	2jsa-11	VAL_A_26_N	VAL_A_26_CA	-9.628	-7.098	1.049	-9.996	-6.564	-0.25	1.45	153.47	124.57
152	2jsa-11	VAL_A_26_CA	VAL_A_26_HA	-9.996	-6.564	-0.25	-9.765	-7.313	-1.008	1.09	134.04	-72.86
153	2jsa-11	VAL_A_26_CA	VAL_A_26_C	-9.996	-6.564	-0.25	-9.156	-5.318	-0.542	1.53	101.00	56.01
154	2jsa-11	VAL_A_26_C	VAL_A_26_O	-9.156	-5.318	-0.542	-9.209	-4.773	-1.644	1.23	153.58	95.55
155	2jsa-11	VAL_A_26_C	ILE_A_27_N	-9.156	-5.318	-0.542	-8.401	-4.904	0.465	1.32	40.53	28.74
156	2jsa-11</											

159	2jsa-11	ILE_A_27_CA	ILE_A_27_C	-7.552	-3.733	0.331	-6.17	-4.164	-0.164	1.53	108.88	-17.32
160	2jsa-11	ILE_A_27_C	ILE_A_27_O	-6.17	-4.164	-0.164	-5.823	-3.939	-1.322	1.23	160.35	32.96
161	2jsa-11	ILE_A_27_C	LYS_A_28_N	-6.17	-4.164	-0.164	-5.418	-4.777	0.74	1.33	47.02	-39.19
162	2jsa-11	LYS_A_28_N	LYS_A_28_H	-5.418	-4.777	0.74	-5.767	-4.928	1.675	1.01	22.13	-156.60
163	2jsa-11	LYS_A_28_N	LYS_A_28_CA	-5.418	-4.777	0.74	-4.082	-5.243	0.409	1.45	103.17	-19.23
164	2jsa-11	LYS_A_28_CA	LYS_A_28_HA	-4.082	-5.243	0.409	-3.424	-4.375	0.361	1.09	92.52	52.84
165	2jsa-11	LYS_A_28_CA	LYS_A_28_C	-4.082	-5.243	0.409	-4.1	-5.889	-0.978	1.53	155.02	-91.60
166	2jsa-11	LYS_A_28_C	LYS_A_28_O	-4.1	-5.889	-0.978	-3.169	-5.71	-1.761	1.23	129.55	10.88
167	2jsa-11	LYS_A_28_C	LYS_A_29_N	-4.1	-5.889	-0.978	-5.169	-6.626	-1.237	1.32	101.28	-145.42
168	2jsa-11	LYS_A_29_N	LYS_A_29_H	-5.169	-6.626	-1.237	-5.896	-6.728	-0.544	1.01	46.65	-172.01
169	2jsa-11	LYS_A_29_N	LYS_A_29_CA	-5.169	-6.626	-1.237	-5.32	-7.301	-2.516	1.45	151.60	-102.61
170	2jsa-11	LYS_A_29_CA	LYS_A_29_HA	-5.32	-7.301	-2.516	-4.381	-7.805	-2.745	1.09	102.13	-28.22
171	2jsa-11	LYS_A_29_CA	LYS_A_29_C	-5.32	-7.301	-2.516	-5.569	-6.261	-3.61	1.53	135.65	103.46
172	2jsa-11	LYS_A_29_C	LYS_A_29_O	-5.569	-6.261	-3.61	-4.961	-6.321	-4.678	1.23	150.23	-5.64
173	2jsa-11	LYS_A_29_C	ASP_A_30_N	-5.569	-6.261	-3.61	-6.463	-5.331	-3.306	1.33	76.74	133.87
174	2jsa-11	ASP_A_30_N	ASP_A_30_H	-6.463	-5.331	-3.306	-6.924	-5.343	-2.408	1.01	27.18	-178.51
175	2jsa-11	ASP_A_30_N	ASP_A_30_CA	-6.463	-5.331	-3.306	-6.799	-4.28	-4.25	1.45	130.55	107.73
176	2jsa-11	ASP_A_30_CA	ASP_A_30_HA	-6.799	-4.28	-4.25	-7.319	-4.719	-5.101	1.09	141.35	-139.83
177	2jsa-11	ASP_A_30_CA	ASP_A_30_C	-6.799	-4.28	-4.25	-5.515	-3.594	-4.723	1.53	108.00	28.11
178	2jsa-11	ASP_A_30_C	ASP_A_30_O	-5.515	-3.594	-4.723	-5.303	-3.426	-5.923	1.23	167.30	38.40
179	2jsa-11	ASP_A_30_C	PHE_A_31_N	-5.515	-3.594	-4.723	-4.693	-3.219	-3.755	1.32	43.03	24.52
180	2jsa-11	PHE_A_31_N	PHE_A_31_H	-4.693	-3.219	-3.755	-4.932	-3.391	-2.789	1.01	16.95	-144.26
181	2jsa-11	PHE_A_31_N	PHE_A_31_CA	-4.693	-3.219	-3.755	-3.435	-2.556	-4.056	1.45	101.95	27.79
182	2jsa-11	PHE_A_31_CA	PHE_A_31_HA	-3.435	-2.556	-4.056	-3.624	-1.534	-4.383	1.09	107.46	100.48
183	2jsa-11	PHE_A_31_CA	PHE_A_31_C	-3.435	-2.556	-4.056	-2.665	-3.309	-5.143	1.53	135.27	-44.36
184	2jsa-11	PHE_A_31_C	PHE_A_31_O	-2.665	-3.309	-5.143	-2.223	-2.713	-6.123	1.23	142.87	53.44
185	2jsa-11	PHE_A_31_C	ASP_A_32_N	-2.665	-3.309	-5.143	-2.528	-4.611	-4.931	1.33	80.80	-83.99
186	2jsa-11	ASP_A_32_N	ASP_A_32_H	-2.528	-4.611	-4.931	-2.917	-5.035	-4.101	1.01	34.73	-132.53
187	2jsa-11	ASP_A_32_N	ASP_A_32_CA	-2.528	-4.611	-4.931	-1.819	-5.452	-5.88	1.45	130.79	-49.87
188	2jsa-11	ASP_A_32_CA	ASP_A_32_HA	-1.819	-5.452	-5.88	-0.772	-5.147	-5.914	1.09	91.79	16.24
189	2jsa-11	ASP_A_32_CA	ASP_A_32_C	-1.819	-5.452	-5.88	-2.451	-5.297	-7.265	1.53	154.83	166.22
190	2jsa-11	ASP_A_32_C	ASP_A_32_O	-2.451	-5.297	-7.265	-1.792	-5.517	-8.28	1.23	145.61	-18.46
191	2jsa-11	ASP_A_32_C	ALA_A_33_N	-2.451	-5.297	-7.265	-3.721	-4.92	-7.262	1.32	89.87	163.47
192	2jsa-11	ALA_A_33_N	ALA_A_33_H	-3.721	-4.92	-7.262	-4.201	-4.758	-6.388	1.01	30.10	161.35
193	2jsa-11	ALA_A_33_N	ALA_A_33_CA	-3.721	-4.92	-7.262	-4.449	-4.733	-8.505	1.45	148.84	165.59
194	2jsa-11	ALA_A_33_CA	ALA_A_33_HA	-4.449	-4.733	-8.505	-4.304	-5.613	-9.132	1.09	125.11	-80.64
195	2jsa-11	ALA_A_33_CA	ALA_A_33_C	-4.449	-4.733	-8.505	-3.887	-3.515	-9.242	1.53	118.79	65.23
196	2jsa-11	ALA_A_33_C	ALA_A_33_O	-3.887	-3.515	-9.242	-3.169	-3.66	-10.23	1.23	143.45	-11.42
197	2jsa-11	ALA_A_33_C	GLU_A_34_N	-3.887	-3.515	-9.242	-4.234	-2.342	-8.732	1.33	67.37	106.48
198	2jsa-11	GLU_A_34_N	GLU_A_34_H	-4.234	-2.342	-8.732	-4.826	-2.298	-7.915	1.01	36.00	175.75
199	2jsa-11	GLU_A_34_N	GLU_A_34_CA	-4.234	-2.342	-8.732	-3.774	-1.101	-9.329	1.45	114.28	69.66
200	2jsa-11	GLU_A_34_CA	GLU_A_34_HA	-3.774	-1.101	-9.329	-4.252	-0.997	-10.303	1.09	153.33	167.73
201	2jsa-11	GLU_A_34_CA	GLU_A_34_C	-3.774	-1.101	-9.329	-2.259	-1.144	-9.54	1.53	97.93	-1.63
202	2jsa-11	GLU_A_34_C	GLU_A_34_O	-2.259	-1.144	-9.54	-1.736	-0.493	-10.443	1.23	137.24	51.22
203	2jsa-11	GLU_A_34_C	CYS_A_35_N	-2.259	-1.144	-9.54	-1.597	-1.916	-8.693	1.32	50.21	-49.39
204	2jsa-11	CYS_A_35_N	CYS_A_35_H	-1.597	-1.916	-8.693	-2.092	-2.424	-7.974	1.01	44.61	-134.26
205	2jsa-11	CYS_A_35_N	CYS_A_35_CA	-1.597	-1.916	-8.693	-0.152	-2.052	-8.775	1.45	93.23	-5.38
206	2jsa-11	CYS_A_35_CA	CYS_A_35_HA	-0.152	-2.052	-8.775	0.278	-1.063	-8.936	1.09	98.49	66.50
207	2jsa-11	CYS_A_35_CA	CYS_A_35_C	-0.152	-2.052	-8.775	0.179	-2.929	-9.984	1.53	142.21	-69.32
208	2jsa-11	CYS_A_35_C	CYS_A_35_O	0.179	-2.929	-9.984	1.161	-2.684	-10.682	1.23	124.59	14.01
209	2jsa-11	CYS_A_35_C	LYS_A_36_N	0.179	-2.929	-9.984	-0.659	-3.933	-10.193	1.32	99.08	-129.85
210	2jsa-11	LYS_A_36_N	LYS_A_36_H	-0.659	-3.933	-10.193	-1.446	-4.075	-9.577	1.01	52.39	-169.77
211	2jsa-11	LYS_A_36_N	LYS_A_36_CA	-0.659	-3.933	-10.193	-0.467	-4.848	-11.306	1.45	139.97	-78.15
212	2jsa-11	LYS_A_36_CA	LYS_A_36_HA	-0.467	-4.848	-11.306	0.599	-5.061	-11.388	1.09	94.31	-11.30
213	2jsa-11	LYS_A_36_CA	LYS_A_36_C	-0.467	-4.848	-11.306	-0.907	-4.166	-12.604	1.53	147.98	122.83
214	2jsa-11	LYS_A_36_C	LYS_A_36_O	-0.907	-4.166	-12.604	-0.818	-4.754	-13.68	1.23	151.07	-81.39
215	2jsa-11	LYS_A_36_C	LYS_A_37_N	-0.907	-4.166	-12.604	-1.372	-2.934	-12.459	1.32	83.72	110.68
216	2jsa-11	LYS_A_37_N	LYS_A_37_H	-1.372	-2.934	-12.459	-1.417	-2.513	-11.542	1.01	24.78	96.10
217	2jsa-11	LYS_A_37_N	LYS_A_37_CA	-1.372	-2.934	-12.459	-1.824	-2.164	-13.605	1.45	142.08	120.41
218	2jsa-11	LYS_A_37_CA	LYS_A_37_HA	-1.824	-2.164	-13.605	-1.717	-2.787	-14.493	1.09	144.55	-80.25
219	2jsa-11	LYS_A_37_CA	LYS_A_37_C	-1.824	-2.164	-13.605	-0.921	-0.943	-13.784	1.53	96.72	53.51
220	2jsa-11	LYS_A_37_C	LYS_A_37_O	-0.921	-0.943	-13.784	-0.433	-0.682	-14.883	1.23	153.27	28.14
221	2jsa-11	LYS_A_37_C	LEU_A_38_N	-0.921	-0.943	-13.784	-0.726	-0.225	-12.687	1.33	34.15	74.81
222	2jsa-11	LEU_A_38_N	LEU_A_38_H	-0.726	-0.225	-12.687	-1.159	-0.498	-11.816	1.01	30.44	-147.77
223	2jsa-11	LEU_A_38_N	LEU_A_38_CA	-0.726	-0.225	-12.687	0.11	0.963	-12.709	1.45	90.87	54.87
224	2jsa-11	LEU_A_38_CA	LEU_A_38_HA	0.11	0.963	-12.709	-0.046	1.469	-13.662	1.09	150.94	107.13
225	2jsa-11	LEU_A_38_CA	LEU_A_38_C	0.11	0.963	-12.709	1.581	0.547	-12.64	1.53	87.42	-15.79
226	2jsa-11	LEU_A_38_C	LEU_A_38_O	1.581	0.547	-12.64	2.4	1.017	-13.428	1.23	129.84	29.85
227	2jsa-11	LEU_A_38_C	PHE_A_39_N	1.581	0.547	-12.64	1.871	-0.329	-11.69	1.32	44.17	-71.68
228	2jsa-11	PHE_A_39_N	PHE_A_39_H	1.871	-0.329	-11.69	1.146	-0.673	-11.077	1.01	52.62	-154.62
229	2jsa-11	PHE_A_39_N	PHE_A_39_CA	1.871	-0.329	-11.69	3.229	-0.813	-11.507	1.45	82.77	-19.62
230	2jsa-11	PHE_A_39_CA	PHE_A_39_HA	3.229	-0.813	-11.507	3.933	0.013	-11.605	1.09	95.16	49.56
231	2jsa-11	PHE_A_39_CA	PHE_A_39_C	3.229	-0.813	-11.507	3.565	-1.901	-12.53	1.53	131.94	-72.84
232	2jsa-11	PHE_A_39_C	PHE_A_39_O	3.565	-1.901	-12.53	4.623	-2.524	-12.453	1.23	86.41	-30.49
233	2jsa-11	PHE_A_39_C	HIS_A_40_N	3.565	-1.901	-12.53	2.645	-2.095	-13.464	1.33	134.81	-168.09
234	2jsa-11	HIS_A_40_N	HIS_A_40_H	2.645	-2.095	-13.464	1.798	-1.546	-13.465	1.01	90.06	147.05
235	2jsa-11	HIS_A_40_N	HIS_A_40_CA	2.645	-2.095	-13.464	2.832	-3.096	-14.501	1.45	135.52	-79.42
236	2jsa-11	HIS_A_40_CA	HIS_A_40_HA	2.832	-3.096	-14.501	2.967	-4.062	-14.015	1.09	63.51	-82.04
237	2jsa-11	HIS_A_40_CA	HIS_A_40_C	2.832	-3.096	-14.501	4.105	-2.787	-15.291	1.53	121.09	13.64
238	2jsa-11	HIS_A_40_C	HIS_A_40_O	4.105	-2.787	-15.291	4.97	-3.647	-15.442	1.23	97.06	-44.83
239	2jsa-11	HIS_A_40_C	THR_A_41_N	4.105	-2.787	-15.291	4.178	-1.555	-15.774	1.33	111.37	86.61
240	2jsa-11	THR_A_41_N	THR_A_41_H	4.178	-1.555	-15.774	3.428	-0.898	-15.61	1.01	80.66	138.78
241	2jsa-11	THR_A_41_N	THR_A_41_CA	4.178	-1.555	-15.774	5.331	-1.122	-16.545	1.45	122.05	20.58
242	2jsa-11	THR_A_41_CA	THR_A_41_HA	5.331	-1.122	-16.545	5.387	-1.716	-17.457	1.09	146.81	-84.61
243	2jsa-11	THR_A_41_CA	THR_A_41_C	5.331	-1.122	-16.545	6.619	-1.353	-15.753	1.53	58.82	-10.17
244	2jsa-11	THR_A_41_C	THR_A_41_O	6.619	-1.353	-15.753	7.707	-1.389	-16.327	1.23	117.80	-1.90
245	2jsa-11	THR_A_41_C	ILE_A_42_N	6.619	-1.353	-15.753	6.455	-1.505	-14.448	1.32	9.72	-137.17
246	2jsa-11	ILE_A_42_N	ILE_A_42_H	6.455	-1.505	-14.448	5.531	-1.465	-14.044	1.01	66.40	177.52
247	2jsa-11	ILE_A_42_N	ILE_A_42_CA	6.455	-1.505	-14.448	7.591	-1.732	-13.572	1.45	52.90	-11.30
248	2jsa-11	ILE_A_42_CA	ILE_A_42_HA	7.591	-1.732	-13.572	8.423	-1.127	-13.934	1.09		

252	2jsa-11	PRO_A_43_N	PRO_A_43_CA	9.355	-3.416	-13.644	9.897	-4.762	-13.721	1.45	93.04	-68.07
253	2jsa-11	PRO_A_43_CA	PRO_A_43_HA	9.897	-4.762	-13.721	9.383	-5.328	-14.497	1.09	135.43	-132.24
254	2jsa-11	PRO_A_43_CA	PRO_A_43_C	9.897	-4.762	-13.721	9.728	-5.498	-12.39	1.53	29.57	-102.93
255	2jsa-11	PRO_A_43_C	PRO_A_43_O	9.728	-5.498	-12.39	8.984	-6.473	-12.306	1.23	86.08	-127.35
256	2jsa-11	PRO_A_43_C	PHE_A_44_N	9.728	-5.498	-12.39	10.433	-5.003	-11.383	1.33	40.54	35.07
257	2jsa-11	PHE_A_44_N	PHE_A_44_H	10.433	-5.003	-11.383	11.026	-4.198	-11.525	1.01	98.08	53.62
258	2jsa-11	PHE_A_44_N	PHE_A_44_CA	10.433	-5.003	-11.383	10.371	-5.601	-10.061	1.45	24.45	-95.92
259	2jsa-11	PHE_A_44_CA	PHE_A_44_HA	10.371	-5.601	-10.061	10.272	-6.683	-10.149	1.09	94.63	-95.23
260	2jsa-11	PHE_A_44_CA	PHE_A_44_C	10.371	-5.601	-10.061	9.194	-5.039	-9.259	1.53	58.41	154.48
261	2jsa-11	PHE_A_44_C	PHE_A_44_O	9.194	-5.039	-9.259	9.041	-5.345	-8.077	1.23	16.14	-116.57
262	2jsa-11	PHE_A_44_C	GLY_A_45_N	9.194	-5.039	-9.259	8.394	-4.228	-9.934	1.32	120.65	134.61
263	2jsa-11	GLY_A_45_N	GLY_A_45_H	8.394	-4.228	-9.934	8.582	-4.02	-10.904	1.01	163.88	47.89
264	2jsa-11	GLY_A_45_N	GLY_A_45_CA	8.394	-4.228	-9.934	7.236	-3.621	-9.3	1.45	64.13	152.34
265	2jsa-11	GLY_A_45_CA	GLY_A_45_C	7.236	-3.621	-9.3	6.273	-4.689	-8.779	1.53	70.08	-132.04
266	2jsa-11	GLY_A_45_C	GLY_A_45_O	6.273	-4.689	-8.779	6.22	-4.951	-7.578	1.23	12.55	-101.44
267	2jsa-11	GLY_A_45_C	THR_A_46_N	6.273	-4.689	-8.779	5.534	-5.278	-9.709	1.33	134.54	-141.44
268	2jsa-11	THR_A_46_N	THR_A_46_H	5.534	-5.278	-9.709	5.63	-5.012	-10.679	1.01	163.75	70.16
269	2jsa-11	THR_A_46_N	THR_A_46_CA	5.534	-5.278	-9.709	4.576	-6.313	-9.359	1.45	76.06	-132.79
270	2jsa-11	THR_A_46_CA	THR_A_46_HA	4.576	-6.313	-9.359	3.674	-5.838	-8.974	1.09	69.31	152.23
271	2jsa-11	THR_A_46_CA	THR_A_46_C	4.576	-6.313	-9.359	5.141	-7.213	-8.258	1.53	43.98	-57.88
272	2jsa-11	THR_A_46_C	THR_A_46_O	5.141	-7.213	-8.258	4.4	-7.693	-7.402	1.23	45.89	-147.07
273	2jsa-11	THR_A_46_C	ARG_A_47_N	5.141	-7.213	-8.258	6.449	-7.417	-8.318	1.33	92.60	-8.86
274	2jsa-11	ARG_A_47_N	ARG_A_47_H	6.449	-7.417	-8.318	6.997	-6.992	-9.052	1.01	136.63	37.80
275	2jsa-11	ARG_A_47_N	ARG_A_47_CA	6.449	-7.417	-8.318	7.122	-8.251	-7.338	1.45	47.56	-51.10
276	2jsa-11	ARG_A_47_CA	ARG_A_47_HA	7.122	-8.251	-7.338	6.62	-9.218	-7.307	1.09	88.37	-117.44
277	2jsa-11	ARG_A_47_CA	ARG_A_47_C	7.122	-8.251	-7.338	7.049	-7.607	-5.953	1.53	25.08	96.47
278	2jsa-11	ARG_A_47_C	ARG_A_47_O	7.049	-7.607	-5.953	6.663	-8.256	-4.981	1.23	37.84	-120.74
279	2jsa-11	ARG_A_47_C	GLU_A_48_N	7.049	-7.607	-5.953	7.425	-6.337	-5.904	1.33	87.88	73.51
280	2jsa-11	GLU_A_48_N	GLU_A_48_H	7.425	-6.337	-5.904	7.731	-5.865	-6.743	1.01	146.16	57.04
281	2jsa-11	GLU_A_48_N	GLU_A_48_CA	7.425	-6.337	-5.904	7.406	-5.598	-4.654	1.45	30.60	91.47
282	2jsa-11	GLU_A_48_CA	GLU_A_48_HA	7.406	-5.598	-4.654	7.914	-6.199	-3.899	1.09	46.19	-49.79
283	2jsa-11	GLU_A_48_CA	GLU_A_48_C	7.406	-5.598	-4.654	5.965	-5.367	-4.195	1.53	72.54	170.89
284	2jsa-11	GLU_A_48_C	GLU_A_48_O	5.965	-5.367	-4.195	5.707	-5.21	-3.002	1.23	14.21	148.68
285	2jsa-11	GLU_A_48_C	CYS_A_49_N	5.965	-5.367	-4.195	5.064	-5.353	-5.166	1.32	137.14	179.11
286	2jsa-11	CYS_A_49_N	CYS_A_49_H	5.064	-5.353	-5.166	5.348	-5.49	-6.125	1.01	161.80	-25.75
287	2jsa-11	CYS_A_49_N	CYS_A_49_CA	5.064	-5.353	-5.166	3.656	-5.143	-4.877	1.45	78.52	171.52
288	2jsa-11	CYS_A_49_CA	CYS_A_49_HA	3.656	-5.143	-4.877	3.537	-4.141	-4.463	1.09	67.69	96.77
289	2jsa-11	CYS_A_49_CA	CYS_A_49_C	3.656	-5.143	-4.877	3.226	-6.162	-3.819	1.53	46.27	-112.88
290	2jsa-11	CYS_A_49_C	CYS_A_49_O	3.226	-6.162	-3.819	2.946	-5.797	-2.678	1.23	21.96	127.49
291	2jsa-11	CYS_A_49_C	ASP_A_50_N	3.226	-6.162	-3.819	3.186	-7.42	-4.236	1.33	108.33	-91.82
292	2jsa-11	ASP_A_50_N	ASP_A_50_H	3.186	-7.42	-4.236	3.429	-7.648	-5.19	1.01	160.75	-43.18
293	2jsa-11	ASP_A_50_N	ASP_A_50_CA	3.186	-7.42	-4.236	2.795	-8.493	-3.339	1.45	51.85	-110.02
294	2jsa-11	ASP_A_50_CA	ASP_A_50_HA	2.795	-8.493	-3.339	1.756	-8.348	-3.043	1.09	74.24	172.06
295	2jsa-11	ASP_A_50_CA	ASP_A_50_C	2.795	-8.493	-3.339	3.696	-8.473	-2.102	1.53	36.08	1.27
296	2jsa-11	ASP_A_50_C	ASP_A_50_O	3.696	-8.473	-2.102	3.307	-8.951	-1.038	1.23	30.08	-129.14
297	2jsa-11	ASP_A_50_C	HIS_A_51_N	3.696	-8.473	-2.102	4.883	-7.914	-2.285	1.32	97.94	25.22
298	2jsa-11	HIS_A_51_N	HIS_A_51_H	4.883	-7.914	-2.285	5.137	-7.541	-3.189	1.01	153.47	55.75
299	2jsa-11	HIS_A_51_N	HIS_A_51_CA	4.883	-7.914	-2.285	5.843	-7.825	-1.197	1.45	41.55	5.30
300	2jsa-11	HIS_A_51_CA	HIS_A_51_HA	5.843	-7.825	-1.197	5.729	-7.825	-0.574	1.09	55.14	-97.32
301	2jsa-11	HIS_A_51_CA	HIS_A_51_C	5.843	-7.825	-1.197	5.528	-6.603	-0.334	1.53	55.63	104.45
302	2jsa-11	HIS_A_51_C	HIS_A_51_O	5.528	-6.603	-0.334	6.231	-6.327	0.637	1.23	37.88	21.44
303	2jsa-11	HIS_A_51_C	TYR_A_52_N	5.528	-6.603	-0.334	4.472	-5.902	-0.719	1.32	106.90	146.42
304	2jsa-11	TYR_A_52_N	TYR_A_52_H	4.472	-5.902	-0.719	3.941	-6.186	-1.529	1.01	143.37	-151.86
305	2jsa-11	TYR_A_52_N	TYR_A_52_CA	4.472	-5.902	-0.719	4.056	-4.715	0.008	1.45	59.97	109.31
306	2jsa-11	TYR_A_52_CA	TYR_A_52_HA	4.056	-4.715	0.008	4.806	-4.447	0.753	1.09	46.91	19.66
307	2jsa-11	TYR_A_52_CA	TYR_A_52_C	4.056	-4.715	0.008	2.703	-4.934	0.688	1.53	63.61	-170.81
308	2jsa-11	TYR_A_52_C	TYR_A_52_O	2.703	-4.934	0.688	2.546	-4.646	1.873	1.23	15.47	118.60
309	2jsa-11	TYR_A_52_C	VAL_A_53_N	2.703	-4.934	0.688	1.761	-5.442	-0.092	1.32	126.08	-151.66
310	2jsa-11	VAL_A_53_N	VAL_A_53_H	1.761	-5.442	-0.092	1.962	-5.655	-1.059	1.01	163.15	-46.66
311	2jsa-11	VAL_A_53_N	VAL_A_53_CA	1.761	-5.442	-0.092	0.426	-5.704	0.42	1.45	69.38	-168.90
312	2jsa-11	VAL_A_53_CA	VAL_A_53_HA	0.426	-5.704	0.42	-0.019	-4.756	0.722	1.09	73.91	115.15
313	2jsa-11	VAL_A_53_CA	VAL_A_53_C	0.426	-5.704	0.42	0.525	-6.596	1.658	1.53	35.94	-83.67
314	2jsa-11	VAL_A_53_C	VAL_A_53_O	0.525	-6.596	1.658	-0.413	-6.672	2.45	1.23	49.92	-175.37
315	2jsa-11	VAL_A_53_C	ASN_A_54_N	0.525	-6.596	1.658	1.671	-7.251	1.787	1.33	84.42	-29.75
316	2jsa-11	ASN_A_54_N	ASN_A_54_H	1.671	-7.251	1.787	2.4	-7.141	1.097	1.01	133.10	8.58
317	2jsa-11	ASN_A_54_N	ASN_A_54_CA	1.671	-7.251	1.787	1.904	-8.135	2.915	1.45	39.02	-75.23
318	2jsa-11	ASN_A_54_CA	ASN_A_54_HA	1.904	-8.135	2.915	1.174	-7.919	3.695	1.09	44.30	163.52
319	2jsa-11	ASN_A_54_CA	ASN_A_54_C	1.904	-8.135	2.915	3.319	-7.907	3.451	1.53	69.50	9.15
320	2jsa-11	ASN_A_54_C	ASN_A_54_O	3.319	-7.907	3.451	4.201	-8.742	3.261	1.23	98.89	-43.43
321	2jsa-11	ASN_A_54_C	SER_A_55_N	3.319	-7.907	3.451	3.49	-6.772	4.113	1.33	60.03	81.43
322	2jsa-11	SER_A_55_N	SER_A_55_H	3.49	-6.772	4.113	2.718	-6.132	4.234	1.01	83.12	140.34
323	2jsa-11	SER_A_55_N	SER_A_55_CA	3.49	-6.772	4.113	4.783	-6.423	4.678	1.45	67.13	15.11
324	2jsa-11	SER_A_55_CA	SER_A_55_HA	4.783	-6.423	4.678	4.937	-7.022	5.575	1.09	34.59	-75.58
325	2jsa-11	SER_A_55_CA	SER_A_55_C	4.783	-6.423	4.678	4.802	-4.944	5.068	1.53	75.23	89.26
326	2jsa-11	SER_A_55_C	SER_A_55_O	4.802	-4.944	5.068	5.505	-4.553	5.999	1.23	40.83	29.08
327	2jsa-11	SER_A_55_C	LYS_A_56_N	4.802	-4.944	5.068	4.021	-4.162	4.337	1.33	123.48	134.96
328	2jsa-11	LYS_A_56_N	LYS_A_56_H	4.021	-4.162	4.337	3.47	-4.553	3.587	1.01	137.99	-144.64
329	2jsa-11	LYS_A_56_N	LYS_A_56_CA	4.021	-4.162	4.337	3.939	-2.735	4.594	1.45	79.81	93.29
330	2jsa-11	LYS_A_56_CA	LYS_A_56_HA	3.939	-2.735	4.594	4.364	-2.545	5.58	1.09	25.27	24.09
331	2jsa-11	LYS_A_56_CA	LYS_A_56_C	3.939	-2.735	4.594	2.47	-2.311	4.632	1.53	88.58	163.90
332	2jsa-11	LYS_A_56_C	LYS_A_56_O	2.47	-2.311	4.632	2.164	-1.119	4.661	1.23	88.65	104.40
333	2jsa-11	LYS_A_56_C	VAL_A_57_N	2.47	-2.311	4.632	1.599	-3.309	4.629	1.32	90.13	-131.11
334	2jsa-11	VAL_A_57_N	VAL_A_57_H	1.599	-3.309	4.629	1.922	-4.265	4.603	1.01	91.48	-71.33
335	2jsa-11	VAL_A_57_N	VAL_A_57_CA	1.599	-3.309	4.629	0.169	-3.055	4.663	1.45	88.66	169.93
336	2jsa-11	VAL_A_57_CA	VAL_A_57_HA	0.169	-3.055	4.663	-0.006	-2.03	4.338	1.09	107.36	99.69
337	2jsa-11	VAL_A_57_HA	VAL_A_57_C	0.169	-3.055	4.663	-0.335	-3.189	6.101	1.53	19.93	-165.11
338	2jsa-11	VAL_A_57_C	VAL_A_57_O	-0.335	-3.189	6.101	-1.035	-2.31	6.602	1.23	65.97	128.53
339	2jsa-11	VAL_A_57_C	ASP_A_58_N	-0.335	-3.189	6.101	0.041	-4.294	6.726	1.32	61.83	-71.21
340	2jsa-11	ASP_A_58_N	ASP_A_58_H	0.041	-4.294	6.726	0.618	-4.975	6.252	1.01	117.97	-49.73
341	2jsa-11	ASP_A_58_N	ASP_A_58_CA	0.041	-4.294	6.726	-0.363	-4.554	8.098	1.45	19.30	-147.24
342	2jsa-11	ASP_A_58_CA	ASP_A_58_HA	-0.363								

345	2jsa-11	ASP_A_58_C	PRO_A_59_N	-0.066	-3.323	8.954	1.144	-2.744	8.728	1.36	99.56	25.57
346	2jsa-11	PRO_A_59_N	PRO_A_59_CA	1.144	-2.744	8.728	1.559	-1.566	9.471	1.45	59.25	70.59
347	2jsa-11	PRO_A_59_CA	PRO_A_59_HA	1.559	-1.566	9.471	1.337	-1.695	10.53	1.09	13.63	-149.84
348	2jsa-11	PRO_A_59_C	PRO_A_59_O	1.559	-1.566	9.471	0.83	-0.317	8.971	1.53	109.07	120.27
349	2jsa-11	PRO_A_59_C	PRO_A_59_O	0.83	-0.317	8.971	0.175	0.376	9.747	1.23	50.86	133.39
350	2jsa-11	PRO_A_59_C	ILE_A_60_N	0.83	-0.317	8.971	0.97	-0.067	7.677	1.33	167.51	60.75
351	2jsa-11	ILE_A_60_N	ILE_A_60_H	0.97	-0.067	7.677	1.525	-0.681	7.097	1.01	125.02	-47.89
352	2jsa-11	ILE_A_60_N	ILE_A_60_CA	0.97	-0.067	7.677	0.333	1.086	7.065	1.45	114.92	118.92
353	2jsa-11	ILE_A_60_CA	ILE_A_60_HA	0.333	1.086	7.065	0.851	1.981	7.411	1.09	71.50	59.94
354	2jsa-11	ILE_A_60_CA	ILE_A_60_C	0.333	1.086	7.065	-1.118	1.174	7.541	1.53	71.87	176.53
355	2jsa-11	ILE_A_60_C	ILE_A_60_O	-1.118	1.174	7.541	-1.52	2.171	8.14	1.23	60.87	111.96
356	2jsa-11	ILE_A_60_C	ILE_A_61_N	-1.118	1.174	7.541	-1.867	0.118	7.257	1.33	102.37	-125.35
357	2jsa-11	ILE_A_61_N	ILE_A_61_H	-1.867	0.118	7.257	-1.471	-0.668	6.761	1.01	119.40	-63.26
358	2jsa-11	ILE_A_61_N	ILE_A_61_CA	-1.867	0.118	7.257	-3.264	0.064	7.651	1.45	74.26	-177.79
359	2jsa-11	ILE_A_61_CA	ILE_A_61_HA	-3.264	0.064	7.651	-3.774	0.916	7.202	1.09	114.33	120.90
360	2jsa-11	ILE_A_61_C	ILE_A_61_O	-3.264	0.064	7.651	-3.369	0.209	9.17	1.53	6.72	125.91
361	2jsa-11	ILE_A_61_C	ILE_A_61_O	-3.369	0.209	9.17	-4.425	0.565	9.691	1.23	64.94	161.37
362	2jsa-11	ILE_A_61_C	HIS_A_62_N	-3.369	0.209	9.17	-2.26	-0.074	9.837	1.32	59.77	-14.32
363	2jsa-11	HIS_A_62_N	HIS_A_62_H	-2.26	-0.074	9.837	-1.427	-0.361	9.342	1.01	119.33	-19.01
364	2jsa-11	HIS_A_62_N	HIS_A_62_CA	-2.26	-0.074	9.837	-2.214	0.02	11.286	1.45	4.13	63.92
365	2jsa-11	HIS_A_62_CA	HIS_A_62_HA	-2.214	0.02	11.286	-3.051	-0.551	11.687	1.09	68.41	-145.70
366	2jsa-11	HIS_A_62_CA	HIS_A_62_C	-2.214	0.02	11.286	-2.393	1.48	11.711	1.53	73.88	96.99
367	2jsa-11	HIS_A_62_C	HIS_A_62_O	-2.393	1.48	11.711	-2.905	1.756	12.795	1.23	28.22	151.67
368	2jsa-11	HIS_A_62_C	GLU_A_63_N	-2.393	1.48	11.711	-1.96	2.375	10.836	1.32	131.35	64.18
369	2jsa-11	GLU_A_63_N	GLU_A_63_H	-1.96	2.375	10.836	-1.548	2.075	9.964	1.01	149.70	-36.06
370	2jsa-11	GLU_A_63_N	GLU_A_63_CA	-1.96	2.375	10.836	-2.066	3.798	11.106	1.45	79.29	94.26
371	2jsa-11	GLU_A_63_CA	GLU_A_63_HA	-2.066	3.798	11.106	-1.905	3.951	12.173	1.09	11.76	43.54
372	2jsa-11	GLU_A_63_CA	GLU_A_63_C	-2.066	3.798	11.106	-3.467	4.304	10.753	1.53	103.33	160.14
373	2jsa-11	GLU_A_63_C	GLU_A_63_O	-3.467	4.304	10.753	-4.174	4.832	11.609	1.23	45.87	143.25
374	2jsa-11	GLU_A_63_C	LEU_A_64_N	-3.467	4.304	10.753	-3.825	4.123	9.491	1.32	162.37	-153.18
375	2jsa-11	LEU_A_64_N	LEU_A_64_H	-3.825	4.123	9.491	-3.191	3.681	8.841	1.01	130.06	-34.88
376	2jsa-11	LEU_A_64_N	LEU_A_64_CA	-3.825	4.123	9.491	-5.128	4.553	9.014	1.45	109.17	161.74
377	2jsa-11	LEU_A_64_CA	LEU_A_64_HA	-5.128	4.553	9.014	-5.164	5.641	9.067	1.09	87.21	91.90
378	2jsa-11	LEU_A_64_CA	LEU_A_64_C	-5.128	4.553	9.014	-6.213	4.007	9.944	1.53	52.56	-153.29
379	2jsa-11	LEU_A_64_C	LEU_A_64_O	-6.213	4.007	9.944	-7.136	4.729	10.319	1.23	72.25	141.97
380	2jsa-11	LEU_A_64_C	GLU_A_65_N	-6.213	4.007	9.944	-6.067	2.737	10.289	1.32	74.90	-83.44
381	2jsa-11	GLU_A_65_N	GLU_A_65_H	-6.067	2.737	10.289	-5.283	2.203	9.942	1.01	110.09	-34.26
382	2jsa-11	GLU_A_65_N	GLU_A_65_CA	-6.067	2.737	10.289	-7.022	2.086	11.169	1.45	52.71	-145.72
383	2jsa-11	GLU_A_65_CA	GLU_A_65_HA	-7.022	2.086	11.169	-8.019	2.241	10.758	1.09	112.16	171.16
384	2jsa-11	GLU_A_65_CA	GLU_A_65_C	-7.022	2.086	11.169	-6.975	2.714	12.563	1.53	24.31	85.72
385	2jsa-11	GLU_A_65_C	GLU_A_65_O	-6.975	2.714	12.563	-7.989	2.772	13.257	1.23	55.66	176.73
386	2jsa-11	GLU_A_65_C	GLY_A_66_N	-6.975	2.714	12.563	-5.786	3.168	12.932	1.33	73.83	20.90
387	2jsa-11	GLY_A_66_N	GLY_A_66_H	-5.786	3.168	12.932	-4.994	3.086	12.31	1.01	128.00	-5.91
388	2jsa-11	GLY_A_66_N	GLY_A_66_CA	-5.786	3.168	12.932	-5.593	3.791	14.232	1.45	26.64	72.79
389	2jsa-11	GLY_A_66_CA	GLY_A_66_C	-5.593	3.791	14.232	-6.264	5.164	14.287	1.53	87.94	116.05
390	2jsa-11	GLY_A_66_C	GLY_A_66_O	-6.264	5.164	14.287	-6.837	5.538	15.308	1.23	33.83	146.87
391	2jsa-11	GLY_A_66_C	GLY_A_67_N	-6.264	5.164	14.287	-6.171	5.878	13.175	1.32	147.08	82.58
392	2jsa-11	GLY_A_67_N	GLY_A_67_H	-6.171	5.878	13.175	-5.684	5.507	12.372	1.01	142.68	-37.30
393	2jsa-11	GLY_A_67_N	GLY_A_67_CA	-6.171	5.878	13.175	-6.762	7.203	13.083	1.45	93.63	114.04
394	2jsa-11	GLY_A_67_CA	GLY_A_67_C	-6.762	7.203	13.083	-5.909	8.125	12.211	1.53	124.77	47.23
395	2jsa-11	GLY_A_67_C	GLY_A_67_O	-5.909	8.125	12.211	-6.366	9.187	11.791	1.23	109.96	113.28
396	2jsa-11	GLY_A_67_C	THR_A_68_N	-5.909	8.125	12.211	-4.683	7.686	11.963	1.33	100.78	-19.70
397	2jsa-11	THR_A_68_N	THR_A_68_H	-4.683	7.686	11.963	-4.373	6.802	12.341	1.01	68.03	-70.68
398	2jsa-11	THR_A_68_N	THR_A_68_CA	-4.683	7.686	11.963	-3.762	8.459	11.148	1.45	124.13	40.01
399	2jsa-11	THR_A_68_CA	THR_A_68_HA	-3.762	8.459	11.148	-3.65	9.449	11.59	1.09	66.08	83.55
400	2jsa-11	THR_A_68_CA	THR_A_68_C	-3.762	8.459	11.148	-4.319	8.634	9.734	1.53	157.56	162.56
401	2jsa-11	THR_A_68_C	THR_A_68_O	-4.319	8.634	9.734	-5.113	7.817	9.27	1.23	112.16	-134.18
402	2jsa-11	THR_A_68_C	ALA_A_69_N	-4.319	8.634	9.734	-3.879	9.704	9.087	1.33	119.22	67.65
403	2jsa-11	ALA_A_69_N	ALA_A_69_H	-3.879	9.704	9.087	-3.225	10.334	9.53	1.01	64.00	43.93
404	2jsa-11	ALA_A_69_N	ALA_A_69_CA	-3.879	9.704	9.087	-4.324	9.996	7.735	1.45	158.51	146.73
405	2jsa-11	ALA_A_69_CA	ALA_A_69_HA	-4.324	9.996	7.735	-5.38	9.74	7.651	1.09	94.42	-166.37
406	2jsa-11	ALA_A_69_CA	ALA_A_69_C	-4.324	9.996	7.735	-3.536	9.133	6.746	1.53	130.24	-47.60
407	2jsa-11	ALA_A_69_C	ALA_A_69_O	-3.536	9.133	6.746	-2.554	8.494	7.12	1.23	72.30	-33.05
408	2jsa-11	ALA_A_69_C	PRO_A_70_N	-3.536	9.133	6.746	-4.009	9.143	5.471	1.36	159.64	178.79
409	2jsa-11	PRO_A_70_N	PRO_A_70_CA	-4.009	9.143	5.471	-3.361	8.37	4.426	1.45	136.01	-50.03
410	2jsa-11	PRO_A_70_CA	PRO_A_70_HA	-3.361	8.37	4.426	-3.133	7.368	4.79	1.09	70.49	-77.18
411	2jsa-11	PRO_A_70_CA	PRO_A_70_C	-3.361	8.37	4.426	-2.054	9.033	3.983	1.53	106.82	26.90
412	2jsa-11	PRO_A_70_C	PRO_A_70_O	-2.054	9.033	3.983	-1.228	8.407	3.322	1.23	122.53	-37.16
413	2jsa-11	PRO_A_70_C	LYS_A_71_N	-2.054	9.033	3.983	-1.909	10.294	4.367	1.33	73.17	83.44
414	2jsa-11	LYS_A_71_N	LYS_A_71_H	-1.909	10.294	4.367	-2.63	10.747	4.911	1.01	57.43	147.86
415	2jsa-11	LYS_A_71_N	LYS_A_71_CA	-1.909	10.294	4.367	-0.719	11.049	4.018	1.45	103.91	32.39
416	2jsa-11	LYS_A_71_CA	LYS_A_71_HA	-0.719	11.049	4.018	-0.13	10.449	3.324	1.09	129.54	-45.53
417	2jsa-11	LYS_A_71_CA	LYS_A_71_C	-0.719	11.049	4.018	0.126	11.271	5.274	1.53	34.82	14.72
418	2jsa-11	LYS_A_71_C	LYS_A_71_O	0.126	11.271	5.274	1.035	12.1	5.277	1.23	89.86	42.36
419	2jsa-11	LYS_A_71_C	ASP_A_72_N	0.126	11.271	5.274	-0.204	10.514	6.311	1.33	38.53	-113.55
420	2jsa-11	ASP_A_72_N	ASP_A_72_H	-0.204	10.514	6.311	-0.964	9.853	6.238	1.01	94.15	-138.99
421	2jsa-11	ASP_A_72_N	ASP_A_72_CA	-0.204	10.514	6.311	0.514	10.617	7.57	1.45	29.95	8.16
422	2jsa-11	ASP_A_72_CA	ASP_A_72_HA	0.514	10.617	7.57	1.346	11.312	7.45	1.09	96.32	39.87
423	2jsa-11	ASP_A_72_CA	ASP_A_72_C	0.514	10.617	7.57	1.042	9.237	7.966	1.53	75.00	-69.06
424	2jsa-11	ASP_A_72_C	ASP_A_72_O	1.042	9.237	7.966	1.689	9.089	9.0	1.23	32.70	-12.88
425	2jsa-11	ASP_A_72_C	VAL_A_73_N	1.042	9.237	7.966	0.745	8.26	7.121	1.33	129.61	-106.91
426	2jsa-11	VAL_A_73_N	VAL_A_73_H	0.745	8.26	7.121	0.207	8.454	6.289	1.01	145.50	160.17
427	2jsa-11	VAL_A_73_N	VAL_A_73_CA	0.745	8.26	7.121	1.182	6.897	7.368	1.45	80.21	-72.22
428	2jsa-11	VAL_A_73_CA	VAL_A_73_HA	1.182	6.897	7.368	1.276	6.756	8.445	1.09	8.94	-56.31
429	2jsa-11	VAL_A_73_CA	VAL_A_73_C	1.182	6.897	7.368	2.561	6.686	6.741	1.53	114.20	-8.70
430	2jsa-11	VAL_A_73_C	VAL_A_73_O	2.561	6.686	6.741	3.414	6.012	7.317	1.23	62.08	-38.31
431	2jsa-11	VAL_A_73_C	CYS_A_74_N	2.561	6.686	6.741	2.737	7.273	5.566	1.33	152.46	73.31
432	2jsa-11	CYS_A_74_N	CYS_A_74_H	2.737	7.273	5.566	1.991	7.812	5.15	1.01	114.32	144.15
433	2jsa-11	CYS_A_74_N	CYS_A_74_CA	2.737	7.273	5.566	3.998	7.158	4.853	1.45	119.38	-5.21
434	2jsa-11	CYS_A_74_CA	CYS_A_74_HA	3.998	7.158	4.853	4.305	6.112	4.866	1.09	89.32	

438	2jsa-11	THR_A_75_N	THR_A_75_H	4.582	8.706	6.605	3.598	8.687	6.831	1.01	77.07	-178.89
439	2jsa-11	THR_A_75_N	THR_A_75_CA	4.582	8.706	6.605	5.467	9.537	7.403	1.45	56.68	43.20
440	2jsa-11	THR_A_75_CA	THR_A_75_HA	5.467	9.537	7.403	6.471	9.484	6.982	1.09	112.72	-3.02
441	2jsa-11	THR_A_75_C	THR_A_75_C	5.467	9.537	7.403	5.533	9.021	8.841	1.53	19.89	-82.71
442	2jsa-11	THR_A_75_C	THR_A_75_O	5.533	9.021	8.841	6.468	9.336	9.576	1.23	53.32	18.62
443	2jsa-11	THR_A_75_C	LYS_A_76_N	5.533	9.021	8.841	4.528	8.236	9.201	1.33	74.24	-142.01
444	2jsa-11	LYS_A_76_N	LYS_A_76_H	4.528	8.236	9.201	3.792	8.019	8.545	1.01	130.53	-163.57
445	2jsa-11	LYS_A_76_N	LYS_A_76_CA	4.528	8.236	9.201	4.46	7.672	10.538	1.45	23.02	-96.87
446	2jsa-11	LYS_A_76_CA	LYS_A_76_HA	4.46	7.672	10.538	4.619	8.48	11.253	1.09	49.03	78.87
447	2jsa-11	LYS_A_76_CA	LYS_A_76_C	4.46	7.672	10.538	5.593	6.662	10.72	1.53	83.16	-41.72
448	2jsa-11	LYS_A_76_C	LYS_A_76_O	5.593	6.662	10.72	6.546	6.916	11.455	1.23	53.31	14.92
449	2jsa-11	LYS_A_76_C	LEU_A_77_N	5.593	6.662	10.72	5.452	5.534	10.037	1.33	121.00	-97.13
450	2jsa-11	LEU_A_77_N	LEU_A_77_H	5.452	5.534	10.037	4.642	5.392	9.451	1.01	125.47	-170.06
451	2jsa-11	LEU_A_77_N	LEU_A_77_CA	5.452	5.534	10.037	6.453	4.483	10.114	1.45	86.96	-46.40
452	2jsa-11	LEU_A_77_CA	LEU_A_77_HA	6.453	4.483	10.114	6.908	4.522	11.104	1.09	24.76	4.90
453	2jsa-11	LEU_A_77_C	LEU_A_77_C	6.453	4.483	10.114	7.553	4.756	9.085	1.53	132.24	13.94
454	2jsa-11	LEU_A_77_C	LEU_A_77_O	7.553	4.756	9.085	8.133	3.825	8.531	1.23	116.80	-58.08
455	2jsa-11	LEU_A_77_C	ASN_A_78_N	7.553	4.756	9.085	7.804	6.037	8.86	1.32	99.78	78.91
456	2jsa-11	ASN_A_78_N	ASN_A_78_H	7.804	6.037	8.86	7.286	6.751	9.352	1.01	60.85	125.96
457	2jsa-11	ASN_A_78_N	ASN_A_78_CA	7.804	6.037	8.86	8.823	6.444	7.909	1.45	130.92	21.77
458	2jsa-11	ASN_A_78_CA	ASN_A_78_HA	8.823	6.444	7.909	8.615	7.461	7.577	1.09	107.74	101.56
459	2jsa-11	ASN_A_78_CA	ASN_A_78_C	8.823	6.444	7.909	8.805	5.492	6.71	1.53	141.55	-91.08
460	2jsa-11	ASN_A_78_C	ASN_A_78_O	8.805	5.492	6.71	9.841	5.24	6.097	1.23	119.90	-13.67
461	2jsa-11	ASN_A_78_C	GLU_A_79_N	8.805	5.492	6.71	7.616	4.99	6.413	1.32	102.96	-157.11
462	2jsa-11	GLU_A_79_N	GLU_A_79_H	7.616	4.99	6.413	6.807	5.243	6.961	1.01	57.12	162.63
463	2jsa-11	GLU_A_79_N	GLU_A_79_CA	7.616	4.99	6.413	7.448	4.071	5.299	1.45	140.02	-100.36
464	2jsa-11	GLU_A_79_CA	GLU_A_79_HA	7.448	4.071	5.299	7.973	3.147	5.541	1.09	77.17	-60.40
465	2jsa-11	GLU_A_79_CA	GLU_A_79_C	7.448	4.071	5.299	8.069	4.659	4.03	1.53	146.02	43.44
466	2jsa-11	GLU_A_79_C	GLU_A_79_O	8.069	4.659	4.03	9.079	4.155	3.539	1.23	113.51	-26.52
467	2jsa-11	GLU_A_79_C	CYS_A_80_N	8.069	4.659	4.03	7.44	5.713	3.535	1.32	111.96	120.83
468	2jsa-11	CYS_A_80_N	CYS_A_80_H	7.44	5.713	3.535	6.615	6.073	3.992	1.01	63.08	156.43
469	2jsa-11	CYS_A_80_N	CYS_A_80_CA	7.44	5.713	3.535	7.918	6.374	2.332	1.45	145.86	54.13
470	2jsa-11	CYS_A_80_CA	CYS_A_80_HA	7.918	6.374	2.332	7.801	5.687	1.494	1.09	140.25	-99.67
471	2jsa-11	CYS_A_80_CA	CYS_A_80_C	7.918	6.374	2.332	9.407	6.676	2.51	1.53	83.32	11.47
472	2jsa-11	CYS_A_80_C	CYS_A_80_O	9.407	6.676	2.51	9.777	7.573	3.266	1.23	52.08	67.58
473	2jsa-11	CYS_A_80_C	PRO_A_81_N	9.407	6.676	2.51	10.245	5.89	1.781	1.36	122.40	-43.17
474	2jsa-11	PRO_A_81_N	PRO_A_81_CA	10.245	5.89	1.781	11.685	6.065	1.85	1.45	87.28	6.93
475	2jsa-11	PRO_A_81_CA	PRO_A_81_HA	11.685	6.065	1.85	11.998	6.176	2.888	1.09	17.74	19.53
476	2jsa-11	PRO_A_81_CA	PRO_A_81_C	11.685	6.065	1.85	12.124	7.308	1.077	1.53	120.39	70.55
477	2jsa-11	PRO_A_81_C	PRO_A_81_O	12.124	7.308	1.077	12.514	8.31	1.674	1.23	60.96	68.73
1	2jsa-12	ARG_A_1_N	ARG_A_1_H	13.725	5.005	-1.373	13.659	5.752	-2.049	1.01	132.03	95.05
2	2jsa-12	ARG_A_1_N	ARG_A_1_CA	13.725	5.005	-1.373	12.511	4.553	-0.716	1.45	63.11	-159.58
3	2jsa-12	ARG_A_1_CA	ARG_A_1_HA	12.511	4.553	-0.716	12.364	3.499	-0.953	1.09	102.56	-97.94
4	2jsa-12	ARG_A_1_CA	ARG_A_1_C	12.511	4.553	-0.716	11.306	5.35	-1.22	1.53	109.23	146.52
5	2jsa-12	ARG_A_1_C	ARG_A_1_O	11.306	5.35	-1.22	10.262	4.775	-1.527	1.23	104.44	-151.16
6	2jsa-12	ARG_A_1_C	SER_A_2_N	11.306	5.35	-1.22	11.49	6.66	-1.288	1.32	92.94	82.00
7	2jsa-12	SER_A_2_N	SER_A_2_H	11.49	6.66	-1.288	12.376	7.064	-1.019	1.01	74.56	24.51
8	2jsa-12	SER_A_2_N	SER_A_2_CA	11.49	6.66	-1.288	10.431	7.542	-1.749	1.45	108.49	140.21
9	2jsa-12	SER_A_2_CA	SER_A_2_HA	10.431	7.542	-1.749	9.499	7.23	-1.279	1.09	64.44	-161.49
10	2jsa-12	SER_A_2_CA	SER_A_2_C	10.431	7.542	-1.749	10.278	7.427	-3.267	1.53	172.81	-143.07
11	2jsa-12	SER_A_2_C	SER_A_2_O	10.278	7.427	-3.267	10.852	8.218	-4.014	1.23	127.39	54.03
12	2jsa-12	SER_A_2_C	ALA_A_3_N	10.278	7.427	-3.267	9.502	6.435	-3.678	1.32	108.07	-128.03
13	2jsa-12	ALA_A_3_N	ALA_A_3_H	9.502	6.435	-3.678	9.063	5.822	-3.007	1.01	48.33	-125.61
14	2jsa-12	ALA_A_3_N	ALA_A_3_CA	9.502	6.435	-3.678	9.267	6.206	-5.094	1.45	166.95	-135.74
15	2jsa-12	ALA_A_3_CA	ALA_A_3_HA	9.267	6.206	-5.094	8.916	7.134	-5.545	1.09	114.44	110.72
16	2jsa-12	ALA_A_3_CA	ALA_A_3_C	9.267	6.206	-5.094	8.178	5.145	-5.261	1.53	96.27	-135.75
17	2jsa-12	ALA_A_3_C	ALA_A_3_O	8.178	5.145	-5.261	7.098	5.433	-5.775	1.23	114.70	165.07
18	2jsa-12	ALA_A_3_C	LEU_A_4_N	8.178	5.145	-5.261	8.499	3.938	-4.816	1.33	70.39	-75.11
19	2jsa-12	LEU_A_4_N	LEU_A_4_H	8.499	3.938	-4.816	9.406	3.772	-4.403	1.01	65.87	-10.37
20	2jsa-12	LEU_A_4_N	LEU_A_4_CA	8.499	3.938	-4.816	7.561	2.832	-4.91	1.45	93.71	-130.30
21	2jsa-12	LEU_A_4_CA	LEU_A_4_HA	7.561	2.832	-4.91	6.789	3.104	-5.63	1.09	131.34	160.59
22	2jsa-12	LEU_A_4_CA	LEU_A_4_C	7.561	2.832	-4.91	6.882	2.629	-3.554	1.53	27.59	-163.35
23	2jsa-12	LEU_A_4_C	LEU_A_4_O	6.882	2.629	-3.554	5.661	2.735	-3.446	1.23	84.96	175.04
24	2jsa-12	LEU_A_4_C	SER_A_5_N	6.882	2.629	-3.554	7.702	2.34	-2.554	1.33	41.00	-19.41
25	2jsa-12	SER_A_5_N	SER_A_5_H	7.702	2.34	-2.554	8.697	2.268	-2.716	1.01	99.22	-4.14
26	2jsa-12	SER_A_5_N	SER_A_5_CA	7.702	2.34	-2.554	7.196	2.122	-1.211	1.45	22.31	-156.69
27	2jsa-12	SER_A_5_CA	SER_A_5_HA	7.196	2.122	-1.211	6.637	1.187	-1.205	1.09	89.68	-120.87
28	2jsa-12	SER_A_5_CA	SER_A_5_C	7.196	2.122	-1.211	6.252	3.26	-0.815	1.53	75.01	129.68
29	2jsa-12	SER_A_5_C	SER_A_5_O	6.252	3.26	-0.815	5.27	3.039	-0.107	1.23	54.88	-167.32
30	2jsa-12	SER_A_5_C	CYS_A_6_N	6.252	3.26	-0.815	6.584	4.452	-1.288	1.32	110.92	74.44
31	2jsa-12	CYS_A_6_N	CYS_A_6_H	6.584	4.452	-1.288	7.407	4.56	-1.864	1.01	124.76	7.48
32	2jsa-12	CYS_A_6_N	CYS_A_6_CA	6.584	4.452	-1.288	5.778	5.625	-0.993	1.45	78.29	124.49
33	2jsa-12	CYS_A_6_CA	CYS_A_6_HA	5.778	5.625	-0.993	5.587	5.648	0.08	1.09	10.16	173.13
34	2jsa-12	CYS_A_6_CA	CYS_A_6_C	5.778	5.625	-0.993	4.441	5.486	-1.723	1.53	118.51	-174.06
35	2jsa-12	CYS_A_6_C	CYS_A_6_O	4.441	5.486	-1.723	3.423	5.171	-1.108	1.23	60.01	-162.81
36	2jsa-12	CYS_A_6_C	GLN_A_7_N	4.441	5.486	-1.723	4.487	5.726	-3.025	1.32	169.37	79.15
37	2jsa-12	GLN_A_7_N	GLN_A_7_H	4.487	5.726	-3.025	5.361	5.98	-3.464	1.01	115.75	16.20
38	2jsa-12	GLN_A_7_N	GLN_A_7_CA	4.487	5.726	-3.025	3.292	5.632	-3.847	1.45	124.44	-175.50
39	2jsa-12	GLN_A_7_CA	GLN_A_7_HA	3.292	5.632	-3.847	2.71	6.541	-3.699	1.09	82.19	122.63
40	2jsa-12	GLN_A_7_CA	GLN_A_7_C	3.292	5.632	-3.847	2.44	4.438	-3.409	1.53	73.37	-125.51
41	2jsa-12	GLN_A_7_C	GLN_A_7_O	2.44	4.438	-3.409	1.246	4.583	-3.157	1.23	78.17	173.08
42	2jsa-12	GLN_A_7_C	MET_A_8_N	2.44	4.438	-3.409	3.09	3.285	-3.334	1.33	86.76	-60.59
43	2jsa-12	MET_A_8_N	MET_A_8_H	3.09	3.285	-3.334	4.074	3.24	-3.558	1.01	102.81	-2.62
44	2jsa-12	MET_A_8_N	MET_A_8_CA	3.09	3.285	-3.334	2.407	2.068	-2.932	1.45	73.93	-119.30
45	2jsa-12	MET_A_8_CA	MET_A_8_HA	2.407	2.068	-2.932	1.759	1.745	-3.747	1.09	138.38	-153.51
46	2jsa-12	MET_A_8_CA	MET_A_8_C	2.407	2.068	-2.932	1.556	2.303	-1.683	1.53	35.25	164.56
47	2jsa-12	MET_A_8_C	MET_A_8_O	1.556	2.303	-1.683	0.437	1.798	-1.586	1.23	85.48	-155.71
48	2jsa-12	MET_A_8_C	CYS_A_9_N	1.556	2.303	-1.683	2.116	3.069	-0.759	1.32	45.76	53.83
49	2jsa-12	CYS_A_9_N	CYS_A_9_H	2.116	3.069	-0.759	3.04	3.451	-0.906	1.01	98.36	22.46
50	2jsa-12	CYS_A_9_N	CYS_A_9_CA	2.116	3.069	-0.759	1.421	3.378	0.479	1.45	31.57	156.03
51	2jsa-12	CYS_A_9_CA	CYS_A_9_HA	1.421	3.378	0.479	1.191	2.441	0.986	1.09	62.28	-103.79
52	2jsa-12	CYS_A_9_CA	CYS_A_9_C	1.421	3.378	0						

54	2jsa-12	CYS_A_9_C	GLU_A_10_N	0.106	4.079	0.131	0.15	4.849	-0.946	1.32	144.39	86.73
55	2jsa-12	GLU_A_10_N	GLU_A_10_H	0.15	4.849	-0.946	1.008	4.939	-1.471	1.01	121.32	5.99
56	2jsa-12	GLU_A_10_N	GLU_A_10_CA	0.15	4.849	-0.946	-1.025	5.576	-1.395	1.45	108.00	148.25
57	2jsa-12	GLU_A_10_CA	GLU_A_10_HA	-1.025	5.576	-1.395	-1.554	5.938	-0.514	1.09	36.04	145.62
58	2jsa-12	GLU_A_10_CA	GLU_A_10_C	-1.025	5.576	-1.395	-1.96	4.646	-2.17	1.53	120.44	-135.15
59	2jsa-12	GLU_A_10_C	GLU_A_10_O	-1.96	4.646	-2.17	-3.065	5.039	-2.541	1.23	107.55	160.42
60	2jsa-12	GLU_A_10_C	LEU_A_11_N	-1.96	4.646	-2.17	-1.483	3.43	-2.392	1.32	99.65	-68.58
61	2jsa-12	LEU_A_11_N	LEU_A_11_H	-1.483	3.43	-2.392	-0.564	3.175	-2.058	1.01	70.70	-15.51
62	2jsa-12	LEU_A_11_N	LEU_A_11_CA	-1.483	3.43	-2.392	-2.263	2.44	-3.116	1.45	119.87	-128.23
63	2jsa-12	LEU_A_11_CA	LEU_A_11_HA	-2.263	2.44	-3.116	-2.958	2.969	-3.768	1.09	126.74	142.72
64	2jsa-12	LEU_A_11_CA	LEU_A_11_C	-2.263	2.44	-3.116	-3.09	1.622	-2.122	1.53	49.49	-135.31
65	2jsa-12	LEU_A_11_C	LEU_A_11_O	-3.09	1.622	-2.122	-4.27	1.367	-2.354	1.23	100.88	-167.81
66	2jsa-12	LEU_A_11_C	VAL_A_12_N	-3.09	1.622	-2.122	-2.436	1.234	-1.037	1.32	35.03	-30.68
67	2jsa-12	VAL_A_12_N	VAL_A_12_H	-2.436	1.234	-1.037	-1.464	1.482	-0.912	1.01	82.90	14.31
68	2jsa-12	VAL_A_12_N	VAL_A_12_CA	-2.436	1.234	-1.037	-3.095	0.449	-0.008	1.45	44.89	-130.01
69	2jsa-12	VAL_A_12_CA	VAL_A_12_HA	-3.095	0.449	-0.008	-3.603	-0.388	-0.486	1.09	116.02	-121.25
70	2jsa-12	VAL_A_12_CA	VAL_A_12_C	-3.095	0.449	-0.008	-4.151	1.313	0.688	1.53	62.97	-140.71
71	2jsa-12	VAL_A_12_C	VAL_A_12_O	-4.151	1.313	0.688	-5.302	0.901	0.824	1.23	83.65	-160.31
72	2jsa-12	VAL_A_12_C	VAL_A_13_N	-4.151	1.313	0.688	-3.721	2.493	1.109	1.32	71.47	69.98
73	2jsa-12	VAL_A_13_N	VAL_A_13_H	-3.721	2.493	1.109	-2.759	2.766	0.963	1.01	98.31	15.84
74	2jsa-12	VAL_A_13_N	VAL_A_13_CA	-3.721	2.493	1.109	-4.614	3.417	1.786	1.45	62.22	134.02
75	2jsa-12	VAL_A_13_CA	VAL_A_13_HA	-4.614	3.417	1.786	-5.036	2.914	2.656	1.09	37.04	-130.00
76	2jsa-12	VAL_A_13_CA	VAL_A_13_C	-4.614	3.417	1.786	-5.764	3.788	0.848	1.53	127.82	162.12
77	2jsa-12	VAL_A_13_C	VAL_A_13_O	-5.764	3.788	0.848	-6.929	3.554	1.165	1.23	75.06	-168.64
78	2jsa-12	VAL_A_13_C	LYS_A_14_N	-5.764	3.788	0.848	-5.397	4.36	-0.29	1.33	149.15	57.32
79	2jsa-12	LYS_A_14_N	LYS_A_14_H	-5.397	4.36	-0.29	-4.419	4.522	-0.485	1.01	101.13	9.41
80	2jsa-12	LYS_A_14_N	LYS_A_14_C	-5.397	4.36	-0.29	-6.384	4.765	-1.277	1.45	132.77	157.69
81	2jsa-12	LYS_A_14_CA	LYS_A_14_HA	-6.384	4.765	-1.277	-6.906	5.641	-0.893	1.09	69.37	120.79
82	2jsa-12	LYS_A_14_CA	LYS_A_14_C	-6.384	4.765	-1.277	-7.415	3.648	-1.45	1.53	96.49	-132.71
83	2jsa-12	LYS_A_14_C	LYS_A_14_O	-7.415	3.648	-1.45	-8.593	3.917	-1.681	1.23	100.82	167.14
84	2jsa-12	LYS_A_14_C	LYS_A_15_N	-7.415	3.648	-1.45	-6.934	2.419	-1.329	1.33	84.76	-68.63
85	2jsa-12	LYS_A_15_N	LYS_A_15_H	-6.934	2.419	-1.329	-5.953	2.273	-1.137	1.01	79.04	-8.47
86	2jsa-12	LYS_A_15_N	LYS_A_15_CA	-6.934	2.419	-1.329	-7.8	1.26	-1.469	1.45	95.53	-126.77
87	2jsa-12	LYS_A_15_CA	LYS_A_15_HA	-7.8	1.26	-1.469	-8.497	1.456	-2.283	1.09	138.35	164.29
88	2jsa-12	LYS_A_15_CA	LYS_A_15_C	-7.8	1.26	-1.469	-8.618	1.083	-0.189	1.53	33.18	-167.29
89	2jsa-12	LYS_A_15_C	LYS_A_15_O	-8.618	1.083	-0.189	-9.807	0.773	-0.245	1.23	92.61	-165.39
90	2jsa-12	LYS_A_15_C	TYR_A_16_N	-8.618	1.083	-0.189	-7.948	1.287	0.937	1.33	31.88	16.93
91	2jsa-12	TYR_A_16_N	TYR_A_16_H	-7.948	1.287	0.937	-6.97	1.539	0.909	1.01	91.59	14.45
92	2jsa-12	TYR_A_16_N	TYR_A_16_CA	-7.948	1.287	0.937	-8.598	1.153	2.229	1.45	27.19	-168.35
93	2jsa-12	TYR_A_16_CA	TYR_A_16_HA	-8.598	1.153	2.229	-9.228	0.264	2.244	1.09	89.21	-125.32
94	2jsa-12	TYR_A_16_CA	TYR_A_16_C	-8.598	1.153	2.229	-9.438	2.391	2.551	1.53	77.85	124.16
95	2jsa-12	TYR_A_16_C	TYR_A_16_O	-9.438	2.391	2.551	-10.666	2.336	2.525	1.23	91.21	-177.44
96	2jsa-12	TYR_A_16_C	GLU_A_17_N	-9.438	2.391	2.551	-8.74	3.478	2.849	1.33	77.01	57.29
97	2jsa-12	GLU_A_17_N	GLU_A_17_H	-8.74	3.478	2.849	-7.73	3.45	2.851	1.01	89.89	-1.59
98	2jsa-12	GLU_A_17_N	GLU_A_17_CA	-8.74	3.478	2.849	-9.406	4.727	3.176	1.45	76.99	118.07
99	2jsa-12	GLU_A_17_CA	GLU_A_17_HA	-9.406	4.727	3.176	-9.71	4.683	4.222	1.09	16.37	-171.76
100	2jsa-12	GLU_A_17_CA	GLU_A_17_C	-9.406	4.727	3.176	-10.661	4.901	2.317	1.53	124.14	172.11
101	2jsa-12	GLU_A_17_C	GLU_A_17_O	-10.661	4.901	2.317	-11.699	5.339	2.811	1.23	66.32	157.12
102	2jsa-12	GLU_A_17_C	GLY_A_18_N	-10.661	4.901	2.317	-10.522	4.55	1.048	1.32	163.43	-68.40
103	2jsa-12	GLY_A_18_N	GLY_A_18_H	-10.522	4.55	1.048	-9.637	4.199	0.711	1.01	109.49	-21.63
104	2jsa-12	GLY_A_18_N	GLY_A_18_CA	-10.522	4.55	1.048	-11.632	4.661	0.116	1.45	129.88	174.29
105	2jsa-12	GLY_A_18_CA	GLY_A_18_C	-11.632	4.661	0.116	-11.986	3.298	-0.482	1.53	113.01	-104.56
106	2jsa-12	GLY_A_18_C	GLY_A_18_O	-11.986	3.298	-0.482	-12.05	3.149	-1.701	1.23	172.42	-113.24
107	2jsa-12	GLY_A_18_C	SER_A_19_N	-11.986	3.298	-0.482	-12.205	2.338	0.405	1.33	47.99	-102.85
108	2jsa-12	SER_A_19_N	SER_A_19_H	-12.205	2.338	0.405	-12.134	2.533	1.394	1.01	11.85	69.99
109	2jsa-12	SER_A_19_N	SER_A_19_CA	-12.205	2.338	0.405	-12.55	0.992	-0.02	1.45	107.01	-104.38
110	2jsa-12	SER_A_19_CA	SER_A_19_HA	-12.55	0.992	-0.02	-12.139	0.833	-1.017	1.09	156.15	-21.15
111	2jsa-12	SER_A_19_CA	SER_A_19_C	-12.55	0.992	-0.02	-14.07	0.838	-0.087	1.53	92.51	-174.21
112	2jsa-12	SER_A_19_C	SER_A_19_O	-14.07	0.838	-0.087	-14.602	0.302	-1.058	1.23	142.13	-134.79
113	2jsa-12	SER_A_19_C	ALA_A_20_N	-14.07	0.838	-0.087	-14.728	1.318	0.959	1.33	37.91	143.89
114	2jsa-12	ALA_A_20_N	ALA_A_20_H	-14.728	1.318	0.959	-14.225	1.746	1.723	1.01	40.84	40.39
115	2jsa-12	ALA_A_20_N	ALA_A_20_CA	-14.728	1.318	0.959	-16.177	1.24	1.032	1.45	87.12	-176.92
116	2jsa-12	ALA_A_20_CA	ALA_A_20_HA	-16.177	1.24	1.032	-16.535	2.005	1.721	1.09	50.79	115.08
117	2jsa-12	ALA_A_20_CA	ALA_A_20_C	-16.177	1.24	1.032	-16.583	-0.13	1.578	1.53	69.09	-106.51
118	2jsa-12	ALA_A_20_C	ALA_A_20_O	-16.583	-0.13	1.578	-17.756	-0.367	1.862	1.23	76.65	-168.58
119	2jsa-12	ALA_A_20_C	ASP_A_21_N	-16.583	-0.13	1.578	-15.59	-0.998	1.709	1.33	84.33	-41.16
120	2jsa-12	ASP_A_21_N	ASP_A_21_H	-15.59	-0.998	1.709	-14.648	-0.735	1.455	1.01	104.56	15.60
121	2jsa-12	ASP_A_21_N	ASP_A_21_CA	-15.59	-0.998	1.709	-15.829	-2.338	2.216	1.45	69.57	-100.11
122	2jsa-12	ASP_A_21_CA	ASP_A_21_HA	-15.829	-2.338	2.216	-16.902	-2.485	2.34	1.09	83.47	-172.20
123	2jsa-12	ASP_A_21_CA	ASP_A_21_C	-15.829	-2.338	2.216	-15.122	-2.503	3.563	1.53	28.32	-13.14
124	2jsa-12	ASP_A_21_C	ASP_A_21_O	-15.122	-2.503	3.563	-15.491	-3.363	4.361	1.23	49.54	-113.22
125	2jsa-12	ASP_A_21_C	LYS_A_22_N	-15.122	-2.503	3.563	-14.118	-1.665	3.774	1.32	80.83	39.85
126	2jsa-12	LYS_A_22_N	LYS_A_22_H	-14.118	-1.665	3.774	-13.869	-0.982	3.073	1.01	133.96	69.97
127	2jsa-12	LYS_A_22_N	LYS_A_22_CA	-14.118	-1.665	3.774	-13.355	-1.708	5.01	1.45	31.73	-3.23
128	2jsa-12	LYS_A_22_CA	LYS_A_22_HA	-13.355	-1.708	5.01	-12.475	-1.076	4.886	1.09	96.53	35.69
129	2jsa-12	LYS_A_22_CA	LYS_A_22_C	-13.355	-1.708	5.01	-12.869	-3.137	5.256	1.53	80.74	-71.22
130	2jsa-12	LYS_A_22_C	LYS_A_22_O	-12.869	-3.137	5.256	-13.301	-3.788	6.205	1.23	39.46	-123.57
131	2jsa-12	LYS_A_22_C	ASP_A_23_N	-12.869	-3.137	5.256	-11.976	-3.582	4.384	1.33	131.15	-26.49
132	2jsa-12	ASP_A_23_N	ASP_A_23_H	-11.976	-3.582	4.384	-11.665	-2.99	3.626	1.01	138.58	62.29
133	2jsa-12	ASP_A_23_N	ASP_A_23_CA	-11.976	-3.582	4.384	-11.426	-4.922	4.495	1.45	85.62	-67.68
134	2jsa-12	ASP_A_23_CA	ASP_A_23_HA	-11.426	-4.922	4.495	-11.445	-5.23	5.541	1.09	16.44	-93.53
135	2jsa-12	ASP_A_23_CA	ASP_A_23_C	-11.426	-4.922	4.495	-9.985	-4.922	3.978	1.53	109.74	0.00
136	2jsa-12	ASP_A_23_C	ASP_A_23_O	-9.985	-4.922	3.978	-9.744	-4.658	2.801	1.23	163.11	47.61
137	2jsa-12	ASP_A_23_C	ALA_A_24_N	-9.985	-4.922	3.978	-9.066	-5.22	4.884	1.32	46.84	-17.97
138	2jsa-12	ALA_A_24_N	ALA_A_24_H	-9.066	-5.22	4.884	-9.337	-5.425	5.835	1.01	19.66	-142.89
139	2jsa-12	ALA_A_24_N	ALA_A_24_CA	-9.066	-5.22	4.884	-7.656	-5.258	4.536	1.45	103.86	-1.54
140	2jsa-12	ALA_A_24_CA	ALA_A_24_HA	-7.656	-5.258	4.536	-7.392	-4.324	4.041	1.09	117.02	74.22
141	2jsa-12	ALA_A_24_CA	ALA_A_24_C	-7.656	-5.258	4.536	-7.407	-6.41	3.561	1.53	129.60	-77.80
142	2jsa-12	ALA_A_24_C	ALA_A_24_O	-7.407	-6.41	3.561	-6.315	-6.537	3.009	1.23	116.66	-6.63
143	2jsa-12	ALA_A_24_C	ASN_A_25_N	-7.407	-6.41	3.561	-8.438	-7.223	3.378	1.33	97.93	-141.74
144	2jsa-12	ASN_A_25_N	ASN_A_25									

147	2jsa-12	ASN_A_25_CA	ASN_A_25_C	-8.344	-8.361	2.479	-8.595	-7.894	1.045	1.53	159.71	118.26
148	2jsa-12	ASN_A_25_C	ASN_A_25_O	-8.595	-7.894	1.045	-7.824	-8.211	0.141	1.23	137.32	-22.35
149	2jsa-12	ASN_A_25_C	VAL_A_26_N	-8.595	-7.894	1.045	-9.678	-7.148	0.88	1.33	97.15	154.44
150	2jsa-12	VAL_A_26_N	VAL_A_26_H	-9.678	-7.148	0.88	-10.268	-6.927	1.669	1.01	38.61	159.47
151	2jsa-12	VAL_A_26_N	VAL_A_26_CA	-9.678	-7.148	0.88	-10.04	-6.634	-0.43	1.45	154.36	125.16
152	2jsa-12	VAL_A_26_CA	VAL_A_26_HA	-10.04	-6.634	-0.43	-9.819	-7.4	-1.173	1.09	132.98	-73.91
153	2jsa-12	VAL_A_26_CA	VAL_A_26_C	-10.04	-6.634	-0.43	-9.186	-5.406	-0.746	1.53	101.93	55.18
154	2jsa-12	VAL_A_26_C	VAL_A_26_O	-9.186	-5.406	-0.746	-9.178	-4.924	-1.878	1.23	156.93	89.05
155	2jsa-12	VAL_A_26_C	ILE_A_27_N	-9.186	-5.406	-0.746	-8.487	-4.932	0.276	1.33	39.57	34.14
156	2jsa-12	ILE_A_27_N	ILE_A_27_H	-8.487	-4.932	0.276	-8.541	-5.378	1.181	1.01	26.40	-96.90
157	2jsa-12	ILE_A_27_N	ILE_A_27_CA	-8.487	-4.932	0.276	-7.63	-3.768	0.121	1.45	96.12	53.64
158	2jsa-12	ILE_A_27_CA	ILE_A_27_HA	-7.63	-3.768	0.121	-8.032	-3.157	-0.687	1.09	137.85	123.34
159	2jsa-12	ILE_A_27_CA	ILE_A_27_C	-7.63	-3.768	0.121	-6.229	-4.223	-0.294	1.53	105.73	-17.99
160	2jsa-12	ILE_A_27_C	ILE_A_27_O	-6.229	-4.223	-0.294	-5.838	-4.067	-1.45	1.23	159.99	21.75
161	2jsa-12	ILE_A_27_C	LYS_A_28_N	-6.229	-4.223	-0.294	-5.511	-4.777	0.673	1.33	43.16	-37.65
162	2jsa-12	LYS_A_28_N	LYS_A_28_H	-5.511	-4.777	0.673	-5.896	-4.873	1.602	1.01	23.13	-166.00
163	2jsa-12	LYS_A_28_N	LYS_A_28_CA	-5.511	-4.777	0.673	-4.163	-5.255	0.423	1.45	99.91	-19.52
164	2jsa-12	LYS_A_28_CA	LYS_A_28_HA	-4.163	-5.255	0.423	-3.498	-4.392	0.4	1.09	91.21	52.38
165	2jsa-12	LYS_A_28_CA	LYS_A_28_C	-4.163	-5.255	0.423	-4.108	-5.921	-0.955	1.53	154.13	-85.28
166	2jsa-12	LYS_A_28_C	LYS_A_28_O	-4.108	-5.921	-0.955	-3.182	-5.682	-1.727	1.23	128.91	14.47
167	2jsa-12	LYS_A_28_C	LYS_A_29_N	-4.108	-5.921	-0.955	-5.115	-6.741	-1.219	1.33	101.49	-140.84
168	2jsa-12	LYS_A_29_N	LYS_A_29_H	-5.115	-6.741	-1.219	-5.843	-6.889	-0.535	1.01	47.36	-168.51
169	2jsa-12	LYS_A_29_N	LYS_A_29_CA	-5.115	-6.741	-1.219	-5.194	-7.442	-2.489	1.45	150.95	-96.43
170	2jsa-12	LYS_A_29_CA	LYS_A_29_HA	-5.194	-7.442	-2.489	-4.243	-7.948	-2.655	1.09	98.76	-28.02
171	2jsa-12	LYS_A_29_CA	LYS_A_29_C	-5.194	-7.442	-2.489	-5.382	-6.426	-3.617	1.53	137.51	100.48
172	2jsa-12	LYS_A_29_C	LYS_A_29_O	-5.382	-6.426	-3.617	-4.634	-6.432	-4.594	1.23	142.56	-0.46
173	2jsa-12	LYS_A_29_C	ASP_A_30_N	-5.382	-6.426	-3.617	-6.385	-5.578	-3.445	1.32	82.54	139.79
174	2jsa-12	ASP_A_30_N	ASP_A_30_H	-6.385	-5.578	-3.445	-6.96	-5.631	-2.616	1.01	34.86	-174.73
175	2jsa-12	ASP_A_30_N	ASP_A_30_CA	-6.385	-5.578	-3.445	-6.681	-4.558	-4.437	1.45	133.05	106.18
176	2jsa-12	ASP_A_30_CA	ASP_A_30_HA	-6.681	-4.558	-4.437	-7.162	-5.025	-5.296	1.09	142.03	-135.85
177	2jsa-12	ASP_A_30_CA	ASP_A_30_C	-6.681	-4.558	-4.437	-5.379	-3.884	-4.873	1.53	106.56	27.37
178	2jsa-12	ASP_A_30_C	ASP_A_30_O	-5.379	-3.884	-4.873	-5.064	-3.843	-6.062	1.23	165.04	7.42
179	2jsa-12	ASP_A_30_C	PHE_A_31_N	-5.379	-3.884	-4.873	-4.656	-3.372	-3.888	1.32	41.97	35.30
180	2jsa-12	PHE_A_31_N	PHE_A_31_H	-4.656	-3.372	-3.888	-4.976	-3.443	-2.933	1.01	18.94	-167.49
181	2jsa-12	PHE_A_31_N	PHE_A_31_CA	-4.656	-3.372	-3.888	-3.395	-2.701	-4.154	1.45	100.55	28.02
182	2jsa-12	PHE_A_31_CA	PHE_A_31_HA	-3.395	-2.701	-4.154	-3.582	-1.684	-4.5	1.09	108.50	100.42
183	2jsa-12	PHE_A_31_CA	PHE_A_31_C	-3.395	-2.701	-4.154	-2.582	-3.461	-5.205	1.53	133.36	-43.07
184	2jsa-12	PHE_A_31_C	PHE_A_31_O	-2.582	-3.461	-5.205	-2.142	-2.879	-6.195	1.23	143.61	52.91
185	2jsa-12	PHE_A_31_C	ASP_A_32_N	-2.582	-3.461	-5.205	-2.406	-4.75	-4.953	1.33	79.04	-82.22
186	2jsa-12	ASP_A_32_N	ASP_A_32_H	-2.406	-4.75	-4.953	-2.795	-5.162	-4.117	1.01	34.13	-133.36
187	2jsa-12	ASP_A_32_N	ASP_A_32_CA	-2.406	-4.75	-4.953	-1.654	-5.596	-5.864	1.45	128.83	-48.37
188	2jsa-12	ASP_A_32_CA	ASP_A_32_HA	-1.654	-5.596	-5.864	-0.604	-5.301	-5.839	1.09	88.69	15.69
189	2jsa-12	ASP_A_32_CA	ASP_A_32_C	-1.654	-5.596	-5.864	-2.207	-5.43	-7.28	1.53	157.82	163.29
190	2jsa-12	ASP_A_32_C	ASP_A_32_O	-2.207	-5.43	-7.28	-1.446	-5.26	-8.232	1.23	140.68	12.59
191	2jsa-12	ASP_A_32_C	ALA_A_33_N	-2.207	-5.43	-7.28	-3.527	-5.486	-7.376	1.32	94.16	-177.57
192	2jsa-12	ALA_A_33_N	ALA_A_33_H	-3.527	-5.486	-7.376	-4.09	-5.631	-6.551	1.01	35.17	-165.56
193	2jsa-12	ALA_A_33_N	ALA_A_33_CA	-3.527	-5.486	-7.376	-4.192	-5.343	-8.661	1.45	152.11	167.86
194	2jsa-12	ALA_A_33_CA	ALA_A_33_HA	-4.192	-5.343	-8.661	-3.902	-6.177	-9.3	1.09	125.89	-70.83
195	2jsa-12	ALA_A_33_CA	ALA_A_33_C	-4.192	-5.343	-8.661	-3.735	-4.044	-9.325	1.53	115.74	70.62
196	2jsa-12	ALA_A_33_C	ALA_A_33_O	-3.735	-4.044	-9.325	-3.104	-4.071	-10.381	1.23	149.12	-2.45
197	2jsa-12	ALA_A_33_C	GLU_A_34_N	-3.735	-4.044	-9.325	-4.071	-2.937	-8.679	1.33	60.82	106.88
198	2jsa-12	GLU_A_34_N	GLU_A_34_H	-4.071	-2.937	-8.679	-4.589	-2.99	-7.814	1.01	31.05	-174.16
199	2jsa-12	GLU_A_34_N	GLU_A_34_CA	-4.071	-2.937	-8.679	-3.703	-1.629	-9.195	1.45	110.79	74.29
200	2jsa-12	GLU_A_34_CA	GLU_A_34_HA	-3.703	-1.629	-9.195	-4.329	-1.42	-10.062	1.09	142.72	161.54
201	2jsa-12	GLU_A_34_CA	GLU_A_34_C	-3.703	-1.629	-9.195	-2.241	-1.628	-9.646	1.53	107.14	0.04
202	2jsa-12	GLU_A_34_C	GLU_A_34_O	-2.241	-1.628	-9.646	-1.918	-1.113	-10.716	1.23	150.40	57.90
203	2jsa-12	GLU_A_34_C	CYS_A_35_N	-2.241	-1.628	-9.646	-1.396	-2.21	-8.808	1.32	50.76	-34.56
204	2jsa-12	CYS_A_35_N	CYS_A_35_H	-1.396	-2.21	-8.808	-1.732	-2.613	-7.945	1.01	31.30	-129.82
205	2jsa-12	CYS_A_35_N	CYS_A_35_CA	-1.396	-2.21	-8.808	0.024	-2.283	-9.107	1.45	101.88	-2.94
206	2jsa-12	CYS_A_35_CA	CYS_A_35_HA	0.024	-2.283	-9.107	0.413	-1.267	-9.177	1.09	93.68	69.05
207	2jsa-12	CYS_A_35_CA	CYS_A_35_C	0.024	-2.283	-9.107	0.194	-2.964	-10.466	1.53	152.68	-75.98
208	2jsa-12	CYS_A_35_C	CYS_A_35_O	0.194	-2.964	-10.466	1.001	-2.528	-11.287	1.23	131.83	28.38
209	2jsa-12	CYS_A_35_C	LYS_A_36_N	0.194	-2.964	-10.466	-0.578	-4.022	-10.663	1.32	98.55	-126.12
210	2jsa-12	LYS_A_36_N	LYS_A_36_H	-0.578	-4.022	-10.663	-1.218	-4.325	-9.943	1.01	44.52	-154.67
211	2jsa-12	LYS_A_36_N	LYS_A_36_CA	-0.578	-4.022	-10.663	-0.523	-4.768	-11.909	1.45	149.02	-85.78
212	2jsa-12	LYS_A_36_CA	LYS_A_36_HA	-0.523	-4.768	-11.909	0.524	-4.873	-12.193	1.09	105.10	-5.73
213	2jsa-12	LYS_A_36_CA	LYS_A_36_C	-0.523	-4.768	-11.909	-1.225	-3.969	-13.008	1.53	135.94	131.30
214	2jsa-12	LYS_A_36_C	LYS_A_36_O	-1.225	-3.969	-13.008	-1.295	-4.411	-14.154	1.23	158.67	-99.00
215	2jsa-12	LYS_A_36_C	LYS_A_37_N	-1.225	-3.969	-13.008	-1.727	-2.805	-12.622	1.33	73.06	113.33
216	2jsa-12	LYS_A_37_N	LYS_A_37_H	-1.727	-2.805	-12.622	-1.632	-2.504	-11.662	1.01	18.20	72.48
217	2jsa-12	LYS_A_37_N	LYS_A_37_CA	-1.727	-2.805	-12.622	-2.42	-1.939	-13.559	1.45	130.19	128.67
218	2jsa-12	LYS_A_37_CA	LYS_A_37_HA	-2.42	-1.939	-13.559	-2.594	-2.504	-14.474	1.09	147.13	-107.12
219	2jsa-12	LYS_A_37_CA	LYS_A_37_C	-2.42	-1.939	-13.559	-1.522	-0.752	-13.911	1.53	103.31	52.89
220	2jsa-12	LYS_A_37_C	LYS_A_37_O	-1.522	-0.752	-13.911	-1.367	-0.413	-15.084	1.23	162.37	65.43
221	2jsa-12	LYS_A_37_C	LEU_A_38_N	-1.522	-0.752	-13.911	-0.955	-0.153	-12.874	1.33	38.50	46.57
222	2jsa-12	LEU_A_38_N	LEU_A_38_H	-0.955	-0.153	-12.874	-1.128	-0.486	-11.936	1.01	21.80	-117.45
223	2jsa-12	LEU_A_38_N	LEU_A_38_CA	-0.955	-0.153	-12.874	-0.076	0.99	-13.059	1.45	97.31	52.44
224	2jsa-12	LEU_A_38_CA	LEU_A_38_HA	-0.076	0.99	-13.059	-0.241	1.384	-14.062	1.09	156.93	112.72
225	2jsa-12	LEU_A_38_CA	LEU_A_38_C	-0.076	0.99	-13.059	1.38	0.528	-12.976	1.53	86.89	-17.60
226	2jsa-12	LEU_A_38_C	LEU_A_38_O	1.38	0.528	-12.976	2.193	0.867	-13.834	1.23	134.25	22.63
227	2jsa-12	LEU_A_38_C	PHE_A_39_N	1.38	0.528	-12.976	1.665	-0.241	-11.935	1.33	38.23	-69.66
228	2jsa-12	PHE_A_39_N	PHE_A_39_H	1.665	-0.241	-11.935	0.946	-0.481	-11.268	1.01	48.65	-161.54
229	2jsa-12	PHE_A_39_N	PHE_A_39_CA	1.665	-0.241	-11.935	3.008	-0.754	-11.728	1.45	81.81	-20.91
230	2jsa-12	PHE_A_39_CA	PHE_A_39_HA	3.008	-0.754	-11.728	3.741	-0.013	-12.051	1.09	107.17	45.31
231	2jsa-12	PHE_A_39_CA	PHE_A_39_C	3.008	-0.754	-11.728	3.222	-2.058	-12.5	1.53	120.29	-80.68
232	2jsa-12	PHE_A_39_C	PHE_A_39_O	3.222	-2.058	-12.5	4.185	-2.781	-12.25	1.23	78.27	-36.90
233	2jsa-12	PHE_A_39_C	HIS_A_40_N	3.222	-2.058	-12.5	2.306	-2.321	-13.421	1.33	134.02	-163.98
234	2jsa-12	HIS_A_40_N	HIS_A_40_H	2.306	-2.321	-13.421	1.539	-1.682	-13.572	1.01	98.60	140.20
235	2jsa-12	HIS_A_40_N	HIS_A_40_CA	2.306	-2.321	-13.421	2.382	-3.525	-14.229	1.45	123.81	-86.39
236	2jsa-12	HIS_A_40_CA	HIS_A_40_HA	2.382	-3.525	-14.229	2.472	-4.377	-13.555	1.09	51.81	-8

240	2jsa-12	THR_A_41_N	THR_A_41_H	3.713	-2.446	-15.924	2.973	-1.759	-15.945	1.01	91.19	137.13
241	2jsa-12	THR_A_41_N	THR_A_41_CA	3.713	-2.446	-15.924	4.852	-2.274	-16.81	1.45	127.57	8.59
242	2jsa-12	THR_A_41_CA	THR_A_41_HA	4.852	-2.274	-16.81	4.78	-3.003	-17.617	1.09	137.77	-95.64
243	2jsa-12	THR_A_41_CA	THR_A_41_C	4.852	-2.274	-16.81	6.158	-2.534	-16.057	1.53	60.51	-11.26
244	2jsa-12	THR_A_41_C	THR_A_41_O	6.158	-2.534	-16.057	7.092	-3.114	-16.607	1.23	116.58	-31.84
245	2jsa-12	THR_A_41_C	ILE_A_42_N	6.158	-2.534	-16.057	6.181	-2.091	-14.808	1.33	19.55	87.03
246	2jsa-12	ILE_A_42_N	ILE_A_42_H	6.181	-2.091	-14.808	5.375	-1.623	-14.419	1.01	67.35	149.86
247	2jsa-12	ILE_A_42_N	ILE_A_42_CA	6.181	-2.091	-14.808	7.358	-2.267	-13.973	1.45	54.95	-8.50
248	2jsa-12	ILE_A_42_CA	ILE_A_42_HA	7.358	-2.267	-13.973	8.236	-2.011	-14.567	1.09	123.00	16.26
249	2jsa-12	ILE_A_42_CA	ILE_A_42_C	7.358	-2.267	-13.973	7.478	-3.741	-13.576	1.53	74.97	-85.35
250	2jsa-12	ILE_A_42_C	ILE_A_42_O	7.478	-3.741	-13.576	6.481	-4.385	-13.257	1.23	74.96	-147.14
251	2jsa-12	ILE_A_42_C	PRO_A_43_N	7.478	-3.741	-13.576	8.742	-4.243	-13.608	1.36	91.35	-21.66
252	2jsa-12	PRO_A_43_N	PRO_A_43_CA	8.742	-4.243	-13.608	9.006	-5.627	-13.256	1.45	75.97	-79.20
253	2jsa-12	PRO_A_43_CA	PRO_A_43_HA	9.006	-5.627	-13.256	8.274	-6.279	-13.731	1.09	115.85	-138.31
254	2jsa-12	PRO_A_43_CA	PRO_A_43_C	9.006	-5.627	-13.256	8.928	-5.831	-11.741	1.53	8.20	-110.92
255	2jsa-12	PRO_A_43_C	PRO_A_43_O	8.928	-5.831	-11.741	7.958	-6.396	-11.237	1.23	65.82	-149.78
256	2jsa-12	PRO_A_43_C	PHE_A_44_N	8.928	-5.831	-11.741	9.961	-5.361	-11.059	1.32	59.00	24.46
257	2jsa-12	PHE_A_44_N	PHE_A_44_H	9.961	-5.361	-11.059	10.725	-4.907	-11.54	1.01	118.42	30.72
258	2jsa-12	PHE_A_44_N	PHE_A_44_CA	9.961	-5.361	-11.059	10.021	-5.485	-9.612	1.45	5.44	-64.18
259	2jsa-12	PHE_A_44_CA	PHE_A_44_HA	10.021	-5.485	-9.612	10.028	-6.538	-9.331	1.09	75.06	-89.62
260	2jsa-12	PHE_A_44_CA	PHE_A_44_C	10.021	-5.485	-9.612	8.833	-4.784	-8.952	1.53	64.43	149.46
261	2jsa-12	PHE_A_44_C	PHE_A_44_O	8.833	-4.784	-8.952	8.498	-5.069	-7.804	1.23	20.96	-139.61
262	2jsa-12	PHE_A_44_C	GLY_A_45_N	8.833	-4.784	-8.952	8.227	-3.878	-9.706	1.33	124.67	123.78
263	2jsa-12	GLY_A_45_N	GLY_A_45_H	8.227	-3.878	-9.706	8.557	-3.694	-10.643	1.01	158.04	29.14
264	2jsa-12	GLY_A_45_N	GLY_A_45_CA	8.227	-3.878	-9.706	7.083	-3.133	-9.209	1.45	70.00	146.93
265	2jsa-12	GLY_A_45_CA	GLY_A_45_C	7.083	-3.133	-9.209	5.999	-4.077	-8.687	1.53	70.04	-138.95
266	2jsa-12	GLY_A_45_C	GLY_A_45_O	5.999	-4.077	-8.687	5.465	-3.875	-7.598	1.23	27.67	159.28
267	2jsa-12	GLY_A_45_C	THR_A_46_N	5.999	-4.077	-8.687	5.704	-5.089	-9.49	1.33	127.30	-106.25
268	2jsa-12	THR_A_46_N	THR_A_46_H	5.704	-5.089	-9.49	6.184	-5.193	-10.373	1.01	150.92	-12.23
269	2jsa-12	THR_A_46_N	THR_A_46_CA	5.704	-5.089	-9.49	4.693	-6.066	-9.124	1.45	75.41	-135.98
270	2jsa-12	THR_A_46_CA	THR_A_46_HA	4.693	-6.066	-9.124	3.822	-5.539	-8.736	1.09	69.14	148.82
271	2jsa-12	THR_A_46_CA	THR_A_46_C	4.693	-6.066	-9.124	5.216	-6.987	-8.02	1.53	43.81	-60.41
272	2jsa-12	THR_A_46_C	THR_A_46_O	5.216	-6.987	-8.02	4.478	-7.343	-7.102	1.23	41.75	-154.25
273	2jsa-12	THR_A_46_C	ARG_A_47_N	5.216	-6.987	-8.02	6.485	-7.347	-8.146	1.33	95.46	-15.84
274	2jsa-12	ARG_A_47_N	ARG_A_47_H	6.485	-7.347	-8.146	7.033	-7.017	-8.928	1.01	140.72	31.06
275	2jsa-12	ARG_A_47_N	ARG_A_47_CA	6.485	-7.347	-8.146	7.115	-8.22	-7.17	1.45	47.81	-54.18
276	2jsa-12	ARG_A_47_CA	ARG_A_47_HA	7.115	-8.22	-7.17	6.525	-9.133	-7.093	1.09	85.95	-122.87
277	2jsa-12	ARG_A_47_CA	ARG_A_47_C	7.115	-8.22	-7.17	7.161	-7.539	-5.8	1.53	26.48	86.14
278	2jsa-12	ARG_A_47_C	ARG_A_47_O	7.161	-7.539	-5.8	6.848	-8.158	-4.785	1.23	34.35	-116.82
279	2jsa-12	ARG_A_47_C	GLU_A_48_N	7.161	-7.539	-5.8	7.555	-6.275	-5.817	1.32	90.74	72.69
280	2jsa-12	GLU_A_48_N	GLU_A_48_H	7.555	-6.275	-5.817	7.798	-5.829	-6.69	1.01	149.81	61.42
281	2jsa-12	GLU_A_48_N	GLU_A_48_CA	7.555	-6.275	-5.817	7.646	-5.504	-4.588	1.45	32.28	83.27
282	2jsa-12	GLU_A_48_CA	GLU_A_48_HA	7.646	-5.504	-4.588	8.159	-6.114	-3.844	1.09	46.97	-49.94
283	2jsa-12	GLU_A_48_CA	GLU_A_48_C	7.646	-5.504	-4.588	6.247	-5.178	-4.061	1.53	69.85	166.88
284	2jsa-12	GLU_A_48_C	GLU_A_48_O	6.247	-5.178	-4.061	6.009	-5.22	-2.855	1.23	11.33	-169.99
285	2jsa-12	GLU_A_48_C	CYS_A_49_N	6.247	-5.178	-4.061	5.358	-4.862	-4.99	1.32	134.56	160.43
286	2jsa-12	CYS_A_49_N	CYS_A_49_H	5.358	-4.862	-4.99	5.624	-4.849	-5.964	1.01	164.71	2.80
287	2jsa-12	CYS_A_49_N	CYS_A_49_CA	5.358	-4.862	-4.99	3.989	-4.529	-4.634	1.45	75.82	166.33
288	2jsa-12	CYS_A_49_CA	CYS_A_49_HA	3.989	-4.529	-4.634	4.009	-3.679	-3.951	1.09	51.22	88.65
289	2jsa-12	CYS_A_49_CA	CYS_A_49_C	3.989	-4.529	-4.634	3.378	-5.727	-3.904	1.53	61.51	-117.02
290	2jsa-12	CYS_A_49_C	CYS_A_49_O	3.378	-5.727	-3.904	2.719	-5.563	-2.878	1.23	33.50	166.03
291	2jsa-12	CYS_A_49_C	ASP_A_50_N	3.378	-5.727	-3.904	3.618	-6.905	-4.462	1.33	114.90	-78.48
292	2jsa-12	ASP_A_50_N	ASP_A_50_H	3.618	-6.905	-4.462	4.167	-6.965	-5.308	1.01	146.86	-6.24
293	2jsa-12	ASP_A_50_N	ASP_A_50_CA	3.618	-6.905	-4.462	3.101	-8.129	-3.876	1.45	66.20	-112.90
294	2jsa-12	ASP_A_50_CA	ASP_A_50_HA	3.101	-8.129	-3.876	2.03	-8.017	-3.706	1.09	81.03	174.03
295	2jsa-12	ASP_A_50_CA	ASP_A_50_C	3.101	-8.129	-3.876	3.813	-8.395	-2.548	1.53	29.78	-20.49
296	2jsa-12	ASP_A_50_C	ASP_A_50_O	3.813	-8.395	-2.548	3.286	-9.099	-1.687	1.23	45.61	-126.82
297	2jsa-12	ASP_A_50_C	HIS_A_51_N	3.813	-8.395	-2.548	4.999	-7.818	-2.423	1.32	84.59	25.94
298	2jsa-12	HIS_A_51_N	HIS_A_51_H	4.999	-7.818	-2.423	5.371	-7.252	-3.172	1.01	137.88	56.69
299	2jsa-12	HIS_A_51_N	HIS_A_51_CA	4.999	-7.818	-2.423	5.788	-7.984	-1.214	1.45	33.70	-11.88
300	2jsa-12	HIS_A_51_CA	HIS_A_51_HA	5.788	-7.984	-1.214	5.445	-8.887	-0.709	1.09	62.40	-110.80
301	2jsa-12	HIS_A_51_CA	HIS_A_51_C	5.788	-7.984	-1.214	5.546	-6.8	-0.276	1.53	52.18	101.55
302	2jsa-12	HIS_A_51_C	HIS_A_51_O	5.546	-6.8	-0.276	6.204	-6.677	0.755	1.23	32.99	108.49
303	2jsa-12	HIS_A_51_C	TYR_A_52_N	5.546	-6.8	-0.276	4.6	-5.96	-0.669	1.32	107.26	13.50
304	2jsa-12	TYR_A_52_N	TYR_A_52_H	4.6	-5.96	-0.669	4.1	-6.124	-1.531	1.01	148.60	-161.84
305	2jsa-12	TYR_A_52_N	TYR_A_52_CA	4.6	-5.96	-0.669	4.263	-4.79	0.124	1.45	56.92	106.07
306	2jsa-12	TYR_A_52_CA	TYR_A_52_HA	4.263	-4.79	0.124	5.064	-4.569	0.83	1.09	49.65	15.42
307	2jsa-12	TYR_A_52_CA	TYR_A_52_C	4.263	-4.79	0.124	2.949	-4.999	0.878	1.53	60.46	-170.96
308	2jsa-12	TYR_A_52_C	TYR_A_52_O	2.949	-4.999	0.878	2.8	-4.546	2.012	1.23	22.81	108.21
309	2jsa-12	TYR_A_52_C	VAL_A_53_N	2.949	-4.999	0.878	2.027	-5.685	0.217	1.33	119.91	-143.35
310	2jsa-12	VAL_A_53_N	VAL_A_53_H	2.027	-5.685	0.217	2.218	-6.027	-0.714	1.01	157.18	-60.82
311	2jsa-12	VAL_A_53_N	VAL_A_53_CA	2.027	-5.685	0.217	0.73	-5.959	0.811	1.45	65.86	-168.07
312	2jsa-12	VAL_A_53_CA	VAL_A_53_HA	0.73	-5.959	0.811	0.442	-5.102	1.42	1.09	56.04	108.58
313	2jsa-12	VAL_A_53_CA	VAL_A_53_C	0.73	-5.959	0.811	0.841	-7.178	1.729	1.53	53.13	-84.80
314	2jsa-12	VAL_A_53_C	VAL_A_53_O	0.841	-7.178	1.729	0.055	-8.117	1.618	1.23	95.18	-129.93
315	2jsa-12	VAL_A_53_C	ASN_A_54_N	0.841	-7.178	1.729	1.825	-7.124	2.615	1.33	48.04	3.14
316	2jsa-12	ASN_A_54_N	ASN_A_54_H	1.825	-7.124	2.615	2.435	-6.319	2.649	1.01	88.07	52.85
317	2jsa-12	ASN_A_54_N	ASN_A_54_CA	1.825	-7.124	2.615	2.049	-8.212	3.552	1.45	49.85	-78.37
318	2jsa-12	ASN_A_54_CA	ASN_A_54_HA	2.049	-8.212	3.552	1.16	-8.341	4.169	1.09	55.52	-171.74
319	2jsa-12	ASN_A_54_CA	ASN_A_54_C	2.049	-8.212	3.552	3.251	-7.876	4.437	1.53	54.66	15.62
320	2jsa-12	ASN_A_54_C	ASN_A_54_O	3.251	-7.876	4.437	4.14	-8.706	4.625	1.23	81.21	-43.03
321	2jsa-12	ASN_A_54_C	SER_A_55_N	3.251	-7.876	4.437	3.239	-6.658	4.959	1.33	66.80	90.56
322	2jsa-12	SER_A_55_N	SER_A_55_H	3.239	-6.658	4.959	2.475	-6.027	4.763	1.01	101.19	140.45
323	2jsa-12	SER_A_55_N	SER_A_55_CA	3.239	-6.658	4.959	4.317	-6.204	5.821	1.45	53.61	22.84
324	2jsa-12	SER_A_55_CA	SER_A_55_HA	4.317	-6.204	5.821	4.173	-6.642	6.809	1.09	25.02	-108.20
325	2jsa-12	SER_A_55_CA	SER_A_55_C	4.317	-6.204	5.821	4.276	-4.68	5.95	1.53	85.16	91.54
326	2jsa-12	SER_A_55_C	SER_A_55_O	4.276	-4.68	5.95	4.709	-4.126	6.959	1.23	34.87	51.99
327	2jsa-12	SER_A_55_C	LYS_A_56_N	4.276	-4.68	5.95	3.753	-4.044	4.911	1.33	141.60	129.43
328	2jsa-12	LYS_A_56_N	LYS_A_56_H	3.753	-4.044	4.911	3.418	-4.563	4.113	1.01	142.26	-122.84
329	2jsa-12	LYS_A_56_N	LYS_A_56_CA	3.753	-4.044	4.911	3.65	-2.594	4.896	1.45	90.59	94.06
330	2jsa-12	LYS_A_56_CA	LYS_A_56_HA	3.65	-2.594	4.896						

333	2jsa-12	LYS_A_56_C	VAL_A_57_N	2.178	-2.193	4.785	1.327	-3.205	4.702	1.32	93.59	-130.06
334	2jsa-12	VAL_A_57_N	VAL_A_57_H	1.327	-3.205	4.702	1.666	-4.156	4.714	1.01	89.32	-70.38
335	2jsa-12	VAL_A_57_N	VAL_A_57_CA	1.327	-3.205	4.702	-0.104	-2.972	4.592	1.45	94.34	170.75
336	2jsa-12	VAL_A_57_CA	VAL_A_57_HA	-0.104	-2.972	4.592	-0.262	-1.942	4.273	1.09	107.02	98.72
337	2jsa-12	VAL_A_57_CA	VAL_A_57_C	-0.104	-2.972	4.592	-0.751	-3.148	5.966	1.53	26.01	-164.78
338	2jsa-12	VAL_A_57_C	VAL_A_57_O	-0.751	-3.148	5.966	-1.598	-2.35	6.364	1.23	71.12	136.71
339	2jsa-12	VAL_A_57_C	ASP_A_58_N	-0.751	-3.148	5.966	-0.327	-4.198	6.655	1.33	58.68	-68.01
340	2jsa-12	ASP_A_58_N	ASP_A_58_H	-0.327	-4.198	6.655	0.373	-4.813	6.265	1.01	112.71	-41.30
341	2jsa-12	ASP_A_58_N	ASP_A_58_CA	-0.327	-4.198	6.655	-0.855	-4.489	7.977	1.45	24.51	-151.14
342	2jsa-12	ASP_A_58_CA	ASP_A_58_HA	-0.855	-4.489	7.977	-1.924	-4.687	7.898	1.09	94.16	-169.51
343	2jsa-12	ASP_A_58_CA	ASP_A_58_C	-0.855	-4.489	7.977	-0.616	-3.287	8.893	1.53	53.22	78.75
344	2jsa-12	ASP_A_58_C	ASP_A_58_O	-0.616	-3.287	8.893	-1.501	-2.892	9.649	1.23	52.04	155.95
345	2jsa-12	ASP_A_58_C	PRO_A_59_N	-0.616	-3.287	8.893	0.619	-2.725	8.793	1.36	94.22	24.47
346	2jsa-12	PRO_A_59_N	PRO_A_59_CA	0.619	-2.725	8.793	0.986	-1.577	9.603	1.45	56.10	72.27
347	2jsa-12	PRO_A_59_CA	PRO_A_59_HA	0.986	-1.577	9.603	0.669	-1.731	10.634	1.09	18.87	-154.09
348	2jsa-12	PRO_A_59_CA	PRO_A_59_C	0.986	-1.577	9.603	0.325	-0.3	9.078	1.53	110.06	117.37
349	2jsa-12	PRO_A_59_C	PRO_A_59_O	0.325	-0.3	9.078	-0.303	0.436	9.838	1.23	51.85	130.47
350	2jsa-12	PRO_A_59_C	ILE_A_60_N	0.325	-0.3	9.078	0.488	-0.078	7.781	1.33	168.01	53.71
351	2jsa-12	ILE_A_60_N	ILE_A_60_H	0.488	-0.078	7.781	1.016	-0.728	7.216	1.01	124.01	-50.91
352	2jsa-12	ILE_A_60_N	ILE_A_60_CA	0.488	-0.078	7.781	-0.085	1.096	7.146	1.45	115.92	116.02
353	2jsa-12	ILE_A_60_CA	ILE_A_60_HA	-0.085	1.096	7.146	0.436	1.974	7.528	1.09	69.49	59.32
354	2jsa-12	ILE_A_60_CA	ILE_A_60_C	-0.085	1.096	7.146	-1.558	1.218	7.544	1.53	74.93	175.27
355	2jsa-12	ILE_A_60_C	ILE_A_60_O	-1.558	1.218	7.544	-2.023	2.303	7.889	1.23	73.71	113.20
356	2jsa-12	ILE_A_60_C	ILE_A_61_N	-1.558	1.218	7.544	-2.25	0.09	7.481	1.32	92.73	-121.53
357	2jsa-12	ILE_A_61_N	ILE_A_61_H	-2.25	0.09	7.481	-1.801	-0.766	7.188	1.01	106.86	-62.32
358	2jsa-12	ILE_A_61_N	ILE_A_61_CA	-2.25	0.09	7.481	-3.66	0.057	7.831	1.45	76.06	-178.66
359	2jsa-12	ILE_A_61_CA	ILE_A_61_HA	-3.66	0.057	7.831	-4.14	0.926	7.38	1.09	114.43	118.91
360	2jsa-12	ILE_A_61_CA	ILE_A_61_C	-3.66	0.057	7.831	-3.808	0.18	9.349	1.53	7.22	140.27
361	2jsa-12	ILE_A_61_C	ILE_A_61_O	-3.808	0.18	9.349	-4.883	0.513	9.846	1.23	66.17	162.79
362	2jsa-12	ILE_A_61_C	HIS_A_62_N	-3.808	0.18	9.349	-2.713	-0.096	10.042	1.32	58.46	-14.15
363	2jsa-12	HIS_A_62_N	HIS_A_62_H	-2.713	-0.096	10.042	-1.864	-0.365	9.566	1.01	118.12	-17.58
364	2jsa-12	HIS_A_62_N	HIS_A_62_CA	-2.713	-0.096	10.042	-2.707	-0.019	11.494	1.45	3.04	85.54
365	2jsa-12	HIS_A_62_CA	HIS_A_62_HA	-2.707	-0.019	11.494	-3.596	-0.531	11.862	1.09	70.27	-150.06
366	2jsa-12	HIS_A_62_CA	HIS_A_62_C	-2.707	-0.019	11.494	-2.794	1.443	11.931	1.53	73.39	93.41
367	2jsa-12	HIS_A_62_C	HIS_A_62_O	-2.794	1.443	11.931	-3.301	1.744	13.012	1.23	28.61	149.30
368	2jsa-12	HIS_A_62_C	GLU_A_63_N	-2.794	1.443	11.931	-2.292	2.316	11.07	1.32	130.53	60.10
369	2jsa-12	GLU_A_63_N	GLU_A_63_H	-2.292	2.316	11.07	-1.891	1.998	10.199	1.01	149.56	-38.42
370	2jsa-12	GLU_A_63_N	GLU_A_63_CA	-2.292	2.316	11.07	-2.306	3.741	11.354	1.45	78.73	90.56
371	2jsa-12	GLU_A_63_CA	GLU_A_63_HA	-2.306	3.741	11.354	-2.128	3.873	12.421	1.09	11.73	36.56
372	2jsa-12	GLU_A_63_CA	GLU_A_63_C	-2.306	3.741	11.354	-3.674	4.337	11.017	1.53	102.73	156.46
373	2jsa-12	GLU_A_63_C	GLU_A_63_O	-3.674	4.337	11.017	-4.286	5.006	11.847	1.23	47.53	132.45
374	2jsa-12	GLU_A_63_C	LEU_A_64_N	-3.674	4.337	11.017	-4.115	4.071	9.795	1.33	157.15	-148.90
375	2jsa-12	LEU_A_64_N	LEU_A_64_H	-4.115	4.071	9.795	-3.558	3.512	9.164	1.01	128.65	-45.10
376	2jsa-12	LEU_A_64_N	LEU_A_64_CA	-4.115	4.071	9.795	-5.398	4.571	9.336	1.45	108.44	158.71
377	2jsa-12	LEU_A_64_CA	LEU_A_64_HA	-5.398	4.571	9.336	-5.392	5.656	9.437	1.09	84.68	89.68
378	2jsa-12	LEU_A_64_CA	LEU_A_64_C	-5.398	4.571	9.336	-6.506	4.026	10.241	1.53	53.76	-153.81
379	2jsa-12	LEU_A_64_C	LEU_A_64_O	-6.506	4.026	10.241	-7.437	4.749	10.593	1.23	73.37	142.17
380	2jsa-12	LEU_A_64_C	GLU_A_65_N	-6.506	4.026	10.241	-6.367	2.757	10.593	1.32	74.58	-83.75
381	2jsa-12	GLU_A_65_N	GLU_A_65_H	-6.367	2.757	10.593	-5.573	2.223	10.268	1.01	108.76	-33.92
382	2jsa-12	GLU_A_65_N	GLU_A_65_CA	-6.367	2.757	10.593	-7.345	2.107	11.45	1.45	53.88	-146.39
383	2jsa-12	GLU_A_65_CA	GLU_A_65_HA	-7.345	2.107	11.45	-8.338	2.335	11.063	1.09	110.80	167.07
384	2jsa-12	GLU_A_65_CA	GLU_A_65_C	-7.345	2.107	11.45	-7.247	2.653	12.875	1.53	21.27	79.82
385	2jsa-12	GLU_A_65_C	GLU_A_65_O	-7.247	2.653	12.875	-8.221	2.615	13.627	1.23	52.35	-177.77
386	2jsa-12	GLU_A_65_C	GLY_A_66_N	-7.247	2.653	12.875	-6.063	3.149	13.205	1.33	75.58	22.73
387	2jsa-12	GLY_A_66_N	GLY_A_66_H	-6.063	3.149	13.205	-5.306	3.148	12.536	1.01	131.47	-0.08
388	2jsa-12	GLY_A_66_N	GLY_A_66_CA	-6.063	3.149	13.205	-5.827	3.703	14.528	1.45	24.47	66.93
389	2jsa-12	GLY_A_66_CA	GLY_A_66_C	-5.827	3.703	14.528	-6.435	5.101	14.654	1.53	85.28	113.50
390	2jsa-12	GLY_A_66_C	GLY_A_66_O	-6.435	5.101	14.654	-6.972	5.456	15.702	1.23	31.56	146.53
391	2jsa-12	GLY_A_66_C	GLY_A_67_N	-6.435	5.101	14.654	-6.332	5.857	13.57	1.33	144.86	82.24
392	2jsa-12	GLY_A_67_N	GLY_A_67_H	-6.332	5.857	13.57	-5.878	5.499	12.742	1.01	145.07	-38.26
393	2jsa-12	GLY_A_67_N	GLY_A_67_CA	-6.332	5.857	13.57	-6.865	7.208	13.547	1.45	90.91	111.53
394	2jsa-12	GLY_A_67_CA	GLY_A_67_C	-6.865	7.208	13.547	-6.003	8.123	12.674	1.53	124.78	46.71
395	2jsa-12	GLY_A_67_C	GLY_A_67_O	-6.003	8.123	12.674	-6.441	9.202	12.278	1.23	108.78	112.09
396	2jsa-12	GLY_A_67_C	THR_A_68_N	-6.003	8.123	12.674	-4.793	7.658	12.4	1.32	101.94	-21.02
397	2jsa-12	THR_A_68_N	THR_A_68_H	-4.793	7.658	12.4	-4.499	6.761	12.76	1.01	69.12	-71.85
398	2jsa-12	THR_A_68_N	THR_A_68_CA	-4.793	7.658	12.4	-3.866	8.42	11.582	1.45	124.28	39.42
399	2jsa-12	THR_A_68_CA	THR_A_68_HA	-3.866	8.42	11.582	-3.755	9.415	12.014	1.09	66.66	83.63
400	2jsa-12	THR_A_68_CA	THR_A_68_C	-3.866	8.42	11.582	-4.415	8.581	10.163	1.53	158.04	163.66
401	2jsa-12	THR_A_68_C	THR_A_68_O	-4.415	8.581	10.163	-5.225	7.772	9.712	1.23	111.50	-135.04
402	2jsa-12	THR_A_68_C	ALA_A_69_N	-4.415	8.581	10.163	-3.952	9.629	9.499	1.32	120.09	66.16
403	2jsa-12	ALA_A_69_N	ALA_A_69_H	-3.952	9.629	9.499	-3.287	10.253	9.934	1.01	64.50	43.18
404	2jsa-12	ALA_A_69_N	ALA_A_69_CA	-3.952	9.629	9.499	-4.386	9.906	8.139	1.45	159.26	147.45
405	2jsa-12	ALA_A_69_CA	ALA_A_69_HA	-4.386	9.906	8.139	-5.42	9.58	8.028	1.09	95.85	-162.50
406	2jsa-12	ALA_A_69_CA	ALA_A_69_C	-4.386	9.906	8.139	-3.521	9.111	7.16	1.53	129.80	-42.59
407	2jsa-12	ALA_A_69_C	ALA_A_69_O	-3.521	9.111	7.16	-2.499	8.547	7.547	1.23	71.66	-28.89
408	2jsa-12	ALA_A_69_C	PRO_A_70_N	-3.521	9.111	7.16	-3.975	9.09	5.878	1.36	160.48	-177.35
409	2jsa-12	PRO_A_70_N	PRO_A_70_CA	-3.975	9.09	5.878	-3.253	8.374	4.84	1.45	135.59	-44.76
410	2jsa-12	PRO_A_70_CA	PRO_A_70_HA	-3.253	8.374	4.84	-2.954	7.391	5.204	1.09	70.49	-73.08
411	2jsa-12	PRO_A_70_CA	PRO_A_70_C	-3.253	8.374	4.84	-1.995	9.137	4.42	1.53	105.93	31.24
412	2jsa-12	PRO_A_70_C	PRO_A_70_O	-1.995	9.137	4.42	-1.092	8.564	3.813	1.23	119.58	-32.40
413	2jsa-12	PRO_A_70_C	LYS_A_71_N	-1.995	9.137	4.42	-1.976	10.417	4.76	1.32	75.13	89.15
414	2jsa-12	LYS_A_71_N	LYS_A_71_H	-1.976	10.417	4.76	-2.755	10.822	5.26	1.01	60.34	152.53
415	2jsa-12	LYS_A_71_N	LYS_A_71_CA	-1.976	10.417	4.76	-0.844	11.264	4.426	1.45	103.29	36.81
416	2jsa-12	LYS_A_71_CA	LYS_A_71_HA	-0.844	11.264	4.426	-0.269	10.767	3.644	1.09	135.82	-40.84
417	2jsa-12	LYS_A_71_CA	LYS_A_71_C	-0.844	11.264	4.426	0.062	11.404	5.651	1.53	36.81	8.78
418	2jsa-12	LYS_A_71_C	LYS_A_71_O	0.062	11.404	5.651	0.978	12.224	5.659	1.23	89.63	41.83
419	2jsa-12	LYS_A_71_C	ASP_A_72_N	0.062	11.404	5.651	-0.226	10.591	6.657	1.33	40.61	-109.51
420	2jsa-12	ASP_A_72_N	ASP_A_72_H	-0.226	10.591	6.657	-0.995	9.941	6.581	1.01	94.32	-139.79
421	2jsa-12	ASP_A_72_N	ASP_A_72_CA	-0.226	10.591	6.657	0.55	10.614	7.884	1.45	32.32	1.70
422	2jsa-12	ASP_A_72_CA	ASP_A_72_HA	0.55	10.614	7.884	1.283	11.419	7.827	1.09	93.0	

426	2jsa-12	VAL_A_73_N	VAL_A_73_H	0.564	8.213	7.68	-0.37	8.325	7.314	1.01	111.26	173.16
427	2jsa-12	VAL_A_73_N	VAL_A_73_CA	0.564	8.213	7.68	1.118	6.873	7.786	1.45	85.82	-67.54
428	2jsa-12	VAL_A_73_CA	VAL_A_73_HA	1.118	6.873	7.786	1.331	6.67	8.836	1.09	15.65	-43.62
429	2jsa-12	VAL_A_73_CA	VAL_A_73_C	1.118	6.873	7.786	2.437	6.808	7.014	1.53	120.31	-2.82
430	2jsa-12	VAL_A_73_C	VAL_A_73_O	2.437	6.808	7.014	3.434	6.301	7.524	1.23	65.49	-26.95
431	2jsa-12	VAL_A_73_C	CYS_A_74_N	2.437	6.808	7.014	2.399	7.329	5.796	1.33	156.79	94.17
432	2jsa-12	CYS_A_74_N	CYS_A_74_H	2.399	7.329	5.796	1.544	7.731	5.441	1.01	110.59	154.82
433	2jsa-12	CYS_A_74_N	CYS_A_74_CA	2.399	7.329	5.796	3.579	7.336	4.949	1.45	125.67	0.34
434	2jsa-12	CYS_A_74_CA	CYS_A_74_HA	3.579	7.336	4.949	4.138	6.417	5.131	1.09	80.40	-58.69
435	2jsa-12	CYS_A_74_CA	CYS_A_74_C	3.579	7.336	4.949	4.454	8.526	5.353	1.53	74.70	53.67
436	2jsa-12	CYS_A_74_C	CYS_A_74_O	4.454	8.526	5.353	4.762	9.383	4.527	1.23	132.21	70.23
437	2jsa-12	CYS_A_74_C	THR_A_75_N	4.454	8.526	5.353	4.828	8.539	6.623	1.32	16.42	1.99
438	2jsa-12	THR_A_75_N	THR_A_75_H	4.828	8.539	6.623	4.537	7.799	7.246	1.01	51.92	-111.47
439	2jsa-12	THR_A_75_N	THR_A_75_CA	4.828	8.539	6.623	5.66	9.608	7.148	1.45	68.82	52.11
440	2jsa-12	THR_A_75_CA	THR_A_75_HA	5.66	9.608	7.148	6.4	9.878	6.394	1.09	133.75	20.05
441	2jsa-12	THR_A_75_CA	THR_A_75_C	5.66	9.608	7.148	6.41	9.138	8.395	1.53	35.37	-32.07
442	2jsa-12	THR_A_75_C	THR_A_75_O	6.41	9.138	8.395	7.639	9.16	8.43	1.23	88.37	1.03
443	2jsa-12	THR_A_75_C	LYS_A_76_N	6.41	9.138	8.395	5.638	8.724	9.39	1.33	41.36	-151.80
444	2jsa-12	LYS_A_76_N	LYS_A_76_H	5.638	8.724	9.39	4.633	8.734	9.292	1.01	95.57	179.43
445	2jsa-12	LYS_A_76_N	LYS_A_76_CA	5.638	8.724	9.39	6.214	8.249	10.636	1.45	30.93	-39.51
446	2jsa-12	LYS_A_76_CA	LYS_A_76_HA	6.214	8.249	10.636	7.088	8.862	10.859	1.09	78.20	35.04
447	2jsa-12	LYS_A_76_CA	LYS_A_76_C	6.214	8.249	10.636	6.692	6.807	10.456	1.53	96.76	-71.66
448	2jsa-12	LYS_A_76_C	LYS_A_76_O	6.692	6.807	10.456	7.736	6.425	10.982	1.23	64.68	-20.10
449	2jsa-12	LYS_A_76_C	LEU_A_77_N	6.692	6.807	10.456	5.904	6.046	9.71	1.33	124.25	-136.00
450	2jsa-12	LEU_A_77_N	LEU_A_77_H	5.904	6.046	9.71	5.06	6.428	9.308	1.01	113.46	155.65
451	2jsa-12	LEU_A_77_N	LEU_A_77_CA	5.904	6.046	9.71	6.233	4.654	9.455	1.45	100.11	-76.70
452	2jsa-12	LEU_A_77_CA	LEU_A_77_HA	6.233	4.654	9.455	6.46	4.18	10.41	1.09	28.82	-64.41
453	2jsa-12	LEU_A_77_CA	LEU_A_77_C	6.233	4.654	9.455	7.493	4.583	8.589	1.53	124.46	-3.23
454	2jsa-12	LEU_A_77_C	LEU_A_77_O	7.493	4.583	8.589	8.031	3.502	8.357	1.23	100.88	-63.54
455	2jsa-12	LEU_A_77_C	ASN_A_78_N	7.493	4.583	8.589	7.927	5.751	8.135	1.33	110.02	69.62
456	2jsa-12	ASN_A_78_N	ASN_A_78_H	7.927	5.751	8.135	7.435	6.602	8.368	1.01	76.67	120.03
457	2jsa-12	ASN_A_78_N	ASN_A_78_CA	7.927	5.751	8.135	9.112	5.834	7.299	1.45	125.14	4.01
458	2jsa-12	ASN_A_78_CA	ASN_A_78_HA	9.112	5.834	7.299	9.324	6.881	7.083	1.09	101.43	78.55
459	2jsa-12	ASN_A_78_CA	ASN_A_78_C	9.112	5.834	7.299	8.867	5.074	5.994	1.53	148.54	-107.87
460	2jsa-12	ASN_A_78_C	ASN_A_78_O	8.867	5.074	5.994	9.781	4.458	5.449	1.23	116.31	-33.98
461	2jsa-12	ASN_A_78_C	GLU_A_79_N	8.867	5.074	5.994	7.628	5.143	5.531	1.32	110.46	176.81
462	2jsa-12	GLU_A_79_N	GLU_A_79_H	7.628	5.143	5.531	6.927	5.67	6.032	1.01	60.26	143.06
463	2jsa-12	GLU_A_79_N	GLU_A_79_CA	7.628	5.143	5.531	7.25	4.469	4.3	1.45	147.88	-119.29
464	2jsa-12	GLU_A_79_CA	GLU_A_79_HA	7.25	4.469	4.3	8.141	3.996	3.888	1.09	112.22	-27.96
465	2jsa-12	GLU_A_79_CA	GLU_A_79_C	7.25	4.469	4.3	6.728	5.483	3.279	1.53	131.84	117.24
466	2jsa-12	GLU_A_79_C	GLU_A_79_O	6.728	5.483	3.279	5.539	5.496	2.966	1.23	104.75	179.37
467	2jsa-12	GLU_A_79_C	CYS_A_80_N	6.728	5.483	3.279	7.643	6.306	2.788	1.33	111.75	41.97
468	2jsa-12	CYS_A_80_N	CYS_A_80_H	7.643	6.306	2.788	8.604	6.237	3.091	1.01	72.54	-4.11
469	2jsa-12	CYS_A_80_N	CYS_A_80_CA	7.643	6.306	2.788	7.29	7.32	1.809	1.45	132.36	109.19
470	2jsa-12	CYS_A_80_CA	CYS_A_80_HA	7.29	7.32	1.809	7.07	6.823	0.864	1.09	150.09	-113.88
471	2jsa-12	CYS_A_80_CA	CYS_A_80_C	7.29	7.32	1.809	8.499	8.235	1.608	1.53	97.55	37.12
472	2jsa-12	CYS_A_80_C	CYS_A_80_O	8.499	8.235	1.608	8.966	8.415	0.484	1.23	156.00	21.08
473	2jsa-12	CYS_A_80_C	PRO_A_81_N	8.499	8.235	1.608	8.985	8.804	2.744	1.36	33.37	49.50
474	2jsa-12	PRO_A_81_N	PRO_A_81_CA	8.985	8.804	2.744	10.131	9.696	2.702	1.45	91.66	37.90
475	2jsa-12	PRO_A_81_CA	PRO_A_81_HA	10.131	9.696	2.702	10.023	10.405	1.881	1.09	138.86	98.66
476	2jsa-12	PRO_A_81_CA	PRO_A_81_C	10.131	9.696	2.702	11.429	8.913	2.498	1.53	97.66	-31.10
477	2jsa-12	PRO_A_81_C	PRO_A_81_O	11.429	8.913	2.498	12.249	8.814	3.41	1.23	42.17	-6.88
1	2jsa-13	ARG_A_1_N	ARG_A_1_H	14.991	3.291	3.617	14.475	4.007	4.108	1.01	60.91	125.78
2	2jsa-13	ARG_A_1_N	ARG_A_1_CA	14.991	3.291	3.617	14.724	3.088	2.203	1.45	166.66	-142.75
3	2jsa-13	ARG_A_1_CA	ARG_A_1_HA	14.724	3.088	2.203	15.645	3.27	1.649	1.09	120.55	11.18
4	2jsa-13	ARG_A_1_CA	ARG_A_1_C	14.724	3.088	2.203	13.65	4.065	1.72	1.53	108.40	137.71
5	2jsa-13	ARG_A_1_C	ARG_A_1_O	13.65	4.065	1.72	12.634	4.256	2.388	1.23	57.13	169.35
6	2jsa-13	ARG_A_1_C	SER_A_2_N	13.65	4.065	1.72	13.91	4.657	0.565	1.32	150.76	66.29
7	2jsa-13	SER_A_2_N	SER_A_2_H	13.91	4.657	0.565	14.766	4.451	0.069	1.01	119.39	-13.53
8	2jsa-13	SER_A_2_N	SER_A_2_CA	13.91	4.657	0.565	12.979	5.61	-0.015	1.45	113.53	134.33
9	2jsa-13	SER_A_2_CA	SER_A_2_HA	12.979	5.61	-0.015	12.005	5.461	0.449	1.09	64.78	-171.30
10	2jsa-13	SER_A_2_CA	SER_A_2_C	12.979	5.61	-0.015	12.848	5.364	-1.519	1.53	169.50	-118.04
11	2jsa-13	SER_A_2_C	SER_A_2_O	12.848	5.364	-1.519	13.839	5.399	-2.247	1.23	126.28	2.02
12	2jsa-13	SER_A_2_C	ALA_A_3_N	12.848	5.364	-1.519	11.616	5.12	-1.942	1.33	108.61	-168.80
13	2jsa-13	ALA_A_3_N	ALA_A_3_H	11.616	5.12	-1.942	10.848	5.105	-1.287	1.01	49.55	-178.88
14	2jsa-13	ALA_A_3_N	ALA_A_3_CA	11.616	5.12	-1.942	11.343	4.869	-3.347	1.45	165.21	-137.40
15	2jsa-13	ALA_A_3_CA	ALA_A_3_HA	11.343	4.869	-3.347	11.679	5.728	-3.929	1.09	122.25	68.64
16	2jsa-13	ALA_A_3_CA	ALA_A_3_C	11.343	4.869	-3.347	9.834	4.708	-3.547	1.53	97.51	-173.91
17	2jsa-13	ALA_A_3_C	ALA_A_3_O	9.834	4.708	-3.547	9.041	5.247	-2.777	1.23	51.23	145.80
18	2jsa-13	ALA_A_3_C	LEU_A_4_N	9.834	4.708	-3.547	9.484	3.965	-4.587	1.33	141.70	-115.22
19	2jsa-13	LEU_A_4_N	LEU_A_4_H	9.484	3.965	-4.587	10.191	3.554	-5.179	1.01	125.90	-30.17
20	2jsa-13	LEU_A_4_N	LEU_A_4_CA	9.484	3.965	-4.587	8.085	3.726	-4.898	1.45	102.36	-170.31
21	2jsa-13	LEU_A_4_CA	LEU_A_4_HA	8.085	3.726	-4.898	7.613	4.69	-5.088	1.09	100.04	116.09
22	2jsa-13	LEU_A_4_CA	LEU_A_4_C	8.085	3.726	-4.898	7.396	3.103	-3.684	1.53	37.42	-137.88
23	2jsa-13	LEU_A_4_C	LEU_A_4_O	7.396	3.103	-3.684	6.17	3.136	-3.575	1.23	84.92	178.46
24	2jsa-13	LEU_A_4_C	SER_A_5_N	7.396	3.103	-3.684	8.212	2.547	-2.8	1.33	48.16	-34.27
25	2jsa-13	SER_A_5_N	SER_A_5_H	8.212	2.547	-2.8	9.211	2.555	-2.954	1.01	98.76	0.46
26	2jsa-13	SER_A_5_N	SER_A_5_CA	8.212	2.547	-2.8	7.696	1.918	-1.596	1.45	34.05	-129.36
27	2jsa-13	SER_A_5_CA	SER_A_5_HA	7.696	1.918	-1.596	7.217	0.981	-1.879	1.09	105.05	-117.08
28	2jsa-13	SER_A_5_CA	SER_A_5_C	7.696	1.918	-1.596	6.651	2.822	-0.938	1.53	64.54	139.14
29	2jsa-13	SER_A_5_C	SER_A_5_O	6.651	2.822	-0.938	5.616	2.346	-0.477	1.23	67.97	-155.30
30	2jsa-13	SER_A_5_C	CYS_A_6_N	6.651	2.822	-0.938	6.96	4.11	-0.917	1.32	89.09	76.51
31	2jsa-13	CYS_A_6_N	CYS_A_6_H	6.96	4.11	-0.917	7.831	4.431	-1.316	1.01	113.26	20.23
32	2jsa-13	CYS_A_6_N	CYS_A_6_CA	6.96	4.11	-0.917	6.061	5.085	-0.324	1.45	65.91	132.68
33	2jsa-13	CYS_A_6_CA	CYS_A_6_HA	6.061	5.085	-0.324	5.861	4.785	0.705	1.09	19.31	-123.69
34	2jsa-13	CYS_A_6_CA	CYS_A_6_C	6.061	5.085	-0.324	4.745	5.062	-1.103	1.53	120.62	-179.00
35	2jsa-13	CYS_A_6_C	CYS_A_6_O	4.745	5.062	-1.103	3.7	4.719	-0.554	1.23	63.47	-161.83
36	2jsa-13	CYS_A_6_C	GLN_A_7_N	4.745	5.062	-1.103	4.839	5.432	-2.372	1.33	163.26	75.75
37	2jsa-13	GLN_A_7_N	GLN_A_7_H	4.839	5.432	-2.372	5.733	5.703	-2.758	1.01	112.45	16.86
38	2jsa-13	GLN_A_7_N	GLN_A_7_CA	4.839	5.432	-2.372	3.669	5.458	-3.233	1.45	126.34	178.73
39	2jsa-13	GLN_A_7_CA	GLN_A_7_HA	3.669	5.458	-3.233	3.108	6.366	-3.011	1.09	78.25	121.71
40	2jsa-13	GLN_A_7_CA	GLN_A_7_C									

42	2jsa-13	GLN_A_7_C	MET_A_8_N	2.77	4.254	-2.944	3.4	3.091	-2.867	1.32	86.67	-61.56
43	2jsa-13	MET_A_8_N	MET_A_8_H	3.4	3.091	-2.867	4.401	3.046	-2.997	1.01	97.39	-2.57
44	2jsa-13	MET_A_8_N	MET_A_8_CA	3.4	3.091	-2.867	2.673	1.861	-2.597	1.45	79.30	-120.59
45	2jsa-13	MET_A_8_CA	MET_A_8_HA	2.673	1.861	-2.597	2.045	1.63	-3.457	1.09	142.11	-159.80
46	2jsa-13	MET_A_8_CA	MET_A_8_C	2.673	1.861	-2.597	1.785	2.011	-1.36	1.53	36.06	170.41
47	2jsa-13	MET_A_8_C	MET_A_8_O	1.785	2.011	-1.36	0.642	1.557	-1.354	1.23	89.72	-158.34
48	2jsa-13	MET_A_8_C	CYS_A_9_N	1.785	2.011	-1.36	2.345	2.648	-0.342	1.33	39.80	-48.68
49	2jsa-13	CYS_A_9_N	CYS_A_9_H	2.345	2.648	-0.342	3.291	2.996	-0.417	1.01	94.26	20.20
50	2jsa-13	CYS_A_9_N	CYS_A_9_CA	2.345	2.648	-0.342	1.618	2.861	0.898	1.45	31.42	163.67
51	2jsa-13	CYS_A_9_CA	CYS_A_9_HA	1.618	2.861	0.898	1.315	1.89	1.29	1.09	68.92	-107.33
52	2jsa-13	CYS_A_9_CA	CYS_A_9_C	1.618	2.861	0.898	0.36	3.674	0.583	1.53	101.88	147.13
53	2jsa-13	CYS_A_9_C	CYS_A_9_O	0.36	3.674	0.583	-0.665	3.517	1.244	1.23	57.48	-171.29
54	2jsa-13	CYS_A_9_C	GLU_A_10_N	0.36	3.674	0.583	0.48	4.524	-0.427	1.33	139.64	81.96
55	2jsa-13	GLU_A_10_N	GLU_A_10_H	0.48	4.524	-0.427	1.354	4.599	-0.927	1.01	119.68	4.90
56	2jsa-13	GLU_A_10_N	GLU_A_10_CA	0.48	4.524	-0.427	-0.635	5.361	-0.836	1.45	106.35	143.11
57	2jsa-13	GLU_A_10_CA	GLU_A_10_HA	-0.635	5.361	-0.836	-1.162	5.684	0.062	1.09	34.54	148.50
58	2jsa-13	GLU_A_10_CA	GLU_A_10_C	-0.635	5.361	-0.836	-1.607	4.561	-1.705	1.53	124.62	-140.54
59	2jsa-13	GLU_A_10_C	GLU_A_10_O	-1.607	4.561	-1.705	-2.695	5.038	-2.026	1.23	105.12	156.33
60	2jsa-13	GLU_A_10_C	LEU_A_11_N	-1.607	4.561	-1.705	-1.181	3.358	-2.061	1.32	105.59	-70.50
61	2jsa-13	LEU_A_11_N	LEU_A_11_H	-1.181	3.358	-2.061	-0.273	3.03	-1.761	1.01	72.74	-19.86
62	2jsa-13	LEU_A_11_N	LEU_A_11_CA	-1.181	3.358	-2.061	-2.002	2.487	-2.885	1.45	124.54	-133.31
63	2jsa-13	LEU_A_11_CA	LEU_A_11_HA	-2.002	2.487	-2.885	-2.667	3.113	-3.479	1.09	123.04	136.73
64	2jsa-13	LEU_A_11_CA	LEU_A_11_C	-2.002	2.487	-2.885	-2.872	1.61	-1.984	1.53	53.89	-134.77
65	2jsa-13	LEU_A_11_C	LEU_A_11_O	-2.872	1.61	-1.984	-4.054	1.409	-2.26	1.23	102.96	-170.35
66	2jsa-13	LEU_A_11_C	VAL_A_12_N	-2.872	1.61	-1.984	-2.254	1.108	-0.924	1.33	36.91	-39.09
67	2jsa-13	VAL_A_12_N	VAL_A_12_H	-2.254	1.108	-0.924	-1.279	1.314	-0.759	1.01	80.60	11.93
68	2jsa-13	VAL_A_12_N	VAL_A_12_CA	-2.254	1.108	-0.924	-2.957	0.256	0.019	1.45	49.51	-129.53
69	2jsa-13	VAL_A_12_CA	VAL_A_12_HA	-2.957	0.256	0.019	-3.485	-0.515	-0.541	1.09	120.93	-124.40
70	2jsa-13	VAL_A_12_CA	VAL_A_12_C	-2.957	0.256	0.019	-3.994	1.088	0.776	1.53	60.34	141.26
71	2jsa-13	VAL_A_12_C	VAL_A_12_O	-3.994	1.088	0.776	-5.152	0.687	0.893	1.23	84.55	-160.90
72	2jsa-13	VAL_A_12_C	VAL_A_13_N	-3.994	1.088	0.776	-3.542	2.231	1.271	1.33	68.06	68.42
73	2jsa-13	VAL_A_13_N	VAL_A_13_H	-3.542	2.231	1.271	-2.577	2.497	1.137	1.01	97.62	15.41
74	2jsa-13	VAL_A_13_N	VAL_A_13_CA	-3.542	2.231	1.271	-4.416	3.123	2.013	1.45	59.28	134.42
75	2jsa-13	VAL_A_13_CA	VAL_A_13_HA	-4.416	3.123	2.013	-4.841	2.57	2.851	1.09	39.77	-127.54
76	2jsa-13	VAL_A_13_CA	VAL_A_13_C	-4.416	3.123	2.013	-5.566	3.572	1.109	1.53	126.21	158.67
77	2jsa-13	VAL_A_13_C	VAL_A_13_O	-5.566	3.572	1.109	-6.733	3.353	1.427	1.23	75.01	-169.37
78	2jsa-13	VAL_A_13_C	LYS_A_14_N	-5.566	3.572	1.109	-5.194	4.195	-0.001	1.33	146.83	59.16
79	2jsa-13	LYS_A_14_N	LYS_A_14_H	-5.194	4.195	-0.001	-4.214	4.342	-0.198	1.01	101.24	8.53
80	2jsa-13	LYS_A_14_N	LYS_A_14_CA	-5.194	4.195	-0.001	-6.18	4.678	-0.953	1.45	130.93	153.90
81	2jsa-13	LYS_A_14_CA	LYS_A_14_HA	-6.18	4.678	-0.953	-6.663	5.556	-0.523	1.09	66.78	118.82
82	2jsa-13	LYS_A_14_CA	LYS_A_14_C	-6.18	4.678	-0.953	-7.254	3.608	-1.155	1.53	97.59	-135.11
83	2jsa-13	LYS_A_14_C	LYS_A_14_O	-7.254	3.608	-1.155	-8.418	3.929	-1.398	1.23	101.38	164.58
84	2jsa-13	LYS_A_14_C	LYS_A_15_N	-7.254	3.608	-1.155	-6.829	2.359	-1.047	1.32	85.32	-71.21
85	2jsa-13	LYS_A_15_N	LYS_A_15_H	-6.829	2.359	-1.047	-5.857	2.169	-0.845	1.01	78.47	-11.06
86	2jsa-13	LYS_A_15_N	LYS_A_15_CA	-6.829	2.359	-1.047	-7.74	1.239	-1.214	1.45	96.60	-129.12
87	2jsa-13	LYS_A_15_CA	LYS_A_15_HA	-7.74	1.239	-1.214	-8.468	1.508	-1.979	1.09	134.59	159.72
88	2jsa-13	LYS_A_15_CA	LYS_A_15_C	-7.74	1.239	-1.214	-8.503	1.009	0.092	1.53	31.39	-163.23
89	2jsa-13	LYS_A_15_C	LYS_A_15_O	-8.503	1.009	0.092	-9.701	1.73	0.074	1.23	90.84	-166.89
90	2jsa-13	LYS_A_15_C	TYR_A_16_N	-8.503	1.009	0.092	-7.777	1.132	1.193	1.32	33.77	9.62
91	2jsa-13	TYR_A_16_N	TYR_A_16_H	-7.777	1.132	1.193	-6.795	1.361	1.132	1.01	93.46	13.13
92	2jsa-13	TYR_A_16_N	TYR_A_16_CA	-7.777	1.132	1.193	-8.37	0.941	2.506	1.45	25.38	-162.15
93	2jsa-13	TYR_A_16_CA	TYR_A_16_HA	-8.37	0.941	2.506	-8.937	0.011	2.532	1.09	88.63	-121.37
94	2jsa-13	TYR_A_16_CA	TYR_A_16_C	-8.37	0.941	2.506	-9.281	2.114	2.872	1.53	76.16	127.83
95	2jsa-13	TYR_A_16_C	TYR_A_16_O	-9.281	2.114	2.872	-10.496	1.951	2.98	1.23	84.97	-172.36
96	2jsa-13	TYR_A_16_C	GLU_A_17_N	-9.281	2.114	2.872	-8.659	3.27	3.054	1.33	82.11	61.72
97	2jsa-13	GLU_A_17_N	GLU_A_17_H	-8.659	3.27	3.054	-7.656	3.33	2.948	1.01	96.02	3.42
98	2jsa-13	GLU_A_17_N	GLU_A_17_CA	-8.659	3.27	3.054	-9.398	4.47	3.407	1.45	75.94	121.63
99	2jsa-13	GLU_A_17_CA	GLU_A_17_HA	-9.398	4.47	3.407	-9.737	4.367	4.438	1.09	18.97	-163.10
100	2jsa-13	GLU_A_17_CA	GLU_A_17_C	-9.398	4.47	3.407	-10.627	4.619	2.508	1.53	125.99	173.09
101	2jsa-13	GLU_A_17_C	GLU_A_17_O	-10.627	4.619	2.508	-11.69	5.034	2.967	1.23	68.09	158.67
102	2jsa-13	GLU_A_17_C	GLY_A_18_N	-10.627	4.619	2.508	-10.441	4.273	1.242	1.33	162.76	-61.74
103	2jsa-13	GLY_A_18_N	GLY_A_18_H	-10.441	4.273	1.242	-9.538	3.94	0.934	1.01	107.75	-20.24
104	2jsa-13	GLY_A_18_N	GLY_A_18_CA	-10.441	4.273	1.242	-11.521	4.363	0.274	1.45	131.77	175.24
105	2jsa-13	GLY_A_18_CA	GLY_A_18_C	-11.521	4.363	0.274	-12.036	2.974	-0.104	1.53	104.31	-110.34
106	2jsa-13	GLY_A_18_C	GLY_A_18_O	-12.036	2.974	-0.104	-12.384	2.73	-1.259	1.23	159.80	-144.96
107	2jsa-13	GLY_A_18_C	SER_A_19_N	-12.036	2.974	-0.104	-12.069	2.099	0.891	1.33	41.35	-92.16
108	2jsa-13	SER_A_19_N	SER_A_19_H	-12.069	2.099	0.891	-11.768	2.369	1.817	1.01	23.59	41.89
109	2jsa-13	SER_A_19_N	SER_A_19_CA	-12.069	2.099	0.891	-12.536	0.74	0.676	1.45	98.51	-108.96
110	2jsa-13	SER_A_19_CA	SER_A_19_HA	-12.536	0.74	0.676	-12.295	0.454	-0.348	1.09	159.94	-49.88
111	2jsa-13	SER_A_19_CA	SER_A_19_C	-12.536	0.74	0.676	-14.053	0.673	0.86	1.53	83.09	-177.47
112	2jsa-13	SER_A_19_C	SER_A_19_O	-14.053	0.673	0.86	-14.774	0.254	-0.045	1.23	137.34	-149.84
113	2jsa-13	SER_A_19_C	ALA_A_20_N	-14.053	0.673	0.86	-14.494	1.092	2.037	1.32	27.33	136.47
114	2jsa-13	ALA_A_20_N	ALA_A_20_H	-14.494	1.092	2.037	-13.843	1.424	2.735	1.01	46.31	27.02
115	2jsa-13	ALA_A_20_N	ALA_A_20_CA	-14.494	1.092	2.037	-15.912	1.084	2.351	1.45	77.51	-179.68
116	2jsa-13	ALA_A_20_CA	ALA_A_20_HA	-15.912	1.084	2.351	-16.089	1.763	3.185	1.09	40.08	104.61
117	2jsa-13	ALA_A_20_CA	ALA_A_20_C	-15.912	1.084	2.351	-16.329	-0.325	2.777	1.53	73.83	-106.49
118	2jsa-13	ALA_A_20_C	ALA_A_20_O	-16.329	-0.325	2.777	-17.487	-0.558	3.12	1.23	73.81	-168.62
119	2jsa-13	ALA_A_20_C	ASP_A_21_N	-16.329	-0.325	2.777	-15.362	-1.23	2.739	1.32	91.64	-43.10
120	2jsa-13	ASP_A_21_N	ASP_A_21_H	-15.362	-1.23	2.739	-14.431	-0.969	2.445	1.01	106.91	15.66
121	2jsa-13	ASP_A_21_N	ASP_A_21_CA	-15.362	-1.23	2.739	-15.614	-2.611	3.116	1.45	74.97	-100.34
122	2jsa-13	ASP_A_21_CA	ASP_A_21_HA	-15.614	-2.611	3.116	-16.685	-2.751	3.258	1.09	82.51	-172.55
123	2jsa-13	ASP_A_21_CA	ASP_A_21_C	-15.614	-2.611	3.116	-14.871	-2.923	4.416	1.53	31.79	-22.78
124	2jsa-13	ASP_A_21_C	ASP_A_21_O	-14.871	-2.923	4.416	-15.16	-3.92	5.077	1.23	57.51	-106.17
125	2jsa-13	ASP_A_21_C	LYS_A_22_N	-14.871	-2.923	4.416	-13.927	-2.053	4.746	1.33	75.58	42.66
126	2jsa-13	LYS_A_22_N	LYS_A_22_H	-13.927	-2.053	4.746	-13.742	-1.255	4.155	1.01	125.81	76.95
127	2jsa-13	LYS_A_22_N	LYS_A_22_CA	-13.927	-2.053	4.746	-13.141	-2.223	5.956	1.45	33.61	-12.20
128	2jsa-13	LYS_A_22_CA	LYS_A_22_HA	-13.141	-2.223	5.956	-12.302	-1.528	5.915	1.09	92.16	39.64
129	2jsa-13	LYS_A_22_CA	LYS_A_22_C	-13.141	-2.223	5.956	-12.568	-3.642	5.991	1.53	88.69	-68.01
130	2jsa-13	LYS_A_22_C	LYS_A_22_O	-12.568	-3.642	5.991	-12.798	-4.385	6.944	1.23	39.22	-107.20
131	2jsa-13	LYS_A_22_C	ASP_A_23_N	-12.568	-3.642	5.991	-11.833	-3.974	4.94	1.32	142.50	-24.31
132	2jsa-13	ASP_A_23_N	ASP_A_23_H	-11.833	-3.974	4.94	-11.686	-3.311				

135	2jsa-13	ASP_A_23_CA	ASP_A_23_C	-11.225	-5.29	4.838	-9.819	-5.154	4.252	1.53	112.53	5.52
136	2jsa-13	ASP_A_23_C	ASP_A_23_O	-9.819	-5.154	4.252	-9.661	-4.785	3.089	1.23	160.96	66.82
137	2jsa-13	ASP_A_23_C	ALA_A_24_N	-9.819	-5.154	4.252	-8.834	-5.459	5.083	1.32	51.13	-17.20
138	2jsa-13	ALA_A_24_N	ALA_A_24_H	-8.834	-5.459	5.083	-9.038	-5.755	6.027	1.01	20.85	-124.57
139	2jsa-13	ALA_A_24_N	ALA_A_24_CA	-8.834	-5.459	5.083	-7.446	-5.375	4.662	1.45	106.84	3.46
140	2jsa-13	ALA_A_24_CA	ALA_A_24_HA	-7.446	-5.375	4.662	-7.285	-4.413	4.176	1.09	116.49	80.50
141	2jsa-13	ALA_A_24_CA	ALA_A_24_C	-7.446	-5.375	4.662	-7.156	-6.485	3.649	1.53	131.44	-75.36
142	2jsa-13	ALA_A_24_C	ALA_A_24_O	-7.156	-6.485	3.649	-6.065	-6.545	3.083	1.23	117.38	-3.15
143	2jsa-13	ALA_A_24_C	ASN_A_25_N	-7.156	-6.485	3.649	-8.153	-7.334	3.45	1.32	98.64	-139.58
144	2jsa-13	ASN_A_25_N	ASN_A_25_H	-8.153	-7.334	3.45	-9.023	-7.222	3.95	1.01	60.32	172.66
145	2jsa-13	ASN_A_25_N	ASN_A_25_CA	-8.153	-7.334	3.45	-8.02	-8.439	2.515	1.45	130.03	-83.14
146	2jsa-13	ASN_A_25_CA	ASN_A_25_HA	-8.02	-8.439	2.515	-7.0	-8.823	2.559	1.09	87.69	-20.63
147	2jsa-13	ASN_A_25_CA	ASN_A_25_C	-8.02	-8.439	2.515	-8.328	-7.943	1.1	1.53	157.58	121.84
148	2jsa-13	ASN_A_25_C	ASN_A_25_O	-8.328	-7.943	1.1	-7.546	-8.164	0.177	1.23	138.64	-15.78
149	2jsa-13	ASN_A_25_C	VAL_A_26_N	-8.328	-7.943	1.1	-9.469	-7.281	0.975	1.33	95.41	149.88
150	2jsa-13	VAL_A_26_N	VAL_A_26_H	-9.469	-7.281	0.975	-10.063	-7.134	1.779	1.01	37.27	166.10
151	2jsa-13	VAL_A_26_N	VAL_A_26_CA	-9.469	-7.281	0.975	-9.89	-6.754	-0.311	1.45	152.32	128.62
152	2jsa-13	VAL_A_26_CA	VAL_A_26_HA	-9.89	-6.754	-0.311	-9.673	-7.499	-1.076	1.09	134.59	-73.76
153	2jsa-13	VAL_A_26_CA	VAL_A_26_C	-9.89	-6.754	-0.311	-9.081	-5.495	-0.631	1.53	102.07	57.28
154	2jsa-13	VAL_A_26_C	VAL_A_26_O	-9.081	-5.495	-0.631	-9.122	-4.994	-1.754	1.23	155.89	94.68
155	2jsa-13	VAL_A_26_C	ILE_A_27_N	-9.081	-5.495	-0.631	-8.363	-5.02	0.377	1.33	40.50	33.49
156	2jsa-13	ILE_A_27_N	ILE_A_27_H	-8.363	-5.02	0.377	-8.376	-5.484	1.274	1.01	27.36	-91.60
157	2jsa-13	ILE_A_27_N	ILE_A_27_CA	-8.363	-5.02	0.377	-7.544	-3.83	0.218	1.45	96.28	55.46
158	2jsa-13	ILE_A_27_CA	ILE_A_27_HA	-7.544	-3.83	0.218	-8.027	-3.183	-0.514	1.09	132.20	126.74
159	2jsa-13	ILE_A_27_CA	ILE_A_27_C	-7.544	-3.83	0.218	-6.178	-4.227	-0.344	1.53	111.56	-16.21
160	2jsa-13	ILE_A_27_C	ILE_A_27_O	-6.178	-4.227	-0.344	-5.899	-4.007	-1.521	1.23	163.20	38.26
161	2jsa-13	ILE_A_27_C	LYS_A_28_N	-6.178	-4.227	-0.344	-5.362	-4.806	0.525	1.33	49.02	-35.36
162	2jsa-13	LYS_A_28_N	LYS_A_28_H	-5.362	-4.806	0.525	-5.658	-4.956	1.479	1.01	19.18	-153.13
163	2jsa-13	LYS_A_28_N	LYS_A_28_CA	-5.362	-4.806	0.525	-4.032	-5.236	0.13	1.45	105.78	-17.92
164	2jsa-13	LYS_A_28_CA	LYS_A_28_HA	-4.032	-5.236	0.13	-3.403	-4.35	0.043	1.09	94.58	54.63
165	2jsa-13	LYS_A_28_CA	LYS_A_28_C	-4.032	-5.236	0.13	-4.101	-5.895	-1.249	1.53	154.34	-95.98
166	2jsa-13	LYS_A_28_C	LYS_A_28_O	-4.101	-5.895	-1.249	-3.189	-5.743	-2.061	1.23	131.29	9.46
167	2jsa-13	LYS_A_28_C	LYS_A_29_N	-4.101	-5.895	-1.249	-5.192	-6.612	-1.473	1.32	99.74	-146.69
168	2jsa-13	LYS_A_29_N	LYS_A_29_H	-5.192	-6.612	-1.473	-5.902	-6.693	-0.759	1.01	45.02	-173.49
169	2jsa-13	LYS_A_29_N	LYS_A_29_CA	-5.192	-6.612	-1.473	-5.393	-7.294	-2.74	1.45	150.70	-106.42
170	2jsa-13	LYS_A_29_CA	LYS_A_29_HA	-5.393	-7.294	-2.74	-4.486	-7.854	-2.969	1.09	102.12	-31.69
171	2jsa-13	LYS_A_29_CA	LYS_A_29_C	-5.393	-7.294	-2.74	-5.59	-6.257	-3.847	1.53	136.36	100.76
172	2jsa-13	LYS_A_29_C	LYS_A_29_O	-5.59	-6.257	-3.847	-4.971	-6.35	-4.906	1.23	149.41	-8.54
173	2jsa-13	LYS_A_29_C	ASP_A_30_N	-5.59	-6.257	-3.847	-6.454	-5.293	-3.565	1.32	77.71	131.87
174	2jsa-13	ASP_A_30_N	ASP_A_30_H	-6.454	-5.293	-3.565	-6.928	-5.28	-2.673	1.01	27.99	178.43
175	2jsa-13	ASP_A_30_N	ASP_A_30_CA	-6.454	-5.293	-3.565	-6.739	-4.24	-4.523	1.45	131.29	105.14
176	2jsa-13	ASP_A_30_CA	ASP_A_30_HA	-6.739	-4.24	-4.523	-7.211	-4.678	-5.402	1.09	143.78	-137.14
177	2jsa-13	ASP_A_30_CA	ASP_A_30_C	-6.739	-4.24	-4.523	-5.433	-3.551	-4.923	1.53	105.16	27.81
178	2jsa-13	ASP_A_30_C	ASP_A_30_O	-5.433	-3.551	-4.923	-5.174	-3.341	-6.107	1.23	164.27	39.04
179	2jsa-13	ASP_A_30_C	PHE_A_31_N	-5.433	-3.551	-4.923	-4.644	-3.217	-3.911	1.33	40.25	22.94
180	2jsa-13	PHE_A_31_N	PHE_A_31_H	-4.644	-3.217	-3.911	-4.921	-3.419	-2.961	1.01	19.84	-143.90
181	2jsa-13	PHE_A_31_N	PHE_A_31_CA	-4.644	-3.217	-3.911	-3.371	-2.557	-4.142	1.45	99.15	27.40
182	2jsa-13	PHE_A_31_CA	PHE_A_31_HA	-3.371	-2.557	-4.142	-3.537	-1.509	-4.393	1.09	103.31	99.00
183	2jsa-13	PHE_A_31_CA	PHE_A_31_C	-3.371	-2.557	-4.142	-2.595	-3.24	-5.27	1.53	137.50	-41.35
184	2jsa-13	PHE_A_31_C	PHE_A_31_O	-2.595	-3.24	-5.27	-2.202	-2.592	-6.238	1.23	141.94	58.76
185	2jsa-13	PHE_A_31_C	ASP_A_32_N	-2.595	-3.24	-5.27	-2.399	-4.54	-5.108	1.32	82.98	-81.43
186	2jsa-13	ASP_A_32_N	ASP_A_32_H	-2.399	-4.54	-5.108	-2.751	-5.009	-4.286	1.01	35.50	-126.89
187	2jsa-13	ASP_A_32_N	ASP_A_32_CA	-2.399	-4.54	-5.108	-1.677	-5.318	-6.101	1.45	133.09	-47.14
188	2jsa-13	ASP_A_32_CA	ASP_A_32_HA	-1.677	-5.318	-6.101	-0.656	-4.941	-6.176	1.09	93.94	20.27
189	2jsa-13	ASP_A_32_CA	ASP_A_32_C	-1.677	-5.318	-6.101	-2.38	-5.188	-7.453	1.53	152.13	169.52
190	2jsa-13	ASP_A_32_C	ASP_A_32_O	-2.38	-5.188	-7.453	-1.76	-5.37	-8.5	1.23	148.32	-16.36
191	2jsa-13	ASP_A_32_C	ALA_A_33_N	-2.38	-5.188	-7.453	-3.665	-4.873	-7.388	1.32	87.19	166.23
192	2jsa-13	ALA_A_33_N	ALA_A_33_H	-3.665	-4.873	-7.388	-4.11	-4.737	-6.492	1.01	27.44	163.01
193	2jsa-13	ALA_A_33_N	ALA_A_33_CA	-3.665	-4.873	-7.388	-4.46	-4.718	-8.595	1.45	146.14	168.97
194	2jsa-13	ALA_A_33_CA	ALA_A_33_HA	-4.46	-4.718	-8.595	-4.317	-5.596	-9.224	1.09	125.26	-80.75
195	2jsa-13	ALA_A_33_CA	ALA_A_33_C	-4.46	-4.718	-8.595	-3.974	-3.487	-9.364	1.53	120.16	68.46
196	2jsa-13	ALA_A_33_C	ALA_A_33_O	-3.974	-3.487	-9.364	-3.321	-3.614	-10.398	1.23	147.24	-11.01
197	2jsa-13	ALA_A_33_C	GLU_A_34_N	-3.974	-3.487	-9.364	-4.312	-2.323	-8.828	1.33	66.14	106.19
198	2jsa-13	GLU_A_34_N	GLU_A_34_H	-4.312	-2.323	-8.828	-4.85	-2.293	-7.974	1.01	32.25	176.81
199	2jsa-13	GLU_A_34_N	GLU_A_34_CA	-4.312	-2.323	-8.828	-3.919	-1.071	-9.451	1.45	115.40	72.57
200	2jsa-13	GLU_A_34_CA	GLU_A_34_HA	-3.919	-1.071	-9.451	-4.425	-1.0	-10.414	1.09	152.05	172.01
201	2jsa-13	GLU_A_34_CA	GLU_A_34_C	-3.919	-1.071	-9.451	-2.409	-1.051	-9.699	1.53	99.33	0.76
202	2jsa-13	GLU_A_34_C	GLU_A_34_O	-2.409	-1.051	-9.699	-1.939	-0.414	-10.639	1.23	139.90	53.58
203	2jsa-13	GLU_A_34_C	CYS_A_35_N	-2.409	-1.051	-9.699	-1.692	-1.759	-8.838	1.33	49.49	-44.64
204	2jsa-13	CYS_A_35_N	CYS_A_35_H	-1.692	-1.759	-8.838	-2.146	-2.26	-8.088	1.01	42.03	-132.18
205	2jsa-13	CYS_A_35_N	CYS_A_35_CA	-1.692	-1.759	-8.838	-0.245	-1.832	-8.951	1.45	94.46	-2.89
206	2jsa-13	CYS_A_35_CA	CYS_A_35_HA	-0.245	-1.832	-8.951	0.144	-0.817	-9.038	1.09	94.58	69.03
207	2jsa-13	CYS_A_35_CA	CYS_A_35_C	-0.245	-1.832	-8.951	0.098	-2.597	-10.231	1.53	146.78	-65.85
208	2jsa-13	CYS_A_35_C	CYS_A_35_O	0.098	-2.597	-10.231	0.837	-2.097	-11.078	1.23	133.51	34.08
209	2jsa-13	CYS_A_35_C	LYS_A_36_N	0.098	-2.597	-10.231	-0.454	-3.797	-10.332	1.32	94.37	-114.70
210	2jsa-13	LYS_A_36_N	LYS_A_36_H	-0.454	-3.797	-10.332	-1.052	-4.145	-9.596	1.01	43.23	-149.80
211	2jsa-13	LYS_A_36_N	LYS_A_36_CA	-0.454	-3.797	-10.332	-0.215	-4.636	-11.493	1.45	143.08	-74.10
212	2jsa-13	LYS_A_36_CA	LYS_A_36_HA	-0.215	-4.636	-11.493	0.837	-4.922	-11.492	1.09	89.95	-15.21
213	2jsa-13	LYS_A_36_CA	LYS_A_36_C	-0.215	-4.636	-11.493	-0.477	-3.825	-12.765	1.53	146.18	107.90
214	2jsa-13	LYS_A_36_C	LYS_A_36_O	-0.477	-3.825	-12.765	-0.042	-4.208	-13.849	1.23	151.87	-41.36
215	2jsa-13	LYS_A_36_C	LYS_A_37_N	-0.477	-3.825	-12.765	-1.188	-2.721	-12.588	1.33	82.32	122.78
216	2jsa-13	LYS_A_37_N	LYS_A_37_H	-1.188	-2.721	-12.588	-1.514	-2.468	-11.666	1.01	24.11	142.19
217	2jsa-13	LYS_A_37_N	LYS_A_37_CA	-1.188	-2.721	-12.588	-1.513	-1.854	-13.708	1.45	140.42	110.55
218	2jsa-13	LYS_A_37_CA	LYS_A_37_HA	-1.513	-1.854	-13.708	-1.319	-2.404	-14.629	1.09	147.66	-70.57
219	2jsa-13	LYS_A_37_CA	LYS_A_37_C	-1.513	-1.854	-13.708	-0.586	-0.636	-13.69	1.53	89.33	52.73
220	2jsa-13	LYS_A_37_C	LYS_A_37_O	-0.586	-0.636	-13.69	0.262	-0.484	-14.567	1.23	135.51	10.16
221	2jsa-13	LYS_A_37_C	LEU_A_38_N	-0.586	-0.636	-13.69	-0.78	0.2	-12.681	1.32	40.38	103.06
222	2jsa-13	LEU_A_38_N	LEU_A_38_H	-0.78	0.2	-12.681	-1.497	0.012	-11.995	1.01	47.22	-165.31
223	2jsa-13	LEU_A_38_N	LEU_A_38_CA	-0.78	0.2	-12.681	0.029	1.4	-12.537	1.45	84.32	56.01
224	2jsa-13	LEU_A_38_CA	LEU_A_38_HA	0.029	1.4	-12.537	-0.153	2.036	-13.403	1.09	142.62	105.97
225	2jsa-13	LEU_A_38_CA	LEU_A_38_C	0.029	1.4	-12.537						

228	2jsa-13	PHE_A_39_N	PHE_A_39_H	1.847	0.067	-11.685	1.149	-0.347	-11.084	1.01	53.48	-149.33
229	2jsa-13	PHE_A_39_N	PHE_A_39_CA	1.847	0.067	-11.685	3.22	-0.397	-11.585	1.45	86.05	-18.67
230	2jsa-13	PHE_A_39_CA	PHE_A_39_HA	3.22	-0.397	-11.585	3.905	0.426	-11.79	1.09	100.84	50.23
231	2jsa-13	PHE_A_39_C	PHE_A_39_C	3.22	-0.397	-11.585	3.484	-1.543	-12.563	1.53	129.75	-77.03
232	2jsa-13	PHE_A_39_C	PHE_A_39_O	3.484	-1.543	-12.563	4.227	-2.472	-12.251	1.23	75.30	-51.35
233	2jsa-13	PHE_A_39_C	HIS_A_40_N	3.484	-1.543	-12.563	2.862	-1.439	-13.728	1.32	151.57	170.51
234	2jsa-13	HIS_A_40_N	HIS_A_40_H	2.862	-1.439	-13.728	2.266	-0.646	-13.917	1.01	100.79	126.93
235	2jsa-13	HIS_A_40_N	HIS_A_40_CA	2.862	-1.439	-13.728	3.021	-2.455	-14.755	1.45	134.96	-81.11
236	2jsa-13	HIS_A_40_CA	HIS_A_40_HA	3.021	-2.455	-14.755	3.281	-3.393	-14.263	1.09	63.19	-74.51
237	2jsa-13	HIS_A_40_CA	HIS_A_40_C	3.021	-2.455	-14.755	4.179	-2.074	-15.679	1.53	127.16	18.21
238	2jsa-13	HIS_A_40_C	HIS_A_40_O	4.179	-2.074	-15.679	3.961	-1.71	-16.835	1.23	159.85	120.92
239	2jsa-13	HIS_A_40_C	THR_A_41_N	4.179	-2.074	-15.679	5.384	-2.169	-15.138	1.32	65.89	-4.51
240	2jsa-13	THR_A_41_N	THR_A_41_H	5.384	-2.169	-15.138	5.489	-2.475	-14.181	1.01	18.68	-71.06
241	2jsa-13	THR_A_41_N	THR_A_41_CA	5.384	-2.169	-15.138	6.576	-1.839	-15.899	1.45	121.60	15.47
242	2jsa-13	THR_A_41_CA	THR_A_41_HA	6.576	-1.839	-15.899	6.799	-2.664	-16.575	1.09	128.34	-74.87
243	2jsa-13	THR_A_41_C	THR_A_41_C	6.576	-1.839	-15.899	7.774	-1.66	-14.965	1.53	52.37	8.50
244	2jsa-13	THR_A_41_C	THR_A_41_O	7.774	-1.66	-14.965	8.881	-2.095	-15.278	1.23	104.74	-21.45
245	2jsa-13	THR_A_41_C	ILE_A_42_N	7.774	-1.66	-14.965	7.511	-1.019	-13.835	1.33	31.51	112.31
246	2jsa-13	ILE_A_42_N	ILE_A_42_H	7.511	-1.019	-13.835	6.576	-0.69	-13.642	1.01	78.98	160.61
247	2jsa-13	ILE_A_42_N	ILE_A_42_C	7.511	-1.019	-13.835	8.555	-0.777	-12.852	1.45	47.47	13.05
248	2jsa-13	ILE_A_42_C	ILE_A_42_HA	8.555	-0.777	-12.852	9.172	0.048	-13.21	1.09	109.16	53.21
249	2jsa-13	ILE_A_42_C	ILE_A_42_C	8.555	-0.777	-12.852	9.448	-2.015	-12.748	1.53	86.10	-54.20
250	2jsa-13	ILE_A_42_C	ILE_A_42_O	9.448	-2.015	-12.748	8.965	-3.143	-12.834	1.23	94.01	-113.18
251	2jsa-13	ILE_A_42_C	PRO_A_43_N	9.448	-2.015	-12.748	10.77	-1.755	-12.561	1.36	82.10	11.13
252	2jsa-13	PRO_A_43_N	PRO_A_43_CA	10.77	-1.755	-12.561	11.735	-2.834	-12.444	1.45	85.38	-48.19
253	2jsa-13	PRO_A_43_C	PRO_A_43_HA	11.735	-2.834	-12.444	11.552	-3.583	-13.214	1.09	134.96	-103.73
254	2jsa-13	PRO_A_43_C	PRO_A_43_C	11.735	-2.834	-12.444	11.638	-3.511	-11.076	1.53	26.56	-98.15
255	2jsa-13	PRO_A_43_C	PRO_A_43_O	11.638	-3.511	-11.076	12.614	-4.082	-10.591	1.23	66.78	-30.33
256	2jsa-13	PRO_A_43_C	PHE_A_44_N	11.638	-3.511	-11.076	10.452	-3.426	-10.491	1.33	63.80	175.90
257	2jsa-13	PHE_A_44_N	PHE_A_44_H	10.452	-3.426	-10.491	9.694	-2.941	-10.948	1.01	116.92	147.39
258	2jsa-13	PHE_A_44_N	PHE_A_44_C	10.452	-3.426	-10.491	10.215	-4.024	-9.188	1.45	26.27	-111.62
259	2jsa-13	PHE_A_44_C	PHE_A_44_HA	10.215	-4.024	-9.188	10.108	-5.104	-9.29	1.09	95.37	-95.66
260	2jsa-13	PHE_A_44_C	PHE_A_44_C	10.215	-4.024	-9.188	8.959	-3.44	-8.538	1.53	64.86	155.06
261	2jsa-13	PHE_A_44_C	PHE_A_44_O	8.959	-3.44	-8.538	8.937	-3.193	-7.333	1.23	11.63	95.09
262	2jsa-13	PHE_A_44_C	GLY_A_45_N	8.959	-3.44	-8.538	7.943	-3.237	-9.364	1.33	128.56	168.70
263	2jsa-13	GLY_A_45_N	GLY_A_45_H	7.943	-3.237	-9.364	8.032	-3.464	-10.344	1.01	166.03	-68.59
264	2jsa-13	GLY_A_45_N	GLY_A_45_C	7.943	-3.237	-9.364	6.687	-2.688	-8.885	1.45	70.74	156.39
265	2jsa-13	GLY_A_45_C	GLY_A_45_C	6.687	-2.688	-8.885	5.689	-3.802	-8.56	1.53	77.74	-131.86
266	2jsa-13	GLY_A_45_C	GLY_A_45_O	5.689	-3.802	-8.56	5.276	-3.955	-7.412	1.23	20.99	-159.67
267	2jsa-13	GLY_A_45_C	THR_A_46_N	5.689	-3.802	-8.56	5.332	-4.552	-9.593	1.33	141.20	-115.45
268	2jsa-13	THR_A_46_N	THR_A_46_H	5.332	-4.552	-9.593	5.714	-4.369	-10.51	1.01	155.21	25.60
269	2jsa-13	THR_A_46_N	THR_A_46_CA	5.332	-4.552	-9.593	4.391	-5.648	-9.432	1.45	83.64	-130.65
270	2jsa-13	THR_A_46_C	THR_A_46_HA	4.391	-5.648	-9.432	3.47	-5.257	-9.0	1.09	66.65	157.00
271	2jsa-13	THR_A_46_C	THR_A_46_C	4.391	-5.648	-9.432	4.953	-6.697	-8.472	1.53	51.11	-61.82
272	2jsa-13	THR_A_46_C	THR_A_46_O	4.953	-6.697	-8.472	4.199	-7.374	-7.775	1.23	55.48	-138.08
273	2jsa-13	THR_A_46_C	ARG_A_47_N	4.953	-6.697	-8.472	6.275	-6.799	-8.465	1.33	89.70	-4.41
274	2jsa-13	ARG_A_47_N	ARG_A_47_H	6.275	-6.799	-8.465	6.834	-6.209	-9.065	1.01	126.44	46.55
275	2jsa-13	ARG_A_47_N	ARG_A_47_CA	6.275	-6.799	-8.465	6.947	-7.754	-7.602	1.45	53.53	-54.87
276	2jsa-13	ARG_A_47_C	ARG_A_47_HA	6.947	-7.754	-7.602	6.446	-8.717	-7.699	1.09	95.11	-117.49
277	2jsa-13	ARG_A_47_C	ARG_A_47_C	6.947	-7.754	-7.602	6.871	-7.298	-6.143	1.53	17.58	99.46
278	2jsa-13	ARG_A_47_C	ARG_A_47_O	6.871	-7.298	-6.143	6.211	-7.935	-5.323	1.23	48.20	-136.02
279	2jsa-13	ARG_A_47_C	GLU_A_48_N	6.871	-7.298	-6.143	7.554	-6.197	-5.864	1.33	77.85	58.19
280	2jsa-13	GLU_A_48_N	GLU_A_48_H	7.554	-6.197	-5.864	8.073	-5.723	-6.59	1.01	135.93	42.41
281	2jsa-13	GLU_A_48_N	GLU_A_48_C	7.554	-6.197	-5.864	7.573	-5.648	-4.52	1.45	22.23	88.02
282	2jsa-13	GLU_A_48_C	GLU_A_48_HA	7.573	-5.648	-4.52	8.091	-6.357	-3.873	1.09	53.62	-53.85
283	2jsa-13	GLU_A_48_C	GLU_A_48_C	7.573	-5.648	-4.52	6.144	-5.474	-3.998	1.53	70.07	173.06
284	2jsa-13	GLU_A_48_C	GLU_A_48_O	6.144	-5.474	-3.998	5.912	-5.506	-2.79	1.23	10.97	-172.15
285	2jsa-13	GLU_A_48_C	CYS_A_49_N	6.144	-5.474	-3.998	5.225	-5.293	-4.934	1.32	134.98	168.86
286	2jsa-13	CYS_A_49_N	CYS_A_49_H	5.225	-5.293	-4.934	5.489	-5.278	-5.909	1.01	164.83	3.25
287	2jsa-13	CYS_A_49_N	CYS_A_49_CA	5.225	-5.293	-4.934	3.826	-5.114	-4.585	1.45	76.10	172.71
288	2jsa-13	CYS_A_49_C	CYS_A_49_HA	3.826	-5.114	-4.585	3.751	-4.276	-3.891	1.09	50.48	95.11
289	2jsa-13	CYS_A_49_C	CYS_A_49_C	3.826	-5.114	-4.585	3.342	-6.38	-3.874	1.53	62.32	-110.92
290	2jsa-13	CYS_A_49_C	CYS_A_49_O	3.342	-6.38	-3.874	2.827	-6.311	-2.759	1.23	24.99	172.37
291	2jsa-13	CYS_A_49_C	ASP_A_50_N	3.342	-6.38	-3.874	3.525	-7.505	-4.549	1.32	120.63	-80.76
292	2jsa-13	ASP_A_50_N	ASP_A_50_H	3.525	-7.505	-4.549	3.955	-7.486	-5.463	1.01	154.78	2.53
293	2jsa-13	ASP_A_50_N	ASP_A_50_CA	3.525	-7.505	-4.549	3.114	-8.785	-3.995	1.45	67.60	-107.80
294	2jsa-13	ASP_A_50_C	ASP_A_50_HA	3.114	-8.785	-3.995	2.033	-8.782	-3.855	1.09	82.62	179.84
295	2jsa-13	ASP_A_50_C	ASP_A_50_C	3.114	-8.785	-3.995	3.811	-9.001	-2.651	1.53	28.50	-17.22
296	2jsa-13	ASP_A_50_C	ASP_A_50_O	3.811	-9.001	-2.651	3.389	-9.842	-1.857	1.23	49.84	-116.65
297	2jsa-13	ASP_A_50_C	HIS_A_51_N	3.811	-9.001	-2.651	4.867	-8.23	-2.436	1.33	80.66	36.13
298	2jsa-13	HIS_A_51_N	HIS_A_51_H	4.867	-8.23	-2.436	5.159	-7.56	-3.134	1.01	133.68	66.45
299	2jsa-13	HIS_A_51_N	HIS_A_51_CA	4.867	-8.23	-2.436	5.626	-8.328	-1.202	1.45	31.81	-7.36
300	2jsa-13	HIS_A_51_C	HIS_A_51_HA	5.626	-8.328	-1.202	5.309	-9.232	-0.682	1.09	61.51	-109.32
301	2jsa-13	HIS_A_51_C	HIS_A_51_C	5.626	-8.328	-1.202	5.303	-7.131	-0.305	1.53	54.11	105.10
302	2jsa-13	HIS_A_51_C	HIS_A_51_O	5.303	-7.131	-0.305	5.909	-6.961	0.752	1.23	30.77	15.67
303	2jsa-13	HIS_A_51_C	TYR_A_52_N	5.303	-7.131	-0.305	4.35	-6.331	-0.76	1.32	110.09	139.99
304	2jsa-13	TYR_A_52_N	TYR_A_52_H	4.35	-6.331	-0.76	3.896	-6.531	-1.639	1.01	150.56	-156.23
305	2jsa-13	TYR_A_52_N	TYR_A_52_C	4.35	-6.331	-0.76	3.94	-5.155	-0.012	1.45	59.01	109.22
306	2jsa-13	TYR_A_52_C	TYR_A_52_HA	3.94	-5.155	-0.012	4.701	-4.891	0.723	1.09	47.62	19.13
307	2jsa-13	TYR_A_52_C	TYR_A_52_C	3.94	-5.155	-0.012	2.599	-5.392	0.688	1.53	62.80	-169.98
308	2jsa-13	TYR_A_52_C	TYR_A_52_O	2.599	-5.392	0.688	2.477	-5.169	1.891	1.23	11.93	118.68
309	2jsa-13	TYR_A_52_C	VAL_A_53_N	2.599	-5.392	0.688	1.629	-5.838	-0.095	1.32	126.26	-155.31
310	2jsa-13	VAL_A_53_N	VAL_A_53_H	1.629	-5.838	-0.095	1.802	-5.998	-1.077	1.01	166.51	-42.76
311	2jsa-13	VAL_A_53_N	VAL_A_53_C	1.629	-5.838	-0.095	0.303	-6.106	0.434	1.45	68.64	-168.57
312	2jsa-13	VAL_A_53_C	VAL_A_53_HA	0.303	-6.106	0.434	-0.153	-5.157	0.717	1.09	74.96	115.66
313	2jsa-13	VAL_A_53_C	VAL_A_53_C	0.303	-6.106	0.434	0.426	-6.968	1.692	1.53	34.69	-81.88
314	2jsa-13	VAL_A_53_C	VAL_A_53_O	0.426	-6.968	1.692	-0.346	-6.806	2.636	1.23	39.88	168.15
315	2jsa-13	VAL_A_53_C	ASN_A_54_N	0.426	-6.968	1.692	1.401	-7.864	1.664	1.32	91.21	-42.58
316	2jsa-13	ASN_A_54_N	ASN_A_54_H	1.401	-7.864	1.664	1.998	-7.941	0.853	1.01	143.42	-7.35
317	2jsa-13	ASN_A_54_N	ASN_A_54_C	1.401	-7.864	1.664	1.635	-8.751	2.791	1.45	39.14	-75.22
318	2jsa-13											

321	2jsa-13	ASN_A_54_C	SER_A_55_N	2.88	-8.287	3.549	3.094	-6.981	3.529	1.32	90.87	80.69
322	2jsa-13	SER_A_55_N	SER_A_55_H	3.094	-6.981	3.529	2.458	-6.369	3.038	1.01	119.09	136.10
323	2jsa-13	SER_A_55_N	SER_A_55_CA	3.094	-6.981	3.529	4.24	-6.399	4.208	1.45	62.15	26.92
324	2jsa-13	SER_A_55_CA	SER_A_55_HA	4.24	-6.399	4.208	4.206	-6.699	5.255	1.09	16.09	-96.47
325	2jsa-13	SER_A_55_CA	SER_A_55_C	4.24	-6.399	4.208	4.173	-4.872	4.134	1.53	92.77	92.51
326	2jsa-13	SER_A_55_C	SER_A_55_O	4.173	-4.872	4.134	4.555	-4.279	3.127	1.23	144.99	57.21
327	2jsa-13	SER_A_55_C	LYS_A_56_N	4.173	-4.872	4.134	3.684	-4.28	5.213	1.32	35.44	129.56
328	2jsa-13	LYS_A_56_N	LYS_A_56_H	3.684	-4.28	5.213	3.388	-4.831	6.006	1.01	38.26	-118.24
329	2jsa-13	LYS_A_56_N	LYS_A_56_CA	3.684	-4.28	5.213	3.562	-2.833	5.283	1.45	87.24	94.82
330	2jsa-13	LYS_A_56_CA	LYS_A_56_HA	3.562	-2.833	5.283	3.842	-2.518	6.289	1.09	22.73	48.37
331	2jsa-13	LYS_A_56_CA	LYS_A_56_C	3.562	-2.833	5.283	2.101	-2.438	5.062	1.53	98.31	164.87
332	2jsa-13	LYS_A_56_C	LYS_A_56_O	2.101	-2.438	5.062	1.766	-1.255	5.071	1.23	89.58	105.81
333	2jsa-13	LYS_A_56_C	VAL_A_57_N	2.101	-2.438	5.062	1.27	-3.451	4.868	1.32	98.42	-129.36
334	2jsa-13	VAL_A_57_N	VAL_A_57_H	1.27	-3.451	4.868	1.616	-4.4	4.874	1.01	89.66	-69.97
335	2jsa-13	VAL_A_57_N	VAL_A_57_CA	1.27	-3.451	4.868	-0.148	-3.225	4.644	1.45	98.87	170.94
336	2jsa-13	VAL_A_57_CA	VAL_A_57_HA	-0.148	-3.225	4.644	-0.286	-2.19	4.331	1.09	106.69	97.59
337	2jsa-13	VAL_A_57_CA	VAL_A_57_C	-0.148	-3.225	4.644	-0.906	-3.429	5.956	1.53	30.89	-164.94
338	2jsa-13	VAL_A_57_C	VAL_A_57_O	-0.906	-3.429	5.956	-2.013	-2.918	6.124	1.23	82.15	155.22
339	2jsa-13	VAL_A_57_C	ASP_A_58_N	-0.906	-3.429	5.956	-0.281	-4.176	6.855	1.33	47.29	-50.08
340	2jsa-13	ASP_A_58_N	ASP_A_58_H	-0.281	-4.176	6.855	0.629	-4.565	6.65	1.01	101.70	-23.15
341	2jsa-13	ASP_A_58_N	ASP_A_58_CA	-0.281	-4.176	6.855	-0.883	-4.453	8.147	1.45	27.15	-155.29
342	2jsa-13	ASP_A_58_CA	ASP_A_58_HA	-0.883	-4.453	8.147	-1.942	-4.667	8.008	1.09	97.33	-168.58
343	2jsa-13	ASP_A_58_CA	ASP_A_58_C	-0.883	-4.453	8.147	-0.713	-3.234	9.057	1.53	53.52	82.06
344	2jsa-13	ASP_A_58_C	ASP_A_58_O	-0.713	-3.234	9.057	-1.639	-2.855	9.77	1.23	54.53	157.74
345	2jsa-13	ASP_A_58_C	PRO_A_59_N	-0.713	-3.234	9.057	0.509	-2.64	8.998	1.36	92.49	25.92
346	2jsa-13	PRO_A_59_N	PRO_A_59_CA	0.509	-2.64	8.998	0.811	-1.472	9.808	1.45	56.12	75.50
347	2jsa-13	PRO_A_59_CA	PRO_A_59_HA	0.811	-1.472	9.808	0.457	-1.623	10.828	1.09	20.67	-156.90
348	2jsa-13	PRO_A_59_CA	PRO_A_59_C	0.811	-1.472	9.808	0.138	-0.221	9.24	1.53	111.79	118.28
349	2jsa-13	PRO_A_59_C	PRO_A_59_O	0.138	-0.221	9.24	-0.559	0.493	9.958	1.23	54.26	134.31
350	2jsa-13	PRO_A_59_C	ILE_A_60_N	0.138	-0.221	9.24	0.369	0.005	7.955	1.33	165.88	44.37
351	2jsa-13	ILE_A_60_N	ILE_A_60_H	0.369	0.005	7.955	0.953	-0.626	7.425	1.01	121.65	-47.22
352	2jsa-13	ILE_A_60_N	ILE_A_60_CA	0.369	0.005	7.955	-0.207	1.156	7.282	1.45	117.60	116.58
353	2jsa-13	ILE_A_60_CA	ILE_A_60_HA	-0.207	1.156	7.282	0.292	2.05	7.657	1.09	69.88	60.83
354	2jsa-13	ILE_A_60_CA	ILE_A_60_C	-0.207	1.156	7.282	-1.69	1.265	7.645	1.53	76.28	175.80
355	2jsa-13	ILE_A_60_C	ILE_A_60_O	-1.69	1.265	7.645	-2.167	2.339	8.006	1.23	72.92	113.95
356	2jsa-13	ILE_A_60_C	ILE_A_61_N	-1.69	1.265	7.645	-2.377	0.137	7.535	1.33	94.76	-121.34
357	2jsa-13	ILE_A_61_N	ILE_A_61_H	-2.377	0.137	7.535	-1.918	-0.71	7.232	1.01	107.46	-61.55
358	2jsa-13	ILE_A_61_N	ILE_A_61_CA	-2.377	0.137	7.535	-3.795	0.092	7.847	1.45	77.60	-178.18
359	2jsa-13	ILE_A_61_CA	ILE_A_61_HA	-3.795	0.092	7.847	-4.285	0.901	7.305	1.09	119.81	121.20
360	2jsa-13	ILE_A_61_CA	ILE_A_61_C	-3.795	0.092	7.847	-3.993	0.347	9.341	1.53	12.19	127.83
361	2jsa-13	ILE_A_61_C	ILE_A_61_O	-3.993	0.347	9.341	-5.038	0.844	9.757	1.23	70.23	154.56
362	2jsa-13	ILE_A_61_C	HIS_A_62_N	-3.993	0.347	9.341	-2.972	-0.003	10.11	1.33	54.53	-18.92
363	2jsa-13	HIS_A_62_N	HIS_A_62_H	-2.972	-0.003	10.11	-2.142	-0.406	9.7	1.01	113.96	-25.90
364	2jsa-13	HIS_A_62_N	HIS_A_62_CA	-2.972	-0.003	10.11	-3.02	0.182	11.55	1.45	7.56	104.55
365	2jsa-13	HIS_A_62_CA	HIS_A_62_HA	-3.02	0.182	11.55	-3.985	-0.181	11.904	1.09	71.05	-159.39
366	2jsa-13	HIS_A_62_CA	HIS_A_62_C	-3.02	0.182	11.55	-2.93	1.673	11.879	1.53	77.58	86.55
367	2jsa-13	HIS_A_62_C	HIS_A_62_O	-2.93	1.673	11.879	-3.212	2.084	13.003	1.23	23.92	124.46
368	2jsa-13	HIS_A_62_C	GLU_A_63_N	-2.93	1.673	11.879	-2.534	2.445	10.877	1.33	139.11	62.84
369	2jsa-13	GLU_A_63_N	GLU_A_63_H	-2.534	2.445	10.877	-2.318	2.039	9.978	1.01	152.91	-61.99
370	2jsa-13	GLU_A_63_N	GLU_A_63_CA	-2.534	2.445	10.877	-2.402	3.882	11.045	1.45	83.36	84.75
371	2jsa-13	GLU_A_63_CA	GLU_A_63_HA	-2.402	3.882	11.045	-2.05	4.072	12.059	1.09	21.53	28.36
372	2jsa-13	GLU_A_63_CA	GLU_A_63_C	-2.402	3.882	11.045	-3.76	4.563	10.871	1.53	96.53	153.37
373	2jsa-13	GLU_A_63_C	GLU_A_63_O	-3.76	4.563	10.871	-4.171	5.361	11.711	1.23	46.90	117.25
374	2jsa-13	GLU_A_63_C	LEU_A_64_N	-3.76	4.563	10.871	-4.421	4.223	9.774	1.33	145.88	-152.78
375	2jsa-13	LEU_A_64_N	LEU_A_64_H	-4.421	4.223	9.774	-4.022	3.559	9.126	1.01	129.91	-59.00
376	2jsa-13	LEU_A_64_N	LEU_A_64_CA	-4.421	4.223	9.774	-5.725	4.792	9.478	1.45	101.75	156.43
377	2jsa-13	LEU_A_64_CA	LEU_A_64_HA	-5.725	4.792	9.478	-5.669	5.868	9.646	1.09	81.14	87.02
378	2jsa-13	LEU_A_64_CA	LEU_A_64_C	-5.725	4.792	9.478	-6.758	4.222	10.452	1.53	50.46	-151.11
379	2jsa-13	LEU_A_64_C	LEU_A_64_O	-6.758	4.222	10.452	-7.761	4.87	10.748	1.23	76.08	147.14
380	2jsa-13	LEU_A_64_C	GLU_A_65_N	-6.758	4.222	10.452	-6.477	3.017	10.925	1.32	69.08	-76.87
381	2jsa-13	GLU_A_65_N	GLU_A_65_H	-6.477	3.017	10.925	-5.632	2.543	10.639	1.01	106.45	-29.29
382	2jsa-13	GLU_A_65_N	GLU_A_65_CA	-6.477	3.017	10.925	-7.369	2.353	11.86	1.45	49.94	-143.34
383	2jsa-13	GLU_A_65_CA	GLU_A_65_HA	-7.369	2.353	11.86	-8.377	2.392	11.449	1.09	112.17	177.78
384	2jsa-13	GLU_A_65_CA	GLU_A_65_C	-7.369	2.353	11.86	-7.369	3.084	13.204	1.53	28.54	90.00
385	2jsa-13	GLU_A_65_C	GLU_A_65_O	-7.369	3.084	13.204	-8.409	3.206	13.849	1.23	58.37	173.31
386	2jsa-13	GLU_A_65_C	GLY_A_66_N	-7.369	3.084	13.204	-6.189	3.55	13.588	1.33	73.16	21.55
387	2jsa-13	GLY_A_66_N	GLY_A_66_H	-6.189	3.55	13.588	-5.374	3.413	13.007	1.01	125.11	-9.54
388	2jsa-13	GLY_A_66_N	GLY_A_66_CA	-6.189	3.55	13.588	-6.039	4.264	14.844	1.45	30.15	78.14
389	2jsa-13	GLY_A_66_CA	GLY_A_66_C	-6.039	4.264	14.844	-6.586	5.69	14.732	1.53	94.19	110.99
390	2jsa-13	GLY_A_66_C	GLY_A_66_O	-6.586	5.69	14.732	-7.399	6.112	15.553	1.23	48.13	152.57
391	2jsa-13	GLY_A_66_C	GLY_A_67_N	-6.586	5.69	14.732	-6.118	6.39	13.71	1.32	140.51	56.23
392	2jsa-13	GLY_A_67_N	GLY_A_67_H	-6.118	6.39	13.71	-5.45	5.978	13.075	1.01	128.98	-31.66
393	2jsa-13	GLY_A_67_N	GLY_A_67_CA	-6.118	6.39	13.71	-6.55	7.759	13.479	1.45	99.14	107.51
394	2jsa-13	GLY_A_67_CA	GLY_A_67_C	-6.55	7.759	13.479	-5.48	8.551	12.723	1.53	119.59	36.51
395	2jsa-13	GLY_A_67_C	GLY_A_67_O	-5.48	8.551	12.723	-5.208	9.703	13.054	1.23	74.38	76.72
396	2jsa-13	GLY_A_67_C	THR_A_68_N	-5.48	8.551	12.723	-4.906	7.901	11.723	1.32	139.07	-48.55
397	2jsa-13	THR_A_68_N	THR_A_68_H	-4.906	7.901	11.723	-5.182	6.954	11.507	1.01	102.35	-106.25
398	2jsa-13	THR_A_68_N	THR_A_68_CA	-4.906	7.901	11.723	-3.873	8.53	10.917	1.45	123.68	31.34
399	2jsa-13	THR_A_68_CA	THR_A_68_HA	-3.873	8.53	10.917	-3.731	9.553	11.266	1.09	71.33	82.10
400	2jsa-13	THR_A_68_CA	THR_A_68_C	-3.873	8.53	10.917	-4.303	8.587	9.449	1.53	163.54	172.45
401	2jsa-13	THR_A_68_C	THR_A_68_O	-4.303	8.587	9.449	-4.533	7.552	8.826	1.23	120.44	-102.53
402	2jsa-13	THR_A_68_C	ALA_A_69_N	-4.303	8.587	9.449	-4.398	9.807	8.94	1.33	112.59	94.45
403	2jsa-13	ALA_A_69_N	ALA_A_69_H	-4.398	9.807	8.94	-4.194	10.614	9.512	1.01	55.50	75.81
404	2jsa-13	ALA_A_69_N	ALA_A_69_CA	-4.398	9.807	8.94	-4.795	10.012	7.558	1.45	162.08	152.69
405	2jsa-13	ALA_A_69_CA	ALA_A_69_HA	-4.795	10.012	7.558	-5.83	9.692	7.44	1.09	96.22	-162.82
406	2jsa-13	ALA_A_69_CA	ALA_A_69_C	-4.795	10.012	7.558	-3.917	9.153	6.646	1.53	126.59	-44.37
407	2jsa-13	ALA_A_69_C	ALA_A_69_O	-3.917	9.153	6.646	-2.865	8.672	7.065	1.23	70.09	-24.57
408	2jsa-13	ALA_A_69_C	PRO_A_70_N	-3.917	9.153	6.646	-4.394	8.982	5.384	1.36	158.12	-160.28
409	2jsa-13	PRO_A_70_N	PRO_A_70_CA	-4.394	8.982	5.384	-3.664	8.189	4.41	1.45	132.10	-47.37
410	2jsa-13	PRO_A_70_CA	PRO_A_70_HA	-3.664	8.189	4.41	-3.319	7.261	4.867	1.09	65.22	-69.61
411	2jsa-											

414	2jsa-13	LYS_A_71_N	LYS_A_71_H	-2.485	10.264	4.067	-3.278	10.691	4.525	1.01	63.05	151.70
415	2jsa-13	LYS_A_71_N	LYS_A_71_CA	-2.485	10.264	4.067	-1.396	11.114	3.618	1.45	108.01	37.97
416	2jsa-13	LYS_A_71_CA	LYS_A_71_HA	-1.396	11.114	3.618	-0.84	10.574	2.852	1.09	134.66	-44.16
417	2jsa-13	LYS_A_71_CA	LYS_A_71_C	-1.396	11.114	3.618	-0.443	11.376	4.786	1.53	40.24	15.37
418	2jsa-13	LYS_A_71_C	LYS_A_71_O	-0.443	11.376	4.786	0.442	12.225	4.692	1.23	94.38	43.81
419	2jsa-13	LYS_A_71_C	ASP_A_72_N	-0.443	11.376	4.786	-0.657	10.632	5.861	1.32	35.76	-106.05
420	2jsa-13	ASP_A_72_N	ASP_A_72_H	-0.657	10.632	5.861	-1.405	9.954	5.869	1.01	89.55	-137.81
421	2jsa-13	ASP_A_72_N	ASP_A_72_CA	-0.657	10.632	5.861	0.171	10.771	7.047	1.45	35.30	9.53
422	2jsa-13	ASP_A_72_CA	ASP_A_72_HA	0.171	10.771	7.047	0.86	11.604	6.905	1.09	97.48	50.40
423	2jsa-13	ASP_A_72_CA	ASP_A_72_C	0.171	10.771	7.047	0.958	9.479	7.269	1.53	81.65	-58.65
424	2jsa-13	ASP_A_72_C	ASP_A_72_O	0.958	9.479	7.269	2.122	9.518	7.666	1.23	71.18	1.92
425	2jsa-13	ASP_A_72_C	VAL_A_73_N	0.958	9.479	7.269	0.294	8.365	7.002	1.32	101.63	-120.80
426	2jsa-13	VAL_A_73_N	VAL_A_73_H	0.294	8.365	7.002	-0.661	8.409	6.677	1.01	108.78	177.36
427	2jsa-13	VAL_A_73_N	VAL_A_73_CA	0.294	8.365	7.002	0.916	7.063	7.169	1.45	83.40	-64.46
428	2jsa-13	VAL_A_73_CA	VAL_A_73_HA	0.916	7.063	7.169	1.113	6.909	8.23	1.09	13.26	-38.02
429	2jsa-13	VAL_A_73_CA	VAL_A_73_C	0.916	7.063	7.169	2.256	7.046	6.429	1.53	118.91	-0.73
430	2jsa-13	VAL_A_73_C	VAL_A_73_O	2.256	7.046	6.429	3.288	6.718	7.013	1.23	61.66	-17.63
431	2jsa-13	VAL_A_73_C	CYS_A_74_N	2.256	7.046	6.429	2.197	7.403	5.155	1.32	164.14	99.38
432	2jsa-13	CYS_A_74_N	CYS_A_74_H	2.197	7.403	5.155	1.314	7.661	4.74	1.01	114.28	163.71
433	2jsa-13	CYS_A_74_N	CYS_A_74_CA	2.197	7.403	5.155	3.392	7.433	4.329	1.45	124.64	1.44
434	2jsa-13	CYS_A_74_CA	CYS_A_74_HA	3.392	7.433	4.329	3.988	6.549	4.556	1.09	77.98	-56.01
435	2jsa-13	CYS_A_74_CA	CYS_A_74_C	3.392	7.433	4.329	4.203	8.675	4.702	1.53	75.89	56.86
436	2jsa-13	CYS_A_74_C	CYS_A_74_O	4.203	8.675	4.702	4.241	9.645	3.947	1.23	127.87	87.76
437	2jsa-13	CYS_A_74_C	THR_A_75_N	4.203	8.675	4.702	4.831	8.606	5.867	1.33	28.47	-6.27
438	2jsa-13	THR_A_75_N	THR_A_75_H	4.831	8.606	5.867	4.755	7.776	6.437	1.01	55.63	-95.23
439	2jsa-13	THR_A_75_N	THR_A_75_CA	4.831	8.606	5.867	5.639	9.713	6.35	1.45	70.59	53.87
440	2jsa-13	THR_A_75_CA	THR_A_75_HA	5.639	9.713	6.35	6.465	9.872	5.656	1.09	129.52	10.90
441	2jsa-13	THR_A_75_CA	THR_A_75_C	5.639	9.713	6.35	6.233	9.382	7.72	1.53	26.40	-29.13
442	2jsa-13	THR_A_75_C	THR_A_75_O	6.233	9.382	7.72	7.451	9.296	7.868	1.23	83.09	-4.04
443	2jsa-13	THR_A_75_C	LYS_A_76_N	6.233	9.382	7.72	5.344	9.205	8.686	1.32	43.18	-168.74
444	2jsa-13	LYS_A_76_N	LYS_A_76_H	5.344	9.205	8.686	4.357	9.29	8.492	1.01	101.08	175.08
445	2jsa-13	LYS_A_76_N	LYS_A_76_CA	5.344	9.205	8.686	5.766	8.886	10.04	1.45	21.34	-37.09
446	2jsa-13	LYS_A_76_CA	LYS_A_76_HA	5.766	8.886	10.04	6.614	9.525	10.289	1.09	76.80	37.00
447	2jsa-13	LYS_A_76_CA	LYS_A_76_C	5.766	8.886	10.04	6.247	7.434	10.091	1.53	88.09	-71.67
448	2jsa-13	LYS_A_76_C	LYS_A_76_O	6.247	7.434	10.091	7.089	7.084	10.916	1.23	47.86	-22.57
449	2jsa-13	LYS_A_76_C	LEU_A_77_N	6.247	7.434	10.091	5.689	6.629	9.198	1.33	132.36	-124.73
450	2jsa-13	LEU_A_77_N	LEU_A_77_H	5.689	6.629	9.198	5.002	6.986	8.549	1.01	129.97	152.54
451	2jsa-13	LEU_A_77_N	LEU_A_77_CA	5.689	6.629	9.198	6.051	5.223	9.132	1.45	92.60	-75.56
452	2jsa-13	LEU_A_77_CA	LEU_A_77_HA	6.051	5.223	9.132	6.088	4.836	10.15	1.09	20.90	-84.54
453	2jsa-13	LEU_A_77_CA	LEU_A_77_C	6.051	5.223	9.132	7.452	5.089	8.532	1.53	113.09	-5.46
454	2jsa-13	LEU_A_77_C	LEU_A_77_O	7.452	5.089	8.532	7.98	3.983	8.418	1.23	95.31	-64.48
455	2jsa-13	LEU_A_77_C	ASN_A_78_N	7.452	5.089	8.532	8.015	6.231	8.164	1.33	106.12	63.76
456	2jsa-13	ASN_A_78_N	ASN_A_78_H	8.015	6.231	8.164	7.523	7.104	8.287	1.01	83.00	119.40
457	2jsa-13	ASN_A_78_N	ASN_A_78_CA	8.015	6.231	8.164	9.345	6.254	7.579	1.45	113.74	0.99
458	2jsa-13	ASN_A_78_CA	ASN_A_78_HA	9.345	6.254	7.579	9.638	7.289	7.4	1.09	99.45	74.19
459	2jsa-13	ASN_A_78_CA	ASN_A_78_C	9.345	6.254	7.579	9.329	5.483	6.257	1.53	149.74	-91.19
460	2jsa-13	ASN_A_78_C	ASN_A_78_O	9.329	5.483	6.257	10.365	4.993	5.809	1.23	111.35	-25.31
461	2jsa-13	ASN_A_78_C	GLU_A_79_N	9.329	5.483	6.257	8.144	5.399	5.672	1.32	116.22	-175.95
462	2jsa-13	GLU_A_79_N	GLU_A_79_H	8.144	5.399	5.672	7.335	5.827	6.099	1.01	64.99	152.12
463	2jsa-13	GLU_A_79_N	GLU_A_79_CA	8.144	5.399	5.672	7.981	4.695	4.411	1.45	150.18	-103.04
464	2jsa-13	GLU_A_79_CA	GLU_A_79_HA	7.981	4.695	4.411	8.84	4.037	4.278	1.09	97.01	-37.45
465	2jsa-13	GLU_A_79_CA	GLU_A_79_C	7.981	4.695	4.411	7.953	5.689	3.249	1.53	139.44	91.61
466	2jsa-13	GLU_A_79_C	GLU_A_79_O	7.953	5.689	3.249	7.942	5.289	2.085	1.23	161.03	-91.58
467	2jsa-13	GLU_A_79_C	CYS_A_80_N	7.953	5.689	3.249	7.942	6.965	3.603	1.32	74.49	90.49
468	2jsa-13	CYS_A_80_N	CYS_A_80_H	7.942	6.965	3.603	7.953	7.222	4.58	1.01	14.75	87.55
469	2jsa-13	CYS_A_80_N	CYS_A_80_CA	7.942	6.965	3.603	7.916	8.02	2.603	1.45	133.46	91.41
470	2jsa-13	CYS_A_80_CA	CYS_A_80_HA	7.916	8.02	2.603	8.419	7.656	1.707	1.09	145.28	-35.89
471	2jsa-13	CYS_A_80_CA	CYS_A_80_C	7.916	8.02	2.603	8.699	9.217	3.147	1.53	69.18	56.81
472	2jsa-13	CYS_A_80_C	CYS_A_80_O	8.699	9.217	3.147	8.534	9.595	4.305	1.23	19.60	113.58
473	2jsa-13	CYS_A_80_C	PRO_A_81_N	8.699	9.217	3.147	9.554	9.795	2.262	1.36	130.61	34.06
474	2jsa-13	PRO_A_81_N	PRO_A_81_CA	9.554	9.795	2.262	10.362	10.942	2.642	1.45	74.85	54.84
475	2jsa-13	PRO_A_81_CA	PRO_A_81_HA	10.362	10.942	2.642	10.809	10.776	3.623	1.09	25.92	-20.37
476	2jsa-13	PRO_A_81_CA	PRO_A_81_C	10.362	10.942	2.642	9.513	12.214	2.704	1.53	87.68	123.72
477	2jsa-13	PRO_A_81_C	PRO_A_81_O	9.513	12.214	2.704	8.286	12.143	2.759	1.23	87.44	-176.69
1	2jsa-14	ARG_A_1_N	ARG_A_1_H	13.785	3.394	-4.024	14.475	4.121	-4.153	1.01	97.33	46.50
2	2jsa-14	ARG_A_1_N	ARG_A_1_CA	13.785	3.394	-4.024	12.457	3.77	-3.568	1.45	71.72	164.19
3	2jsa-14	ARG_A_1_CA	ARG_A_1_HA	12.457	3.77	-3.568	11.735	3.47	-4.327	1.09	134.15	-157.44
4	2jsa-14	ARG_A_1_CA	ARG_A_1_C	12.457	3.77	-3.568	12.372	5.284	-3.37	1.53	82.56	93.21
5	2jsa-14	ARG_A_1_C	ARG_A_1_O	12.372	5.284	-3.37	12.68	5.791	-2.293	1.23	28.85	58.72
6	2jsa-14	ARG_A_1_C	SER_A_2_N	12.372	5.284	-3.37	11.953	5.964	-4.427	1.32	142.92	121.64
7	2jsa-14	SER_A_2_N	SER_A_2_H	11.953	5.964	-4.427	11.718	5.481	-5.282	1.01	147.86	-115.94
8	2jsa-14	SER_A_2_N	SER_A_2_CA	11.953	5.964	-4.427	11.822	7.41	-4.383	1.45	88.26	95.18
9	2jsa-14	SER_A_2_CA	SER_A_2_HA	11.822	7.41	-4.383	12.039	7.742	-3.367	1.09	21.32	56.83
10	2jsa-14	SER_A_2_CA	SER_A_2_C	11.822	7.41	-4.383	10.391	7.819	-4.736	1.53	103.34	164.05
11	2jsa-14	SER_A_2_C	SER_A_2_O	10.391	7.819	-4.736	10.151	8.945	-5.167	1.23	110.52	102.03
12	2jsa-14	SER_A_2_C	ALA_A_3_N	10.391	7.819	-4.736	9.477	6.88	-4.54	1.32	81.49	-134.23
13	2jsa-14	ALA_A_3_N	ALA_A_3_H	9.477	6.88	-4.54	9.747	5.974	-4.183	1.01	69.31	-73.41
14	2jsa-14	ALA_A_3_N	ALA_A_3_CA	9.477	6.88	-4.54	8.075	7.128	-4.832	1.45	101.59	169.97
15	2jsa-14	ALA_A_3_CA	ALA_A_3_HA	8.075	7.128	-4.832	7.726	7.948	-4.204	1.09	54.83	113.06
16	2jsa-14	ALA_A_3_CA	ALA_A_3_C	8.075	7.128	-4.832	7.26	5.877	-4.494	1.53	77.24	-123.08
17	2jsa-14	ALA_A_3_C	ALA_A_3_O	7.26	5.877	-4.494	6.319	5.941	-3.703	1.23	50.01	176.11
18	2jsa-14	ALA_A_3_C	LEU_A_4_N	7.26	5.877	-4.494	7.649	4.771	-5.11	1.32	117.72	-70.62
19	2jsa-14	LEU_A_4_N	LEU_A_4_H	7.649	4.771	-5.11	8.432	4.793	-5.748	1.01	129.16	1.61
20	2jsa-14	LEU_A_4_N	LEU_A_4_CA	7.649	4.771	-5.11	6.966	3.509	-4.885	1.45	81.09	-118.42
21	2jsa-14	LEU_A_4_CA	LEU_A_4_HA	6.966	3.509	-4.885	6.049	3.512	-5.473	1.09	122.67	179.81
22	2jsa-14	LEU_A_4_CA	LEU_A_4_C	6.966	3.509	-4.885	6.573	3.403	-3.409	1.53	15.42	-164.91
23	2jsa-14	LEU_A_4_C	LEU_A_4_O	6.573	3.403	-3.409	5.431	3.079	-3.089	1.23	74.91	-164.16
24	2jsa-14	LEU_A_4_C	SER_A_5_N	6.573	3.403	-3.409	7.543	3.683	-2.55	1.33	49.61	16.10
25	2jsa-14	SER_A_5_N	SER_A_5_H	7.543	3.683	-2.55	8.46	3.944	-2.884	1.01	109.31	15.89
26	2jsa-14	SER_A_5_N	SER_A_5_CA	7.543	3.683	-2.55	7.312	3.623	-1.117	1.45	9.46	-165.44
27	2jsa-14	SER_A_5_CA	SER_A_5_HA	7.312	3.623	-1.117	7.188	2.578	-0.834	1.09		

30	2jsa-14	SER_A_5_C	CYS_A_6_N	6.032	4.382	-0.76	6.07	5.685	-0.997	1.32	100.30	88.33
31	2jsa-14	CYS_A_6_N	CYS_A_6_H	6.07	5.685	-0.997	6.901	6.108	-1.385	1.01	112.59	26.98
32	2jsa-14	CYS_A_6_N	CYS_A_6_CA	6.07	5.685	-0.997	4.925	6.532	-0.707	1.45	78.49	143.51
33	2jsa-14	CYS_A_6_CA	CYS_A_6_HA	4.925	6.532	-0.707	4.668	6.413	0.346	1.09	15.05	-155.15
34	2jsa-14	CYS_A_6_CA	CYS_A_6_C	4.925	6.532	-0.707	3.745	6.05	-1.554	1.53	123.60	-157.78
35	2jsa-14	CYS_A_6_C	CYS_A_6_O	3.745	6.05	-1.554	2.77	5.521	-1.022	1.23	64.38	-151.52
36	2jsa-14	CYS_A_6_C	GLN_A_7_N	3.745	6.05	-1.554	3.871	6.253	-2.858	1.33	169.62	58.17
37	2jsa-14	GLN_A_7_N	GLN_A_7_H	3.871	6.253	-2.858	4.701	6.697	-3.226	1.01	111.35	28.14
38	2jsa-14	GLN_A_7_N	GLN_A_7_CA	3.871	6.253	-2.858	2.827	5.847	-3.783	1.45	129.55	-158.75
39	2jsa-14	GLN_A_7_CA	GLN_A_7_HA	2.827	5.847	-3.783	2.089	6.647	-3.83	1.09	92.47	132.69
40	2jsa-14	GLN_A_7_CA	GLN_A_7_C	2.827	5.847	-3.783	2.133	4.581	-3.276	1.53	70.65	-118.73
41	2jsa-14	GLN_A_7_C	GLN_A_7_O	2.133	4.581	-3.276	0.939	4.6	-2.978	1.23	75.99	179.09
42	2jsa-14	GLN_A_7_C	MET_A_8_N	2.133	4.581	-3.276	2.909	3.51	-3.195	1.33	86.50	-54.07
43	2jsa-14	MET_A_8_N	MET_A_8_H	2.909	3.51	-3.195	3.882	3.566	-3.459	1.01	105.16	3.29
44	2jsa-14	MET_A_8_N	MET_A_8_CA	2.909	3.51	-3.195	2.383	2.238	-2.729	1.45	71.30	-112.47
45	2jsa-14	MET_A_8_CA	MET_A_8_HA	2.383	2.238	-2.729	1.768	1.804	-3.517	1.09	136.31	-144.79
46	2jsa-14	MET_A_8_CA	MET_A_8_C	2.383	2.238	-2.729	1.526	2.426	-1.476	1.53	35.00	167.63
47	2jsa-14	MET_A_8_C	MET_A_8_O	1.526	2.426	-1.476	0.423	1.887	-1.388	1.23	85.90	-153.96
48	2jsa-14	MET_A_8_C	CYS_A_9_N	1.526	2.426	-1.476	2.064	3.19	-0.537	1.32	44.86	54.85
49	2jsa-14	CYS_A_9_N	CYS_A_9_H	2.064	3.19	-0.537	2.976	3.602	-0.677	1.01	97.96	24.31
50	2jsa-14	CYS_A_9_N	CYS_A_9_CA	2.064	3.19	-0.537	1.363	3.454	0.707	1.45	31.05	159.36
51	2jsa-14	CYS_A_9_CA	CYS_A_9_HA	1.363	3.454	0.707	1.136	2.499	1.182	1.09	64.18	-103.37
52	2jsa-14	CYS_A_9_CA	CYS_A_9_C	1.363	3.454	0.707	0.046	4.159	0.376	1.53	102.49	151.84
53	2jsa-14	CYS_A_9_C	CYS_A_9_O	0.046	4.159	0.376	-0.954	3.97	1.066	1.23	55.86	-169.30
54	2jsa-14	CYS_A_9_C	GLU_A_10_N	0.046	4.159	0.376	0.089	4.958	-0.68	1.32	142.85	86.92
55	2jsa-14	GLU_A_10_N	GLU_A_10_H	0.089	4.958	-0.68	0.948	5.066	-1.201	1.01	121.04	7.17
56	2jsa-14	GLU_A_10_N	GLU_A_10_CA	0.089	4.958	-0.68	-1.088	5.692	-1.112	1.45	107.30	148.05
57	2jsa-14	GLU_A_10_CA	GLU_A_10_HA	-1.088	5.692	-1.112	-1.627	6.018	-0.222	1.09	35.29	148.83
58	2jsa-14	GLU_A_10_CA	GLU_A_10_C	-1.088	5.692	-1.112	-2.011	4.784	-1.927	1.53	122.19	-135.47
59	2jsa-14	GLU_A_10_C	GLU_A_10_O	-2.011	4.784	-1.927	-3.107	5.191	-2.31	1.23	108.14	159.63
60	2jsa-14	GLU_A_10_C	LEU_A_11_N	-2.011	4.784	-1.927	-1.534	3.572	-2.169	1.32	100.53	-68.52
61	2jsa-14	LEU_A_11_N	LEU_A_11_H	-1.534	3.572	-2.169	-0.623	3.306	-1.823	1.01	69.97	-16.28
62	2jsa-14	LEU_A_11_N	LEU_A_11_CA	-1.534	3.572	-2.169	-2.302	2.603	-2.931	1.45	121.64	-128.40
63	2jsa-14	LEU_A_11_CA	LEU_A_11_HA	-2.302	2.603	-2.931	-3.001	3.15	-3.564	1.09	125.50	141.96
64	2jsa-14	LEU_A_11_CA	LEU_A_11_C	-2.302	2.603	-2.931	-3.123	1.74	-1.971	1.53	51.13	-133.57
65	2jsa-14	LEU_A_11_C	LEU_A_11_O	-3.123	1.74	-1.971	-4.276	1.418	-2.251	1.23	103.16	-164.40
66	2jsa-14	LEU_A_11_C	VAL_A_12_N	-3.123	1.74	-1.971	-2.494	1.389	-0.859	1.32	32.93	-29.16
67	2jsa-14	VAL_A_12_N	VAL_A_12_H	-2.494	1.389	-0.859	-1.544	1.69	-0.695	1.01	80.65	17.58
68	2jsa-14	VAL_A_12_N	VAL_A_12_CA	-2.494	1.389	-0.859	-3.151	0.568	0.145	1.45	46.32	-128.67
69	2jsa-14	VAL_A_12_CA	VAL_A_12_HA	-3.151	0.568	0.145	-3.667	-0.247	-0.361	1.09	117.68	-122.34
70	2jsa-14	VAL_A_12_CA	VAL_A_12_C	-3.151	0.568	0.145	-4.197	1.408	0.88	1.53	61.28	141.23
71	2jsa-14	VAL_A_12_C	VAL_A_12_O	-4.197	1.408	0.88	-5.345	0.991	1.023	1.23	83.32	-160.04
72	2jsa-14	VAL_A_12_C	VAL_A_13_N	-4.197	1.408	0.88	-3.763	2.578	1.326	1.33	70.33	69.65
73	2jsa-14	VAL_A_13_N	VAL_A_13_H	-3.763	2.578	1.326	-2.804	2.857	1.171	1.01	98.82	16.22
74	2jsa-14	VAL_A_13_N	VAL_A_13_CA	-3.763	2.578	1.326	-4.647	3.481	2.043	1.45	60.43	134.39
75	2jsa-14	VAL_A_13_CA	VAL_A_13_HA	-4.647	3.481	2.043	-5.06	2.95	2.9	1.09	38.13	-127.87
76	2jsa-14	VAL_A_13_CA	VAL_A_13_C	-4.647	3.481	2.043	-5.806	3.885	1.129	1.53	126.67	160.78
77	2jsa-14	VAL_A_13_C	VAL_A_13_O	-5.806	3.885	1.129	-6.969	3.655	1.459	1.23	74.45	-168.81
78	2jsa-14	VAL_A_13_C	LYS_A_14_N	-5.806	3.885	1.129	-5.449	4.478	-0.001	1.33	148.51	58.95
79	2jsa-14	LYS_A_14_N	LYS_A_14_H	-5.449	4.478	-0.001	-4.472	4.634	-0.207	1.01	101.76	9.07
80	2jsa-14	LYS_A_14_N	LYS_A_14_CA	-5.449	4.478	-0.001	-6.445	4.915	-0.964	1.45	131.52	156.31
81	2jsa-14	LYS_A_14_CA	LYS_A_14_HA	-6.445	4.915	-0.964	-6.955	5.785	-0.551	1.09	67.73	120.38
82	2jsa-14	LYS_A_14_CA	LYS_A_14_C	-6.445	4.915	-0.964	-7.487	3.81	-1.15	1.53	96.98	-133.32
83	2jsa-14	LYS_A_14_C	LYS_A_14_O	-7.487	3.81	-1.15	-8.664	4.093	-1.367	1.23	100.16	166.48
84	2jsa-14	LYS_A_14_C	LYS_A_15_N	-7.487	3.81	-1.15	-7.017	2.575	-1.057	1.32	85.97	-69.16
85	2jsa-14	LYS_A_15_N	LYS_A_15_H	-7.017	2.575	-1.057	-6.036	2.416	-0.875	1.01	79.62	-9.21
86	2jsa-14	LYS_A_15_N	LYS_A_15_CA	-7.017	2.575	-1.057	-7.894	1.427	-1.213	1.45	96.16	-127.38
87	2jsa-14	LYS_A_15_CA	LYS_A_15_HA	-7.894	1.427	-1.213	-8.605	1.651	-2.008	1.09	136.84	162.51
88	2jsa-14	LYS_A_15_CA	LYS_A_15_C	-7.894	1.427	-1.213	-8.689	1.22	0.077	1.53	32.49	-165.41
89	2jsa-14	LYS_A_15_C	LYS_A_15_O	-8.689	1.22	0.077	-9.878	0.905	0.034	1.23	92.00	-165.16
90	2jsa-14	LYS_A_15_C	TYR_A_16_N	-8.689	1.22	0.077	-8.003	1.406	1.195	1.32	32.45	15.17
91	2jsa-14	TYR_A_16_N	TYR_A_16_H	-8.003	1.406	1.195	-7.027	1.664	1.155	1.01	92.27	14.81
92	2jsa-14	TYR_A_16_N	TYR_A_16_CA	-8.003	1.406	1.195	-8.63	1.244	2.495	1.45	26.48	-165.51
93	2jsa-14	TYR_A_16_CA	TYR_A_16_HA	-8.63	1.244	2.495	-9.2	0.316	2.525	1.09	88.42	-121.56
94	2jsa-14	TYR_A_16_CA	TYR_A_16_C	-8.63	1.244	2.495	-9.547	2.427	2.814	1.53	77.97	127.78
95	2jsa-14	TYR_A_16_C	TYR_A_16_O	-9.547	2.427	2.814	-10.766	2.274	2.873	1.23	87.25	-172.85
96	2jsa-14	TYR_A_16_C	GLU_A_17_N	-9.547	2.427	2.814	-8.924	3.581	3.008	1.33	81.59	61.64
97	2jsa-14	GLU_A_17_N	GLU_A_17_H	-8.924	3.581	3.008	-7.917	3.634	2.941	1.01	93.80	3.01
98	2jsa-14	GLU_A_17_N	GLU_A_17_CA	-8.924	3.581	3.008	-9.669	4.789	3.319	1.45	77.64	121.66
99	2jsa-14	GLU_A_17_CA	GLU_A_17_HA	-9.669	4.789	3.319	-9.941	4.756	4.374	1.09	14.56	-173.08
100	2jsa-14	GLU_A_17_CA	GLU_A_17_C	-9.669	4.789	3.319	-10.955	4.847	2.491	1.53	122.75	177.42
101	2jsa-14	GLU_A_17_C	GLU_A_17_O	-10.955	4.847	2.491	-12.006	5.236	2.999	1.23	65.62	159.69
102	2jsa-14	GLU_A_17_C	GLY_A_18_N	-10.955	4.847	2.491	-10.83	4.455	1.232	1.32	161.90	-72.31
103	2jsa-14	GLY_A_18_N	GLY_A_18_H	-10.83	4.455	1.232	-9.934	4.148	0.882	1.01	110.28	-18.91
104	2jsa-14	GLY_A_18_N	GLY_A_18_CA	-10.83	4.455	1.232	-11.969	4.457	0.332	1.45	128.31	179.90
105	2jsa-14	GLY_A_18_CA	GLY_A_18_C	-11.969	4.457	0.332	-12.265	3.047	-0.183	1.53	109.67	-101.86
106	2jsa-14	GLY_A_18_C	GLY_A_18_O	-12.265	3.047	-0.183	-12.429	2.842	-1.385	1.23	167.68	-128.66
107	2jsa-14	GLY_A_18_C	SER_A_19_N	-12.265	3.047	-0.183	-12.323	2.11	0.752	1.32	45.12	-93.54
108	2jsa-14	SER_A_19_N	SER_A_19_H	-12.323	2.11	0.752	-12.177	2.351	1.722	1.01	16.20	58.79
109	2jsa-14	SER_A_19_N	SER_A_19_CA	-12.323	2.11	0.752	-12.596	0.725	0.409	1.45	103.66	-101.15
110	2jsa-14	SER_A_19_CA	SER_A_19_HA	-12.596	0.725	0.409	-12.083	0.498	-0.526	1.09	149.04	-23.87
111	2jsa-14	SER_A_19_CA	SER_A_19_C	-12.596	0.725	0.409	-14.099	0.522	0.206	1.53	97.62	-172.31
112	2jsa-14	SER_A_19_C	SER_A_19_O	-14.099	0.522	0.206	-14.528	0.039	-0.839	1.23	148.28	-131.61
113	2jsa-14	SER_A_19_C	ALA_A_20_N	-14.099	0.522	0.206	-14.857	0.902	1.225	1.33	39.76	153.37
114	2jsa-14	ALA_A_20_N	ALA_A_20_H	-14.857	0.902	1.225	-14.434	1.291	2.056	1.01	34.67	42.60
115	2jsa-14	ALA_A_20_N	ALA_A_20_CA	-14.857	0.902	1.225	-16.303	0.768	1.172	1.45	92.09	-174.71
116	2jsa-14	ALA_A_20_CA	ALA_A_20_HA	-16.303	0.768	1.172	-16.745	1.462	1.886	1.09	49.05	122.49
117	2jsa-14	ALA_A_20_CA	ALA_A_20_C	-16.303	0.768	1.172	-16.694	-0.655	1.575	1.53	74.73	-105.36
118	2jsa-14	ALA_A_20_C	ALA_A_20_O	-16.694	-0.655	1.575	-17.875	-0.955	1.739	1.23	82.33	-165.75
119	2jsa-14	ALA_A_20_C	ASP_A_21_N	-16.694	-0.655	1.575	-15.679	-1.494	1.722	1.33	83.63	-39.58
120	2jsa-14	ASP_A_21_N	ASP_A_21_H	-15.679	-1.494	1.722	-14.731	-1.179	1.569			

123	2jsa-14	ASP_A_21_CA	ASP_A_21_C	-15.902	-2.878	2.103	-15.245	-3.143	3.459	1.53	27.58	-21.97
124	2jsa-14	ASP_A_21_C	ASP_A_21_O	-15.245	-3.143	3.459	-15.449	-4.198	4.056	1.23	60.94	-100.94
125	2jsa-14	ASP_A_21_C	LYS_A_22_N	-15.245	-3.143	3.459	-14.47	-2.164	3.905	1.33	70.34	51.63
126	2jsa-14	LYS_A_22_N	LYS_A_22_H	-14.47	-2.164	3.905	-14.348	-1.323	3.36	1.01	122.67	81.75
127	2jsa-14	LYS_A_22_N	LYS_A_22_CA	-14.47	-2.164	3.905	-13.782	-2.277	5.18	1.45	28.67	-9.33
128	2jsa-14	LYS_A_22_CA	LYS_A_22_HA	-13.782	-2.277	5.18	-12.958	-1.563	5.183	1.09	89.84	40.91
129	2jsa-14	LYS_A_22_CA	LYS_A_22_C	-13.782	-2.277	5.18	-13.183	-3.679	5.309	1.53	85.16	-66.87
130	2jsa-14	LYS_A_22_C	LYS_A_22_O	-13.183	-3.679	5.309	-13.655	-4.489	6.106	1.23	49.63	-120.23
131	2jsa-14	LYS_A_22_C	ASP_A_23_N	-13.183	-3.679	5.309	-12.153	-3.924	4.512	1.33	126.97	-13.38
132	2jsa-14	ASP_A_23_N	ASP_A_23_H	-12.153	-3.924	4.512	-11.818	-3.211	3.88	1.01	128.74	64.83
133	2jsa-14	ASP_A_23_N	ASP_A_23_CA	-12.153	-3.924	4.512	-11.485	-5.214	4.527	1.45	89.41	-62.62
134	2jsa-14	ASP_A_23_CA	ASP_A_23_HA	-11.485	-5.214	4.527	-11.499	-5.61	5.543	1.09	21.31	-92.02
135	2jsa-14	ASP_A_23_CA	ASP_A_23_C	-11.485	-5.214	4.527	-10.04	-5.041	4.056	1.53	107.93	6.83
136	2jsa-14	ASP_A_23_C	ASP_A_23_O	-10.04	-5.041	4.056	-9.792	-4.789	2.877	1.23	163.31	45.46
137	2jsa-14	ASP_A_23_C	ALA_A_24_N	-10.04	-5.041	4.056	-9.121	-5.182	5.001	1.33	44.53	-8.72
138	2jsa-14	ALA_A_24_N	ALA_A_24_H	-9.121	-5.182	5.001	-9.396	-5.388	5.951	1.01	19.88	-143.16
139	2jsa-14	ALA_A_24_N	ALA_A_24_CA	-9.121	-5.182	5.001	-7.707	-5.044	4.697	1.45	102.08	5.57
140	2jsa-14	ALA_A_24_CA	ALA_A_24_HA	-7.707	-5.044	4.697	-7.537	-4.063	4.253	1.09	114.03	80.17
141	2jsa-14	ALA_A_24_CA	ALA_A_24_C	-7.707	-5.044	4.697	-7.302	-6.112	3.681	1.53	131.65	-69.23
142	2jsa-14	ALA_A_24_C	ALA_A_24_O	-7.302	-6.112	3.681	-6.219	-6.044	3.1	1.23	118.17	3.59
143	2jsa-14	ALA_A_24_C	ASN_A_25_N	-7.302	-6.112	3.681	-8.192	-7.075	3.494	1.32	98.12	-132.74
144	2jsa-14	ASN_A_25_N	ASN_A_25_H	-8.192	-7.075	3.494	-9.062	-7.068	4.006	1.01	59.52	179.54
145	2jsa-14	ASN_A_25_N	ASN_A_25_CA	-8.192	-7.075	3.494	-7.941	-8.156	2.556	1.45	130.21	-76.93
146	2jsa-14	ASN_A_25_CA	ASN_A_25_HA	-7.941	-8.156	2.556	-6.902	-8.474	2.648	1.09	85.16	-17.02
147	2jsa-14	ASN_A_25_CA	ASN_A_25_C	-7.941	-8.156	2.556	-8.21	-7.664	1.132	1.53	158.51	118.67
148	2jsa-14	ASN_A_25_C	ASN_A_25_O	-8.21	-7.664	1.132	-7.47	-7.996	0.208	1.23	138.72	-24.16
149	2jsa-14	ASN_A_25_C	VAL_A_26_N	-8.21	-7.664	1.132	-9.27	-6.879	1.002	1.33	95.63	143.48
150	2jsa-14	VAL_A_26_N	VAL_A_26_H	-9.27	-6.879	1.002	-9.833	-6.647	1.808	1.01	37.07	157.60
151	2jsa-14	VAL_A_26_N	VAL_A_26_CA	-9.27	-6.879	1.002	-9.645	-6.338	-0.293	1.45	153.06	124.73
152	2jsa-14	VAL_A_26_CA	VAL_A_26_HA	-9.645	-6.338	-0.293	-9.361	-7.057	-1.062	1.09	134.85	-68.45
153	2jsa-14	VAL_A_26_CA	VAL_A_26_C	-9.645	-6.338	-0.293	-8.869	-5.043	-0.544	1.53	99.44	59.07
154	2jsa-14	VAL_A_26_C	VAL_A_26_O	-8.869	-5.043	-0.544	-8.965	-4.456	-1.62	1.23	151.07	99.29
155	2jsa-14	VAL_A_26_C	ILE_A_27_N	-8.869	-5.043	-0.544	-8.116	-4.636	0.468	1.33	40.22	28.39
156	2jsa-14	ILE_A_27_N	ILE_A_27_H	-8.116	-4.636	0.468	-8.082	-5.17	1.325	1.01	31.98	-86.36
157	2jsa-14	ILE_A_27_N	ILE_A_27_CA	-8.116	-4.636	0.468	-7.325	-3.422	0.371	1.45	93.83	56.91
158	2jsa-14	ILE_A_27_CA	ILE_A_27_HA	-7.325	-3.422	0.371	-7.771	-2.789	-0.396	1.09	134.73	125.17
159	2jsa-14	ILE_A_27_CA	ILE_A_27_C	-7.325	-3.422	0.371	-5.909	-3.777	-0.085	1.53	107.35	-14.07
160	2jsa-14	ILE_A_27_C	ILE_A_27_O	-5.909	-3.777	-0.085	-5.39	-3.184	-1.031	1.23	140.20	48.81
161	2jsa-14	ILE_A_27_C	LYS_A_28_N	-5.909	-3.777	-0.085	-5.322	-4.742	0.607	1.32	58.51	-58.69
162	2jsa-14	LYS_A_28_N	LYS_A_28_H	-5.322	-4.742	0.607	-5.808	-5.186	1.373	1.01	40.67	-137.59
163	2jsa-14	LYS_A_28_N	LYS_A_28_CA	-5.322	-4.742	0.607	-3.976	-5.183	0.285	1.45	102.81	-18.14
164	2jsa-14	LYS_A_28_CA	LYS_A_28_HA	-3.976	-5.183	0.285	-3.342	-4.3	0.204	1.09	94.26	54.32
165	2jsa-14	LYS_A_28_CA	LYS_A_28_C	-3.976	-5.183	0.285	-3.984	-5.877	-1.079	1.53	153.03	-90.66
166	2jsa-14	LYS_A_28_C	LYS_A_28_O	-3.984	-5.877	-1.079	-2.995	-5.834	-1.808	1.23	126.37	2.49
167	2jsa-14	LYS_A_28_C	LYS_A_29_N	-3.984	-5.877	-1.079	-5.113	-6.501	-1.383	1.33	103.26	-151.07
168	2jsa-14	LYS_A_29_N	LYS_A_29_H	-5.113	-6.501	-1.383	-5.887	-6.495	-0.735	1.01	50.06	179.56
169	2jsa-14	LYS_A_29_N	LYS_A_29_CA	-5.113	-6.501	-1.383	-5.263	-7.203	-2.646	1.45	150.39	-102.06
170	2jsa-14	LYS_A_29_CA	LYS_A_29_HA	-5.263	-7.203	-2.646	-4.337	-7.745	-2.843	1.09	100.40	-30.34
171	2jsa-14	LYS_A_29_CA	LYS_A_29_C	-5.263	-7.203	-2.646	-5.454	-6.184	-3.772	1.53	137.36	100.62
172	2jsa-14	LYS_A_29_C	LYS_A_29_O	-5.454	-6.184	-3.772	-4.78	-6.254	-4.799	1.23	146.58	-5.93
173	2jsa-14	LYS_A_29_C	ASP_A_30_N	-5.454	-6.184	-3.772	-6.375	-5.261	-3.54	1.32	79.91	134.94
174	2jsa-14	ASP_A_30_N	ASP_A_30_H	-6.375	-5.261	-3.54	-6.891	-5.264	-2.672	1.01	30.73	-179.67
175	2jsa-14	ASP_A_30_N	ASP_A_30_CA	-6.375	-5.261	-3.54	-6.664	-4.228	-4.522	1.45	132.47	105.63
176	2jsa-14	ASP_A_30_CA	ASP_A_30_HA	-6.664	-4.228	-4.522	-7.12	-4.687	-5.399	1.09	143.58	-134.81
177	2jsa-14	ASP_A_30_CA	ASP_A_30_C	-6.664	-4.228	-4.522	-5.361	-3.531	-4.919	1.53	105.04	28.14
178	2jsa-14	ASP_A_30_C	ASP_A_30_O	-5.361	-3.531	-4.919	-5.065	-3.389	-6.105	1.23	164.53	25.63
179	2jsa-14	ASP_A_30_C	PHE_A_31_N	-5.361	-3.531	-4.919	-4.617	-3.115	-3.905	1.32	40.05	29.21
180	2jsa-14	PHE_A_31_N	PHE_A_31_H	-4.617	-3.115	-3.905	-4.922	-3.266	-2.954	1.01	19.69	-153.66
181	2jsa-14	PHE_A_31_N	PHE_A_31_CA	-4.617	-3.115	-3.905	-3.353	-2.436	-4.134	1.45	99.07	28.24
182	2jsa-14	PHE_A_31_CA	PHE_A_31_HA	-3.353	-2.436	-4.134	-3.534	-1.455	-4.572	1.09	113.70	100.45
183	2jsa-14	PHE_A_31_CA	PHE_A_31_C	-3.353	-2.436	-4.134	-2.451	-3.254	-5.06	1.53	127.25	-42.20
184	2jsa-14	PHE_A_31_C	PHE_A_31_O	-2.451	-3.254	-5.06	-1.749	-2.695	-5.902	1.23	133.18	38.53
185	2jsa-14	PHE_A_31_C	ASP_A_32_N	-2.451	-3.254	-5.06	-2.498	-4.565	-4.872	1.33	81.84	-92.05
186	2jsa-14	ASP_A_32_N	ASP_A_32_H	-2.498	-4.565	-4.872	-3.098	-4.956	-4.179	1.01	45.13	-146.91
187	2jsa-14	ASP_A_32_N	ASP_A_32_CA	-2.498	-4.565	-4.872	-1.693	-5.466	-5.679	1.45	123.74	-48.22
188	2jsa-14	ASP_A_32_CA	ASP_A_32_HA	-1.693	-5.466	-5.679	-0.65	-5.152	-5.629	1.09	87.37	16.75
189	2jsa-14	ASP_A_32_CA	ASP_A_32_C	-1.693	-5.466	-5.679	-2.182	-5.42	-7.129	1.53	161.29	174.63
190	2jsa-14	ASP_A_32_C	ASP_A_32_O	-2.182	-5.42	-7.129	-1.401	-5.615	-8.058	1.23	139.09	-14.02
191	2jsa-14	ASP_A_32_C	ALA_A_33_N	-2.182	-5.42	-7.129	-3.474	-5.16	-7.275	1.33	96.32	168.62
192	2jsa-14	ALA_A_33_N	ALA_A_33_H	-3.474	-5.16	-7.275	-4.057	-5.009	-6.464	1.01	36.60	165.48
193	2jsa-14	ALA_A_33_N	ALA_A_33_CA	-3.474	-5.16	-7.275	-4.077	-5.087	-8.595	1.45	155.29	173.10
194	2jsa-14	ALA_A_33_CA	ALA_A_33_HA	-4.077	-5.087	-8.595	-3.8	-5.979	-9.157	1.09	121.04	-72.75
195	2jsa-14	ALA_A_33_CA	ALA_A_33_C	-4.077	-5.087	-8.595	-3.531	-3.861	-9.332	1.53	118.77	65.99
196	2jsa-14	ALA_A_33_C	ALA_A_33_O	-3.531	-3.861	-9.332	-2.732	-3.993	-10.257	1.23	138.80	-9.38
197	2jsa-14	ALA_A_33_C	GLU_A_34_N	-3.531	-3.861	-9.332	-3.987	-2.696	-8.895	1.33	70.75	111.38
198	2jsa-14	GLU_A_34_N	GLU_A_34_H	-3.987	-2.696	-8.895	-4.644	-2.663	-8.129	1.01	40.66	177.12
199	2jsa-14	GLU_A_34_N	GLU_A_34_CA	-3.987	-2.696	-8.895	-3.556	-1.448	-9.501	1.45	114.65	70.95
200	2jsa-14	GLU_A_34_CA	GLU_A_34_HA	-3.556	-1.448	-9.501	-3.989	-1.39	-10.499	1.09	156.36	172.37
201	2jsa-14	GLU_A_34_CA	GLU_A_34_C	-3.556	-1.448	-9.501	-2.032	-1.423	-9.636	1.53	95.06	0.94
202	2jsa-14	GLU_A_34_C	GLU_A_34_O	-2.032	-1.423	-9.636	-1.502	-0.966	-10.648	1.23	145.34	40.77
203	2jsa-14	GLU_A_34_C	CYS_A_35_N	-2.032	-1.423	-9.636	-1.37	-1.918	-8.6	1.33	38.59	-36.79
204	2jsa-14	CYS_A_35_N	CYS_A_35_H	-1.37	-1.918	-8.6	-1.871	-2.276	-7.8	1.01	37.59	-144.45
205	2jsa-14	CYS_A_35_N	CYS_A_35_CA	-1.37	-1.918	-8.6	0.082	-1.959	-8.59	1.45	89.61	-1.62
206	2jsa-14	CYS_A_35_CA	CYS_A_35_HA	0.082	-1.959	-8.59	0.454	-0.942	-8.715	1.09	96.58	69.91
207	2jsa-14	CYS_A_35_CA	CYS_A_35_C	0.082	-1.959	-8.59	0.549	-2.797	-9.782	1.53	141.17	-60.87
208	2jsa-14	CYS_A_35_C	CYS_A_35_O	0.549	-2.797	-9.782	1.33	-2.328	-10.608	1.23	132.20	30.99
209	2jsa-14	CYS_A_35_C	LYS_A_36_N	0.549	-2.797	-9.782	0.049	-4.023	-9.835	1.33	92.29	-112.19
210	2jsa-14	LYS_A_36_N	LYS_A_36_H	0.049	-4.023	-9.835	-0.589	-4.342	-9.121	1.01	44.97	-153.43
211	2jsa-14	LYS_A_36_N	LYS_A_36_CA	0.049	-4.023	-9.835	0.404	-4.931	-10.912	1.45	137.85	-68.65
212	2jsa-14	LYS_A_36_CA	LYS_A_36_HA	0.404	-4.931	-10.912	1.488	-5.048	-10.912	1.09	90.00	-6.16
213	2jsa-14	LYS_A_36_CA	LYS_A_36_C	0.404								

216	2jsa-14	LYS_A_37_N	LYS_A_37_H	-0.66	-3.164	-12.16	-0.866	-2.766	-11.255	1.01	26.34	117.37
217	2jsa-14	LYS_A_37_N	LYS_A_37_CA	-0.66	-3.164	-12.16	-1.104	-2.461	-13.351	1.45	145.08	122.28
218	2jsa-14	LYS_A_37_CA	LYS_A_37_HA	-1.104	-2.461	-13.351	-1.057	-3.155	-14.19	1.09	140.34	-86.13
219	2jsa-14	LYS_A_37_CA	LYS_A_37_C	-1.104	-2.461	-13.351	-0.141	-1.309	-13.647	1.53	101.15	50.11
220	2jsa-14	LYS_A_37_C	LYS_A_37_O	-0.141	-1.309	-13.647	0.675	-1.396	-14.563	1.23	138.14	-6.09
221	2jsa-14	LYS_A_37_C	LEU_A_38_N	-0.141	-1.309	-13.647	-0.267	-0.256	-12.853	1.32	53.18	96.82
222	2jsa-14	LEU_A_38_N	LEU_A_38_H	-0.267	-0.256	-12.853	-0.96	-0.253	-12.118	1.01	43.32	179.75
223	2jsa-14	LEU_A_38_N	LEU_A_38_CA	-0.267	-0.256	-12.853	0.581	0.912	-13.017	1.45	96.48	54.02
224	2jsa-14	LEU_A_38_CA	LEU_A_38_HA	0.581	0.912	-13.017	0.481	1.261	-14.045	1.09	160.55	105.99
225	2jsa-14	LEU_A_38_CA	LEU_A_38_C	0.581	0.912	-13.017	2.041	0.509	-12.804	1.53	81.99	-15.43
226	2jsa-14	LEU_A_38_C	LEU_A_38_O	2.041	0.509	-12.804	2.907	0.848	-13.61	1.23	130.91	21.38
227	2jsa-14	LEU_A_38_C	PHE_A_39_N	2.041	0.509	-12.804	2.272	-0.207	-11.713	1.33	34.59	-72.12
228	2jsa-14	PHE_A_39_N	PHE_A_39_H	2.272	-0.207	-11.713	1.512	-0.448	-11.093	1.01	52.13	-162.41
229	2jsa-14	PHE_A_39_N	PHE_A_39_CA	2.272	-0.207	-11.713	3.612	-0.66	-11.383	1.45	76.87	-18.68
230	2jsa-14	PHE_A_39_CA	PHE_A_39_HA	3.612	-0.66	-11.383	4.341	0.097	-11.674	1.09	105.48	46.08
231	2jsa-14	PHE_A_39_CA	PHE_A_39_C	3.612	-0.66	-11.383	3.934	-1.98	-12.086	1.53	117.36	-76.29
232	2jsa-14	PHE_A_39_C	PHE_A_39_O	3.934	-1.98	-12.086	4.644	-2.822	-11.538	1.23	63.55	-49.86
233	2jsa-14	PHE_A_39_C	HIS_A_40_N	3.934	-1.98	-12.086	3.396	-2.119	-13.289	1.33	155.21	-165.51
234	2jsa-14	HIS_A_40_N	HIS_A_40_H	3.396	-2.119	-13.289	2.822	-1.385	-13.677	1.01	112.61	128.03
235	2jsa-14	HIS_A_40_N	HIS_A_40_CA	3.396	-2.119	-13.289	3.618	-3.323	-14.072	1.45	122.60	-79.55
236	2jsa-14	HIS_A_40_CA	HIS_A_40_HA	3.618	-3.323	-14.072	3.794	-4.147	-13.38	1.09	50.60	-77.94
237	2jsa-14	HIS_A_40_CA	HIS_A_40_C	3.618	-3.323	-14.072	4.874	-3.154	-14.93	1.53	124.10	7.66
238	2jsa-14	HIS_A_40_C	HIS_A_40_O	4.874	-3.154	-14.93	5.631	-4.104	-15.121	1.23	98.94	-51.45
239	2jsa-14	HIS_A_40_C	THR_A_41_N	4.874	-3.154	-14.93	5.057	-1.937	-15.421	1.33	111.75	81.45
240	2jsa-14	THR_A_41_N	THR_A_41_H	5.057	-1.937	-15.421	4.394	-1.202	-15.22	1.01	78.52	132.05
241	2jsa-14	THR_A_41_N	THR_A_41_CA	5.057	-1.937	-15.421	6.208	-1.631	-16.253	1.45	124.94	14.89
242	2jsa-14	THR_A_41_CA	THR_A_41_HA	6.208	-1.631	-16.253	6.237	-2.336	-17.084	1.09	139.67	-87.64
243	2jsa-14	THR_A_41_CA	THR_A_41_C	6.208	-1.631	-16.253	7.502	-1.794	-15.453	1.53	58.48	-7.18
244	2jsa-14	THR_A_41_C	THR_A_41_O	7.502	-1.794	-15.453	8.565	-2.029	-16.025	1.23	117.72	-12.47
245	2jsa-14	THR_A_41_C	ILE_A_42_N	7.502	-1.794	-15.453	7.369	-1.662	-14.141	1.33	8.13	135.22
246	2jsa-14	ILE_A_42_N	ILE_A_42_H	7.369	-1.662	-14.141	6.463	-1.47	-13.738	1.01	66.48	168.03
247	2jsa-14	ILE_A_42_N	ILE_A_42_CA	7.369	-1.662	-14.141	8.515	-1.791	-13.257	1.45	52.53	-6.42
248	2jsa-14	ILE_A_42_CA	ILE_A_42_HA	8.515	-1.791	-13.257	9.284	-1.098	-13.598	1.09	108.23	42.02
249	2jsa-14	ILE_A_42_CA	ILE_A_42_C	8.515	-1.791	-13.257	9.083	-3.207	-13.368	1.53	94.16	-68.14
250	2jsa-14	ILE_A_42_C	ILE_A_42_O	9.083	-3.207	-13.368	8.331	-4.176	-13.457	1.23	94.15	-127.81
251	2jsa-14	ILE_A_42_C	PRO_A_43_N	9.083	-3.207	-13.368	10.441	-3.284	-13.36	1.36	89.66	-3.25
252	2jsa-14	PRO_A_43_N	PRO_A_43_CA	10.441	-3.284	-13.36	11.117	-4.567	-13.459	1.45	93.91	-62.22
253	2jsa-14	PRO_A_43_CA	PRO_A_43_HA	11.117	-4.567	-13.459	10.659	-5.171	-14.242	1.09	135.93	-127.17
254	2jsa-14	PRO_A_43_CA	PRO_A_43_C	11.117	-4.567	-13.459	11.031	-5.336	-12.139	1.53	30.38	-96.38
255	2jsa-14	PRO_A_43_C	PRO_A_43_O	11.031	-5.336	-12.139	11.556	-6.442	-12.025	1.23	84.68	-64.61
256	2jsa-14	PRO_A_43_C	PHE_A_44_N	11.031	-5.336	-12.139	10.364	-4.719	-11.174	1.33	43.28	137.23
257	2jsa-14	PHE_A_44_N	PHE_A_44_H	10.364	-4.719	-11.174	9.958	-3.809	-11.338	1.01	99.35	114.04
258	2jsa-14	PHE_A_44_N	PHE_A_44_CA	10.364	-4.719	-11.174	10.202	-5.332	-9.867	1.45	25.88	-104.80
259	2jsa-14	PHE_A_44_CA	PHE_A_44_HA	10.202	-5.332	-9.867	10.116	-6.413	-9.973	1.09	95.58	-94.55
260	2jsa-14	PHE_A_44_CA	PHE_A_44_C	10.202	-5.332	-9.867	8.964	-4.784	-9.154	1.53	62.23	156.12
261	2jsa-14	PHE_A_44_C	PHE_A_44_O	8.964	-4.784	-9.154	8.845	-4.895	-7.936	1.23	7.61	-136.99
262	2jsa-14	PHE_A_44_C	GLY_A_45_N	8.964	-4.784	-9.154	8.073	-4.206	-9.946	1.32	126.71	147.03
263	2jsa-14	GLY_A_45_N	GLY_A_45_H	8.073	-4.206	-9.946	8.237	-4.15	-10.941	1.01	170.12	18.85
264	2jsa-14	GLY_A_45_N	GLY_A_45_CA	8.073	-4.206	-9.946	6.848	-3.642	-9.406	1.45	68.18	155.28
265	2jsa-14	GLY_A_45_CA	GLY_A_45_C	6.848	-3.642	-9.406	5.934	-4.739	-8.856	1.53	68.93	-129.80
266	2jsa-14	GLY_A_45_C	GLY_A_45_O	5.934	-4.739	-8.856	5.585	-4.728	-7.676	1.23	16.48	178.19
267	2jsa-14	GLY_A_45_C	THR_A_46_N	5.934	-4.739	-8.856	5.572	-5.66	-9.736	1.32	131.65	-111.46
268	2jsa-14	THR_A_46_N	THR_A_46_H	5.572	-5.66	-9.736	5.898	-5.606	-10.691	1.01	160.91	9.41
269	2jsa-14	THR_A_46_N	THR_A_46_CA	5.572	-5.66	-9.736	4.706	-6.762	-9.354	1.45	74.75	-128.16
270	2jsa-14	THR_A_46_CA	THR_A_46_HA	4.706	-6.762	-9.354	3.74	-6.359	-9.049	1.09	73.75	157.35
271	2jsa-14	THR_A_46_CA	THR_A_46_C	4.706	-6.762	-9.354	5.299	-7.517	-8.162	1.53	38.85	-51.85
272	2jsa-14	THR_A_46_C	THR_A_46_O	5.299	-7.517	-8.162	4.564	-8.013	-7.309	1.23	46.11	-145.99
273	2jsa-14	THR_A_46_C	ARG_A_47_N	5.299	-7.517	-8.162	6.621	-7.579	-8.14	1.32	89.05	-2.69
274	2jsa-14	ARG_A_47_N	ARG_A_47_H	6.621	-7.579	-8.14	7.163	-7.148	-8.875	1.01	136.71	38.49
275	2jsa-14	ARG_A_47_N	ARG_A_47_CA	6.621	-7.579	-8.14	7.321	-8.264	-7.067	1.45	42.39	-44.38
276	2jsa-14	ARG_A_47_CA	ARG_A_47_HA	7.321	-8.264	-7.067	6.924	-9.276	-6.989	1.09	85.90	-111.42
277	2jsa-14	ARG_A_47_CA	ARG_A_47_C	7.321	-8.264	-7.067	7.098	-7.538	-5.739	1.53	29.77	107.07
278	2jsa-14	ARG_A_47_C	ARG_A_47_O	7.098	-7.538	-5.739	6.75	-8.162	-4.737	1.23	35.49	-119.15
279	2jsa-14	ARG_A_47_C	GLU_A_48_N	7.098	-7.538	-5.739	7.307	-6.23	-5.774	1.33	91.51	80.92
280	2jsa-14	GLU_A_48_N	GLU_A_48_H	7.307	-6.23	-5.774	7.592	-5.783	-6.634	1.01	148.35	57.48
281	2jsa-14	GLU_A_48_N	GLU_A_48_CA	7.307	-6.23	-5.774	7.133	-5.412	-4.586	1.45	35.14	102.01
282	2jsa-14	GLU_A_48_CA	GLU_A_48_HA	7.133	-5.412	-4.586	7.646	-5.905	-3.759	1.09	40.71	-43.86
283	2jsa-14	GLU_A_48_CA	GLU_A_48_C	7.133	-5.412	-4.586	5.649	-5.299	-4.232	1.53	76.62	175.65
284	2jsa-14	GLU_A_48_C	GLU_A_48_O	5.649	-5.299	-4.232	5.298	-5.072	-3.075	1.23	19.86	147.11
285	2jsa-14	GLU_A_48_C	CYS_A_49_N	5.649	-5.299	-4.232	4.816	-5.462	-5.25	1.33	140.18	-168.93
286	2jsa-14	CYS_A_49_N	CYS_A_49_H	4.816	-5.462	-5.25	5.175	-5.646	-6.176	1.01	156.46	-27.14
287	2jsa-14	CYS_A_49_N	CYS_A_49_CA	4.816	-5.462	-5.25	3.378	-5.381	-5.06	1.45	82.49	176.78
288	2jsa-14	CYS_A_49_CA	CYS_A_49_HA	3.378	-5.381	-5.06	3.131	-4.367	-4.744	1.09	73.15	103.69
289	2jsa-14	CYS_A_49_CA	CYS_A_49_C	3.378	-5.381	-5.06	2.985	-6.349	-3.943	1.53	43.09	-112.10
290	2jsa-14	CYS_A_49_C	CYS_A_49_O	2.985	-6.349	-3.943	2.369	-5.947	-2.958	1.23	36.75	146.87
291	2jsa-14	CYS_A_49_C	ASP_A_50_N	2.985	-6.349	-3.943	3.358	-7.607	-4.134	1.33	98.28	-73.48
292	2jsa-14	ASP_A_50_N	ASP_A_50_H	3.358	-7.607	-4.134	3.864	-7.866	-4.969	1.01	145.75	-27.11
293	2jsa-14	ASP_A_50_N	ASP_A_50_CA	3.358	-7.607	-4.134	3.051	-8.635	-3.156	1.45	47.65	-106.63
294	2jsa-14	ASP_A_50_CA	ASP_A_50_HA	3.051	-8.635	-3.156	2.014	-8.527	-2.839	1.09	73.09	174.05
295	2jsa-14	ASP_A_50_CA	ASP_A_50_C	3.051	-8.635	-3.156	3.983	-8.48	-1.951	1.53	38.10	9.44
296	2jsa-14	ASP_A_50_C	ASP_A_50_O	3.983	-8.48	-1.951	3.721	-9.032	-0.884	1.23	29.80	-115.39
297	2jsa-14	ASP_A_50_C	HIS_A_51_N	3.983	-8.48	-1.951	5.051	-7.724	-2.163	1.33	99.20	35.29
298	2jsa-14	HIS_A_51_N	HIS_A_51_H	5.051	-7.724	-2.163	5.203	-7.299	-3.067	1.01	153.47	70.32
299	2jsa-14	HIS_A_51_N	HIS_A_51_CA	5.051	-7.724	-2.163	6.023	-7.49	-1.109	1.45	43.49	13.54
300	2jsa-14	HIS_A_51_CA	HIS_A_51_HA	6.023	-7.49	-1.109	6.037	-8.368	-0.462	1.09	53.62	-89.09
301	2jsa-14	HIS_A_51_CA	HIS_A_51_C	6.023	-7.49	-1.109	5.584	-6.291	-0.265	1.53	56.54	110.11
302	2jsa-14	HIS_A_51_C	HIS_A_51_O	5.584	-6.291	-0.265	6.286	-5.89	0.662	1.23	41.09	29.74
303	2jsa-14	HIS_A_51_C	TYR_A_52_N	5.584	-6.291	-0.265	4.426	-5.752	-0.616	1.32	105.37	155.04
304	2jsa-14	TYR_A_52_N	TYR_A_52_H	4.426	-5.752	-0.616	3.902	-6.133	-1.391	1.01	140.11	-143.98
305	2jsa-14	TYR_A_52_N	TYR_A_52_CA	4.426	-5.752	-0.616	3.886	-4.608	0.097	1.45	60.59	

309	2jsa-14	TYR_A_52_C	VAL_A_53_N	2.584	-4.972	0.812	1.746	-5.718	0.106	1.33	122.18	-138.32
310	2jsa-14	VAL_A_53_N	VAL_A_53_H	1.746	-5.718	0.106	1.987	-6.004	-0.832	1.01	158.26	-49.88
311	2jsa-14	VAL_A_53_N	VAL_A_53_CA	1.746	-5.718	0.106	0.471	-6.139	0.66	1.45	67.58	-161.73
312	2jsa-14	VAL_A_53_CA	VAL_A_53_HA	0.471	-6.139	0.66	0.081	-5.331	1.28	1.09	55.35	115.77
313	2jsa-14	VAL_A_53_CA	VAL_A_53_C	0.471	-6.139	0.66	0.686	-7.362	1.553	1.53	54.28	-80.03
314	2jsa-14	VAL_A_53_C	VAL_A_53_O	0.686	-7.362	1.553	-0.025	-8.358	1.43	1.23	95.74	-125.52
315	2jsa-14	VAL_A_53_C	ASN_A_54_N	0.686	-7.362	1.553	1.671	-7.246	2.432	1.33	48.45	6.72
316	2jsa-14	ASN_A_54_N	ASN_A_54_H	1.671	-7.246	2.432	2.216	-6.396	2.477	1.01	87.45	57.33
317	2jsa-14	ASN_A_54_N	ASN_A_54_CA	1.671	-7.246	2.432	1.989	-8.33	3.346	1.45	51.02	-73.65
318	2jsa-14	ASN_A_54_CA	ASN_A_54_HA	1.989	-8.33	3.346	1.146	-8.489	4.018	1.09	51.93	-169.32
319	2jsa-14	ASN_A_54_CA	ASN_A_54_C	1.989	-8.33	3.346	3.235	-7.961	4.154	1.53	58.13	16.50
320	2jsa-14	ASN_A_54_C	ASN_A_54_O	3.235	-7.961	4.154	4.158	-8.763	4.281	1.23	84.07	-40.99
321	2jsa-14	ASN_A_54_C	SER_A_55_N	3.235	-7.961	4.154	3.221	-6.745	4.681	1.33	66.57	90.66
322	2jsa-14	SER_A_55_N	SER_A_55_H	3.221	-6.745	4.681	2.427	-6.138	4.537	1.01	98.20	142.60
323	2jsa-14	SER_A_55_N	SER_A_55_CA	3.221	-6.745	4.681	4.337	-6.259	5.473	1.45	56.95	23.53
324	2jsa-14	SER_A_55_CA	SER_A_55_HA	4.337	-6.259	5.473	4.224	-6.636	6.49	1.09	21.16	-106.69
325	2jsa-14	SER_A_55_CA	SER_A_55_C	4.337	-6.259	5.473	4.325	-4.73	5.514	1.53	88.46	90.45
326	2jsa-14	SER_A_55_C	SER_A_55_O	4.325	-4.73	5.514	4.875	-4.125	6.433	1.23	41.66	47.73
327	2jsa-14	SER_A_55_C	LYS_A_56_N	4.325	-4.73	5.514	3.692	-4.149	4.505	1.33	139.58	137.45
328	2jsa-14	LYS_A_56_N	LYS_A_56_H	3.692	-4.149	4.505	3.263	-4.71	3.783	1.01	135.63	-127.41
329	2jsa-14	LYS_A_56_N	LYS_A_56_CA	3.692	-4.149	4.505	3.601	-2.701	4.414	1.45	93.59	93.60
330	2jsa-14	LYS_A_56_CA	LYS_A_56_HA	3.601	-2.701	4.414	4.081	-2.276	5.296	1.09	36.01	41.52
331	2jsa-14	LYS_A_56_CA	LYS_A_56_C	3.601	-2.701	4.414	2.128	-2.285	4.439	1.53	89.06	164.23
332	2jsa-14	LYS_A_56_C	LYS_A_56_O	2.128	-2.285	4.439	1.817	-1.098	4.518	1.23	86.32	104.68
333	2jsa-14	LYS_A_56_C	VAL_A_57_N	2.128	-2.285	4.439	1.262	-3.285	4.371	1.32	92.94	-130.89
334	2jsa-14	VAL_A_57_N	VAL_A_57_H	1.262	-3.285	4.371	1.59	-4.238	4.308	1.01	93.58	-71.01
335	2jsa-14	VAL_A_57_N	VAL_A_57_CA	1.262	-3.285	4.371	-0.17	-3.038	4.386	1.45	89.41	170.21
336	2jsa-14	VAL_A_57_CA	VAL_A_57_HA	-0.17	-3.038	4.386	-0.343	-1.999	4.105	1.09	104.94	99.45
337	2jsa-14	VAL_A_57_CA	VAL_A_57_C	-0.17	-3.038	4.386	-0.703	-3.24	5.805	1.53	21.88	-159.24
338	2jsa-14	VAL_A_57_C	VAL_A_57_O	-0.703	-3.24	5.805	-1.435	-2.398	6.323	1.23	65.10	131.00
339	2jsa-14	VAL_A_57_C	ASP_A_58_N	-0.703	-3.24	5.805	-0.318	-4.363	6.393	1.32	63.65	-71.08
340	2jsa-14	ASP_A_58_N	ASP_A_58_H	-0.318	-4.363	6.393	0.283	-5.012	5.906	1.01	118.84	-47.20
341	2jsa-14	ASP_A_58_N	ASP_A_58_CA	-0.318	-4.363	6.393	-0.748	-4.687	7.743	1.45	21.74	-143.00
342	2jsa-14	ASP_A_58_CA	ASP_A_58_HA	-0.748	-4.687	7.743	-1.818	-4.895	7.736	1.09	90.37	-169.00
343	2jsa-14	ASP_A_58_CA	ASP_A_58_C	-0.748	-4.687	7.743	-0.455	-3.502	8.665	1.53	52.94	76.11
344	2jsa-14	ASP_A_58_C	ASP_A_58_O	-0.455	-3.502	8.665	-1.293	-3.126	9.484	1.23	48.28	155.83
345	2jsa-14	ASP_A_58_C	PRO_A_59_N	-0.455	-3.502	8.665	0.768	-2.932	8.498	1.36	97.06	24.99
346	2jsa-14	PRO_A_59_N	PRO_A_59_CA	0.768	-2.932	8.498	1.183	-1.797	9.305	1.45	56.27	69.92
347	2jsa-14	PRO_A_59_CA	PRO_A_59_HA	1.183	-1.797	9.305	0.935	-1.973	10.352	1.09	16.20	-144.64
348	2jsa-14	PRO_A_59_CA	PRO_A_59_C	1.183	-1.797	9.305	0.483	-0.515	8.849	1.53	107.34	118.64
349	2jsa-14	PRO_A_59_C	PRO_A_59_O	0.483	-0.515	8.849	-0.183	0.15	9.642	1.23	49.88	135.04
350	2jsa-14	PRO_A_59_C	ILE_A_60_N	0.483	-0.515	8.849	0.658	-0.205	7.573	1.32	164.41	60.55
351	2jsa-14	ILE_A_60_N	ILE_A_60_H	0.658	-0.205	7.573	1.219	-0.798	6.978	1.01	126.09	-46.59
352	2jsa-14	ILE_A_60_N	ILE_A_60_CA	0.658	-0.205	7.573	0.052	0.986	7.002	1.45	113.14	116.97
353	2jsa-14	ILE_A_60_CA	ILE_A_60_HA	0.052	0.986	7.002	0.599	1.854	7.372	1.09	70.17	57.78
354	2jsa-14	ILE_A_60_CA	ILE_A_60_C	0.052	0.986	7.002	-1.392	1.103	7.493	1.53	71.28	175.37
355	2jsa-14	ILE_A_60_C	ILE_A_60_O	-1.392	1.103	7.493	-1.775	2.118	8.072	1.23	61.91	110.67
356	2jsa-14	ILE_A_60_C	ILE_A_61_N	-1.392	1.103	7.493	-2.156	0.049	7.242	1.33	100.91	-125.94
357	2jsa-14	ILE_A_61_N	ILE_A_61_H	-2.156	0.049	7.242	-1.774	-0.754	6.762	1.01	118.36	-64.56
358	2jsa-14	ILE_A_61_N	ILE_A_61_CA	-2.156	0.049	7.242	-3.551	0.023	7.651	1.45	73.66	-178.93
359	2jsa-14	ILE_A_61_CA	ILE_A_61_HA	-3.551	0.023	7.651	-4.055	0.87	7.187	1.09	115.21	120.75
360	2jsa-14	ILE_A_61_CA	ILE_A_61_C	-3.551	0.023	7.651	-3.637	0.204	9.167	1.53	7.53	115.41
361	2jsa-14	ILE_A_61_C	ILE_A_61_O	-3.637	0.204	9.167	-4.653	0.664	9.685	1.23	65.09	155.64
362	2jsa-14	ILE_A_61_C	HIS_A_62_N	-3.637	0.204	9.167	-2.555	-0.165	9.838	1.33	59.59	-18.83
363	2jsa-14	HIS_A_62_N	HIS_A_62_H	-2.555	-0.165	9.838	-1.754	-0.536	9.347	1.01	119.08	-24.85
364	2jsa-14	HIS_A_62_N	HIS_A_62_CA	-2.555	-0.165	9.838	-2.495	-0.047	11.285	1.45	5.23	63.05
365	2jsa-14	HIS_A_62_CA	HIS_A_62_HA	-2.495	-0.047	11.285	-3.355	-0.571	11.701	1.09	67.56	-148.65
366	2jsa-14	HIS_A_62_CA	HIS_A_62_C	-2.495	-0.047	11.285	-2.604	1.425	11.685	1.53	74.84	94.23
367	2jsa-14	HIS_A_62_C	HIS_A_62_O	-2.604	1.425	11.685	-3.093	1.744	12.768	1.23	28.33	146.88
368	2jsa-14	HIS_A_62_C	GLU_A_63_N	-2.604	1.425	11.685	-2.139	2.285	10.789	1.33	132.50	61.60
369	2jsa-14	GLU_A_63_N	GLU_A_63_H	-2.139	2.285	10.789	-1.751	1.952	9.918	1.01	149.59	-40.64
370	2jsa-14	GLU_A_63_N	GLU_A_63_CA	-2.139	2.285	10.789	-2.177	3.716	11.036	1.45	80.21	91.52
371	2jsa-14	GLU_A_63_CA	GLU_A_63_HA	-2.177	3.716	11.036	-1.904	3.886	12.078	1.09	17.15	31.91
372	2jsa-14	GLU_A_63_CA	GLU_A_63_C	-2.177	3.716	11.036	-3.592	4.255	10.816	1.53	98.27	159.15
373	2jsa-14	GLU_A_63_C	GLU_A_63_O	-3.592	4.255	10.816	-4.136	4.95	11.673	1.23	45.84	128.05
374	2jsa-14	GLU_A_63_C	LEU_A_64_N	-3.592	4.255	10.816	-4.147	3.914	9.662	1.33	150.56	-148.43
375	2jsa-14	LEU_A_64_N	LEU_A_64_H	-4.147	3.914	9.662	-3.64	3.34	9.003	1.01	130.71	-48.55
376	2jsa-14	LEU_A_64_N	LEU_A_64_CA	-4.147	3.914	9.662	-5.488	4.354	9.319	1.45	103.66	161.83
377	2jsa-14	LEU_A_64_CA	LEU_A_64_HA	-5.488	4.354	9.319	-5.502	5.444	9.346	1.09	88.58	90.74
378	2jsa-14	LEU_A_64_CA	LEU_A_64_C	-5.488	4.354	9.319	-6.473	3.85	10.375	1.53	46.34	-152.90
379	2jsa-14	LEU_A_64_C	LEU_A_64_O	-6.473	3.85	10.375	-7.418	4.552	10.733	1.23	73.09	143.39
380	2jsa-14	LEU_A_64_C	GLU_A_65_N	-6.473	3.85	10.375	-6.219	2.638	10.845	1.32	69.22	-78.16
381	2jsa-14	GLU_A_65_N	GLU_A_65_H	-6.219	2.638	10.845	-5.423	2.117	10.505	1.01	109.67	-33.21
382	2jsa-14	GLU_A_65_N	GLU_A_65_CA	-6.219	2.638	10.845	-7.071	2.033	11.854	1.45	46.00	-144.62
383	2jsa-14	GLU_A_65_CA	GLU_A_65_HA	-7.071	2.033	11.854	-8.106	2.143	11.532	1.09	107.19	173.93
384	2jsa-14	GLU_A_65_CA	GLU_A_65_C	-7.071	2.033	11.854	-6.905	2.755	13.193	1.53	28.95	77.05
385	2jsa-14	GLU_A_65_C	GLU_A_65_O	-6.905	2.755	13.193	-7.83	2.789	14.003	1.23	48.81	177.89
386	2jsa-14	GLU_A_65_C	GLY_A_66_N	-6.905	2.755	13.193	-5.72	3.317	13.383	1.33	81.76	25.37
387	2jsa-14	GLY_A_66_N	GLY_A_66_H	-5.72	3.317	13.383	-5.005	3.25	12.672	1.01	134.71	-5.35
388	2jsa-14	GLY_A_66_N	GLY_A_66_CA	-5.72	3.317	13.383	-5.422	4.037	14.609	1.45	32.44	67.52
389	2jsa-14	GLY_A_66_CA	GLY_A_66_C	-5.422	4.037	14.609	-6.044	5.434	14.589	1.53	90.75	114.00
390	2jsa-14	GLY_A_66_C	GLY_A_66_O	-6.044	5.434	14.589	-6.569	5.899	15.6	1.23	34.75	138.47
391	2jsa-14	GLY_A_66_C	GLY_A_67_N	-6.044	5.434	14.589	-5.964	6.067	13.428	1.32	151.21	82.80
392	2jsa-14	GLY_A_67_N	GLY_A_67_H	-5.964	6.067	13.428	-5.516	5.624	12.638	1.01	141.43	-44.68
393	2jsa-14	GLY_A_67_N	GLY_A_67_CA	-5.964	6.067	13.428	-6.512	7.402	13.262	1.45	96.56	112.32
394	2jsa-14	GLY_A_67_CA	GLY_A_67_C	-6.512	7.402	13.262	-5.629	8.248	12.345	1.53	126.87	43.77
395	2jsa-14	GLY_A_67_C	GLY_A_67_O	-5.629	8.248	12.345	-6.04	9.315	11.89	1.23	111.70	111.07
396	2jsa-14	GLY_A_67_C	THR_A_68_N	-5.629	8.248	12.345	-4.429	7.741	12.098	1.33	100.74	-22.90
397	2jsa-14	THR_A_68_N	THR_A_68_H	-4.429	7.741	12.098	-4.156	6.858	12.505	1.01	66.23	-72.82
398	2jsa-14	THR_A_68_N	THR_A_68_CA	-4.429	7.741	12.098	-3.484	8.438	11.242	1.45	126.09	36.41

402	2jsa-14	THR_A_68_C	ALA_A_69_N	-4.053	8.587	9.83	-3.766	9.732	9.229	1.32	116.98	75.93
403	2jsa-14	ALA_A_69_N	ALA_A_69_H	-3.766	9.732	9.229	-3.21	10.43	9.703	1.01	62.02	51.46
404	2jsa-14	ALA_A_69_N	ALA_A_69_CA	-3.766	9.732	9.229	-4.24	10.011	7.884	1.45	157.76	149.52
405	2jsa-14	ALA_A_69_CA	ALA_A_69_HA	-4.24	10.011	7.884	-5.297	9.753	7.825	1.09	93.10	-166.28
406	2jsa-14	ALA_A_69_CA	ALA_A_69_C	-4.24	10.011	7.884	-3.473	9.141	6.886	1.53	130.71	-48.60
407	2jsa-14	ALA_A_69_C	ALA_A_69_O	-3.473	9.141	6.886	-2.468	8.526	7.238	1.23	73.37	-31.46
408	2jsa-14	ALA_A_69_C	PRO_A_70_N	-3.473	9.141	6.886	-3.99	9.117	5.628	1.36	157.64	-177.34
409	2jsa-14	PRO_A_70_N	PRO_A_70_CA	-3.99	9.117	5.628	-3.365	8.333	4.577	1.45	136.35	-51.44
410	2jsa-14	PRO_A_70_CA	PRO_A_70_HA	-3.365	8.333	4.577	-3.108	7.342	4.953	1.09	69.83	-75.46
411	2jsa-14	PRO_A_70_CA	PRO_A_70_C	-3.365	8.333	4.577	-2.086	9.009	4.076	1.53	109.10	27.86
412	2jsa-14	PRO_A_70_C	PRO_A_70_O	-2.086	9.009	4.076	-1.218	8.353	3.502	1.23	117.81	-37.08
413	2jsa-14	PRO_A_70_C	LYS_A_71_N	-2.086	9.009	4.076	-2.011	10.31	4.312	1.32	79.74	86.70
414	2jsa-14	LYS_A_71_N	LYS_A_71_H	-2.011	10.31	4.312	-2.763	10.785	4.79	1.01	61.75	147.72
415	2jsa-14	LYS_A_71_N	LYS_A_71_CA	-2.011	10.31	4.312	-0.853	11.081	3.892	1.45	106.80	33.66
416	2jsa-14	LYS_A_71_CA	LYS_A_71_HA	-0.853	11.081	3.892	-0.341	10.522	3.109	1.09	135.93	-47.51
417	2jsa-14	LYS_A_71_CA	LYS_A_71_C	-0.853	11.081	3.892	0.114	11.223	5.069	1.53	39.71	8.35
418	2jsa-14	LYS_A_71_C	LYS_A_71_O	0.114	11.223	5.069	1.072	11.992	5.001	1.23	93.17	38.75
419	2jsa-14	LYS_A_71_C	ASP_A_72_N	0.114	11.223	5.069	-0.17	10.469	6.121	1.33	37.45	-110.64
420	2jsa-14	ASP_A_72_N	ASP_A_72_H	-0.17	10.469	6.121	-0.975	9.859	6.108	1.01	90.74	-142.85
421	2jsa-14	ASP_A_72_N	ASP_A_72_CA	-0.17	10.469	6.121	0.663	10.501	7.312	1.45	34.99	2.20
422	2jsa-14	ASP_A_72_CA	ASP_A_72_HA	0.663	10.501	7.312	1.418	11.279	7.198	1.09	96.00	45.86
423	2jsa-14	ASP_A_72_CA	ASP_A_72_C	0.663	10.501	7.312	1.34	9.141	7.492	1.53	83.24	-63.54
424	2jsa-14	ASP_A_72_C	ASP_A_72_O	1.34	9.141	7.492	2.481	9.067	7.946	1.23	68.34	-3.71
425	2jsa-14	ASP_A_72_C	VAL_A_73_N	1.34	9.141	7.492	0.61	8.098	7.125	1.32	106.08	-124.99
426	2jsa-14	VAL_A_73_N	VAL_A_73_H	0.61	8.098	7.125	-0.321	8.233	6.759	1.01	111.26	171.75
427	2jsa-14	VAL_A_73_N	VAL_A_73_CA	0.61	8.098	7.125	1.127	6.745	7.24	1.45	85.46	-69.09
428	2jsa-14	VAL_A_73_CA	VAL_A_73_HA	1.127	6.745	7.24	1.374	6.558	8.285	1.09	16.51	-37.13
429	2jsa-14	VAL_A_73_CA	VAL_A_73_C	1.127	6.745	7.24	2.412	6.623	6.42	1.53	122.43	-5.42
430	2jsa-14	VAL_A_73_C	VAL_A_73_O	2.412	6.623	6.42	3.376	5.996	6.859	1.23	69.11	-33.04
431	2jsa-14	VAL_A_73_C	CYS_A_74_N	2.412	6.623	6.42	2.386	7.232	5.243	1.33	152.62	92.44
432	2jsa-14	CYS_A_74_N	CYS_A_74_H	2.386	7.232	5.243	1.56	7.731	4.947	1.01	107.05	148.86
433	2jsa-14	CYS_A_74_N	CYS_A_74_CA	2.386	7.232	5.243	3.537	7.199	4.357	1.45	127.58	-1.64
434	2jsa-14	CYS_A_74_CA	CYS_A_74_HA	3.537	7.199	4.357	3.94	6.186	4.356	1.09	90.05	-68.31
435	2jsa-14	CYS_A_74_CA	CYS_A_74_C	3.537	7.199	4.357	4.601	8.146	4.917	1.53	68.54	41.67
436	2jsa-14	CYS_A_74_C	CYS_A_74_O	4.601	8.146	4.917	4.96	9.131	4.273	1.23	121.56	69.97
437	2jsa-14	CYS_A_74_C	THR_A_75_N	4.601	8.146	4.917	5.074	7.813	6.108	1.32	25.91	-35.15
438	2jsa-14	THR_A_75_N	THR_A_75_H	5.074	7.813	6.108	4.733	6.987	6.579	1.01	62.21	-112.43
439	2jsa-14	THR_A_75_N	THR_A_75_CA	5.074	7.813	6.108	6.09	8.622	6.761	1.45	63.31	38.53
440	2jsa-14	THR_A_75_CA	THR_A_75_HA	6.09	8.622	6.761	6.99	8.619	6.145	1.09	124.39	-0.19
441	2jsa-14	THR_A_75_CA	THR_A_75_C	6.09	8.622	6.761	6.45	8.027	8.124	1.53	27.03	-58.82
442	2jsa-14	THR_A_75_C	THR_A_75_O	6.45	8.027	8.124	7.603	7.677	8.369	1.23	78.51	-16.89
443	2jsa-14	THR_A_75_C	LYS_A_76_N	6.45	8.027	8.124	5.44	7.932	8.977	1.33	49.94	-174.63
444	2jsa-14	LYS_A_76_N	LYS_A_76_H	5.44	7.932	8.977	4.517	8.24	8.708	1.01	105.45	161.55
445	2jsa-14	LYS_A_76_N	LYS_A_76_CA	5.44	7.932	8.977	5.635	7.386	10.31	1.45	23.51	-70.35
446	2jsa-14	LYS_A_76_CA	LYS_A_76_HA	5.635	7.386	10.31	6.502	7.878	10.753	1.09	66.04	29.57
447	2jsa-14	LYS_A_76_CA	LYS_A_76_C	5.635	7.386	10.31	5.953	5.893	10.203	1.53	94.01	-77.98
448	2jsa-14	LYS_A_76_C	LYS_A_76_O	5.953	5.893	10.203	6.561	5.318	11.104	1.23	42.89	-43.40
449	2jsa-14	LYS_A_76_C	LEU_A_77_N	5.953	5.893	10.203	5.525	5.308	9.094	1.32	146.83	-126.19
450	2jsa-14	LEU_A_77_N	LEU_A_77_H	5.525	5.308	9.094	5.031	5.844	8.395	1.01	133.80	132.66
451	2jsa-14	LEU_A_77_N	LEU_A_77_CA	5.525	5.308	9.094	5.755	3.892	8.857	1.45	99.38	-80.77
452	2jsa-14	LEU_A_77_CA	LEU_A_77_HA	5.755	3.892	8.857	5.77	3.386	9.823	1.09	27.66	-88.30
453	2jsa-14	LEU_A_77_CA	LEU_A_77_C	5.755	3.892	8.857	7.131	3.705	8.213	1.53	114.88	-7.74
454	2jsa-14	LEU_A_77_C	LEU_A_77_O	7.131	3.705	8.213	7.447	2.623	7.721	1.23	113.58	-73.72
455	2jsa-14	LEU_A_77_C	ASN_A_78_N	7.131	3.705	8.213	7.912	4.775	8.239	1.32	88.88	53.87
456	2jsa-14	ASN_A_78_N	ASN_A_78_H	7.912	4.775	8.239	7.587	5.632	8.663	1.01	65.17	110.77
457	2jsa-14	ASN_A_78_N	ASN_A_78_CA	7.912	4.775	8.239	9.246	4.742	7.664	1.45	113.31	-1.42
458	2jsa-14	ASN_A_78_CA	ASN_A_78_HA	9.246	4.742	7.664	9.644	5.756	7.627	1.09	91.95	68.57
459	2jsa-14	ASN_A_78_CA	ASN_A_78_C	9.246	4.742	7.664	9.173	4.161	6.251	1.53	157.49	-97.16
460	2jsa-14	ASN_A_78_C	ASN_A_78_O	9.173	4.161	6.251	10.127	3.542	5.781	1.23	112.45	-32.98
461	2jsa-14	ASN_A_78_C	GLU_A_79_N	9.173	4.161	6.251	8.032	4.378	5.613	1.33	118.78	169.23
462	2jsa-14	GLU_A_79_N	GLU_A_79_H	8.032	4.378	5.613	7.289	4.894	6.062	1.01	63.60	145.22
463	2jsa-14	GLU_A_79_N	GLU_A_79_CA	8.032	4.378	5.613	7.824	3.884	4.263	1.45	158.34	-112.83
464	2jsa-14	GLU_A_79_CA	GLU_A_79_HA	7.824	3.884	4.263	8.329	2.922	4.174	1.09	94.68	-62.30
465	2jsa-14	GLU_A_79_CA	GLU_A_79_C	7.824	3.884	4.263	8.439	4.845	3.245	1.53	131.74	57.38
466	2jsa-14	GLU_A_79_C	GLU_A_79_O	8.439	4.845	3.245	9.38	4.487	2.538	1.23	125.08	-20.83
467	2jsa-14	GLU_A_79_C	CYS_A_80_N	8.439	4.845	3.245	7.881	6.046	3.201	1.33	91.90	114.92
468	2jsa-14	CYS_A_80_N	CYS_A_80_H	7.881	6.046	3.201	7.109	6.271	3.812	1.01	52.77	163.75
469	2jsa-14	CYS_A_80_N	CYS_A_80_CA	7.881	6.046	3.201	8.363	7.062	2.281	1.45	129.29	64.62
470	2jsa-14	CYS_A_80_CA	CYS_A_80_HA	8.363	7.062	2.281	8.101	6.759	1.268	1.09	158.42	-130.85
471	2jsa-14	CYS_A_80_CA	CYS_A_80_C	8.363	7.062	2.281	9.888	7.125	2.39	1.53	85.92	2.37
472	2jsa-14	CYS_A_80_C	CYS_A_80_O	9.888	7.125	2.39	10.463	6.665	3.375	1.23	36.78	-38.66
473	2jsa-14	CYS_A_80_C	PRO_A_81_N	9.888	7.125	2.39	10.516	7.712	1.336	1.36	140.80	43.07
474	2jsa-14	PRO_A_81_N	PRO_A_81_CA	10.516	7.712	1.336	11.963	7.84	1.305	1.45	91.22	5.06
475	2jsa-14	PRO_A_81_CA	PRO_A_81_HA	11.963	7.84	1.305	12.428	6.903	1.612	1.09	73.64	-63.61
476	2jsa-14	PRO_A_81_CA	PRO_A_81_C	11.963	7.84	1.305	12.436	8.948	2.247	1.53	51.98	66.88
477	2jsa-14	PRO_A_81_C	PRO_A_81_O	12.436	8.948	2.247	13.633	9.21	2.352	1.23	85.10	12.35
1	2jsa-15	ARG_A_1_N	ARG_A_1_H	13.763	1.432	2.232	14.415	2.167	1.997	1.01	103.45	48.42
2	2jsa-15	ARG_A_1_N	ARG_A_1_CA	13.763	1.432	2.232	12.354	1.765	2.35	1.45	85.34	166.70
3	2jsa-15	ARG_A_1_CA	ARG_A_1_HA	12.354	1.765	2.35	11.8	1.181	1.615	1.09	132.40	-133.49
4	2jsa-15	ARG_A_1_CA	ARG_A_1_C	12.354	1.765	2.35	12.135	3.253	2.072	1.53	100.47	98.37
5	2jsa-15	ARG_A_1_C	ARG_A_1_O	12.135	3.253	2.072	11.525	3.956	2.876	1.23	49.18	130.95
6	2jsa-15	ARG_A_1_C	SER_A_2_N	12.135	3.253	2.072	12.646	3.69	0.929	1.33	149.53	40.54
7	2jsa-15	SER_A_2_N	SER_A_2_H	12.646	3.69	0.929	13.136	3.055	0.315	1.01	127.43	-52.34
8	2jsa-15	SER_A_2_N	SER_A_2_CA	12.646	3.69	0.929	12.514	5.082	0.534	1.45	105.77	95.42
9	2jsa-15	SER_A_2_CA	SER_A_2_HA	12.514	5.082	0.534	11.56	5.454	0.907	1.09	69.98	158.70
10	2jsa-15	SER_A_2_CA	SER_A_2_C	12.514	5.082	0.534	12.522	5.196	-0.992	1.53	175.72	85.99
11	2jsa-15	SER_A_2_C	SER_A_2_O	12.522	5.196	-0.992	13.551	5.506	-1.589	1.23	119.05	16.77
12	2jsa-15	SER_A_2_C	ALA_A_3_N	12.522	5.196	-0.992	11.362	4.94	-1.578	1.32	116.26	-167.55
13	2jsa-15	ALA_A_3_N	ALA_A_3_H	11.362	4.94	-1.578	10.556	4.691	-1.023	1.01	56.66	-162.83
14	2jsa-15	ALA_A_3_N	ALA_A_3_CA	11.362	4.94	-1.578	11.222	5.01	-3.023	1.45	173.82	153.43
15	2jsa-15	ALA_A_3_CA	ALA_A_3_HA	11.222	5.01	-3.023	11.589	5.978				

18	2jsa-15	ALA_A_3_C	LEU_A_4_N	9.742	4.895	-3.394	9.492	4.183	-4.483	1.32	145.28	-109.35
19	2jsa-15	LEU_A_4_N	LEU_A_4_H	9.492	4.183	-4.483	10.251	3.764	-5.002	1.01	120.91	-28.90
20	2jsa-15	LEU_A_4_N	LEU_A_4_CA	9.492	4.183	-4.483	8.131	3.989	-4.954	1.45	108.91	-171.89
21	2jsa-15	LEU_A_4_CA	LEU_A_4_HA	8.131	3.989	-4.954	7.714	4.968	-5.189	1.09	102.45	113.07
22	2jsa-15	LEU_A_4_CA	LEU_A_4_C	8.131	3.989	-4.954	7.288	3.382	-3.831	1.53	42.77	-144.24
23	2jsa-15	LEU_A_4_C	LEU_A_4_O	7.288	3.382	-3.831	6.06	3.452	-3.864	1.23	91.54	176.74
24	2jsa-15	LEU_A_4_C	SER_A_5_N	7.288	3.382	-3.831	7.981	2.801	-2.862	1.33	43.02	-39.98
25	2jsa-15	SER_A_5_N	SER_A_5_H	7.981	2.801	-2.862	8.991	2.783	-2.899	1.01	92.10	-1.02
26	2jsa-15	SER_A_5_N	SER_A_5_CA	7.981	2.801	-2.862	7.312	2.182	-1.731	1.45	38.86	-137.22
27	2jsa-15	SER_A_5_CA	SER_A_5_HA	7.312	2.182	-1.731	6.804	1.285	-2.084	1.09	108.90	-119.52
28	2jsa-15	SER_A_5_CA	SER_A_5_C	7.312	2.182	-1.731	6.269	3.141	-1.152	1.53	67.77	137.40
29	2jsa-15	SER_A_5_C	SER_A_5_O	6.269	3.141	-1.152	5.117	2.761	-0.951	1.23	80.59	-161.74
30	2jsa-15	SER_A_5_C	CYS_A_6_N	6.269	3.141	-1.152	6.711	4.364	-0.901	1.32	79.08	70.13
31	2jsa-15	CYS_A_6_N	CYS_A_6_H	6.711	4.364	-0.901	7.673	4.607	-1.092	1.01	100.90	14.18
32	2jsa-15	CYS_A_6_N	CYS_A_6_CA	6.711	4.364	-0.901	5.83	5.379	-0.349	1.45	67.67	130.96
33	2jsa-15	CYS_A_6_CA	CYS_A_6_HA	5.83	5.379	-0.349	5.593	5.105	0.679	1.09	19.41	-130.86
34	2jsa-15	CYS_A_6_CA	CYS_A_6_C	5.83	5.379	-0.349	4.535	5.385	-1.163	1.53	122.15	179.73
35	2jsa-15	CYS_A_6_C	CYS_A_6_O	4.535	5.385	-1.163	3.444	5.302	-0.601	1.23	62.81	-175.65
36	2jsa-15	CYS_A_6_C	GLN_A_7_N	4.535	5.385	-1.163	4.698	5.486	-2.475	1.33	171.68	31.78
37	2jsa-15	GLN_A_7_N	GLN_A_7_H	4.698	5.486	-2.475	5.626	5.552	-2.868	1.01	112.90	4.07
38	2jsa-15	GLN_A_7_N	GLN_A_7_CA	4.698	5.486	-2.475	3.555	5.505	-3.372	1.45	128.12	179.05
39	2jsa-15	GLN_A_7_CA	GLN_A_7_HA	3.555	5.505	-3.372	3.009	6.433	-3.202	1.09	81.03	120.47
40	2jsa-15	GLN_A_7_CA	GLN_A_7_C	3.555	5.505	-3.372	2.621	4.332	-3.064	1.53	78.39	-128.53
41	2jsa-15	GLN_A_7_C	GLN_A_7_O	2.621	4.332	-3.064	1.424	4.525	-2.857	1.23	80.31	170.84
42	2jsa-15	GLN_A_7_C	MET_A_8_N	2.621	4.332	-3.064	3.202	3.142	-3.045	1.32	89.18	-63.98
43	2jsa-15	MET_A_8_N	MET_A_8_H	3.202	3.142	-3.045	4.192	3.057	-3.226	1.01	100.32	-4.91
44	2jsa-15	MET_A_8_N	MET_A_8_CA	3.202	3.142	-3.045	2.437	1.939	-2.767	1.45	78.97	-122.45
45	2jsa-15	MET_A_8_CA	MET_A_8_HA	2.437	1.939	-2.767	1.786	1.735	-3.617	1.09	141.25	-162.60
46	2jsa-15	MET_A_8_CA	MET_A_8_C	2.437	1.939	-2.767	1.577	2.113	-1.513	1.53	34.98	168.56
47	2jsa-15	MET_A_8_C	MET_A_8_O	1.577	2.113	-1.513	0.438	1.653	-1.468	1.23	87.90	-158.01
48	2jsa-15	MET_A_8_C	CYS_A_9_N	1.577	2.113	-1.513	2.157	2.78	-0.526	1.32	41.85	48.99
49	2jsa-15	CYS_A_9_N	CYS_A_9_H	2.157	2.78	-0.526	3.098	3.132	-0.633	1.01	96.08	20.51
50	2jsa-15	CYS_A_9_N	CYS_A_9_CA	2.157	2.78	-0.526	1.458	3.02	0.725	1.45	30.57	161.05
51	2jsa-15	CYS_A_9_CA	CYS_A_9_HA	1.458	3.02	0.725	1.165	2.058	1.145	1.09	67.33	-106.94
52	2jsa-15	CYS_A_9_CA	CYS_A_9_C	1.458	3.02	0.725	0.193	3.825	0.422	1.53	101.42	147.53
53	2jsa-15	CYS_A_9_C	CYS_A_9_O	0.193	3.825	0.422	-0.82	3.677	1.104	1.23	56.33	-171.69
54	2jsa-15	CYS_A_9_C	GLU_A_10_N	0.193	3.825	0.422	0.292	4.66	-0.603	1.33	140.64	83.24
55	2jsa-15	GLU_A_10_N	GLU_A_10_H	0.292	4.66	-0.603	1.157	4.73	-1.12	1.01	120.78	4.63
56	2jsa-15	GLU_A_10_N	GLU_A_10_CA	0.292	4.66	-0.603	-0.832	5.487	-1.005	1.45	106.07	143.66
57	2jsa-15	GLU_A_10_CA	GLU_A_10_HA	-0.832	5.487	-1.005	-1.346	5.819	-0.103	1.09	34.15	147.14
58	2jsa-15	GLU_A_10_CA	GLU_A_10_C	-0.832	5.487	-1.005	-1.816	4.674	-1.847	1.53	123.41	-140.44
59	2jsa-15	GLU_A_10_C	GLU_A_10_O	-1.816	4.674	-1.847	-2.897	5.156	-2.184	1.23	105.89	155.97
60	2jsa-15	GLU_A_10_C	LEU_A_11_N	-1.816	4.674	-1.847	-1.407	3.454	-2.163	1.32	103.80	-71.47
61	2jsa-15	LEU_A_11_N	LEU_A_11_H	-1.407	3.454	-2.163	-0.505	3.123	-1.852	1.01	72.06	-20.15
62	2jsa-15	LEU_A_11_N	LEU_A_11_CA	-1.407	3.454	-2.163	-2.24	2.569	-2.959	1.45	123.22	-133.27
63	2jsa-15	LEU_A_11_CA	LEU_A_11_HA	-2.24	2.569	-2.959	-2.927	3.184	-3.54	1.09	122.22	138.17
64	2jsa-15	LEU_A_11_CA	LEU_A_11_C	-2.24	2.569	-2.959	-3.077	1.688	-2.029	1.53	52.57	-133.53
65	2jsa-15	LEU_A_11_C	LEU_A_11_O	-3.077	1.688	-2.029	-4.239	1.406	-2.316	1.23	103.50	-166.36
66	2jsa-15	LEU_A_11_C	VAL_A_12_N	-3.077	1.688	-2.029	-2.454	1.28	-0.934	1.32	34.22	-33.22
67	2jsa-15	VAL_A_12_N	VAL_A_12_H	-2.454	1.28	-0.934	-1.496	1.552	-0.763	1.01	80.26	15.85
68	2jsa-15	VAL_A_12_N	VAL_A_12_CA	-2.454	1.28	-0.934	-3.127	0.438	0.041	1.45	47.87	-128.63
69	2jsa-15	VAL_A_12_CA	VAL_A_12_HA	-3.127	0.438	0.041	-3.675	-0.337	-0.494	1.09	119.41	-125.26
70	2jsa-15	VAL_A_12_CA	VAL_A_12_C	-3.127	0.438	0.041	-4.136	1.279	0.824	1.53	59.20	140.19
71	2jsa-15	VAL_A_12_C	VAL_A_12_O	-4.136	1.279	0.824	-5.193	0.784	1.213	1.23	71.57	-154.91
72	2jsa-15	VAL_A_12_C	VAL_A_13_N	-4.136	1.279	0.824	-3.775	2.536	1.032	1.32	80.96	73.98
73	2jsa-15	VAL_A_13_N	VAL_A_13_H	-3.775	2.536	1.032	-2.89	2.876	0.683	1.01	110.21	21.02
74	2jsa-15	VAL_A_13_N	VAL_A_13_CA	-3.775	2.536	1.032	-4.637	3.451	1.763	1.45	59.82	133.29
75	2jsa-15	VAL_A_13_CA	VAL_A_13_HA	-4.637	3.451	1.763	-4.983	2.951	2.668	1.09	33.90	-124.68
76	2jsa-15	VAL_A_13_CA	VAL_A_13_C	-4.637	3.451	1.763	-5.86	3.785	0.907	1.53	124.03	164.73
77	2jsa-15	VAL_A_13_C	VAL_A_13_O	-5.86	3.785	0.907	-6.995	3.547	1.319	1.23	70.44	-168.16
78	2jsa-15	VAL_A_13_C	LYS_A_14_N	-5.86	3.785	0.907	-5.589	4.332	-0.269	1.33	152.57	63.64
79	2jsa-15	LYS_A_14_N	LYS_A_14_H	-5.589	4.332	-0.269	-4.631	4.5	-0.543	1.01	105.73	9.95
80	2jsa-15	LYS_A_14_N	LYS_A_14_CA	-5.589	4.332	-0.269	-6.653	4.701	-1.186	1.45	129.15	160.87
81	2jsa-15	LYS_A_14_CA	LYS_A_14_HA	-6.653	4.701	-1.186	-7.202	5.534	-0.747	1.09	66.25	123.39
82	2jsa-15	LYS_A_14_CA	LYS_A_14_C	-6.653	4.701	-1.186	-7.626	3.529	-1.332	1.53	95.47	-129.70
83	2jsa-15	LYS_A_14_C	LYS_A_14_O	-7.626	3.529	-1.332	-8.826	3.732	-1.507	1.23	98.18	170.40
84	2jsa-15	LYS_A_14_C	LYS_A_15_N	-7.626	3.529	-1.332	-7.07	2.329	-1.253	1.32	86.58	-65.14
85	2jsa-15	LYS_A_15_N	LYS_A_15_H	-7.07	2.329	-1.253	-6.074	2.238	-1.107	1.01	81.69	-5.22
86	2jsa-15	LYS_A_15_N	LYS_A_15_CA	-7.07	2.329	-1.253	-7.874	1.123	-1.373	1.45	94.73	-123.69
87	2jsa-15	LYS_A_15_CA	LYS_A_15_HA	-7.874	1.123	-1.373	-8.628	1.295	-2.14	1.09	134.76	167.15
88	2jsa-15	LYS_A_15_CA	LYS_A_15_C	-7.874	1.123	-1.373	-8.603	0.868	-0.053	1.53	30.33	-160.72
89	2jsa-15	LYS_A_15_C	LYS_A_15_O	-8.603	0.868	-0.053	-9.77	0.48	-0.05	1.23	89.86	-161.61
90	2jsa-15	LYS_A_15_C	TYR_A_16_N	-8.603	0.868	-0.053	-7.885	1.097	1.037	1.33	34.66	17.69
91	2jsa-15	TYR_A_16_N	TYR_A_16_H	-7.885	1.097	1.037	-6.929	1.414	0.959	1.01	94.43	18.35
92	2jsa-15	TYR_A_16_N	TYR_A_16_CA	-7.885	1.097	1.037	-8.45	0.897	2.361	1.45	24.36	-160.51
93	2jsa-15	TYR_A_16_CA	TYR_A_16_HA	-8.45	0.897	2.361	-9.018	-0.033	2.392	1.09	88.37	-121.41
94	2jsa-15	TYR_A_16_CA	TYR_A_16_C	-8.45	0.897	2.361	-9.351	2.069	2.756	1.53	75.04	127.55
95	2jsa-15	TYR_A_16_C	TYR_A_16_O	-9.351	2.069	2.756	-10.572	1.929	2.805	1.23	87.72	-173.46
96	2jsa-15	TYR_A_16_C	GLU_A_17_N	-9.351	2.069	2.756	-8.714	3.198	3.027	1.32	78.19	60.57
97	2jsa-15	GLU_A_17_N	GLU_A_17_H	-8.714	3.198	3.027	-7.706	3.241	2.965	1.01	93.52	2.44
98	2jsa-15	GLU_A_17_N	GLU_A_17_CA	-8.714	3.198	3.027	-9.441	4.394	3.416	1.45	74.47	121.29
99	2jsa-15	GLU_A_17_CA	GLU_A_17_HA	-9.441	4.394	3.416	-9.68	4.313	4.476	1.09	13.39	-161.28
100	2jsa-15	GLU_A_17_CA	GLU_A_17_C	-9.441	4.394	3.416	-10.752	4.495	2.633	1.53	120.77	175.59
101	2jsa-15	GLU_A_17_C	GLU_A_17_O	-10.752	4.495	2.633	-11.786	4.859	3.192	1.23	62.98	160.61
102	2jsa-15	GLU_A_17_C	GLY_A_18_N	-10.752	4.495	2.633	-10.665	4.168	1.352	1.32	165.20	-75.10
103	2jsa-15	GLY_A_18_N	GLY_A_18_H	-10.665	4.168	1.352	-9.78	3.878	0.96	1.01	112.83	-18.14
104	2jsa-15	GLY_A_18_N	GLY_A_18_CA	-10.665	4.168	1.352	-11.832	4.218	0.486	1.45	126.55	177.55
105	2jsa-15	GLY_A_18_CA	GLY_A_18_C	-11.832	4.218	0.486	-12.197	2.823	-0.023	1.53	109.44	-104.66
106	2jsa-15	GLY_A_18_C	GLY_A_18_O	-12.197	2.823	-0.023	-12.315	2.609	-1.228	1.23	168.54	-118.87
107	2jsa-15	GLY_A_18_C	SER_A_19_N	-12.197	2.823	-0.023	-12.366	1.908	0.922	1.33	44.56	-100.46
108	2jsa-15	SER_A_19_N	SER_A_19_H	-12.366	1.908	0.922	-12.253	2.155	1.895	1.01	15.60	65.42
109	2jsa-15	SER_A_1										

111	2jsa-15	SER_A_19_CA	SER_A_19_C	-12.715	0.54	0.584	-14.237	0.378	0.564	1.53	90.75	-173.92
112	2jsa-15	SER_A_19_C	SER_A_19_O	-14.237	0.378	0.564	-14.796	-0.15	-0.396	1.23	141.31	-136.63
113	2jsa-15	SER_A_19_C	ALA_A_20_N	-14.237	0.378	0.564	-14.864	0.842	1.635	1.32	36.07	143.50
114	2jsa-15	ALA_A_20_N	ALA_A_20_H	-14.864	0.842	1.635	-14.339	1.264	2.388	1.01	41.81	38.79
115	2jsa-15	ALA_A_20_N	ALA_A_20_CA	-14.864	0.842	1.635	-16.309	0.755	1.753	1.45	85.34	-176.55
116	2jsa-15	ALA_A_20_CA	ALA_A_20_HA	-16.309	0.755	1.753	-16.65	1.517	2.454	1.09	49.98	114.11
117	2jsa-15	ALA_A_20_CA	ALA_A_20_C	-16.309	0.755	1.753	-16.69	-0.62	2.308	1.53	68.74	-105.49
118	2jsa-15	ALA_A_20_C	ALA_A_20_O	-16.69	-0.62	2.308	-17.841	-0.847	2.676	1.23	72.58	-168.84
119	2jsa-15	ALA_A_20_C	ASP_A_21_N	-16.69	-0.62	2.308	-15.7	-1.5	2.35	1.33	88.18	-41.63
120	2jsa-15	ASP_A_21_N	ASP_A_21_H	-15.7	-1.5	2.35	-14.777	-1.244	2.03	1.01	108.47	15.50
121	2jsa-15	ASP_A_21_N	ASP_A_21_CA	-15.7	-1.5	2.35	-15.917	-2.845	2.853	1.45	69.74	-99.17
122	2jsa-15	ASP_A_21_CA	ASP_A_21_HA	-15.917	-2.845	2.853	-16.975	-2.975	3.077	1.09	78.13	-172.99
123	2jsa-15	ASP_A_21_CA	ASP_A_21_C	-15.917	-2.845	2.853	-15.088	-3.05	4.122	1.53	33.94	-13.89
124	2jsa-15	ASP_A_21_C	ASP_A_21_O	-15.088	-3.05	4.122	-15.279	-4.03	4.842	1.23	54.20	-101.03
125	2jsa-15	ASP_A_21_C	LYS_A_22_N	-15.088	-3.05	4.122	-14.185	-2.111	4.359	1.32	79.69	46.12
126	2jsa-15	LYS_A_22_N	LYS_A_22_H	-14.185	-2.111	4.359	-14.082	-1.333	3.723	1.01	129.02	82.46
127	2jsa-15	LYS_A_22_N	LYS_A_22_CA	-14.185	-2.111	4.359	-13.326	-2.175	5.529	1.45	36.36	-4.26
128	2jsa-15	LYS_A_22_CA	LYS_A_22_HA	-13.326	-2.175	5.529	-12.474	-1.516	5.36	1.09	98.92	37.72
129	2jsa-15	LYS_A_22_CA	LYS_A_22_C	-13.326	-2.175	5.529	-12.788	-3.6	5.683	1.53	84.23	-69.32
130	2jsa-15	LYS_A_22_C	LYS_A_22_O	-12.788	-3.6	5.683	-13.081	-4.274	6.669	1.23	36.70	-113.50
131	2jsa-15	LYS_A_22_C	ASP_A_23_N	-12.788	-3.6	5.683	-12.012	-4.015	4.693	1.32	138.37	-28.14
132	2jsa-15	ASP_A_23_N	ASP_A_23_H	-12.012	-4.015	4.693	-11.815	-3.407	3.911	1.01	140.74	72.05
133	2jsa-15	ASP_A_23_N	ASP_A_23_CA	-12.012	-4.015	4.693	-11.43	-5.347	4.707	1.45	89.45	-66.40
134	2jsa-15	ASP_A_23_CA	ASP_A_23_HA	-11.43	-5.347	4.707	-11.456	-5.737	5.725	1.09	21.00	-93.81
135	2jsa-15	ASP_A_23_CA	ASP_A_23_C	-11.43	-5.347	4.707	-9.983	-5.272	4.216	1.53	108.72	2.97
136	2jsa-15	ASP_A_23_C	ASP_A_23_O	-9.983	-5.272	4.216	-9.736	-5.027	3.036	1.23	163.57	44.77
137	2jsa-15	ASP_A_23_C	ALA_A_24_N	-9.983	-5.272	4.216	-9.065	-5.487	5.146	1.32	45.39	-13.18
138	2jsa-15	ALA_A_24_N	ALA_A_24_H	-9.065	-5.487	5.146	-9.34	-5.682	6.098	1.01	19.50	-144.66
139	2jsa-15	ALA_A_24_N	ALA_A_24_CA	-9.065	-5.487	5.146	-7.649	-5.447	4.822	1.45	102.88	1.62
140	2jsa-15	ALA_A_24_CA	ALA_A_24_HA	-7.649	-5.447	4.822	-7.411	-4.467	4.409	1.09	112.27	76.35
141	2jsa-15	ALA_A_24_CA	ALA_A_24_C	-7.649	-5.447	4.822	-7.343	-6.506	3.762	1.53	133.88	-73.88
142	2jsa-15	ALA_A_24_C	ALA_A_24_O	-7.343	-6.506	3.762	-6.275	-6.486	3.15	1.23	119.81	1.07
143	2jsa-15	ALA_A_24_C	ASN_A_25_N	-7.343	-6.506	3.762	-8.296	-7.406	3.577	1.32	98.03	-136.64
144	2jsa-15	ASN_A_25_N	ASN_A_25_H	-8.296	-7.406	3.577	-9.148	-7.361	4.117	1.01	57.67	176.98
145	2jsa-15	ASN_A_25_N	ASN_A_25_CA	-8.296	-7.406	3.577	-8.142	-8.471	2.602	1.45	132.18	-81.77
146	2jsa-15	ASN_A_25_CA	ASN_A_25_HA	-8.142	-8.471	2.602	-7.118	-8.844	2.642	1.09	87.90	-20.01
147	2jsa-15	ASN_A_25_CA	ASN_A_25_C	-8.142	-8.471	2.602	-8.442	-7.926	1.204	1.53	156.01	118.83
148	2jsa-15	ASN_A_25_C	ASN_A_25_O	-8.442	-7.926	1.204	-7.589	-7.968	0.32	1.23	135.99	-2.82
149	2jsa-15	ASN_A_25_C	VAL_A_26_N	-8.442	-7.926	1.204	-9.659	-7.424	1.049	1.33	96.72	157.58
150	2jsa-15	VAL_A_26_N	VAL_A_26_H	-9.659	-7.424	1.049	-10.309	-7.421	1.821	1.01	40.10	179.74
151	2jsa-15	VAL_A_26_N	VAL_A_26_CA	-9.659	-7.424	1.049	-10.084	-6.87	-0.226	1.45	151.29	127.49
152	2jsa-15	VAL_A_26_CA	VAL_A_26_HA	-10.084	-6.87	-0.226	-9.82	-7.576	-1.013	1.09	136.24	-69.50
153	2jsa-15	VAL_A_26_CA	VAL_A_26_C	-10.084	-6.87	-0.226	-9.329	-5.565	-0.485	1.53	99.75	59.95
154	2jsa-15	VAL_A_26_C	VAL_A_26_O	-9.329	-5.565	-0.485	-9.432	-4.99	-1.568	1.23	151.66	100.16
155	2jsa-15	VAL_A_26_C	ILE_A_27_N	-9.329	-5.565	-0.485	-8.588	-5.135	0.526	1.33	40.28	30.13
156	2jsa-15	ILE_A_27_N	ILE_A_27_H	-8.588	-5.135	0.526	-8.55	-5.66	1.388	1.01	31.41	-85.86
157	2jsa-15	ILE_A_27_N	ILE_A_27_CA	-8.588	-5.135	0.526	-7.816	-3.908	0.42	1.45	94.18	57.82
158	2jsa-15	ILE_A_27_CA	ILE_A_27_HA	-7.816	-3.908	0.42	-8.298	-3.268	-0.319	1.09	132.69	126.98
159	2jsa-15	ILE_A_27_CA	ILE_A_27_C	-7.816	-3.908	0.42	-6.413	-4.237	-0.094	1.53	109.63	-13.20
160	2jsa-15	ILE_A_27_C	ILE_A_27_O	-6.413	-4.237	-0.094	-6.0	-3.743	-1.142	1.23	148.43	50.10
161	2jsa-15	ILE_A_27_C	LYS_A_28_N	-6.413	-4.237	-0.094	-5.717	-5.068	0.669	1.33	54.86	-50.05
162	2jsa-15	LYS_A_28_N	LYS_A_28_H	-5.717	-5.068	0.669	-6.119	-5.436	1.519	1.01	32.67	-137.53
163	2jsa-15	LYS_A_28_N	LYS_A_28_CA	-5.717	-5.068	0.669	-4.369	-5.466	0.304	1.45	104.56	-16.45
164	2jsa-15	LYS_A_28_CA	LYS_A_28_HA	-4.369	-5.466	0.304	-3.73	-4.584	0.356	1.09	87.27	54.08
165	2jsa-15	LYS_A_28_CA	LYS_A_28_C	-4.369	-5.466	0.304	-4.362	-5.961	-1.144	1.53	161.13	-89.19
166	2jsa-15	LYS_A_28_C	LYS_A_28_O	-4.362	-5.961	-1.144	-3.438	-5.666	-1.9	1.23	127.93	17.71
167	2jsa-15	LYS_A_28_C	LYS_A_29_N	-4.362	-5.961	-1.144	-5.404	-6.703	-1.488	1.32	105.05	-144.55
168	2jsa-15	LYS_A_29_N	LYS_A_29_H	-5.404	-6.703	-1.488	-6.128	-6.905	-0.814	1.01	48.12	-164.41
169	2jsa-15	LYS_A_29_N	LYS_A_29_CA	-5.404	-6.703	-1.488	-5.53	-7.24	-2.832	1.45	157.69	-103.20
170	2jsa-15	LYS_A_29_CA	LYS_A_29_HA	-5.53	-7.24	-2.832	-4.581	-7.705	-3.1	1.09	104.23	-26.10
171	2jsa-15	LYS_A_29_CA	LYS_A_29_C	-5.53	-7.24	-2.832	-5.779	-6.094	-3.813	1.53	129.91	102.26
172	2jsa-15	LYS_A_29_C	LYS_A_29_O	-5.779	-6.094	-3.813	-5.105	-5.992	-4.838	1.23	146.37	8.61
173	2jsa-15	LYS_A_29_C	ASP_A_30_N	-5.779	-6.094	-3.813	-6.748	-5.26	-3.466	1.32	74.81	139.28
174	2jsa-15	ASP_A_30_N	ASP_A_30_H	-6.748	-5.26	-3.466	-7.261	-5.405	-2.608	1.01	31.85	-164.22
175	2jsa-15	ASP_A_30_N	ASP_A_30_CA	-6.748	-5.26	-3.466	-7.094	-4.125	-4.304	1.45	125.23	106.95
176	2jsa-15	ASP_A_30_CA	ASP_A_30_HA	-7.094	-4.125	-4.304	-7.647	-4.48	-5.173	1.09	142.90	-147.30
177	2jsa-15	ASP_A_30_CA	ASP_A_30_C	-7.094	-4.125	-4.304	-5.814	-3.419	-4.755	1.53	107.15	28.88
178	2jsa-15	ASP_A_30_C	ASP_A_30_O	-5.814	-3.419	-4.755	-5.633	-3.153	-5.941	1.23	164.82	55.77
179	2jsa-15	ASP_A_30_C	PHE_A_31_N	-5.814	-3.419	-4.755	-4.957	-3.138	-3.783	1.33	42.86	18.15
180	2jsa-15	PHE_A_31_N	PHE_A_31_H	-4.957	-3.138	-3.783	-5.171	-3.388	-2.828	1.01	19.01	-130.56
181	2jsa-15	PHE_A_31_N	PHE_A_31_CA	-4.957	-3.138	-3.783	-3.699	-2.47	-4.065	1.45	101.20	27.97
182	2jsa-15	PHE_A_31_CA	PHE_A_31_HA	-3.699	-2.47	-4.065	-3.879	-1.415	-4.271	1.09	100.90	99.68
183	2jsa-15	PHE_A_31_CA	PHE_A_31_C	-3.699	-2.47	-4.065	-2.991	-3.114	-5.26	1.53	141.31	-42.29
184	2jsa-15	PHE_A_31_C	PHE_A_31_O	-2.991	-3.114	-5.26	-2.791	-2.47	-6.288	1.23	146.74	72.75
185	2jsa-15	PHE_A_31_C	ASP_A_32_N	-2.991	-3.114	-5.26	-2.631	-4.376	-5.082	1.32	82.28	-74.08
186	2jsa-15	ASP_A_32_N	ASP_A_32_H	-2.631	-4.376	-5.082	-2.826	-4.842	-4.208	1.01	30.03	-112.71
187	2jsa-15	ASP_A_32_N	ASP_A_32_CA	-2.631	-4.376	-5.082	-1.95	-5.115	-6.132	1.45	136.26	-47.34
188	2jsa-15	ASP_A_32_CA	ASP_A_32_HA	-1.95	-5.115	-6.132	-0.912	-4.784	-6.185	1.09	92.79	17.69
189	2jsa-15	ASP_A_32_CA	ASP_A_32_C	-1.95	-5.115	-6.132	-2.647	-4.854	-7.468	1.53	150.88	159.47
190	2jsa-15	ASP_A_32_C	ASP_A_32_O	-2.647	-4.854	-7.468	-1.99	-4.694	-8.494	1.23	146.61	13.69
191	2jsa-15	ASP_A_32_C	ALA_A_33_N	-2.647	-4.854	-7.468	-3.971	-4.82	-7.411	1.33	87.54	178.53
192	2jsa-15	ALA_A_33_N	ALA_A_33_H	-3.971	-4.82	-7.411	-4.445	-4.962	-6.531	1.01	29.35	-163.32
193	2jsa-15	ALA_A_33_N	ALA_A_33_CA	-3.971	-4.82	-7.411	-4.766	-4.581	-8.604	1.45	145.17	163.27
194	2jsa-15	ALA_A_33_CA	ALA_A_33_HA	-4.766	-4.581	-8.604	-4.684	-5.448	-9.259	1.09	126.95	-84.60
195	2jsa-15	ALA_A_33_CA	ALA_A_33_C	-4.766	-4.581	-8.604	-4.212	-3.362	-9.344	1.53	118.93	65.56
196	2jsa-15	ALA_A_33_C	ALA_A_33_O	-4.212	-3.362	-9.344	-3.754	-3.476	-10.481	1.23	157.46	-13.98
197	2jsa-15	ALA_A_33_C	GLU_A_34_N	-4.212	-3.362	-9.344	-4.274	-2.223	-8.671	1.32	59.46	93.12
198	2jsa-15	GLU_A_34_N	GLU_A_34_H	-4.274	-2.223	-8.671	-4.665	-2.203	-7.74	1.01	22.81	177.07
199	2jsa-15	GLU_A_34_N	GLU_A_34_CA	-4.274	-2.223	-8.671	-3.784	-0.984	-9.25	1.45	113.49	68.42
200	2jsa-15	GLU_A_34_CA	GLU_A_34_HA	-3.784	-0.984	-9.25	-4.008	-0.999	-10.316	1.09	168.11	-176.17
201	2jsa-15	GLU_A_34_CA	GLU_A_34_C	-3.784	-0.984							

204	2jsa-15	CYS_A_35_N	CYS_A_35_H	-1.663	-2.011	-8.745	-2.199	-2.857	-8.62	1.01	82.89	-122.36
205	2jsa-15	CYS_A_35_N	CYS_A_35_CA	-1.663	-2.011	-8.745	-0.225	-2.061	-8.55	1.45	82.28	-1.99
206	2jsa-15	CYS_A_35_CA	CYS_A_35_HA	-0.225	-2.061	-8.55	0.139	-1.042	-8.416	1.09	82.94	70.34
207	2jsa-15	CYS_A_35_CA	CYS_A_35_C	-0.225	-2.061	-8.55	0.412	-2.642	-9.814	1.53	145.70	-42.37
208	2jsa-15	CYS_A_35_C	CYS_A_35_O	0.412	-2.642	-9.814	1.179	-1.965	-10.496	1.23	123.69	41.43
209	2jsa-15	CYS_A_35_C	LYS_A_36_N	0.412	-2.642	-9.814	0.07	-3.893	-10.089	1.33	101.97	-105.29
210	2jsa-15	LYS_A_36_N	LYS_A_36_H	0.07	-3.893	-10.089	-0.567	-4.39	-9.483	1.01	53.13	-142.04
211	2jsa-15	LYS_A_36_N	LYS_A_36_CA	0.07	-3.893	-10.089	0.598	-4.574	-11.258	1.45	143.60	-52.21
212	2jsa-15	LYS_A_36_CA	LYS_A_36_HA	0.598	-4.574	-11.258	1.687	-4.557	-11.195	1.09	86.69	0.89
213	2jsa-15	LYS_A_36_CA	LYS_A_36_C	0.598	-4.574	-11.258	0.193	-3.805	-12.517	1.53	145.38	117.77
214	2jsa-15	LYS_A_36_C	LYS_A_36_O	0.193	-3.805	-12.517	0.907	-3.824	-13.518	1.23	144.49	-1.52
215	2jsa-15	LYS_A_36_C	LYS_A_37_N	0.193	-3.805	-12.517	-0.954	-3.146	-12.426	1.33	86.06	150.12
216	2jsa-15	LYS_A_37_N	LYS_A_37_H	-0.954	-3.146	-12.426	-1.49	-3.175	-11.571	1.01	32.12	-176.90
217	2jsa-15	LYS_A_37_N	LYS_A_37_CA	-0.954	-3.146	-12.426	-1.463	-2.372	-13.545	1.45	140.38	123.33
218	2jsa-15	LYS_A_37_CA	LYS_A_37_HA	-1.463	-2.372	-13.545	-1.226	-2.91	-14.463	1.09	147.36	-66.23
219	2jsa-15	LYS_A_37_CA	LYS_A_37_C	-1.463	-2.372	-13.545	-0.741	-1.024	-13.598	1.53	91.99	61.83
220	2jsa-15	LYS_A_37_C	LYS_A_37_O	-0.741	-1.024	-13.598	-0.173	-0.659	-14.625	1.23	146.68	32.73
221	2jsa-15	LYS_A_37_C	LEU_A_38_N	-0.741	-1.024	-13.598	-0.788	-0.32	-12.476	1.33	32.16	93.82
222	2jsa-15	LEU_A_38_N	LEU_A_38_H	-0.788	-0.32	-12.476	-1.275	-0.682	-11.668	1.01	36.91	-143.38
223	2jsa-15	LEU_A_38_N	LEU_A_38_CA	-0.788	-0.32	-12.476	-0.145	0.98	-12.63	1.45	86.21	-63.68
224	2jsa-15	LEU_A_38_CA	LEU_A_38_HA	-0.145	0.98	-12.38	-0.547	1.614	-13.17	1.09	136.46	122.38
225	2jsa-15	LEU_A_38_CA	LEU_A_38_C	-0.145	0.98	-12.38	1.356	0.822	-12.63	1.53	99.41	-6.01
226	2jsa-15	LEU_A_38_C	LEU_A_38_O	1.356	0.822	-12.63	1.908	1.448	-13.534	1.23	137.29	48.59
227	2jsa-15	LEU_A_38_C	PHE_A_39_N	1.356	0.822	-12.63	1.974	-0.019	-11.814	1.32	51.98	-53.69
228	2jsa-15	PHE_A_39_N	PHE_A_39_H	1.974	-0.019	-11.814	1.457	-0.501	-11.093	1.01	44.43	-137.01
229	2jsa-15	PHE_A_39_N	PHE_A_39_CA	1.974	-0.019	-11.814	3.401	-0.267	-11.935	1.45	94.78	-9.86
230	2jsa-15	PHE_A_39_CA	PHE_A_39_HA	3.401	-0.267	-11.935	3.908	0.639	-12.268	1.09	107.78	60.77
231	2jsa-15	PHE_A_39_CA	PHE_A_39_C	3.401	-0.267	-11.935	3.677	-1.403	-12.922	1.53	130.17	-76.34
232	2jsa-15	PHE_A_39_C	PHE_A_39_O	3.677	-1.403	-12.922	4.659	-2.13	-12.777	1.23	83.23	-36.51
233	2jsa-15	PHE_A_39_C	HIS_A_40_N	3.677	-1.403	-12.922	2.793	-1.522	-13.902	1.33	137.69	-172.33
234	2jsa-15	HIS_A_40_N	HIS_A_40_H	2.793	-1.522	-13.902	2.008	-0.889	-13.958	1.01	93.18	141.12
235	2jsa-15	HIS_A_40_N	HIS_A_40_CA	2.793	-1.522	-13.902	2.93	-2.558	-14.912	1.45	134.02	-82.47
236	2jsa-15	HIS_A_40_CA	HIS_A_40_HA	2.93	-2.558	-14.912	2.915	-3.524	-14.407	1.09	62.40	-90.89
237	2jsa-15	HIS_A_40_CA	HIS_A_40_C	2.93	-2.558	-14.912	4.282	-2.415	-15.614	1.53	117.31	6.04
238	2jsa-15	HIS_A_40_C	HIS_A_40_O	4.282	-2.415	-15.614	4.759	-3.356	-16.246	1.23	120.92	-63.12
239	2jsa-15	HIS_A_40_C	THR_A_41_N	4.282	-2.415	-15.614	4.861	-1.231	-15.477	1.33	84.07	63.94
240	2jsa-15	THR_A_41_N	THR_A_41_H	4.861	-1.231	-15.477	4.411	-0.503	-14.941	1.01	57.94	121.72
241	2jsa-15	THR_A_41_N	THR_A_41_CA	4.861	-1.231	-15.477	6.15	-0.953	-16.09	1.45	114.93	12.17
242	2jsa-15	THR_A_41_CA	THR_A_41_HA	6.15	-0.953	-16.09	6.563	-1.885	-16.476	1.09	110.74	-66.10
243	2jsa-15	THR_A_41_CA	THR_A_41_C	6.15	-0.953	-16.09	7.127	-0.401	-15.05	1.53	47.18	29.47
244	2jsa-15	THR_A_41_C	THR_A_41_O	7.127	-0.401	-15.05	7.449	0.786	-15.065	1.23	90.70	74.82
245	2jsa-15	THR_A_41_C	ILE_A_42_N	7.127	-0.401	-15.05	7.572	-1.289	-14.173	1.33	48.56	-63.38
246	2jsa-15	ILE_A_42_N	ILE_A_42_H	7.572	-1.289	-14.173	7.266	-2.25	-14.221	1.01	92.72	-107.66
247	2jsa-15	ILE_A_42_N	ILE_A_42_CA	7.572	-1.289	-14.173	8.506	-0.905	-13.129	1.45	44.05	22.35
248	2jsa-15	ILE_A_42_CA	ILE_A_42_HA	8.506	-0.905	-13.129	9.146	-0.114	-13.522	1.09	111.12	51.02
249	2jsa-15	ILE_A_42_CA	ILE_A_42_C	8.506	-0.905	-13.129	9.4	-2.098	-12.786	1.53	77.04	-53.15
250	2jsa-15	ILE_A_42_C	ILE_A_42_O	9.4	-2.098	-12.786	8.939	-3.238	-12.767	1.23	89.11	-112.02
251	2jsa-15	ILE_A_42_C	PRO_A_43_N	9.4	-2.098	-12.786	10.696	-1.787	-12.517	1.36	78.59	13.49
252	2jsa-15	PRO_A_43_N	PRO_A_43_CA	10.696	-1.787	-12.517	11.659	-2.821	-12.177	1.45	76.47	-47.04
253	2jsa-15	PRO_A_43_CA	PRO_A_43_HA	11.659	-2.821	-12.177	11.554	-3.667	-12.856	1.09	128.54	-97.07
254	2jsa-15	PRO_A_43_CA	PRO_A_43_C	11.659	-2.821	-12.177	11.446	-3.317	-10.745	1.53	20.65	-113.24
255	2jsa-15	PRO_A_43_C	PRO_A_43_O	11.446	-3.317	-10.745	11.763	-2.616	-9.787	1.23	38.77	65.67
256	2jsa-15	PRO_A_43_C	PHE_A_44_N	11.446	-3.317	-10.745	10.909	-4.526	-10.646	1.33	85.72	-113.95
257	2jsa-15	PHE_A_44_N	PHE_A_44_H	10.909	-4.526	-10.646	10.673	-5.047	-11.478	1.01	145.49	-114.37
258	2jsa-15	PHE_A_44_N	PHE_A_44_CA	10.909	-4.526	-10.646	10.65	-5.125	-9.349	1.45	26.71	-113.38
259	2jsa-15	PHE_A_44_CA	PHE_A_44_HA	10.65	-5.125	-9.349	10.528	-6.203	-9.457	1.09	95.69	-96.46
260	2jsa-15	PHE_A_44_CA	PHE_A_44_C	10.65	-5.125	-9.349	9.395	-4.526	-8.709	1.53	65.29	154.49
261	2jsa-15	PHE_A_44_C	PHE_A_44_O	9.395	-4.526	-8.709	8.974	-4.959	-7.637	1.23	29.40	-134.19
262	2jsa-15	PHE_A_44_C	GLY_A_45_N	9.395	-4.526	-8.709	8.834	-3.541	-9.394	1.32	121.14	119.66
263	2jsa-15	GLY_A_45_N	GLY_A_45_H	8.834	-3.541	-9.394	9.236	-3.237	-10.269	1.01	150.06	37.10
264	2jsa-15	GLY_A_45_N	GLY_A_45_CA	8.834	-3.541	-9.394	7.636	-2.879	-8.906	1.45	70.38	151.08
265	2jsa-15	GLY_A_45_CA	GLY_A_45_C	7.636	-2.879	-8.906	6.564	-3.899	-8.518	1.53	75.31	-136.42
266	2jsa-15	GLY_A_45_C	GLY_A_45_O	6.564	-3.899	-8.518	6.134	-3.945	-7.366	1.23	20.58	-173.89
267	2jsa-15	GLY_A_45_C	THR_A_46_N	6.564	-3.899	-8.518	6.164	-4.692	-9.501	1.32	137.90	-116.77
268	2jsa-15	THR_A_46_N	THR_A_46_H	6.164	-4.692	-9.501	6.563	-4.598	-10.424	1.01	156.05	13.26
269	2jsa-15	THR_A_46_N	THR_A_46_CA	6.164	-4.692	-9.501	5.151	-5.709	-9.276	1.45	81.09	-134.89
270	2jsa-15	THR_A_46_CA	THR_A_46_HA	5.151	-5.709	-9.276	4.242	-5.225	-8.918	1.09	70.83	151.97
271	2jsa-15	THR_A_46_CA	THR_A_46_C	5.151	-5.709	-9.276	5.614	-6.695	-8.201	1.53	45.38	-64.85
272	2jsa-15	THR_A_46_C	THR_A_46_O	5.614	-6.695	-8.201	4.803	-7.196	-7.423	1.23	50.78	-148.29
273	2jsa-15	THR_A_46_C	ARG_A_47_N	5.614	-6.695	-8.201	6.915	-6.944	-8.193	1.32	89.65	-10.83
274	2jsa-15	ARG_A_47_N	ARG_A_47_H	6.915	-6.944	-8.193	7.523	-6.497	-8.864	1.01	131.64	36.32
275	2jsa-15	ARG_A_47_N	ARG_A_47_CA	6.915	-6.944	-8.193	7.495	-7.86	-7.227	1.45	48.30	-57.66
276	2jsa-15	ARG_A_47_CA	ARG_A_47_HA	7.495	-7.86	-7.227	6.986	-8.82	-7.314	1.09	94.58	-117.93
277	2jsa-15	ARG_A_47_CA	ARG_A_47_C	7.495	-7.86	-7.227	7.307	-7.324	-5.806	1.53	21.79	109.33
278	2jsa-15	ARG_A_47_C	ARG_A_47_O	7.307	-7.324	-5.806	6.924	-8.067	-4.904	1.23	42.82	-117.27
279	2jsa-15	ARG_A_47_C	GLU_A_48_N	7.307	-7.324	-5.806	7.585	-6.037	-5.652	1.33	83.33	77.81
280	2jsa-15	GLU_A_48_N	GLU_A_48_H	7.585	-6.037	-5.652	7.896	-5.486	-6.439	1.01	141.20	60.56
281	2jsa-15	GLU_A_48_N	GLU_A_48_CA	7.585	-6.037	-5.652	7.45	-5.393	-4.357	1.45	26.94	101.84
282	2jsa-15	GLU_A_48_CA	GLU_A_48_HA	7.45	-5.393	-4.357	7.954	-6.015	-3.617	1.09	47.25	-50.98
283	2jsa-15	GLU_A_48_CA	GLU_A_48_C	7.45	-5.393	-4.357	5.974	-5.283	-3.969	1.53	75.31	175.74
284	2jsa-15	GLU_A_48_C	GLU_A_48_O	5.974	-5.283	-3.969	5.631	-5.352	-2.789	1.23	16.52	-168.63
285	2jsa-15	GLU_A_48_C	CYS_A_49_N	5.974	-5.283	-3.969	5.139	-5.115	-4.984	1.33	140.00	168.62
286	2jsa-15	CYS_A_49_N	CYS_A_49_H	5.139	-5.115	-4.984	5.491	-5.069	-5.929	1.01	159.41	7.45
287	2jsa-15	CYS_A_49_N	CYS_A_49_CA	5.139	-5.115	-4.984	3.708	-4.995	-4.765	1.45	81.33	175.21
288	2jsa-15	CYS_A_49_CA	CYS_A_49_HA	3.708	-4.995	-4.765	3.517	-4.048	-4.26	1.09	62.40	101.40
289	2jsa-15	CYS_A_49_CA	CYS_A_49_C	3.708	-4.995	-4.765	3.266	-6.135	-3.845	1.53	53.04	-111.19
290	2jsa-15	CYS_A_49_C	CYS_A_49_O	3.266	-6.135	-3.845	2.842	-5.896	-2.715	1.23	23.30	150.59
291	2jsa-15	CYS_A_49_C	ASP_A_50_N	3.266	-6.135	-3.845	3.381	-7.349	-4.362	1.32	112.98	-84.59
292	2jsa-15	ASP_A_50_N	ASP_A_50_H	3.381	-7.349	-4.362	3.738	-7.471	-5.299	1.01	158.07	-18.87
293	2jsa-15	ASP_A_50_N	ASP_A_50_CA	3.381	-7.349	-4.362	2.999	-8.526	-3.602			

297	2jsa-15	ASP_A_50_C	HIS_A_51_N	3.764	-8.543	-2.277	4.955	-7.964	-2.311	1.32	91.47	25.93
298	2jsa-15	HIS_A_51_N	HIS_A_51_H	4.955	-7.964	-2.311	5.297	-7.553	-3.168	1.01	148.04	50.24
299	2jsa-15	HIS_A_51_N	HIS_A_51_CA	4.955	-7.964	-2.311	5.794	-7.906	-1.126	1.45	35.36	3.95
300	2jsa-15	HIS_A_51_CA	HIS_A_51_HA	5.794	-7.906	-1.126	5.602	-8.8	-0.533	1.09	57.04	-102.12
301	2jsa-15	HIS_A_51_CA	HIS_A_51_C	5.794	-7.906	-1.126	5.405	-6.69	-0.282	1.53	56.53	107.74
302	2jsa-15	HIS_A_51_C	HIS_A_51_O	5.405	-6.69	-0.282	6.1	-6.344	0.672	1.23	39.14	26.47
303	2jsa-15	HIS_A_51_C	TYR_A_52_N	5.405	-6.69	-0.282	4.294	-6.076	-0.662	1.33	106.67	151.07
304	2jsa-15	TYR_A_52_N	TYR_A_52_H	4.294	-6.076	-0.662	3.772	-6.416	-1.456	1.01	141.88	-146.92
305	2jsa-15	TYR_A_52_N	TYR_A_52_CA	4.294	-6.076	-0.662	3.804	-4.907	0.047	1.45	60.78	112.74
306	2jsa-15	TYR_A_52_CA	TYR_A_52_HA	3.804	-4.907	0.047	4.531	-4.587	0.794	1.09	46.76	23.76
307	2jsa-15	TYR_A_52_CA	TYR_A_52_C	3.804	-4.907	0.047	2.462	-5.197	0.721	1.53	63.85	-167.81
308	2jsa-15	TYR_A_52_C	TYR_A_52_O	2.462	-5.197	0.721	2.223	-4.766	1.848	1.23	23.62	119.01
309	2jsa-15	TYR_A_52_C	VAL_A_53_N	2.462	-5.197	0.721	1.62	-5.926	0.001	1.33	122.88	-139.11
310	2jsa-15	VAL_A_53_N	VAL_A_53_H	1.62	-5.926	0.001	1.884	-6.247	-0.919	1.01	155.69	-50.57
311	2jsa-15	VAL_A_53_N	VAL_A_53_CA	1.62	-5.926	0.001	0.308	-6.278	0.515	1.45	69.27	-164.98
312	2jsa-15	VAL_A_53_CA	VAL_A_53_HA	0.308	-6.278	0.515	-0.054	-5.453	1.129	1.09	55.72	113.69
313	2jsa-15	VAL_A_53_CA	VAL_A_53_C	0.308	-6.278	0.515	0.429	-7.516	1.406	1.53	54.39	-84.42
314	2jsa-15	VAL_A_53_C	VAL_A_53_O	0.429	-7.516	1.406	-0.289	-8.496	1.214	1.23	98.98	-126.23
315	2jsa-15	VAL_A_53_C	ASN_A_54_N	0.429	-7.516	1.406	1.343	-7.43	2.362	1.33	43.84	5.38
316	2jsa-15	ASN_A_54_N	ASN_A_54_H	1.343	-7.43	2.362	1.898	-6.592	2.462	1.01	84.32	56.48
317	2jsa-15	ASN_A_54_N	ASN_A_54_CA	1.343	-7.43	2.362	1.567	-8.531	3.283	1.45	50.66	-78.50
318	2jsa-15	ASN_A_54_CA	ASN_A_54_HA	1.567	-8.531	3.283	0.684	-8.658	3.909	1.09	54.94	-171.82
319	2jsa-15	ASN_A_54_CA	ASN_A_54_C	1.567	-8.531	3.283	2.784	-8.219	4.157	1.53	55.18	14.38
320	2jsa-15	ASN_A_54_C	ASN_A_54_O	2.784	-8.219	4.157	3.629	-9.083	4.382	1.23	79.45	-45.64
321	2jsa-15	ASN_A_54_C	SER_A_55_N	2.784	-8.219	4.157	2.832	-6.981	4.626	1.32	69.27	87.78
322	2jsa-15	SER_A_55_N	SER_A_55_H	2.832	-6.981	4.626	2.101	-6.322	4.4	1.01	102.93	137.97
323	2jsa-15	SER_A_55_N	SER_A_55_CA	2.832	-6.981	4.626	3.931	-6.544	5.472	1.45	54.42	21.68
324	2jsa-15	SER_A_55_CA	SER_A_55_HA	3.931	-6.544	5.472	3.812	-7.005	6.453	1.09	25.89	-104.47
325	2jsa-15	SER_A_55_CA	SER_A_55_C	3.931	-6.544	5.472	3.89	-5.023	5.637	1.53	83.81	91.54
326	2jsa-15	SER_A_55_C	SER_A_55_O	3.89	-5.023	5.637	4.296	-4.497	6.671	1.23	32.73	52.34
327	2jsa-15	SER_A_55_C	LYS_A_56_N	3.89	-5.023	5.637	3.398	-4.36	4.601	1.32	141.45	126.58
328	2jsa-15	LYS_A_56_N	LYS_A_56_H	3.398	-4.36	4.601	3.083	-4.859	3.781	1.01	144.26	-122.26
329	2jsa-15	LYS_A_56_N	LYS_A_56_CA	3.398	-4.36	4.601	3.3	-2.911	4.618	1.45	89.33	93.87
330	2jsa-15	LYS_A_56_CA	LYS_A_56_HA	3.3	-2.911	4.618	3.695	-2.557	5.571	1.09	29.10	41.87
331	2jsa-15	LYS_A_56_CA	LYS_A_56_C	3.3	-2.911	4.618	1.826	-2.503	4.544	1.53	92.77	164.53
332	2jsa-15	LYS_A_56_C	LYS_A_56_O	1.826	-2.503	4.544	1.502	-1.319	4.618	1.23	86.55	105.30
333	2jsa-15	LYS_A_56_C	VAL_A_57_N	1.826	-2.503	4.544	0.974	-3.506	4.399	1.32	96.29	-130.35
334	2jsa-15	VAL_A_57_N	VAL_A_57_H	0.974	-3.506	4.399	1.312	-4.456	4.346	1.01	93.01	-70.41
335	2jsa-15	VAL_A_57_N	VAL_A_57_CA	0.974	-3.506	4.399	-0.456	-3.267	4.314	1.45	93.36	170.51
336	2jsa-15	VAL_A_57_CA	VAL_A_57_HA	-0.456	-3.267	4.314	-0.615	-2.224	4.041	1.09	104.51	98.67
337	2jsa-15	VAL_A_57_CA	VAL_A_57_C	-0.456	-3.267	4.314	-1.091	-3.501	5.687	1.53	26.24	-159.77
338	2jsa-15	VAL_A_57_C	VAL_A_57_O	-1.091	-3.501	5.687	-2.188	-3.015	5.959	1.23	77.23	156.11
339	2jsa-15	VAL_A_57_C	ASP_A_58_N	-1.091	-3.501	5.687	-0.373	-4.245	6.516	1.33	51.28	-46.02
340	2jsa-15	ASP_A_58_N	ASP_A_58_H	-0.373	-4.245	6.516	0.522	-4.612	6.225	1.01	106.74	-22.30
341	2jsa-15	ASP_A_58_N	ASP_A_58_CA	-0.373	-4.245	6.516	-0.852	-4.549	7.854	1.45	22.98	-147.60
342	2jsa-15	ASP_A_58_CA	ASP_A_58_HA	-0.852	-4.549	7.854	-1.915	-4.786	7.807	1.09	92.47	-167.43
343	2jsa-15	ASP_A_58_CA	ASP_A_58_C	-0.852	-4.549	7.854	-0.63	-3.335	8.758	1.53	53.78	79.64
344	2jsa-15	ASP_A_58_C	ASP_A_58_O	-0.63	-3.335	8.758	-1.518	-2.951	9.517	1.23	51.89	156.61
345	2jsa-15	ASP_A_58_C	PRO_A_59_N	-0.63	-3.335	8.758	0.593	-2.751	8.645	1.36	94.77	25.53
346	2jsa-15	PRO_A_59_N	PRO_A_59_CA	0.593	-2.751	8.645	0.944	-1.588	9.444	1.45	56.67	73.21
347	2jsa-15	PRO_A_59_CA	PRO_A_59_HA	0.944	-1.588	9.444	0.637	-1.739	10.479	1.09	18.29	-153.81
348	2jsa-15	PRO_A_59_CA	PRO_A_59_C	0.944	-1.588	9.444	0.255	-0.331	8.913	1.53	110.33	118.73
349	2jsa-15	PRO_A_59_C	PRO_A_59_O	0.255	-0.331	8.913	-0.377	0.403	9.672	1.23	51.92	130.73
350	2jsa-15	PRO_A_59_C	ILE_A_60_N	0.255	-0.331	8.913	0.401	-0.118	7.613	1.33	168.76	55.57
351	2jsa-15	ILE_A_60_N	ILE_A_60_H	0.401	-0.118	7.613	0.935	-0.763	7.049	1.01	123.96	-50.38
352	2jsa-15	ILE_A_60_N	ILE_A_60_CA	0.401	-0.118	7.613	-0.2	1.039	6.972	1.45	116.18	117.45
353	2jsa-15	ILE_A_60_CA	ILE_A_60_HA	-0.2	1.039	6.972	0.327	1.928	7.319	1.09	71.44	59.34
354	2jsa-15	ILE_A_60_CA	ILE_A_60_C	-0.2	1.039	6.972	-1.659	1.162	7.414	1.53	73.20	175.18
355	2jsa-15	ILE_A_60_C	ILE_A_60_O	-1.659	1.162	7.414	-2.101	2.236	7.812	1.23	70.73	112.37
356	2jsa-15	ILE_A_60_C	ILE_A_61_N	-1.659	1.162	7.414	-2.368	0.046	7.322	1.33	93.98	-122.43
357	2jsa-15	ILE_A_61_N	ILE_A_61_H	-2.368	0.046	7.322	-1.939	-0.803	6.981	1.01	109.72	-63.19
358	2jsa-15	ILE_A_61_N	ILE_A_61_CA	-2.368	0.046	7.322	-3.769	0.016	6.708	1.45	74.60	-178.77
359	2jsa-15	ILE_A_61_CA	ILE_A_61_HA	-3.769	0.016	7.708	-4.276	0.838	7.203	1.09	117.60	121.67
360	2jsa-15	ILE_A_61_CA	ILE_A_61_C	-3.769	0.016	7.708	-3.884	0.255	9.215	1.53	9.98	115.70
361	2jsa-15	ILE_A_61_C	ILE_A_61_O	-3.884	0.255	9.215	-4.91	0.735	9.694	1.23	67.08	154.93
362	2jsa-15	ILE_A_61_C	HIS_A_62_N	-3.884	0.255	9.215	-2.817	-0.089	9.92	1.32	57.84	-17.87
363	2jsa-15	HIS_A_62_N	HIS_A_62_H	-2.817	-0.089	9.92	-2.007	-0.478	9.459	1.01	117.16	-25.65
364	2jsa-15	HIS_A_62_N	HIS_A_62_CA	-2.817	-0.089	9.92	-2.784	0.082	11.362	1.45	6.89	79.08
365	2jsa-15	HIS_A_62_CA	HIS_A_62_HA	-2.784	0.082	11.362	-3.736	-0.264	11.763	1.09	68.40	-160.03
366	2jsa-15	HIS_A_62_CA	HIS_A_62_C	-2.784	0.082	11.362	-2.644	1.568	11.7	1.53	77.24	84.62
367	2jsa-15	HIS_A_62_C	HIS_A_62_O	-2.644	1.568	11.7	-2.928	1.983	12.822	1.23	24.14	124.39
368	2jsa-15	HIS_A_62_C	GLU_A_63_N	-2.644	1.568	11.7	-2.205	2.327	10.707	1.32	138.56	59.96
369	2jsa-15	GLU_A_63_N	GLU_A_63_H	-2.205	2.327	10.707	-1.991	1.917	9.809	1.01	152.75	-62.44
370	2jsa-15	GLU_A_63_N	GLU_A_63_CA	-2.205	2.327	10.707	-2.022	3.758	10.884	1.45	83.01	82.71
371	2jsa-15	GLU_A_63_CA	GLU_A_63_HA	-2.022	3.758	10.884	-1.66	3.929	11.898	1.09	21.55	25.28
372	2jsa-15	GLU_A_63_CA	GLU_A_63_C	-2.022	3.758	10.884	-3.357	4.488	10.72	1.53	96.15	151.33
373	2jsa-15	GLU_A_63_C	GLU_A_63_O	-3.357	4.488	10.72	-3.794	5.202	11.622	1.23	42.86	121.47
374	2jsa-15	GLU_A_63_C	LEU_A_64_N	-3.357	4.488	10.72	-3.969	4.283	9.563	1.32	150.85	-161.48
375	2jsa-15	LEU_A_64_N	LEU_A_64_H	-3.969	4.283	9.563	-3.551	3.682	8.867	1.01	133.55	-55.18
376	2jsa-15	LEU_A_64_N	LEU_A_64_CA	-3.969	4.283	9.563	-5.246	4.912	9.269	1.45	101.67	153.78
377	2jsa-15	LEU_A_64_CA	LEU_A_64_HA	-5.246	4.912	9.269	-5.139	5.985	9.432	1.09	81.40	84.31
378	2jsa-15	LEU_A_64_CA	LEU_A_64_C	-5.246	4.912	9.269	-6.301	4.396	10.249	1.53	50.16	-153.94
379	2jsa-15	LEU_A_64_C	LEU_A_64_O	-6.301	4.396	10.249	-7.049	5.179	10.83	1.23	61.78	133.69
380	2jsa-15	LEU_A_64_C	GLU_A_65_N	-6.301	4.396	10.249	-6.327	3.079	10.402	1.33	83.37	-91.13
381	2jsa-15	GLU_A_65_N	GLU_A_65_H	-6.327	3.079	10.402	-5.68	2.495	9.892	1.01	120.33	-42.07
382	2jsa-15	GLU_A_65_N	GLU_A_65_CA	-6.327	3.079	10.402	-7.278	2.449	11.301	1.45	51.76	-146.48
383	2jsa-15	GLU_A_65_CA	GLU_A_65_HA	-7.278	2.449	11.301	-8.281	2.739	10.988	1.09	106.69	163.87
384	2jsa-15	GLU_A_65_CA	GLU_A_65_C	-7.278	2.449	11.301	-7.061	2.941	12.734	1.53	20.57	66.20
385	2jsa-15	GLU_A_65_C	GLU_A_65_O	-7.061	2.941	12.734	-7.994	2.966	13.533	1.23	49.43	178.47
386	2jsa-15	GLU_A_65_C	GLY_A_66_N	-7.061	2.941	12.734	-5.822	3.318	13.013	1.32	77.84	16.92
387	2jsa-15	GLY_A_66_N	GLY_A_66									

390	2jsa-15	GLY_A_66_C	GLY_A_66_O	-5.957	5.242	14.537	-6.474	5.583	15.6	1.23	30.23	146.59
391	2jsa-15	GLY_A_66_C	GLY_A_67_N	-5.957	5.242	14.537	-5.777	6.047	13.5	1.33	141.50	77.40
392	2jsa-15	GLY_A_67_N	GLY_A_67_H	-5.777	6.047	13.5	-5.345	5.699	12.656	1.01	146.68	-38.85
393	2jsa-15	GLY_A_67_N	GLY_A_67_CA	-5.777	6.047	13.5	-6.192	7.438	13.551	1.45	87.99	106.61
394	2jsa-15	GLY_A_67_CA	GLY_A_67_C	-6.192	7.438	13.551	-5.375	8.29	12.577	1.53	129.53	46.20
395	2jsa-15	GLY_A_67_C	GLY_A_67_O	-5.375	8.29	12.577	-5.798	9.381	12.195	1.23	108.08	111.19
396	2jsa-15	GLY_A_67_C	THR_A_68_N	-5.375	8.29	12.577	-4.219	7.76	12.203	1.33	106.39	-24.63
397	2jsa-15	THR_A_68_N	THR_A_68_H	-4.219	7.76	12.203	-3.934	6.858	12.557	1.01	69.48	-72.47
398	2jsa-15	THR_A_68_N	THR_A_68_CA	-4.219	7.76	12.203	-3.34	8.458	11.281	1.45	129.40	38.45
399	2jsa-15	THR_A_68_CA	THR_A_68_HA	-3.34	8.458	11.281	-3.076	9.424	11.713	1.09	66.67	74.71
400	2jsa-15	THR_A_68_CA	THR_A_68_C	-3.34	8.458	11.281	-4.054	8.716	9.953	1.53	150.24	160.13
401	2jsa-15	THR_A_68_C	THR_A_68_O	-4.054	8.716	9.953	-5.101	8.128	9.683	1.23	102.67	-150.68
402	2jsa-15	THR_A_68_C	ALA_A_69_N	-4.054	8.716	9.953	-3.46	9.595	9.159	1.33	126.81	55.95
403	2jsa-15	ALA_A_69_N	ALA_A_69_H	-3.46	9.595	9.159	-2.6	10.041	9.447	1.01	73.44	27.41
404	2jsa-15	ALA_A_69_N	ALA_A_69_CA	-3.46	9.595	9.159	-4.026	9.937	7.866	1.45	152.91	148.86
405	2jsa-15	ALA_A_69_CA	ALA_A_69_HA	-4.026	9.937	7.866	-5.081	9.666	7.863	1.09	90.16	-165.59
406	2jsa-15	ALA_A_69_CA	ALA_A_69_C	-4.026	9.937	7.866	-3.317	9.132	6.774	1.53	135.51	-48.63
407	2jsa-15	ALA_A_69_C	ALA_A_69_O	-3.317	9.132	6.774	-2.257	8.556	7.012	1.23	78.84	-28.52
408	2jsa-15	ALA_A_69_C	PRO_A_70_N	-3.317	9.132	6.774	-3.946	9.12	5.568	1.36	152.45	-178.91
409	2jsa-15	PRO_A_70_N	PRO_A_70_CA	-3.946	9.12	5.568	-3.386	8.398	4.439	1.45	141.02	-52.20
410	2jsa-15	PRO_A_70_CA	PRO_A_70_HA	-3.386	8.398	4.439	-3.051	7.411	4.757	1.09	73.03	-71.25
411	2jsa-15	PRO_A_70_CA	PRO_A_70_C	-3.386	8.398	4.439	-2.191	9.147	3.846	1.53	112.81	32.08
412	2jsa-15	PRO_A_70_C	PRO_A_70_O	-2.191	9.147	3.846	-1.613	8.712	2.851	1.23	143.98	-36.96
413	2jsa-15	PRO_A_70_C	LYS_A_71_N	-2.191	9.147	3.846	-1.857	10.26	4.483	1.33	61.27	73.30
414	2jsa-15	LYS_A_71_N	LYS_A_71_H	-1.857	10.26	4.483	-2.377	10.558	5.296	1.01	36.40	150.18
415	2jsa-15	LYS_A_71_N	LYS_A_71_CA	-1.857	10.26	4.483	-0.741	11.073	4.03	1.45	108.16	36.07
416	2jsa-15	LYS_A_71_CA	LYS_A_71_HA	-0.741	11.073	4.03	-0.251	10.548	3.21	1.09	138.79	-46.97
417	2jsa-15	LYS_A_71_CA	LYS_A_71_C	-0.741	11.073	4.03	0.275	11.214	5.166	1.53	42.08	7.90
418	2jsa-15	LYS_A_71_C	LYS_A_71_O	0.275	11.214	5.166	1.249	11.955	5.043	1.23	95.74	37.26
419	2jsa-15	LYS_A_71_C	ASP_A_72_N	0.275	11.214	5.166	0.012	10.492	6.245	1.32	35.46	-110.01
420	2jsa-15	ASP_A_72_N	ASP_A_72_H	0.012	10.492	6.245	-0.809	9.905	6.277	1.01	88.18	-144.44
421	2jsa-15	ASP_A_72_N	ASP_A_72_CA	0.012	10.492	6.245	0.891	10.528	7.401	1.45	37.27	2.35
422	2jsa-15	ASP_A_72_CA	ASP_A_72_HA	0.891	10.528	7.401	1.667	11.276	7.236	1.09	98.70	43.95
423	2jsa-15	ASP_A_72_CA	ASP_A_72_C	0.891	10.528	7.401	1.529	9.151	7.593	1.53	82.79	-65.14
424	2jsa-15	ASP_A_72_C	ASP_A_72_O	1.529	9.151	7.593	2.508	9.013	8.325	1.23	53.48	-8.02
425	2jsa-15	ASP_A_72_C	VAL_A_73_N	1.529	9.151	7.593	0.949	8.166	6.924	1.32	120.34	-120.49
426	2jsa-15	VAL_A_73_N	VAL_A_73_H	0.949	8.166	6.924	0.146	8.352	6.341	1.01	125.27	166.96
427	2jsa-15	VAL_A_73_N	VAL_A_73_CA	0.949	8.166	6.924	1.448	6.804	7.011	1.45	86.57	-69.88
428	2jsa-15	VAL_A_73_CA	VAL_A_73_HA	1.448	6.804	7.011	1.598	6.559	8.063	1.09	15.27	-58.52
429	2jsa-15	VAL_A_73_CA	VAL_A_73_C	1.448	6.804	7.011	2.803	6.716	6.306	1.53	117.44	-3.72
430	2jsa-15	VAL_A_73_C	VAL_A_73_O	2.803	6.716	6.306	3.758	6.17	6.855	1.23	63.48	-29.76
431	2jsa-15	VAL_A_73_C	CYS_A_74_N	2.803	6.716	6.306	2.842	7.262	5.099	1.33	155.61	85.91
432	2jsa-15	CYS_A_74_N	CYS_A_74_H	2.842	7.262	5.099	2.017	7.695	4.71	1.01	112.66	152.31
433	2jsa-15	CYS_A_74_N	CYS_A_74_CA	2.842	7.262	5.099	4.064	7.252	4.312	1.45	122.78	-0.47
434	2jsa-15	CYS_A_74_CA	CYS_A_74_HA	4.064	7.252	4.312	4.617	6.342	4.549	1.09	77.45	-58.71
435	2jsa-15	CYS_A_74_CA	CYS_A_74_C	4.064	7.252	4.312	4.911	8.456	4.725	1.53	74.33	54.87
436	2jsa-15	CYS_A_74_C	CYS_A_74_O	4.911	8.456	4.725	5.354	9.229	3.876	1.23	133.62	60.18
437	2jsa-15	CYS_A_74_C	THR_A_75_N	4.911	8.456	4.725	5.111	8.58	6.03	1.33	10.22	31.80
438	2jsa-15	THR_A_75_N	THR_A_75_H	5.111	8.58	6.03	4.717	7.907	6.672	1.01	50.54	-120.35
439	2jsa-15	THR_A_75_N	THR_A_75_CA	5.111	8.58	6.03	5.897	9.678	6.565	1.45	68.39	54.40
440	2jsa-15	THR_A_75_CA	THR_A_75_HA	5.897	9.678	6.565	6.769	9.827	5.928	1.09	125.76	9.70
441	2jsa-15	THR_A_75_CA	THR_A_75_C	5.897	9.678	6.565	6.394	9.341	7.972	1.53	23.11	-34.14
442	2jsa-15	THR_A_75_C	THR_A_75_O	6.394	9.341	7.972	7.6	9.288	8.213	1.23	78.71	-2.52
443	2jsa-15	THR_A_75_C	LYS_A_76_N	6.394	9.341	7.972	5.44	9.122	8.865	1.32	47.62	-167.07
444	2jsa-15	LYS_A_76_N	LYS_A_76_H	5.44	9.122	8.865	4.469	9.183	8.597	1.01	105.40	176.41
445	2jsa-15	LYS_A_76_N	LYS_A_76_CA	5.44	9.122	8.865	5.766	8.792	10.242	1.45	18.62	-45.35
446	2jsa-15	LYS_A_76_CA	LYS_A_76_HA	5.766	8.792	10.242	6.495	9.52	10.6	1.09	70.84	44.96
447	2jsa-15	LYS_A_76_CA	LYS_A_76_C	5.766	8.792	10.242	6.425	7.411	10.29	1.53	88.20	-64.49
448	2jsa-15	LYS_A_76_C	LYS_A_76_O	6.425	7.411	10.29	7.26	7.147	11.152	1.23	45.45	-17.55
449	2jsa-15	LYS_A_76_C	LEU_A_77_N	6.425	7.411	10.29	6.025	6.567	9.349	1.33	135.21	-115.36
450	2jsa-15	LEU_A_77_N	LEU_A_77_H	6.025	6.567	9.349	5.335	6.853	8.67	1.01	132.27	157.49
451	2jsa-15	LEU_A_77_N	LEU_A_77_CA	6.025	6.567	9.349	6.566	5.221	9.272	1.45	93.04	-68.10
452	2jsa-15	LEU_A_77_CA	LEU_A_77_HA	6.566	5.221	9.272	6.864	4.919	10.276	1.09	22.91	-45.38
453	2jsa-15	LEU_A_77_CA	LEU_A_77_C	6.566	5.221	9.272	7.822	5.231	8.399	1.53	124.80	0.46
454	2jsa-15	LEU_A_77_C	LEU_A_77_O	7.822	5.231	8.399	8.281	4.179	7.954	1.23	111.19	-66.43
455	2jsa-15	LEU_A_77_C	ASN_A_78_N	7.822	5.231	8.399	8.342	6.428	8.176	1.32	99.70	66.52
456	2jsa-15	ASN_A_78_N	ASN_A_78_H	8.342	6.428	8.176	7.911	7.251	8.572	1.01	66.91	117.64
457	2jsa-15	ASN_A_78_N	ASN_A_78_CA	8.342	6.428	8.176	9.535	6.588	7.364	1.45	124.00	7.64
458	2jsa-15	ASN_A_78_CA	ASN_A_78_HA	9.535	6.588	7.364	9.708	7.65	7.189	1.09	99.24	80.75
459	2jsa-15	ASN_A_78_CA	ASN_A_78_C	9.535	6.588	7.364	9.339	5.866	6.03	1.53	150.72	-105.19
460	2jsa-15	ASN_A_78_C	ASN_A_78_O	9.339	5.866	6.03	10.31	5.511	5.363	1.23	122.83	-20.08
461	2jsa-15	ASN_A_78_C	GLU_A_79_N	9.339	5.866	6.03	8.076	5.669	5.68	1.33	105.31	-171.13
462	2jsa-15	GLU_A_79_N	GLU_A_79_H	8.076	5.669	5.68	7.327	5.988	6.278	1.01	53.70	156.93
463	2jsa-15	GLU_A_79_N	GLU_A_79_CA	8.076	5.669	5.68	7.74	4.995	4.437	1.45	148.79	-116.50
464	2jsa-15	GLU_A_79_CA	GLU_A_79_HA	7.74	4.995	4.437	8.546	4.299	4.202	1.09	102.44	-40.81
465	2jsa-15	GLU_A_79_CA	GLU_A_79_C	7.74	4.995	4.437	7.632	6.009	3.296	1.53	138.21	96.08
466	2jsa-15	GLU_A_79_C	GLU_A_79_O	7.632	6.009	3.296	6.725	5.924	2.47	1.23	132.20	-174.65
467	2jsa-15	GLU_A_79_C	CYS_A_80_N	7.632	6.009	3.296	8.57	6.944	3.288	1.32	90.35	44.91
468	2jsa-15	CYS_A_80_N	CYS_A_80_H	8.57	6.944	3.288	9.287	6.953	4.0	1.01	45.20	0.72
469	2jsa-15	CYS_A_80_N	CYS_A_80_CA	8.57	6.944	3.288	8.592	7.973	2.261	1.45	134.94	88.78
470	2jsa-15	CYS_A_80_CA	CYS_A_80_HA	8.592	7.973	2.261	8.753	7.492	1.296	1.09	152.27	-71.49
471	2jsa-15	CYS_A_80_CA	CYS_A_80_C	8.592	7.973	2.261	9.772	8.906	2.542	1.53	79.42	38.33
472	2jsa-15	CYS_A_80_C	CYS_A_80_O	9.772	8.906	2.542	9.995	9.303	3.685	1.23	21.72	60.68
473	2jsa-15	CYS_A_80_C	PRO_A_81_N	9.772	8.906	2.542	10.513	9.239	1.452	1.36	143.30	24.20
474	2jsa-15	PRO_A_81_N	PRO_A_81_CA	10.513	9.239	1.452	11.664	10.119	1.57	1.45	85.34	37.40
475	2jsa-15	PRO_A_81_CA	PRO_A_81_HA	11.664	10.119	1.57	12.271	9.827	2.427	1.09	38.17	-25.69
476	2jsa-15	PRO_A_81_CA	PRO_A_81_C	11.664	10.119	1.57	11.225	11.574	1.758	1.53	82.95	106.79
477	2jsa-15	PRO_A_81_C	PRO_A_81_O	11.225	11.574	1.758	11.249	12.093	2.873	1.23	24.98	87.35

Table 1. A reversible spherical geometric conversion of Caenopore-5 backbone structure coordinate matrix to three independent vectors of ρ , θ and ϕ [1–3].

Bond ID	Model ID	Atom_Initial	Atom_Final	X _i	Y _i	Z _i	X _f	Y _f	Z _f	ρ (Å)	θ (°)	φ (°)
1	2jsa-1	ARG_A_1_C	SER_A_2_N	13.875	5.84	-0.967	12.838	6.548	-0.544	1.32	71.38	145.68
2	2jsa-1	SER_A_2_C	ALA_A_3_N	12.226	7.489	-2.715	11.022	7.04	-3.037	1.32	104.07	-159.55
3	2jsa-1	ALA_A_3_C	LEU_A_4_N	9.201	6.358	-4.5	8.901	5.473	-5.439	1.32	135.14	-108.73
4	2jsa-1	LEU_A_4_C	SER_A_5_N	7.055	4.298	-4.374	8.012	3.981	-3.514	1.33	49.53	-18.33
5	2jsa-1	SER_A_5_C	CYS_A_6_N	6.482	3.925	-1.609	6.528	5.245	-1.501	1.33	85.33	88.00
6	2jsa-1	CYS_A_6_C	GLN_A_7_N	4.155	5.681	-1.669	4.218	5.929	-2.969	1.32	168.86	75.75
7	2jsa-1	GLN_A_7_C	MET_A_8_N	2.299	4.459	-3.356	2.995	3.332	-3.33	1.32	88.88	-58.30
8	2jsa-1	MET_A_8_C	CYS_A_9_N	1.584	2.284	-1.611	2.224	2.929	-0.647	1.32	43.31	45.22
9	2jsa-1	CYS_A_9_C	GLU_A_10_N	0.277	3.938	0.372	0.291	4.739	-0.684	1.33	142.81	89.00
10	2jsa-1	GLU_A_10_C	LEU_A_11_N	-1.841	4.661	-1.885	-1.395	3.451	-2.188	1.32	103.22	-69.77
11	2jsa-1	LEU_A_11_C	VAL_A_12_N	-3.025	1.65	-2.036	-2.379	1.215	-0.965	1.32	36.02	-33.96
12	2jsa-1	VAL_A_12_C	VAL_A_13_N	-4.052	1.199	0.802	-3.584	2.341	1.285	1.33	68.63	67.72
13	2jsa-1	VAL_A_13_C	LYS_A_14_N	-5.599	3.701	1.179	-5.246	4.324	0.064	1.33	147.29	60.46
14	2jsa-1	LYS_A_14_C	LYS_A_15_N	-7.323	3.755	-1.069	-6.89	2.505	-1.009	1.32	87.40	-70.89
15	2jsa-1	LYS_A_15_C	TYR_A_16_N	-8.512	1.1	0.138	-7.769	1.272	1.221	1.32	35.15	13.03
16	2jsa-1	TYR_A_16_C	GLU_A_17_N	-9.301	2.135	2.94	-8.762	3.332	3.124	1.33	82.02	65.76
17	2jsa-1	GLU_A_17_C	GLY_A_18_N	-10.75	4.629	2.524	-10.513	4.202	1.292	1.33	158.38	-60.97
18	2jsa-1	GLY_A_18_C	SER_A_19_N	-11.817	2.915	-0.347	-12.397	2.05	0.472	1.32	51.82	-123.84
19	2jsa-1	SER_A_19_C	ALA_A_20_N	-14.232	0.591	-0.222	-14.936	0.126	0.799	1.32	39.57	-146.55
20	2jsa-1	ALA_A_20_C	ASP_A_21_N	-16.849	-1.012	1.781	-16.008	-2.0	2.049	1.32	78.33	-49.60
21	2jsa-1	ASP_A_21_C	LYS_A_22_N	-15.378	-2.846	4.242	-14.303	-2.108	4.009	1.32	100.13	34.47
22	2jsa-1	LYS_A_22_C	ASP_A_23_N	-12.574	-3.179	5.345	-12.424	-3.986	4.305	1.32	141.72	-79.47
23	2jsa-1	ASP_A_23_C	ALA_A_24_N	-10.258	-5.077	4.099	-9.423	-5.274	5.108	1.32	40.37	-13.27
24	2jsa-1	ALA_A_24_C	ASN_A_25_N	-7.485	-6.235	3.993	-8.369	-7.183	3.718	1.33	101.98	-133.00
25	2jsa-1	ASN_A_25_C	VAL_A_26_N	-8.27	-7.88	1.388	-9.483	-7.415	1.131	1.32	101.19	159.03
26	2jsa-1	VAL_A_26_C	ILE_A_27_N	-9.229	-5.618	-0.49	-8.604	-5.064	0.539	1.33	39.06	41.55
27	2jsa-1	ILE_A_27_C	LYS_A_28_N	-6.549	-3.949	-0.136	-5.8	-4.82	0.525	1.33	60.08	-49.31
28	2jsa-1	LYS_A_28_C	LYS_A_29_N	-4.442	-5.715	-1.284	-5.567	-6.33	-1.618	1.32	104.60	-151.34
29	2jsa-1	LYS_A_29_C	ASP_A_30_N	-5.841	-5.887	-3.995	-6.722	-4.933	-3.733	1.32	78.59	132.72
30	2jsa-1	ASP_A_30_C	PHE_A_31_N	-5.601	-3.237	-5.069	-4.735	-3.088	-4.077	1.33	41.53	9.76
31	2jsa-1	PHE_A_31_C	ASP_A_32_N	-2.675	-3.299	-5.403	-2.437	-4.572	-5.121	1.33	77.72	-79.41
32	2jsa-1	ASP_A_32_C	ALA_A_33_N	-2.482	-5.415	-7.403	-3.751	-5.038	-7.337	1.33	87.15	163.45
33	2jsa-1	ALA_A_33_C	GLU_A_34_N	-3.907	-4.071	-9.564	-3.938	-2.778	-9.278	1.32	77.53	91.37
34	2jsa-1	GLU_A_34_C	CYS_A_35_N	-1.814	-1.866	-10.085	-1.329	-2.056	-8.867	1.32	23.15	-21.39
35	2jsa-1	CYS_A_35_C	LYS_A_36_N	0.704	-3.081	-9.682	-0.141	-3.967	-10.188	1.32	112.45	-133.64
36	2jsa-1	LYS_A_36_C	LYS_A_37_N	0.202	-4.282	-12.577	-1.013	-3.891	-12.935	1.33	105.67	162.16
37	2jsa-1	LYS_A_37_C	LEU_A_38_N	-0.537	-1.909	-14.265	-0.983	-1.017	-13.393	1.32	48.83	116.57
38	2jsa-1	LEU_A_38_C	PHE_A_39_N	1.117	0.21	-13.48	1.695	-0.732	-12.75	1.32	56.55	-58.47
39	2jsa-1	PHE_A_39_C	HIS_A_40_N	3.462	-2.336	-13.343	2.835	-2.665	-14.463	1.33	147.70	-152.31
40	2jsa-1	HIS_A_40_C	THR_A_41_N	4.39	-3.95	-15.832	4.835	-2.749	-16.172	1.33	104.87	69.67
41	2jsa-1	THR_A_41_C	ILE_A_42_N	7.143	-1.953	-15.97	7.172	-2.427	-14.733	1.33	21.00	-86.50
42	2jsa-1	ILE_A_42_C	PRO_A_43_N	9.052	-3.044	-13.317	10.341	-2.671	-13.096	1.36	80.65	16.14
43	2jsa-1	PRO_A_43_C	PHE_A_44_N	11.156	-4.007	-11.2	10.599	-5.189	-10.982	1.32	80.53	-115.23
44	2jsa-1	PHE_A_44_C	GLY_A_45_N	9.153	-4.975	-9.005	8.552	-4.087	-9.784	1.33	126.00	124.09
45	2jsa-1	GLY_A_45_C	THR_A_46_N	6.3	-4.305	-8.821	5.774	-5.089	-9.75	1.32	134.54	-123.86
46	2jsa-1	THR_A_46_C	ARG_A_47_N	5.218	-7.016	-8.342	6.518	-7.27	-8.365	1.32	90.99	-11.06
47	2jsa-1	ARG_A_47_C	GLU_A_48_N	6.99	-7.606	-5.986	7.502	-6.396	-5.82	1.32	82.80	67.06
48	2jsa-1	GLU_A_48_C	CYS_A_49_N	5.998	-5.451	-4.135	5.17	-5.255	-5.15	1.32	140.03	166.68
49	2jsa-1	CYS_A_49_C	ASP_A_50_N	3.218	-6.02	-3.944	3.151	-7.255	-4.419	1.32	111.01	-93.11
50	2jsa-1	ASP_A_50_C	HIS_A_51_N	3.474	-8.423	-2.309	4.698	-7.922	-2.393	1.33	93.63	22.26
51	2jsa-1	HIS_A_51_C	TYR_A_52_N	5.294	-6.713	-0.361	4.268	-5.972	-0.752	1.32	107.17	144.16
52	2jsa-1	TYR_A_52_C	VAL_A_53_N	2.505	-4.985	0.649	1.58	-5.52	-0.134	1.32	126.23	-149.96
53	2jsa-1	VAL_A_53_C	ASN_A_54_N	0.301	-6.666	1.59	1.445	-7.317	1.747	1.33	83.20	-29.64
54	2jsa-1	ASN_A_54_C	SER_A_55_N	3.041	-7.968	3.465	3.193	-6.805	4.081	1.32	62.29	82.55
55	2jsa-1	SER_A_55_C	LYS_A_56_N	4.416	-4.987	5.164	3.7	-4.171	4.404	1.33	125.00	131.27
56	2jsa-1	LYS_A_56_C	VAL_A_57_N	2.087	-2.381	4.741	1.245	-3.403	4.699	1.32	91.82	-129.48
57	2jsa-1	VAL_A_57_C	ASP_A_58_N	-0.728	-3.355	6.123	-0.263	-4.409	6.778	1.33	60.38	-66.19
58	2jsa-1	ASP_A_58_C	PRO_A_59_N	-0.444	-3.455	9.009	0.754	-2.841	8.815	1.36	98.20	27.14
59	2jsa-1	PRO_A_59_C	ILE_A_60_N	0.365	-0.425	9.062	0.518	-0.171	7.77	1.33	167.07	58.94
60	2jsa-1	ILE_A_60_C	ILE_A_61_N	-1.604	1.007	7.59	-2.289	-0.104	7.36	1.33	99.99	-121.66
61	2jsa-1	ILE_A_61_C	HIS_A_62_N	-3.828	-0.063	9.244	-2.727	-0.321	9.933	1.32	58.65	-13.19
62	2jsa-1	HIS_A_62_C	GLU_A_63_N	-2.935	1.23	11.802	-2.237	2.124	11.117	1.33	121.13	52.02
63	2jsa-1	GLU_A_63_C	LEU_A_64_N	-3.791	4.014	11.205	-4.263	3.861	9.976	1.33	158.01	-162.04
64	2jsa-1	LEU_A_64_C	GLU_A_65_N	-6.606	3.506	10.527	-6.11	2.437	11.132	1.32	62.82	-65.11
65	2jsa-1	GLU_A_65_C	GLY_A_66_N	-7.161	2.334	13.341	-6.161	3.109	13.738	1.33	72.58	37.78
66	2jsa-1	GLY_A_66_C	GLY_A_67_N	-6.909	5.206	14.781	-6.627	5.802	13.632	1.32	150.15	64.68
67	2jsa-1	GLY_A_67_C	THR_A_68_N	-6.14	8.017	12.683	-5.35	7.441	11.788	1.33	132.47	-36.10
68	2jsa-1	THR_A_68_C	ALA_A_69_N	-4.673	8.439	9.656	-4.196	9.561	9.137	1.33	113.06	66.97
69	2jsa-1	ALA_A_69_C	PRO_A_70_N	-3.498	9.178	6.838	-3.871	9.124	5.531	1.36	163.91	-171.76
70	2jsa-1	PRO_A_70_C	LYS_A_71_N	-1.813	9.285	4.195	-1.778	10.488	4.748	1.32	65.32	88.33
71	2jsa-1	LYS_A_71_C	ASP_A_72_N	0.179	11.509	5.773	-0.236	10.771	6.792	1.32	39.72	-119.35
72	2jsa-1	ASP_A_72_C	VAL_A_73_N	1.211	9.455	8.239	0.694	8.432	7.575	1.32	120.08	-116.81
73	2jsa-1	VAL_A_73_C	CYS_A_74_N	2.633	7.119	6.913	2.577	7.533	5.656	1.32	161.62	97.70
74	2jsa-1	CYS_A_74_C	THR_A_75_N	4.65	8.74	5.343	5.17	8.554	6.547	1.32	24.64	-19.68
75	2jsa-1	THR_A_75_C	LYS_A_76_N	6.512	9.086	8.527	5.56	8.916	9.433	1.33	46.87	-169.88
76	2jsa-1	LYS_A_76_C	LEU_A_77_N	6.209	6.975	10.749	5.66	6.299	9.75	1.33	138.92	-129.08
77	2jsa-1	LEU_A_77_C	ASN_A_78_N	7.224	4.646	8.888	7.981	5.726	8.761	1.32	95.50	54.97
78	2jsa-1	ASN_A_78_C	GLU_A_79_N	9.189	4.72	6.904	8.019	4.713	6.283	1.32	117.96	-179.66
79	2jsa-1	GLU_A_79_C	CYS_A_80_N	8.022	4.661	3.835	7.544	5.897	3.846	1.33	89.52	111.14
80	2jsa-1	CYS_A_80_C	PRO_A_81_N	9.16	6.755	2.264	10.051	6.958	3.27	1.36	42.25	12.83
1	2jsa-2	ARG_A_1_C	SER_A_2_N	13.384	4.161	-0.108	14.105	5.075	-0.74	1.32	118.50	51.73
2	2jsa-2	SER_A_2_C	ALA_A_3_N	13.216	5.968	-2.835	11.964	5.663	-3.139	1.32	103.27	-166.31
3	2jsa-2	ALA_A_3_C	LEU_A_4_N	10.047	5.404	-4.616	9.535	4.549	-5.489	1.32	131.22	-120.91
4	2jsa-2	LEU_A_4_C	SER_A_5_N	7.467	3.713	-4.516	8.326	3.26	-3.614	1.33	47.11	-27.81
5	2jsa-2	SER_A_5_C	CYS_A_6_N	6.827	3.364	-1.685	7.101	4.657	-1.597	1.32	86.19	78.04
6	2jsa-2	CYS_A_6_C	GLN_A_7_N	4.833	5.495	-1.585	4.85	5.65	-2.9	1.32	173.24	83.74
7	2jsa-2	GLN_A_7_C	MET_A_8_N	2.773	4.404	-3.256	3.415	3.245	-3.231	1.33	88.92	-61.02
8	2jsa-2	MET_A_8_C	CYS_A_9_N	1.919	2.22	-1.57	2.539	2.888	-0.61	1.32	43.51	47.13
9	2jsa-2	CYS_A_9_C	GLU_A_10_N	0.601	3.937	0.387	0.639	4.717	-0.685	1.33	143.93	87.21
10	2jsa-2	GLU_A_10_C	LEU_A_11_N	-1.506	4.676	-1.865	-1.082	3.461	-2.181	1.33	103.80	-70.76
11	2jsa-2	LEU_A_11_C	VAL_A_12_N	-2.775	1.726	-1.971	-2.117	1.216	-0.94	1.33	38.92	-37.78
12	2jsa-2											

13	2jsa-2	VAL_A_13_C	LYS_A_14_N	-5.345	3.773	1.114	-4.96	4.374	-0.002	1.32	147.40	57.36
14	2jsa-2	LYS_A_14_C	LYS_A_15_N	-6.998	3.779	-1.192	-6.569	2.533	-1.058	1.32	84.19	-71.00
15	2jsa-2	LYS_A_15_C	TYR_A_16_N	-8.283	1.194	0.033	-7.617	1.393	1.162	1.33	31.62	16.64
16	2jsa-2	TYR_A_16_C	GLU_A_17_N	-9.163	2.421	2.773	-8.524	3.564	2.979	1.33	81.06	60.79
17	2jsa-2	GLU_A_17_C	GLY_A_18_N	-10.429	4.96	2.33	-10.199	4.567	1.086	1.32	159.90	-59.66
18	2jsa-2	GLY_A_18_C	SER_A_19_N	-11.643	3.298	-0.446	-11.906	2.407	0.499	1.33	44.51	-106.45
19	2jsa-2	SER_A_19_C	ALA_A_20_N	-13.836	0.929	0.247	-14.367	1.331	1.392	1.32	30.19	142.87
20	2jsa-2	ALA_A_20_C	ASP_A_21_N	-16.186	-0.148	2.044	-15.194	-1.027	2.025	1.33	90.82	-41.54
21	2jsa-2	ASP_A_21_C	LYS_A_22_N	-14.792	-2.661	3.783	-13.949	-1.725	4.195	1.33	71.89	47.99
22	2jsa-2	LYS_A_22_C	ASP_A_23_N	-12.705	-3.238	5.638	-12.088	-3.713	4.565	1.33	144.03	-37.59
23	2jsa-2	ASP_A_23_C	ALA_A_24_N	-10.02	-4.929	4.16	-9.151	-5.303	5.086	1.32	45.61	-23.29
24	2jsa-2	ALA_A_24_C	ASN_A_25_N	-7.339	-6.369	3.86	-8.322	-7.201	3.55	1.32	103.53	-139.76
25	2jsa-2	ASN_A_25_C	VAL_A_26_N	-8.346	-7.834	1.201	-9.498	-7.21	1.004	1.32	98.55	151.56
26	2jsa-2	VAL_A_26_C	ILE_A_27_N	-9.121	-5.391	-0.569	-8.48	-4.893	0.479	1.33	37.76	37.84
27	2jsa-2	ILE_A_27_C	LYS_A_28_N	-6.332	-3.946	-0.158	-5.556	-4.647	0.656	1.33	52.10	-42.09
28	2jsa-2	LYS_A_28_C	LYS_A_29_N	-4.218	-5.679	-1.095	-5.276	-6.439	-1.328	1.32	100.14	-144.31
29	2jsa-2	LYS_A_29_C	ASP_A_30_N	-5.611	-6.129	-3.719	-6.432	-5.127	-3.443	1.32	77.97	129.33
30	2jsa-2	ASP_A_30_C	PHE_A_31_N	-5.378	-3.466	-4.875	-4.561	-3.112	-3.894	1.32	42.23	23.43
31	2jsa-2	PHE_A_31_C	ASP_A_32_N	-2.542	-3.265	-5.289	-2.409	-4.567	-5.087	1.32	81.23	-84.17
32	2jsa-2	ASP_A_32_C	ALA_A_33_N	-2.473	-5.321	-7.399	-3.746	-4.959	-7.316	1.33	86.41	164.13
33	2jsa-2	ALA_A_33_C	GLU_A_34_N	-4.141	-3.582	-9.283	-4.432	-2.432	-8.694	1.32	63.59	104.20
34	2jsa-2	GLU_A_34_C	CYS_A_35_N	-2.599	-1.133	-9.668	-1.824	-1.878	-8.893	1.33	54.21	-43.87
35	2jsa-2	CYS_A_35_C	LYS_A_36_N	-0.133	-2.784	-10.365	-0.817	-3.916	-10.43	1.32	92.81	-121.14
36	2jsa-2	LYS_A_36_C	LYS_A_37_N	-0.906	-4.033	-12.86	-1.569	-2.895	-12.716	1.32	83.76	120.23
37	2jsa-2	LYS_A_37_C	LEU_A_38_N	-0.968	-0.809	-13.815	-0.858	-0.241	-12.622	1.33	25.87	79.04
38	2jsa-2	LEU_A_38_C	PHE_A_39_N	1.425	0.6	-12.704	1.962	-0.269	-11.86	1.33	50.44	-58.29
39	2jsa-2	PHE_A_39_C	HIS_A_40_N	3.461	-1.903	-12.923	2.574	-1.944	-13.907	1.33	137.94	-177.35
40	2jsa-2	HIS_A_40_C	THR_A_41_N	3.825	-2.979	-15.725	4.399	-1.787	-15.794	1.32	92.99	64.29
41	2jsa-2	THR_A_41_C	ILE_A_42_N	6.769	-1.178	-15.672	7.101	-2.074	-14.755	1.32	46.18	-69.67
42	2jsa-2	ILE_A_42_C	PRO_A_43_N	8.9	-3.143	-13.511	10.247	-3.046	-13.352	1.36	83.29	4.12
43	2jsa-2	PRO_A_43_C	PHE_A_44_N	10.874	-4.646	-11.593	10.151	-5.741	-11.414	1.32	82.23	-123.44
44	2jsa-2	PHE_A_44_C	GLY_A_45_N	8.825	-5.445	-9.365	8.364	-4.406	-10.047	1.33	120.96	113.93
45	2jsa-2	GLY_A_45_C	THR_A_46_N	6.149	-4.356	-8.981	5.733	-5.311	-9.8	1.33	128.18	-113.54
46	2jsa-2	THR_A_46_C	ARG_A_47_N	5.007	-7.125	-8.322	6.277	-7.502	-8.329	1.32	90.30	-16.53
47	2jsa-2	ARG_A_47_C	GLU_A_48_N	6.748	-7.756	-5.939	7.476	-6.655	-5.821	1.33	84.89	56.53
48	2jsa-2	GLU_A_48_C	CYS_A_49_N	6.115	-5.603	-4.079	5.211	-5.463	-5.037	1.32	136.32	171.20
49	2jsa-2	CYS_A_49_C	ASP_A_50_N	3.261	-6.3	-3.877	3.395	-7.506	-4.409	1.32	113.67	-83.66
50	2jsa-2	ASP_A_50_C	HIS_A_51_N	3.674	-8.863	-2.409	4.756	-8.109	-2.289	1.32	84.80	34.87
51	2jsa-2	HIS_A_51_C	TYR_A_52_N	5.338	-6.934	-0.234	4.411	-6.106	-0.694	1.33	110.31	138.23
52	2jsa-2	TYR_A_52_C	VAL_A_53_N	2.698	-5.008	0.687	1.755	-5.547	-0.072	1.33	124.95	-150.25
53	2jsa-2	VAL_A_53_C	ASN_A_54_N	0.441	-6.554	1.711	1.555	-7.246	1.897	1.32	81.93	-31.85
54	2jsa-2	ASN_A_54_C	SER_A_55_N	3.116	-7.825	3.672	3.381	-6.556	3.948	1.33	77.98	78.20
55	2jsa-2	SER_A_55_C	LYS_A_56_N	4.565	-4.749	5.088	4.066	-3.845	4.258	1.32	128.79	118.90
56	2jsa-2	LYS_A_56_C	VAL_A_57_N	2.433	-2.104	4.73	1.608	-3.137	4.646	1.32	93.64	-128.61
57	2jsa-2	VAL_A_57_C	ASP_A_58_N	-0.322	-3.17	6.129	0.092	-4.293	6.696	1.32	64.65	-69.76
58	2jsa-2	ASP_A_58_C	PRO_A_59_N	-0.075	-3.419	8.961	1.106	-2.771	8.777	1.36	97.78	28.75
59	2jsa-2	PRO_A_59_C	ILE_A_60_N	0.663	-0.374	9.102	0.756	-0.108	7.807	1.33	167.72	70.73
60	2jsa-2	ILE_A_60_C	ILE_A_61_N	-1.395	1.027	7.697	-2.079	-0.068	7.397	1.33	103.08	-121.99
61	2jsa-2	ILE_A_61_C	HIS_A_62_N	-3.592	-0.088	9.303	-2.476	-0.338	9.973	1.33	59.64	-12.63
62	2jsa-2	HIS_A_62_C	GLU_A_63_N	-2.73	1.172	11.87	-2.265	2.113	11.061	1.33	127.62	63.70
63	2jsa-2	GLU_A_63_C	LEU_A_64_N	-3.881	3.951	10.972	-4.204	3.736	9.705	1.33	162.97	-146.35
64	2jsa-2	LEU_A_64_C	GLU_A_65_N	-6.586	3.636	10.189	-6.396	2.427	10.697	1.33	67.46	-81.07
65	2jsa-2	GLU_A_65_C	GLY_A_66_N	-7.366	2.706	12.928	-6.187	3.16	13.33	1.33	72.35	21.06
66	2jsa-2	GLY_A_66_C	GLY_A_67_N	-6.851	5.283	14.378	-6.818	5.821	13.168	1.32	155.99	86.49
67	2jsa-2	GLY_A_67_C	THR_A_68_N	-6.668	7.979	11.997	-5.421	7.573	11.805	1.33	98.33	-18.03
68	2jsa-2	THR_A_68_C	ALA_A_69_N	-5.03	8.459	9.555	-4.487	9.429	8.834	1.32	122.97	60.76
69	2jsa-2	ALA_A_69_C	PRO_A_70_N	-4.131	8.695	6.541	-4.674	8.528	5.305	1.36	155.32	-162.90
70	2jsa-2	PRO_A_70_C	LYS_A_71_N	-2.802	8.28	3.73	-2.588	9.538	4.085	1.32	74.45	80.35
71	2jsa-2	LYS_A_71_C	ASP_A_72_N	-0.538	10.659	4.77	-0.935	10.2	5.949	1.33	27.24	-130.86
72	2jsa-2	ASP_A_72_C	VAL_A_73_N	0.441	9.199	7.688	-0.241	8.096	7.417	1.32	101.80	-121.73
73	2jsa-2	VAL_A_73_C	CYS_A_74_N	1.728	6.672	7.559	2.02	6.095	6.403	1.32	150.78	-63.16
74	2jsa-2	CYS_A_74_C	THR_A_75_N	4.212	7.116	6.466	3.662	8.296	6.216	1.33	100.87	114.99
75	2jsa-2	THR_A_75_C	LYS_A_76_N	5.002	9.353	7.973	4.177	9.259	9.005	1.32	38.82	-173.50
76	2jsa-2	LYS_A_76_C	LEU_A_77_N	5.336	7.712	10.483	4.87	6.793	9.649	1.33	128.99	-116.89
77	2jsa-2	LEU_A_77_C	ASN_A_78_N	6.722	5.407	8.896	7.213	6.596	8.577	1.33	103.93	67.56
78	2jsa-2	ASN_A_78_C	GLU_A_79_N	8.515	5.664	6.743	7.334	5.303	6.263	1.32	111.24	-163.00
79	2jsa-2	GLU_A_79_C	CYS_A_80_N	6.85	4.985	3.884	7.775	5.787	3.379	1.32	112.42	40.93
80	2jsa-2	CYS_A_80_C	PRO_A_81_N	8.67	7.523	1.952	8.824	8.387	2.992	1.36	40.16	79.89
1	2jsa-3	ARG_A_1_C	SER_A_2_N	13.816	2.625	-2.435	12.949	3.538	-2.847	1.32	108.12	133.52
2	2jsa-3	SER_A_2_C	ALA_A_3_N	11.925	5.751	-3.011	10.736	5.187	-3.172	1.33	96.98	-154.62
3	2jsa-3	ALA_A_3_C	LEU_A_4_N	8.433	4.981	-3.93	8.599	3.9	-4.678	1.32	124.37	-81.27
4	2jsa-3	LEU_A_4_C	SER_A_5_N	6.904	2.615	-3.496	7.745	2.106	-2.607	1.33	47.88	-31.18
5	2jsa-3	SER_A_5_C	CYS_A_6_N	6.262	2.762	-0.778	6.615	4.032	-0.91	1.32	95.72	74.47
6	2jsa-3	CYS_A_6_C	GLN_A_7_N	4.473	5.062	-1.354	4.67	5.339	-2.635	1.33	165.14	54.58
7	2jsa-3	GLN_A_7_C	MET_A_8_N	2.598	4.197	-3.263	3.156	2.999	-3.171	1.32	86.02	-65.03
8	2jsa-3	MET_A_8_C	CYS_A_9_N	1.479	2.05	-1.643	2.031	2.79	-0.692	1.33	44.15	53.28
9	2jsa-3	CYS_A_9_C	GLU_A_10_N	0.038	3.853	0.172	0.147	4.657	-0.876	1.33	142.25	82.28
10	2jsa-3	GLU_A_10_C	LEU_A_11_N	-1.936	4.579	-2.162	-1.481	3.367	-2.449	1.33	102.50	-69.42
11	2jsa-3	LEU_A_11_C	VAL_A_12_N	-3.136	1.589	-2.282	-2.526	1.202	-1.172	1.32	33.06	-32.39
12	2jsa-3	VAL_A_12_C	VAL_A_13_N	-4.23	1.265	0.566	-3.75	2.412	1.024	1.33	69.78	67.29
13	2jsa-3	VAL_A_13_C	LYS_A_14_N	-5.791	3.73	0.877	-5.475	4.296	-0.278	1.32	150.70	60.83
14	2jsa-3	LYS_A_14_C	LYS_A_15_N	-7.567	3.622	-1.323	-7.106	2.383	-1.221	1.33	85.59	-69.59
15	2jsa-3	LYS_A_15_C	TYR_A_16_N	-8.748	1.083	0.017	-8.019	1.306	1.101	1.33	35.12	17.01
16	2jsa-3	TYR_A_16_C	GLU_A_17_N	-9.486	2.395	2.746	-8.844	3.547	2.876	1.33	84.37	60.87
17	2jsa-3	GLU_A_17_C	GLY_A_18_N	-10.881	4.821	2.402	-10.814	4.38	1.155	1.32	160.32	-81.36
18	2jsa-3	GLY_A_18_C	SER_A_19_N	-12.343	2.94	-0.124	-12.367	2.051	0.859	1.33	42.14	-91.55
19	2jsa-3	SER_A_19_C	ALA_A_20_N	-14.202	0.477	0.501	-14.886	0.898	1.555	1.33	37.31	148.39
20	2jsa-3	ALA_A_20_C	ASP_A_21_N	-16.722	-0.613	2.074	-15.713	-1.465	2.186	1.33	85.15	-40.18
21	2jsa-3	ASP_A_21_C	LYS_A_22_N	-15.238	-3.048	3.972	-14.405	-2.082	4.333	1.33	74.20	49.23
22	2jsa-3	LYS_A_22_C	ASP_A_23_N	-13.044	-3.54	5.727	-12.156	-3.848	4.792	1.33	134.85	-19.13
23	2jsa-3	ASP_A_23_C	ALA_A_24_N	-10.043	-4.949	4.298	-9.099	-5.308	5.156	1.33	49.65	-20.82
24	2jsa-3	ALA_A_24_C	ASN_A_25_N	-7.307	-6.319	3.856	-8.283	-7.168</				

26	2jsa-3	VAL_A_26_C	ILE_A_27_N	-8.916	-5.39	-0.592	-8.347	-4.826	0.462	1.32	37.24	44.75
27	2jsa-3	ILE_A_27_C	LYS_A_28_N	-6.158	-4.016	-0.23	-5.401	-4.724	0.594	1.32	51.52	-43.08
28	2jsa-3	LYS_A_28_C	LYS_A_29_N	-4.151	-5.866	-1.152	-5.263	-6.557	-1.36	1.33	99.03	-148.14
29	2jsa-3	LYS_A_29_C	ASP_A_30_N	-5.635	-6.277	-3.749	-6.707	-5.504	-3.67	1.32	86.58	144.21
30	2jsa-3	ASP_A_30_C	PHE_A_31_N	-5.689	-3.794	-5.07	-4.974	-3.346	-4.049	1.32	39.57	32.07
31	2jsa-3	PHE_A_31_C	ASP_A_32_N	-2.886	-3.34	-5.347	-2.6	-4.611	-5.11	1.32	79.69	-77.32
32	2jsa-3	ASP_A_32_C	ALA_A_33_N	-2.464	-5.305	-7.439	-3.779	-5.145	-7.433	1.32	89.74	173.06
33	2jsa-3	ALA_A_33_C	GLU_A_34_N	-4.057	-3.814	-9.452	-4.078	-2.68	-8.767	1.32	58.87	91.06
34	2jsa-3	GLU_A_34_C	CYS_A_35_N	-2.133	-1.335	-9.401	-1.502	-2.296	-8.742	1.33	60.18	-56.71
35	2jsa-3	CYS_A_35_C	LYS_A_36_N	0.472	-2.876	-10.013	-0.086	-4.009	-10.415	1.33	107.66	-127.22
36	2jsa-3	LYS_A_36_C	LYS_A_37_N	-0.095	-3.746	-12.833	-1.143	-2.967	-12.606	1.33	80.14	143.38
37	2jsa-3	LYS_A_37_C	LEU_A_38_N	-0.796	-0.79	-13.637	-0.728	-0.157	-12.475	1.32	28.72	83.87
38	2jsa-3	LEU_A_38_C	PHE_A_39_N	1.517	0.772	-12.602	2.054	-0.152	-11.82	1.32	53.81	-59.84
39	2jsa-3	PHE_A_39_C	HIS_A_40_N	3.614	-1.62	-13.025	2.725	-1.583	-14.007	1.33	137.82	177.62
40	2jsa-3	HIS_A_40_C	THR_A_41_N	4.115	-2.483	-15.795	4.694	-1.291	-15.78	1.33	89.35	64.09
41	2jsa-3	THR_A_41_C	ILE_A_42_N	7.013	-0.609	-15.384	7.392	-1.531	-14.512	1.32	48.82	-67.65
42	2jsa-3	ILE_A_42_C	PRO_A_43_N	9.191	-2.479	-13.176	10.505	-2.25	-12.907	1.36	78.60	9.89
43	2jsa-3	PRO_A_43_C	PHE_A_44_N	11.175	-3.874	-11.187	10.441	-4.974	-11.113	1.32	86.80	-123.71
44	2jsa-3	PHE_A_44_C	GLY_A_45_N	9.051	-4.803	-9.09	8.582	-3.748	-9.74	1.32	119.38	113.97
45	2jsa-3	GLY_A_45_C	THR_A_46_N	6.416	-3.762	-8.577	5.805	-4.55	-9.447	1.32	131.10	-127.79
46	2jsa-3	THR_A_46_C	ARG_A_47_N	5.203	-6.451	-8.024	6.399	-6.962	-8.281	1.33	101.18	-23.13
47	2jsa-3	ARG_A_47_C	GLU_A_48_N	7.015	-7.448	-5.962	7.245	-6.149	-5.83	1.33	84.29	79.96
48	2jsa-3	GLU_A_48_C	CYS_A_49_N	5.881	-5.307	-3.98	4.976	-4.992	-4.895	1.32	133.68	160.81
49	2jsa-3	CYS_A_49_C	ASP_A_50_N	3.079	-5.981	-3.767	3.452	-7.148	-4.27	1.32	112.32	-72.27
50	2jsa-3	ASP_A_50_C	HIS_A_51_N	3.688	-8.513	-2.27	4.934	-8.069	-2.196	1.32	86.80	19.61
51	2jsa-3	HIS_A_51_C	TYR_A_52_N	5.367	-6.869	-0.119	4.338	-6.152	-0.548	1.33	108.88	145.13
52	2jsa-3	TYR_A_52_C	VAL_A_53_N	2.581	-5.129	0.834	1.633	-5.66	0.077	1.32	124.86	-150.75
53	2jsa-3	VAL_A_53_C	ASN_A_54_N	0.401	-6.725	1.885	1.54	-7.388	2.035	1.33	83.51	-30.20
54	2jsa-3	ASN_A_54_C	SER_A_55_N	3.188	-7.954	3.733	3.369	-6.763	4.283	1.32	65.46	81.36
55	2jsa-3	SER_A_55_C	LYS_A_56_N	4.649	-4.895	5.204	3.903	-4.126	4.426	1.32	125.99	134.13
56	2jsa-3	LYS_A_56_C	VAL_A_57_N	2.322	-2.294	4.691	1.466	-3.302	4.605	1.33	93.72	-130.34
57	2jsa-3	VAL_A_57_C	ASP_A_58_N	-0.499	-3.241	6.04	-0.047	-4.309	6.681	1.33	61.07	-67.06
58	2jsa-3	ASP_A_58_C	PRO_A_59_N	-0.279	-3.35	8.905	0.904	-2.702	8.729	1.36	97.43	28.71
59	2jsa-3	PRO_A_59_C	ILE_A_60_N	0.44	-0.298	8.948	0.625	-0.038	7.662	1.32	166.06	54.57
60	2jsa-3	ILE_A_60_C	ILE_A_61_N	-1.523	1.084	7.436	-2.19	-0.025	7.156	1.32	102.21	-121.02
61	2jsa-3	ILE_A_61_C	HIS_A_62_N	-3.77	0.014	9.007	-2.687	-0.238	9.727	1.32	57.08	-13.10
62	2jsa-3	HIS_A_62_C	GLU_A_63_N	-2.949	1.346	11.562	-2.221	2.23	10.897	1.32	120.14	50.53
63	2jsa-3	GLU_A_63_C	LEU_A_64_N	-3.776	4.12	10.88	-4.255	3.775	9.693	1.33	153.56	-144.24
64	2jsa-3	LEU_A_64_C	GLU_A_65_N	-6.608	3.554	10.274	-6.309	2.34	10.714	1.33	70.61	-76.16
65	2jsa-3	GLU_A_65_C	GLY_A_66_N	-7.321	2.464	12.94	-6.179	2.871	13.475	1.33	66.19	19.62
66	2jsa-3	GLY_A_66_C	GLY_A_67_N	-6.888	4.988	14.506	-6.585	5.633	13.39	1.32	147.44	64.84
67	2jsa-3	GLY_A_67_C	THR_A_68_N	-6.157	7.906	12.554	-5.291	7.405	11.686	1.32	130.94	-30.05
68	2jsa-3	THR_A_68_C	ALA_A_69_N	-4.473	8.409	9.606	-4.404	9.658	9.171	1.32	109.18	86.84
69	2jsa-3	ALA_A_69_C	PRO_A_70_N	-3.6	9.178	6.925	-3.904	9.087	5.603	1.36	166.50	-163.34
70	2jsa-3	PRO_A_70_C	LYS_A_71_N	-1.776	9.159	4.373	-1.827	10.442	4.702	1.33	75.63	92.28
71	2jsa-3	LYS_A_71_C	ASP_A_72_N	0.138	11.431	5.742	-0.277	10.674	6.747	1.32	40.66	-118.73
72	2jsa-3	ASP_A_72_C	VAL_A_73_N	1.184	9.362	8.185	0.616	8.309	7.616	1.32	115.43	-118.34
73	2jsa-3	VAL_A_73_C	CYS_A_74_N	2.516	6.993	6.858	2.401	7.522	5.649	1.32	155.88	102.26
74	2jsa-3	CYS_A_74_C	THR_A_75_N	4.412	8.773	5.161	5.013	8.647	6.335	1.32	27.61	-11.84
75	2jsa-3	THR_A_75_C	LYS_A_76_N	6.496	9.268	8.184	5.628	8.972	9.14	1.32	43.81	-161.17
76	2jsa-3	LYS_A_76_C	LEU_A_77_N	6.565	7.1	10.381	6.014	6.373	9.42	1.33	136.49	-127.16
77	2jsa-3	LEU_A_77_C	ASN_A_78_N	7.631	4.9	8.354	8.242	6.057	8.142	1.33	99.20	62.16
78	2jsa-3	ASN_A_78_C	GLU_A_79_N	9.229	5.336	6.038	7.992	5.362	5.563	1.33	111.00	178.80
79	2jsa-3	GLU_A_79_C	CYS_A_80_N	7.373	5.642	3.211	7.754	6.888	3.453	1.33	79.48	73.00
80	2jsa-3	CYS_A_80_C	PRO_A_81_N	8.159	9.232	3.014	9.426	9.5	2.598	1.36	107.81	11.94
1	2jsa-4	ARG_A_1_C	SER_A_2_N	13.831	5.809	1.973	13.569	5.572	0.696	1.32	164.54	-137.87
2	2jsa-4	SER_A_2_C	ALA_A_3_N	12.335	5.701	-1.41	11.19	5.171	-1.813	1.32	107.71	-155.16
3	2jsa-4	ALA_A_3_C	LEU_A_4_N	9.563	4.281	-3.389	9.387	3.389	-4.353	1.33	136.68	-101.16
4	2jsa-4	LEU_A_4_C	SER_A_5_N	7.318	2.598	-3.348	8.059	2.103	-2.367	1.33	42.25	-33.74
5	2jsa-4	SER_A_5_C	CYS_A_6_N	6.496	2.9	-0.667	7.006	4.123	-0.632	1.33	88.49	67.36
6	2jsa-4	CYS_A_6_C	GLN_A_7_N	4.93	5.255	-1.138	5.145	5.456	-2.43	1.33	167.17	43.07
7	2jsa-4	GLN_A_7_C	MET_A_8_N	3.066	4.336	-3.075	3.606	3.127	-0.038	1.32	88.40	-65.93
8	2jsa-4	MET_A_8_C	CYS_A_9_N	1.936	2.163	-1.513	2.43	3.015	-0.628	1.32	48.06	59.89
9	2jsa-4	CYS_A_9_C	GLU_A_10_N	0.429	4.05	0.249	0.509	4.84	-0.811	1.32	143.16	84.22
10	2jsa-4	GLU_A_10_C	LEU_A_11_N	-1.593	4.707	-2.06	-1.125	3.499	-2.338	1.32	102.11	-68.82
11	2jsa-4	LEU_A_11_C	VAL_A_12_N	-2.764	1.715	-2.115	-2.123	1.295	-1.033	1.33	35.31	-33.23
12	2jsa-4	VAL_A_12_C	VAL_A_13_N	-3.858	1.361	0.672	-3.419	2.521	1.138	1.32	69.41	69.27
13	2jsa-4	VAL_A_13_C	LYS_A_14_N	-5.46	3.821	0.883	-5.087	4.367	-0.264	1.32	150.04	55.66
14	2jsa-4	LYS_A_14_C	LYS_A_15_N	-7.106	3.668	-1.428	-6.648	2.439	-1.242	1.32	81.93	-69.56
15	2jsa-4	LYS_A_15_C	TYR_A_16_N	-8.301	1.088	-0.075	-7.616	1.339	1.032	1.33	33.39	20.12
16	2jsa-4	TYR_A_16_C	GLU_A_17_N	-9.222	2.325	2.61	-8.68	3.53	2.72	1.33	85.24	65.78
17	2jsa-4	GLU_A_17_C	GLY_A_18_N	-10.74	4.686	2.077	-10.515	4.334	0.819	1.33	161.63	-57.41
18	2jsa-4	GLY_A_18_C	SER_A_19_N	-11.824	2.843	-0.633	-11.966	1.942	0.328	1.32	43.51	-98.96
19	2jsa-4	SER_A_19_C	ALA_A_20_N	-13.686	0.267	-0.132	-14.438	0.733	0.853	1.32	41.93	148.21
20	2jsa-4	ALA_A_20_C	ASP_A_21_N	-16.217	-0.799	1.491	-15.788	-0.948	2.736	1.33	20.04	-19.15
21	2jsa-4	ASP_A_21_C	LYS_A_22_N	-15.082	-2.253	4.664	-13.947	-1.587	4.517	1.32	96.37	30.40
22	2jsa-4	LYS_A_22_C	ASP_A_23_N	-12.378	-2.982	5.747	-12.018	-3.586	4.623	1.33	147.97	-59.20
23	2jsa-4	ASP_A_23_C	ALA_A_24_N	-9.999	-4.875	4.2	-9.118	-5.145	5.153	1.33	44.04	-17.04
24	2jsa-4	ALA_A_24_C	ASN_A_25_N	-7.352	-6.268	3.912	-8.349	-7.1	3.654	1.32	101.24	-140.15
25	2jsa-4	ASN_A_25_C	VAL_A_26_N	-8.401	-7.765	1.314	-9.577	-7.196	1.091	1.33	99.69	154.18
26	2jsa-4	VAL_A_26_C	ILE_A_27_N	-9.156	-5.423	-0.523	-8.461	-4.945	0.499	1.33	39.53	34.52
27	2jsa-4	ILE_A_27_C	LYS_A_28_N	-6.286	-4.082	-0.168	-5.462	-4.614	0.723	1.33	47.75	-32.85
28	2jsa-4	LYS_A_28_C	LYS_A_29_N	-4.131	-5.684	-1.011	-5.167	-6.483	-1.22	1.32	99.08	-142.36
29	2jsa-4	LYS_A_29_C	ASP_A_30_N	-5.527	-6.196	-3.609	-6.417	-5.247	-3.36	1.32	79.17	133.16
30	2jsa-4	ASP_A_30_C	PHE_A_31_N	-5.412	-3.602	-4.844	-4.602	-3.166	-3.891	1.32	43.99	28.29
31	2jsa-4	PHE_A_31_C	ASP_A_32_N	-2.593	-3.346	-5.298	-2.461	-4.64	-5.049	1.32	79.16	-84.18
32	2jsa-4	ASP_A_32_C	ALA_A_33_N	-2.526	-5.488	-7.33	-3.834	-5.297	-7.242	1.32	86.19	171.69
33	2jsa-4	ALA_A_33_C	GLU_A_34_N	-4.24	-4.053	-9.294	-4.52	-2.864	-8.781	1.32	67.22	103.25
34	2jsa-4	GLU_A_34_C	CYS_A_35_N	-2.73	-1.709	-9.989	-1.815	-1.856	-9.042	1.33	44.38	-9.13
35	2jsa-4	CYS_A_35_C	LYS_A_36_N	-0.238	-2.89	-10.555	-0.726	-4.107	-10.365	1.32	81.75	-111.85
36	2jsa-4	LYS_A_36_C	LYS_A_37_N	-0.906	-4.47	-12.765	-1.71	-3.418	-12.735	1.32	88.70	127.39
37	2jsa-4	LYS_A_37_C	LEU_A_38_N	-1.173	-1.453	-14.068	-1.217	-0.64	-13.022	1.33	37.90	93

39	2jsa-4	PHE_A_39_C	HIS_A_40_N	2.905	-2.596	-13.815	2.042	-2.736	-14.81	1.32	138.70	-170.79
40	2jsa-4	HIS_A_40_C	THR_A_41_N	3.234	-4.196	-16.355	3.797	-3.089	-16.818	1.33	110.45	63.04
41	2jsa-4	THR_A_41_C	ILE_A_42_N	6.229	-3.357	-16.681	6.243	-2.606	-15.589	1.33	34.52	88.93
42	2jsa-4	ILE_A_42_C	PRO_A_43_N	7.56	-4.175	-14.276	8.863	-4.525	-14.101	1.36	82.61	-15.04
43	2jsa-4	PRO_A_43_C	PHE_A_44_N	8.919	-6.195	-12.298	9.932	-6.03	-11.461	1.32	50.80	9.25
44	2jsa-4	PHE_A_44_C	GLY_A_45_N	8.554	-5.554	-9.481	8.196	-4.468	-10.15	1.32	120.33	108.24
45	2jsa-4	GLY_A_45_C	THR_A_46_N	5.947	-4.567	-9.162	5.442	-5.448	-10.013	1.32	129.96	-119.82
46	2jsa-4	THR_A_46_C	ARG_A_47_N	4.848	-7.222	-8.433	6.11	-7.621	-8.494	1.32	92.64	-17.55
47	2jsa-4	ARG_A_47_C	GLU_A_48_N	6.726	-7.676	-6.125	7.421	-6.548	-6.154	1.33	91.25	58.36
48	2jsa-4	GLU_A_48_C	CYS_A_49_N	6.16	-5.345	-4.435	5.254	-5.073	-5.363	1.33	134.45	163.29
49	2jsa-4	CYS_A_49_C	ASP_A_50_N	3.257	-5.894	-4.275	3.505	-7.079	-4.814	1.33	114.00	-78.18
50	2jsa-4	ASP_A_50_C	HIS_A_51_N	3.704	-8.607	-2.931	4.726	-7.808	-2.664	1.32	78.37	38.02
51	2jsa-4	HIS_A_51_C	TYR_A_52_N	5.311	-6.799	-0.522	4.447	-5.892	-0.954	1.33	109.03	133.61
52	2jsa-4	TYR_A_52_C	VAL_A_53_N	2.809	-4.858	0.562	1.846	-5.426	-0.148	1.32	122.42	-149.47
53	2jsa-4	VAL_A_53_C	ASN_A_54_N	0.643	-6.459	1.697	1.79	-7.106	1.841	1.32	83.76	-29.43
54	2jsa-4	ASN_A_54_C	SER_A_55_N	3.46	-7.662	3.522	3.669	-6.434	3.973	1.32	70.10	80.34
55	2jsa-4	SER_A_55_C	LYS_A_56_N	4.897	-4.617	5.052	4.173	-3.767	4.337	1.33	122.63	130.42
56	2jsa-4	LYS_A_56_C	VAL_A_57_N	2.53	-2.023	4.764	1.704	-3.049	4.615	1.33	96.45	-128.84
57	2jsa-4	VAL_A_57_C	ASP_A_58_N	-0.285	-3.096	6.015	0.154	-4.197	6.607	1.32	63.46	-68.26
58	2jsa-4	ASP_A_58_C	PRO_A_59_N	-0.113	-3.344	8.872	1.067	-2.682	8.741	1.36	95.53	29.29
59	2jsa-4	PRO_A_59_C	ILE_A_60_N	0.586	-0.293	9.067	0.798	0.038	7.802	1.32	162.74	57.36
60	2jsa-4	ILE_A_60_C	ILE_A_61_N	-1.353	1.158	7.601	-2.019	0.076	7.225	1.33	106.49	-121.61
61	2jsa-4	ILE_A_61_C	HIS_A_62_N	-3.634	0.047	9.046	-2.564	-0.223	9.779	1.32	56.41	-14.16
62	2jsa-4	HIS_A_62_C	GLU_A_63_N	-2.769	1.316	11.658	-2.316	2.208	10.789	1.33	130.98	63.08
63	2jsa-4	GLU_A_63_C	LEU_A_64_N	-3.831	4.131	10.85	-4.367	3.806	9.683	1.32	151.76	-148.77
64	2jsa-4	LEU_A_64_C	GLU_A_65_N	-6.708	3.527	10.287	-6.303	2.361	10.77	1.33	68.63	-70.85
65	2jsa-4	GLU_A_65_C	GLY_A_66_N	-7.29	2.337	13.011	-6.157	2.784	13.534	1.33	66.76	21.53
66	2jsa-4	GLY_A_66_C	GLY_A_67_N	-6.874	4.847	14.665	-6.406	5.647	13.718	1.33	135.62	59.67
67	2jsa-4	GLY_A_67_C	THR_A_68_N	-5.999	7.892	12.801	-5.298	7.347	11.818	1.32	137.91	-37.86
68	2jsa-4	THR_A_68_C	ALA_A_69_N	-4.734	8.271	9.62	-4.589	9.487	9.116	1.32	112.37	83.20
69	2jsa-4	ALA_A_69_C	PRO_A_70_N	-4.014	9.008	6.8	-4.369	9.032	5.488	1.36	164.83	176.13
70	2jsa-4	PRO_A_70_C	LYS_A_71_N	-2.286	9.119	4.185	-2.311	10.401	4.52	1.33	75.36	91.12
71	2jsa-4	LYS_A_71_C	ASP_A_72_N	-0.315	11.317	5.569	-0.864	10.744	6.63	1.32	36.79	-133.77
72	2jsa-4	ASP_A_72_C	VAL_A_73_N	0.528	9.381	8.087	-0.137	8.334	7.621	1.32	110.59	-122.42
73	2jsa-4	VAL_A_73_C	CYS_A_74_N	1.847	6.993	7.189	1.989	7.476	5.964	1.32	157.66	73.62
74	2jsa-4	CYS_A_74_C	THR_A_75_N	4.015	8.791	5.834	4.114	8.889	7.151	1.32	6.04	44.71
75	2jsa-4	THR_A_75_C	LYS_A_76_N	5.504	9.592	9.041	4.744	9.001	9.95	1.32	46.64	-142.13
76	2jsa-4	LYS_A_76_C	LEU_A_77_N	5.944	7.162	10.999	5.438	6.455	10.0	1.32	138.97	-125.59
77	2jsa-4	LEU_A_77_C	ASN_A_78_N	7.272	5.264	8.933	7.688	6.509	8.749	1.33	97.98	71.52
78	2jsa-4	ASN_A_78_C	GLU_A_79_N	8.893	6.13	6.667	7.686	5.722	6.251	1.33	108.29	-163.48
79	2jsa-4	GLU_A_79_C	CYS_A_80_N	7.018	6.162	3.928	7.812	7.212	3.771	1.33	96.80	52.90
80	2jsa-4	CYS_A_80_C	PRO_A_81_N	8.375	9.472	3.119	8.663	10.25	2.042	1.36	142.39	69.69
1	2jsa-5	ARG_A_1_C	SER_A_2_N	13.136	3.863	-0.521	12.151	4.637	-0.092	1.32	71.10	141.84
2	2jsa-5	SER_A_2_C	ALA_A_3_N	11.851	6.475	-1.674	10.728	5.943	-2.134	1.33	110.31	-154.65
3	2jsa-5	ALA_A_3_C	LEU_A_4_N	8.937	5.501	-3.722	9.054	4.236	-4.095	1.32	106.36	-84.72
4	2jsa-5	LEU_A_4_C	SER_A_5_N	7.213	3.052	-3.033	8.049	2.789	-2.04	1.32	41.43	-17.46
5	2jsa-5	SER_A_5_C	CYS_A_6_N	6.516	3.442	-0.252	6.799	4.704	-0.539	1.32	102.51	77.36
6	2jsa-5	CYS_A_6_C	GLN_A_7_N	4.638	5.682	-1.009	4.841	5.763	-2.317	1.33	170.51	21.75
7	2jsa-5	GLN_A_7_C	MET_A_8_N	2.863	4.465	-2.946	3.509	3.309	-2.918	1.32	88.79	-60.80
8	2jsa-5	MET_A_8_C	CYS_A_9_N	1.905	2.21	-1.414	2.446	2.853	-0.39	1.32	39.37	49.92
9	2jsa-5	CYS_A_9_C	GLU_A_10_N	0.428	3.845	0.503	0.538	4.675	-0.524	1.33	140.81	82.45
10	2jsa-5	GLU_A_10_C	LEU_A_11_N	-1.553	4.641	-1.798	-1.106	3.438	-2.125	1.32	104.29	-69.62
11	2jsa-5	LEU_A_11_C	VAL_A_12_N	-2.755	1.654	-1.995	-2.131	1.233	-0.904	1.33	34.60	-34.01
12	2jsa-5	VAL_A_12_C	VAL_A_13_N	-3.825	1.232	0.844	-3.368	2.394	1.289	1.33	70.38	68.53
13	2jsa-5	VAL_A_13_C	LYS_A_14_N	-5.401	3.724	1.166	-5.068	4.35	0.046	1.33	147.66	61.99
14	2jsa-5	LYS_A_14_C	LYS_A_15_N	-7.128	3.714	-1.084	-6.659	2.477	-1.002	1.33	86.45	-69.24
15	2jsa-5	LYS_A_15_C	TYR_A_16_N	-8.333	1.11	0.116	-7.644	1.275	1.235	1.32	32.34	13.47
16	2jsa-5	TYR_A_16_C	GLU_A_17_N	-9.113	2.318	2.908	-8.419	3.403	3.219	1.32	76.42	57.40
17	2jsa-5	GLU_A_17_C	GLY_A_18_N	-10.309	4.872	2.704	-10.16	4.502	1.44	1.33	162.49	-68.07
18	2jsa-5	GLY_A_18_C	SER_A_19_N	-11.682	3.314	-0.082	-11.863	2.363	0.823	1.33	46.93	-100.78
19	2jsa-5	SER_A_19_C	ALA_A_20_N	-13.808	0.916	0.515	-14.337	1.305	1.666	1.33	29.70	143.67
20	2jsa-5	ALA_A_20_C	ASP_A_21_N	-16.185	-0.189	2.189	-15.191	-1.065	2.204	1.33	89.35	-41.39
21	2jsa-5	ASP_A_21_C	LYS_A_22_N	-14.816	-2.838	3.828	-14.006	-1.923	4.339	1.32	67.31	48.48
22	2jsa-5	LYS_A_22_C	ASP_A_23_N	-12.782	-3.559	5.661	-12.046	-3.902	4.615	1.32	142.18	-24.99
23	2jsa-5	ASP_A_23_C	ALA_A_24_N	-9.997	-5.088	4.052	-9.081	-5.32	4.982	1.33	45.46	-14.21
24	2jsa-5	ALA_A_24_C	ASN_A_25_N	-7.299	-6.296	3.642	-8.242	-7.198	3.413	1.32	99.95	-136.27
25	2jsa-5	ASN_A_25_C	VAL_A_26_N	-8.289	-7.745	1.043	-9.434	-7.096	0.885	1.33	96.85	150.45
26	2jsa-5	VAL_A_26_C	ILE_A_27_N	-9.018	-5.255	-0.651	-8.305	-4.83	0.383	1.33	38.76	30.80
27	2jsa-5	ILE_A_27_C	LYS_A_28_N	-6.108	-3.976	-0.22	-5.389	-4.735	0.596	1.33	52.03	-46.55
28	2jsa-5	LYS_A_28_C	LYS_A_29_N	-4.06	-5.774	-1.158	-5.103	-6.552	-1.412	1.33	101.05	-143.28
29	2jsa-5	LYS_A_29_C	ASP_A_30_N	-5.443	-6.154	-3.789	-6.341	-5.22	-3.509	1.33	77.81	133.87
30	2jsa-5	ASP_A_30_C	PHE_A_31_N	-5.314	-3.523	-4.919	-4.502	-3.135	-3.947	1.32	42.80	25.54
31	2jsa-5	PHE_A_31_C	ASP_A_32_N	-2.487	-3.285	-5.349	-2.291	-4.572	-5.104	1.32	79.34	-81.34
32	2jsa-5	ASP_A_32_C	ALA_A_33_N	-2.39	-5.423	-7.383	-3.672	-5.106	-7.274	1.33	85.28	166.11
33	2jsa-5	ALA_A_33_C	GLU_A_34_N	-4.162	-3.858	-9.306	-4.346	-2.68	-8.73	1.32	64.21	98.88
34	2jsa-5	GLU_A_34_C	CYS_A_35_N	-2.579	-1.456	-9.899	-1.698	-1.832	-8.983	1.33	46.28	-23.11
35	2jsa-5	CYS_A_35_C	LYS_A_36_N	-0.076	-2.849	-10.461	-0.694	-4.016	-10.342	1.33	84.85	-117.90
36	2jsa-5	LYS_A_36_C	LYS_A_37_N	-0.674	-4.353	-12.752	-1.521	-3.338	-12.826	1.32	93.20	129.84
37	2jsa-5	LYS_A_37_C	LEU_A_38_N	-0.791	-1.376	-14.069	-0.933	-0.574	-13.024	1.32	37.93	100.04
38	2jsa-5	LEU_A_38_C	PHE_A_39_N	1.329	0.305	-13.209	1.802	-0.782	-12.617	1.33	63.46	-66.48
39	2jsa-5	PHE_A_39_C	HIS_A_40_N	3.22	-2.591	-13.49	2.353	-2.768	-14.477	1.33	138.12	-168.46
40	2jsa-5	HIS_A_40_C	THR_A_41_N	3.562	-4.221	-16.016	4.209	-3.104	-16.315	1.33	103.04	59.92
41	2jsa-5	THR_A_41_C	ILE_A_42_N	6.65	-3.243	-16.164	6.622	-2.442	-15.109	1.32	37.22	92.00
42	2jsa-5	ILE_A_42_C	PRO_A_43_N	8.195	-3.871	-13.924	9.54	-4.005	-13.772	1.36	83.58	-5.69
43	2jsa-5	PRO_A_43_C	PHE_A_44_N	9.9	-5.796	-12.127	10.222	-4.929	-11.178	1.33	44.26	69.63
44	2jsa-5	PHE_A_44_C	GLY_A_45_N	8.874	-4.475	-9.172	7.874	-4.235	-10.005	1.32	129.01	166.50
45	2jsa-5	GLY_A_45_C	THR_A_46_N	5.622	-4.454	-9.04	5.286	-5.434	-9.867	1.33	128.60	-108.92
46	2jsa-5	THR_A_46_C	ARG_A_47_N	4.822	-7.357	-8.422	6.122	-7.602	-8.498	1.33	93.29	-10.67
47	2jsa-5	ARG_A_47_C	GLU_A_48_N	6.807	-7.831	-6.159	7.421	-6.658	-6.105	1.33	87.66	62.37
48	2jsa-5	GLU_A_48_C	CYS_A_49_N	6.137	-5.565	-4.332	5.222	-5.359	-5.268	1.33	134.94	167.31
49	2jsa-5	CYS_A_49_C	ASP_A_50_N	3.233	-6.193	-4.173	3.334	-7.358	-4.795	1.32	118.01	-85.05
50	2jsa-5	ASP_A_50_C	HIS_A_51_N	3.5	-8.858	-2.884	4.619	-8.176	-			

52	2jsa-5	TYR_A_52_C	VAL_A_53_N	2.679	-5.144	0.429	1.727	-5.677	-0.322	1.32	124.54	-150.76
53	2jsa-5	VAL_A_53_C	ASN_A_54_N	0.416	-6.669	1.471	1.529	-7.364	1.655	1.33	82.02	-31.98
54	2jsa-5	ASN_A_54_C	SER_A_55_N	3.123	-8.009	3.377	3.363	-6.822	3.915	1.33	66.05	78.57
55	2jsa-5	SER_A_55_C	LYS_A_56_N	4.669	-5.072	5.012	3.945	-4.209	4.314	1.33	121.78	129.99
56	2jsa-5	LYS_A_56_C	VAL_A_57_N	2.389	-2.38	4.706	1.514	-3.365	4.567	1.32	96.02	-131.62
57	2jsa-5	VAL_A_57_C	ASP_A_58_N	-0.493	-3.331	5.942	-0.072	-4.431	6.548	1.32	62.77	-69.06
58	2jsa-5	ASP_A_58_C	PRO_A_59_N	-0.321	-3.587	8.817	0.891	-2.981	8.705	1.36	94.72	26.57
59	2jsa-5	PRO_A_59_C	ILE_A_60_N	0.52	-0.575	9.049	0.693	-0.288	7.767	1.33	165.35	58.92
60	2jsa-5	ILE_A_60_C	ILE_A_61_N	-1.385	0.971	7.631	-2.112	-0.111	7.401	1.32	100.01	-123.90
61	2jsa-5	ILE_A_61_C	HIS_A_62_N	-3.631	0.048	9.295	-2.556	-0.285	9.994	1.32	58.15	-17.21
62	2jsa-5	HIS_A_62_C	GLU_A_63_N	-2.559	1.354	11.8	-2.175	2.173	10.832	1.32	136.94	64.88
63	2jsa-5	GLU_A_63_C	LEU_A_64_N	-3.522	4.213	10.703	-4.087	3.748	9.599	1.32	146.46	-140.55
64	2jsa-5	LEU_A_64_C	GLU_A_65_N	-6.45	3.804	10.178	-6.319	2.57	10.643	1.33	69.46	-83.94
65	2jsa-5	GLU_A_65_C	GLY_A_66_N	-7.101	2.75	12.957	-5.868	3.142	13.241	1.32	77.62	17.64
66	2jsa-5	GLY_A_66_C	GLY_A_67_N	-6.2	5.231	14.495	-5.978	5.955	13.407	1.33	145.16	72.95
67	2jsa-5	GLY_A_67_C	THR_A_68_N	-5.772	8.087	12.201	-4.54	7.668	11.95	1.33	100.92	-18.78
68	2jsa-5	THR_A_68_C	ALA_A_69_N	-4.451	8.379	9.607	-4.144	9.417	8.844	1.32	125.18	73.52
69	2jsa-5	ALA_A_69_C	PRO_A_70_N	-3.968	8.823	6.49	-4.59	8.679	5.289	1.36	152.00	-166.97
70	2jsa-5	PRO_A_70_C	LYS_A_71_N	-2.847	8.811	3.562	-2.689	10.017	4.091	1.33	66.49	82.54
71	2jsa-5	LYS_A_71_C	ASP_A_72_N	-0.667	11.225	4.697	-0.848	10.541	5.817	1.32	32.28	-104.82
72	2jsa-5	ASP_A_72_C	VAL_A_73_N	0.804	9.423	7.211	0.102	8.313	7.028	1.33	97.93	-122.31
73	2jsa-5	VAL_A_73_C	CYS_A_74_N	2.126	7.009	6.671	2.222	7.339	5.392	1.32	164.96	73.78
74	2jsa-5	CYS_A_74_C	THR_A_75_N	4.212	8.684	5.119	4.627	8.736	6.377	1.33	18.39	7.14
75	2jsa-5	THR_A_75_C	LYS_A_76_N	5.755	9.68	8.337	4.777	9.682	9.231	1.33	47.57	179.88
76	2jsa-5	LYS_A_76_C	LEU_A_77_N	5.301	7.985	10.895	4.495	7.164	10.237	1.33	119.77	-134.47
77	2jsa-5	LEU_A_77_C	ASN_A_78_N	6.043	5.298	10.035	6.749	6.198	9.367	1.32	120.28	51.89
78	2jsa-5	ASN_A_78_C	GLU_A_79_N	8.124	5.015	7.745	7.451	5.475	6.7	1.33	142.04	145.65
79	2jsa-5	GLU_A_79_C	CYS_A_80_N	8.265	5.335	4.396	7.82	6.475	3.888	1.33	112.54	111.32
80	2jsa-5	CYS_A_80_C	PRO_A_81_N	9.983	7.436	3.388	10.043	7.948	4.647	1.36	22.27	83.32
1	2jsa-6	ARG_A_1_C	SER_A_2_N	13.524	3.618	-1.098	12.724	4.398	-1.81	1.32	122.51	135.73
2	2jsa-6	SER_A_2_C	ALA_A_3_N	11.665	6.481	-2.525	10.501	5.857	-2.625	1.32	94.33	-151.81
3	2jsa-6	ALA_A_3_C	LEU_A_4_N	8.345	5.315	-3.616	8.638	4.275	-4.382	1.32	125.33	-74.27
4	2jsa-6	LEU_A_4_C	SER_A_5_N	6.953	2.915	-3.27	7.73	2.492	-2.283	1.33	41.87	-28.56
5	2jsa-6	SER_A_5_C	CYS_A_6_N	6.113	3.216	-0.599	6.533	4.471	-0.589	1.32	89.57	71.50
6	2jsa-6	CYS_A_6_C	GLN_A_7_N	4.391	5.451	-1.137	4.601	5.698	-2.423	1.33	165.85	49.63
7	2jsa-6	GLN_A_7_C	MET_A_8_N	2.605	4.44	-3.076	3.215	3.265	-3.041	1.32	88.49	-62.56
8	2jsa-6	MET_A_8_C	CYS_A_9_N	1.532	2.238	-1.572	1.933	3.129	-0.677	1.33	47.51	65.77
9	2jsa-6	CYS_A_9_C	GLU_A_10_N	-0.168	4.076	0.055	-0.029	5.022	-0.863	1.33	133.83	81.64
10	2jsa-6	GLU_A_10_C	LEU_A_11_N	-2.077	4.788	-2.183	-1.563	3.587	-2.405	1.33	99.64	-66.83
11	2jsa-6	LEU_A_11_C	VAL_A_12_N	-3.124	1.734	-2.182	-2.441	1.223	-1.169	1.32	40.10	-36.80
12	2jsa-6	VAL_A_12_C	VAL_A_13_N	-4.149	1.225	0.565	-3.738	2.415	0.976	1.32	71.92	70.95
13	2jsa-6	VAL_A_13_C	LYS_A_14_N	-5.842	3.625	0.803	-5.551	4.162	-0.373	1.33	152.55	61.55
14	2jsa-6	LYS_A_14_C	LYS_A_15_N	-7.631	3.382	-1.368	-7.132	2.163	-1.232	1.32	84.11	-67.74
15	2jsa-6	LYS_A_15_C	TYR_A_16_N	-8.7	0.852	0.088	-7.943	1.107	1.146	1.33	37.05	18.62
16	2jsa-6	TYR_A_16_C	GLU_A_17_N	-9.348	2.228	2.823	-8.681	3.358	3.006	1.32	82.06	59.45
17	2jsa-6	GLU_A_17_C	GLY_A_18_N	-10.661	4.71	2.504	-10.573	4.259	1.261	1.33	159.71	-78.96
18	2jsa-6	GLY_A_18_C	SER_A_19_N	-12.088	2.904	-0.122	-12.149	1.98	0.825	1.32	44.36	-93.78
19	2jsa-6	SER_A_19_C	ALA_A_20_N	-14.011	0.44	0.459	-14.657	0.904	1.519	1.33	36.88	144.31
20	2jsa-6	ALA_A_20_C	ASP_A_21_N	-16.495	-0.564	2.145	-15.497	-1.432	2.237	1.33	86.02	-41.01
21	2jsa-6	ASP_A_21_C	LYS_A_22_N	-14.966	-2.969	4.047	-14.058	-2.042	4.31	1.32	78.54	45.59
22	2jsa-6	LYS_A_22_C	ASP_A_23_N	-12.689	-3.501	5.695	-11.776	-3.843	4.798	1.32	132.62	-20.54
23	2jsa-6	ASP_A_23_C	ALA_A_24_N	-9.733	-5.046	4.25	-8.752	-5.304	5.103	1.33	49.94	-14.73
24	2jsa-6	ALA_A_24_C	ASN_A_25_N	-7.093	-6.347	3.66	-8.078	-7.22	3.505	1.33	96.72	-138.45
25	2jsa-6	ASN_A_25_C	VAL_A_26_N	-8.286	-7.821	1.156	-9.415	-7.135	1.051	1.33	94.54	148.72
26	2jsa-6	VAL_A_26_C	ILE_A_27_N	-9.03	-5.35	-0.556	-8.267	-4.904	0.432	1.33	41.81	30.31
27	2jsa-6	ILE_A_27_C	LYS_A_28_N	-6.062	-4.147	-0.264	-5.323	-4.838	0.591	1.32	49.80	-43.08
28	2jsa-6	LYS_A_28_C	LYS_A_29_N	-4.045	-5.925	-1.171	-5.082	-6.717	-1.396	1.32	99.78	-142.63
29	2jsa-6	LYS_A_29_C	ASP_A_30_N	-5.479	-6.318	-3.764	-6.46	-5.461	-3.518	1.33	79.31	138.86
30	2jsa-6	ASP_A_30_C	PHE_A_31_N	-5.492	-3.72	-4.915	-4.733	-3.249	-3.937	1.32	42.41	31.82
31	2jsa-6	PHE_A_31_C	ASP_A_32_N	-2.712	-3.29	-5.337	-2.538	-4.59	-5.151	1.32	81.93	-82.38
32	2jsa-6	ASP_A_32_C	ALA_A_33_N	-2.541	-5.299	-7.479	-3.864	-5.271	-7.412	1.32	87.10	178.79
33	2jsa-6	ALA_A_33_C	GLU_A_34_N	-4.237	-3.956	-9.426	-4.171	-2.824	-8.74	1.33	58.83	86.66
34	2jsa-6	GLU_A_34_C	CYS_A_35_N	-2.279	-1.616	-9.717	-1.472	-1.699	-8.671	1.32	37.80	-5.87
35	2jsa-6	CYS_A_35_C	LYS_A_36_N	0.288	-2.611	-10.056	-0.539	-3.628	-10.247	1.32	98.29	-129.12
36	2jsa-6	LYS_A_36_C	LYS_A_37_N	-0.438	-3.755	-12.676	-1.664	-3.431	-13.061	1.33	106.89	165.20
37	2jsa-6	LYS_A_37_C	LEU_A_38_N	-1.112	-1.37	-14.23	-0.897	-0.9	-13.01	1.32	22.96	65.42
38	2jsa-6	LEU_A_38_C	PHE_A_39_N	1.283	0.157	-13.243	1.925	-0.837	-12.648	1.32	63.31	-57.14
39	2jsa-6	PHE_A_39_C	HIS_A_40_N	3.459	-2.542	-13.535	2.633	-2.835	-14.529	1.33	138.60	-160.47
40	2jsa-6	HIS_A_40_C	THR_A_41_N	3.992	-4.329	-15.894	4.401	-3.28	-16.591	1.32	121.76	68.70
41	2jsa-6	THR_A_41_C	ILE_A_42_N	6.837	-3.426	-16.377	6.712	-2.744	-15.248	1.32	31.56	100.39
42	2jsa-6	ILE_A_42_C	PRO_A_43_N	8.156	-4.204	-13.943	9.487	-4.411	-13.755	1.36	82.05	-8.84
43	2jsa-6	PRO_A_43_C	PHE_A_44_N	9.703	-6.133	-12.013	10.598	-5.728	-11.124	1.32	47.86	24.35
44	2jsa-6	PHE_A_44_C	GLY_A_45_N	9.277	-5.244	-9.107	8.651	-4.435	-9.949	1.32	129.46	127.73
45	2jsa-6	GLY_A_45_C	THR_A_46_N	6.434	-4.493	-8.889	5.887	-5.379	-9.709	1.33	128.22	-121.69
46	2jsa-6	THR_A_46_C	ARG_A_47_N	5.341	-7.149	-8.104	6.63	-7.454	-8.159	1.33	92.38	-13.31
47	2jsa-6	ARG_A_47_C	GLU_A_48_N	7.136	-7.602	-5.768	7.573	-6.352	-5.724	1.32	88.10	70.73
48	2jsa-6	GLU_A_48_C	CYS_A_49_N	6.08	-5.265	-4.118	5.282	-5.004	-5.143	1.32	140.68	161.89
49	2jsa-6	CYS_A_49_C	ASP_A_50_N	3.223	-5.852	-4.2	3.506	-7.051	-4.685	1.32	111.49	-76.72
50	2jsa-6	ASP_A_50_C	HIS_A_51_N	3.617	-8.492	-2.729	4.753	-7.838	-2.538	1.32	81.71	29.93
51	2jsa-6	HIS_A_51_C	TYR_A_52_N	5.215	-6.763	-0.399	4.259	-5.954	-0.832	1.33	109.07	139.76
52	2jsa-6	TYR_A_52_C	VAL_A_53_N	2.519	-4.942	0.581	1.646	-5.654	-0.118	1.33	121.82	-140.80
53	2jsa-6	VAL_A_53_C	ASN_A_54_N	0.394	-6.775	1.642	1.585	-7.305	1.873	1.32	79.95	-23.99
54	2jsa-6	ASN_A_54_C	SER_A_55_N	3.196	-7.857	3.612	3.352	-6.627	4.077	1.32	69.44	82.77
55	2jsa-6	SER_A_55_C	LYS_A_56_N	4.485	-4.776	5.203	3.754	-3.958	4.459	1.33	124.14	131.79
56	2jsa-6	LYS_A_56_C	VAL_A_57_N	2.065	-2.223	4.701	1.249	-3.263	4.618	1.32	93.59	-128.12
57	2jsa-6	VAL_A_57_C	ASP_A_58_N	-0.858	-3.256	5.836	-0.181	-3.994	6.704	1.33	49.08	-47.47
58	2jsa-6	ASP_A_58_C	PRO_A_59_N	-0.46	-3.014	8.914	0.765	-2.442	8.778	1.36	95.74	25.03
59	2jsa-6	PRO_A_59_C	ILE_A_60_N	0.448	-0.013	8.996	0.602	0.181	7.695	1.32	169.22	51.56
60	2jsa-6	ILE_A_60_C	ILE_A_61_N	-1.468	1.432	7.427	-2.129	0.284	7.421	1.32	90.26	-119.93
61	2jsa-6	ILE_A_61_C	HIS_A_62_N	-3.69	0.436	9.282	-2.599	0.191	9.994	1.33	57.51	-12.66
62	2jsa-6	HIS_A_62_C	GLU_A_63_N	-2.652	1.83	11.796	-2.249	2.652	10.839	1.32	136.27	63.88
63	2jsa-6	GLU_A_63_C	LEU_A_64_N	-3.632	4.671	10.745	-4.177	4.266	9.606	1.33</		

65	2jsa-6	GLU_A_65_C	GLY_A_66_N	-7.065	2.969	12.97	-5.858	3.443	13.24	1.32	78.24	21.44
66	2jsa-6	GLY_A_66_C	GLY_A_67_N	-6.125	5.472	14.601	-5.907	6.219	13.528	1.33	144.05	73.73
67	2jsa-6	GLY_A_67_C	THR_A_68_N	-5.53	8.422	12.504	-4.322	7.934	12.265	1.32	100.40	-22.00
68	2jsa-6	THR_A_68_C	ALA_A_69_N	-4.004	8.747	9.976	-3.665	9.846	9.317	1.33	119.81	72.86
69	2jsa-6	ALA_A_69_C	PRO_A_70_N	-3.362	9.269	6.973	-3.889	9.215	5.721	1.36	157.07	-174.15
70	2jsa-6	PRO_A_70_C	LYS_A_71_N	-1.997	9.204	4.15	-1.83	10.422	4.643	1.32	68.15	82.19
71	2jsa-6	LYS_A_71_C	ASP_A_72_N	0.285	11.349	5.41	-0.097	10.738	6.523	1.33	32.92	-122.01
72	2jsa-6	ASP_A_72_C	VAL_A_73_N	1.438	9.406	7.861	0.745	8.365	7.421	1.33	109.38	-123.65
73	2jsa-6	VAL_A_73_C	CYS_A_74_N	2.622	6.967	6.757	2.616	7.524	5.555	1.32	155.14	90.62
74	2jsa-6	CYS_A_74_C	THR_A_75_N	4.767	8.602	5.304	5.143	8.398	6.558	1.32	18.84	-28.48
75	2jsa-6	THR_A_75_C	LYS_A_76_N	6.183	8.949	8.706	5.098	8.423	9.256	1.33	65.48	-154.14
76	2jsa-6	LYS_A_76_C	LEU_A_77_N	5.955	6.778	10.831	5.764	5.827	9.927	1.33	132.98	-101.36
77	2jsa-6	LEU_A_77_C	ASN_A_78_N	7.809	4.752	9.164	8.213	6.003	9.003	1.32	96.98	72.10
78	2jsa-6	ASN_A_78_C	GLU_A_79_N	9.331	5.677	6.866	8.106	5.358	6.474	1.33	107.21	-165.40
79	2jsa-6	GLU_A_79_C	CYS_A_80_N	8.432	5.638	4.064	7.742	6.744	3.829	1.32	100.22	121.96
80	2jsa-6	CYS_A_80_C	PRO_A_81_N	9.679	7.839	2.88	10.259	8.395	1.784	1.36	143.76	43.79
1	2jsa-7	ARG_A_1_C	SER_A_2_N	12.624	4.584	-0.334	12.748	5.903	-0.375	1.33	91.77	84.63
2	2jsa-7	SER_A_2_C	ALA_A_3_N	11.668	6.516	-2.48	10.656	5.776	-2.907	1.32	108.81	-143.82
3	2jsa-7	ALA_A_3_C	LEU_A_4_N	9.063	4.984	-4.568	8.962	3.988	-5.436	1.33	130.93	-95.79
4	2jsa-7	LEU_A_4_C	SER_A_5_N	7.067	2.772	-4.515	7.907	2.623	-3.501	1.33	40.08	-10.06
5	2jsa-7	SER_A_5_C	CYS_A_6_N	6.459	2.949	-1.559	6.828	4.218	-1.467	1.32	86.02	73.79
6	2jsa-7	CYS_A_6_C	GLN_A_7_N	4.619	5.197	-1.562	4.678	5.468	-2.857	1.32	167.91	77.72
7	2jsa-7	GLN_A_7_C	MET_A_8_N	2.573	4.308	-3.329	3.17	3.126	-3.362	1.32	91.43	-63.20
8	2jsa-7	MET_A_8_C	CYS_A_9_N	1.616	2.068	-1.778	2.169	2.837	-0.851	1.33	45.62	54.28
9	2jsa-7	CYS_A_9_C	GLU_A_10_N	0.191	3.816	0.138	0.254	4.722	-0.828	1.33	136.77	86.02
10	2jsa-7	GLU_A_10_C	LEU_A_11_N	-1.894	4.637	-2.0	-1.455	3.425	-2.302	1.32	103.19	-70.09
11	2jsa-7	LEU_A_11_C	VAL_A_12_N	-3.07	1.616	-2.088	-2.4	1.227	-1.012	1.33	35.75	-30.14
12	2jsa-7	VAL_A_12_C	VAL_A_13_N	-4.017	1.223	0.806	-3.553	2.39	1.228	1.32	71.43	68.32
13	2jsa-7	VAL_A_13_C	LYS_A_14_N	-5.57	3.749	1.158	-5.244	4.393	0.047	1.32	146.99	63.15
14	2jsa-7	LYS_A_14_C	LYS_A_15_N	-7.342	3.815	-1.043	-6.893	2.569	-1.062	1.32	90.82	-70.18
15	2jsa-7	LYS_A_15_C	TYR_A_16_N	-8.522	1.18	0.093	-7.776	1.324	1.178	1.32	35.00	10.93
16	2jsa-7	TYR_A_16_C	GLU_A_17_N	-9.191	2.286	2.943	-8.516	3.38	3.267	1.33	75.85	58.33
17	2jsa-7	GLU_A_17_C	GLY_A_18_N	-10.446	4.825	2.841	-10.351	4.397	1.591	1.32	160.67	-77.49
18	2jsa-7	GLY_A_18_C	SER_A_19_N	-11.927	3.208	0.125	-11.972	2.237	1.025	1.32	47.20	-92.65
19	2jsa-7	SER_A_19_C	ALA_A_20_N	-13.93	0.849	0.566	-14.572	1.258	1.649	1.32	35.10	147.50
20	2jsa-7	ALA_A_20_C	ASP_A_21_N	-16.523	-0.13	2.081	-15.585	-1.064	2.138	1.32	87.53	-44.88
21	2jsa-7	ASP_A_21_C	LYS_A_22_N	-15.285	-2.78	3.837	-14.302	-1.977	4.217	1.32	73.33	39.24
22	2jsa-7	LYS_A_22_C	ASP_A_23_N	-13.096	-3.625	5.541	-12.189	-3.936	4.627	1.32	133.63	-18.93
23	2jsa-7	ASP_A_23_C	ALA_A_24_N	-10.166	-5.17	4.077	-9.243	-5.375	5.005	1.32	45.53	-12.52
24	2jsa-7	ALA_A_24_C	ASN_A_25_N	-7.499	-6.395	3.649	-8.436	-7.316	3.484	1.32	97.16	-135.49
25	2jsa-7	ASN_A_25_C	VAL_A_26_N	-8.562	-7.898	1.125	-9.573	-7.046	1.04	1.32	93.68	139.88
26	2jsa-7	VAL_A_26_C	ILE_A_27_N	-9.147	-5.228	-0.52	-8.386	-4.822	0.485	1.32	40.64	28.08
27	2jsa-7	ILE_A_27_C	LYS_A_28_N	-6.159	-4.057	-0.128	-5.515	-4.901	0.666	1.33	53.21	-52.66
28	2jsa-7	LYS_A_28_C	LYS_A_29_N	-4.208	-5.982	-1.079	-5.239	-6.773	-1.334	1.32	101.10	-142.50
29	2jsa-7	LYS_A_29_C	ASP_A_30_N	-5.659	-6.346	-3.693	-6.593	-5.462	-3.374	1.32	76.07	136.58
30	2jsa-7	ASP_A_30_C	PHE_A_31_N	-5.684	-3.698	-4.781	-4.862	-3.289	-3.825	1.33	43.84	26.45
31	2jsa-7	PHE_A_31_C	ASP_A_32_N	-2.897	-3.313	-5.302	-2.64	-4.598	-5.106	1.33	81.49	-78.69
32	2jsa-7	ASP_A_32_C	ALA_A_33_N	-2.638	-5.164	-7.473	-3.957	-5.05	-7.428	1.32	88.05	175.06
33	2jsa-7	ALA_A_33_C	GLU_A_34_N	-4.127	-3.669	-9.423	-4.042	-2.528	-8.756	1.32	59.76	85.74
34	2jsa-7	GLU_A_34_C	CYS_A_35_N	-1.977	-1.486	-9.559	-1.303	-1.747	-8.447	1.33	33.02	-21.17
35	2jsa-7	CYS_A_35_C	LYS_A_36_N	0.515	-2.692	-9.733	-0.399	-3.556	-10.151	1.33	108.38	-136.61
36	2jsa-7	LYS_A_36_C	LYS_A_37_N	-0.196	-3.461	-12.573	-1.402	-3.088	-12.977	1.33	107.75	162.81
37	2jsa-7	LYS_A_37_C	LEU_A_38_N	-0.815	-0.919	-13.912	-0.479	-0.676	-12.653	1.33	18.23	35.87
38	2jsa-7	LEU_A_38_C	PHE_A_39_N	1.719	0.368	-12.652	2.411	-0.417	-11.839	1.33	52.16	-48.60
39	2jsa-7	PHE_A_39_C	HIS_A_40_N	4.037	-1.93	-12.894	3.076	-2.192	-13.768	1.33	131.27	-164.75
40	2jsa-7	HIS_A_40_C	THR_A_41_N	4.519	-3.428	-15.295	4.832	-2.375	-16.036	1.33	124.00	73.45
41	2jsa-7	THR_A_41_C	ILE_A_42_N	7.176	-1.694	-15.82	7.577	-2.477	-14.829	1.33	41.60	-62.88
42	2jsa-7	ILE_A_42_C	PRO_A_43_N	9.386	-3.241	-13.392	10.718	-3.021	-13.227	1.36	83.03	9.38
43	2jsa-7	PRO_A_43_C	PHE_A_44_N	11.418	-4.326	-11.263	10.886	-5.497	-10.948	1.32	76.24	-114.43
44	2jsa-7	PHE_A_44_C	GLY_A_45_N	9.452	-5.119	-8.988	8.844	-4.301	-9.835	1.33	129.73	126.62
45	2jsa-7	GLY_A_45_C	THR_A_46_N	6.569	-4.437	-8.913	6.074	-5.277	-9.811	1.33	132.65	-120.51
46	2jsa-7	THR_A_46_C	ARG_A_47_N	5.468	-7.153	-8.357	6.775	-7.369	-8.311	1.33	88.01	-9.38
47	2jsa-7	ARG_A_47_C	GLU_A_48_N	7.206	-7.64	-5.916	7.497	-6.35	-5.835	1.32	86.49	77.29
48	2jsa-7	GLU_A_48_C	CYS_A_49_N	5.934	-5.415	-4.199	5.121	-5.206	-5.223	1.32	140.66	165.58
49	2jsa-7	CYS_A_49_C	ASP_A_50_N	3.16	-6.097	-4.125	3.546	-7.319	-4.462	1.33	104.73	-72.47
50	2jsa-7	ASP_A_50_C	HIS_A_51_N	3.903	-8.556	-2.397	5.091	-7.97	-2.429	1.33	91.38	26.26
51	2jsa-7	HIS_A_51_C	TYR_A_52_N	5.656	-6.733	-0.405	4.53	-6.102	-0.707	1.33	103.17	150.73
52	2jsa-7	TYR_A_52_C	VAL_A_53_N	2.797	-5.15	0.754	1.878	-5.798	0.054	1.32	121.90	-144.81
53	2jsa-7	VAL_A_53_C	ASN_A_54_N	0.688	-7.302	1.553	1.616	-7.199	2.493	1.32	44.81	6.33
54	2jsa-7	ASN_A_54_C	SER_A_55_N	3.035	-7.924	4.332	3.1	-6.657	4.714	1.32	73.24	87.06
55	2jsa-7	SER_A_55_C	LYS_A_56_N	4.045	-4.679	5.794	3.649	-3.98	4.74	1.33	142.68	119.53
56	2jsa-7	LYS_A_56_C	VAL_A_57_N	1.986	-2.204	4.692	1.189	-3.248	4.515	1.33	97.67	-127.36
57	2jsa-7	VAL_A_57_C	ASP_A_58_N	-0.921	-3.372	5.72	-0.227	-4.15	6.537	1.32	51.92	-48.27
58	2jsa-7	ASP_A_58_C	PRO_A_59_N	-0.572	-3.331	8.803	0.638	-2.714	8.741	1.36	92.61	27.02
59	2jsa-7	PRO_A_59_C	ILE_A_60_N	0.235	-0.315	9.097	0.412	-0.042	7.813	1.32	165.78	57.04
60	2jsa-7	ILE_A_60_C	ILE_A_61_N	-1.68	1.182	7.594	-2.339	0.042	7.454	1.32	96.07	-120.03
61	2jsa-7	ILE_A_61_C	HIS_A_62_N	-3.926	0.103	9.299	-2.858	-0.204	10.021	1.33	56.99	-16.04
62	2jsa-7	HIS_A_62_C	GLU_A_63_N	-2.891	1.37	11.882	-2.525	2.219	10.934	1.32	135.72	66.68
63	2jsa-7	GLU_A_63_C	LEU_A_64_N	-3.873	4.262	10.962	-4.442	3.956	9.804	1.33	150.84	-151.73
64	2jsa-7	LEU_A_64_C	GLU_A_65_N	-6.796	3.883	10.418	-6.619	2.606	10.724	1.33	76.65	-82.11
65	2jsa-7	GLU_A_65_C	GLY_A_66_N	-7.459	2.537	13.022	-6.249	2.917	13.407	1.33	73.11	17.43
66	2jsa-7	GLY_A_66_C	GLY_A_67_N	-6.648	4.919	14.777	-6.236	5.757	13.837	1.32	135.19	63.82
67	2jsa-7	GLY_A_67_C	THR_A_68_N	-5.728	8.045	13.095	-5.16	7.549	12.005	1.33	145.32	-41.13
68	2jsa-7	THR_A_68_C	ALA_A_69_N	-4.629	8.472	9.799	-4.397	9.662	9.265	1.32	113.77	78.97
69	2jsa-7	ALA_A_69_C	PRO_A_70_N	-3.892	9.127	6.946	-4.356	9.028	5.671	1.36	159.59	-167.96
70	2jsa-7	PRO_A_70_C	LYS_A_71_N	-2.392	9.047	4.193	-2.341	10.313	4.579	1.32	73.06	87.69
71	2jsa-7	LYS_A_71_C	ASP_A_72_N	-0.275	11.309	5.394	-0.665	10.691	6.499	1.32	33.48	-122.25
72	2jsa-7	ASP_A_72_C	VAL_A_73_N	0.885	9.416	7.875	0.203	8.341	7.51	1.32	106.00	-122.39
73	2jsa-7	VAL_A_73_C	CYS_A_74_N	2.15	7.005	6.917	2.138	7.409	5.656	1.32	162.23	91.70
74	2jsa-7	CYS_A_74_C	THR_A_75_N	4.143	8.703	5.273	4.604	8.701	6.515	1.32	20.36	-0.25
75	2jsa-7	THR_A_75_C	LYS_A_76_N	6.089	9.429	8.322	5.297	9.06	9.317	1.32	41.29	-155.02
76	2jsa-7	LYS_A_76_C	LEU_A_77_N	6.268	7.19	10.534	5.744	6.501				

78	2jsa-7	ASN_A_78_C	GLU_A_79_N	8.958	5.506	6.062	7.734	5.616	5.565	1.33	112.02	174.86
79	2jsa-7	GLU_A_79_C	CYS_A_80_N	6.872	6.152	3.337	7.662	7.209	3.21	1.33	95.50	53.23
80	2jsa-7	CYS_A_80_C	PRO_A_81_N	8.211	9.503	2.678	8.347	10.413	1.677	1.36	137.41	81.50
1	2jsa-8	ARG_A_1_C	SER_A_2_N	13.936	6.737	0.31	13.944	5.905	-0.721	1.32	141.10	-89.45
2	2jsa-8	SER_A_2_C	ALA_A_3_N	12.039	6.029	-2.247	10.732	5.833	-2.349	1.33	94.41	-171.47
3	2jsa-8	ALA_A_3_C	LEU_A_4_N	8.64	5.77	-3.589	8.78	4.569	-4.131	1.33	114.14	-83.35
4	2jsa-8	LEU_A_4_C	SER_A_5_N	6.948	3.349	-3.096	7.732	3.395	-2.029	1.32	36.35	-3.36
5	2jsa-8	SER_A_5_C	CYS_A_6_N	6.038	3.954	-0.358	6.121	5.194	-0.818	1.33	110.31	86.17
6	2jsa-8	CYS_A_6_C	GLN_A_7_N	3.873	5.82	-1.455	4.078	5.994	-2.752	1.32	168.29	40.32
7	2jsa-8	GLN_A_7_C	MET_A_8_N	2.27	4.444	-3.322	3.018	3.358	-3.194	1.32	84.46	-55.44
8	2jsa-8	MET_A_8_C	CYS_A_9_N	1.563	2.226	-1.567	2.05	3.037	-0.64	1.32	45.58	59.02
9	2jsa-8	CYS_A_9_C	GLU_A_10_N	0.034	4.006	0.28	0.127	4.904	-0.69	1.33	137.05	84.09
10	2jsa-8	GLU_A_10_C	LEU_A_11_N	-1.988	4.811	-1.919	-1.553	3.586	-2.175	1.32	101.14	-70.45
11	2jsa-8	LEU_A_11_C	VAL_A_12_N	-3.195	1.8	-1.983	-2.523	1.274	-0.969	1.33	40.08	-38.05
12	2jsa-8	VAL_A_12_C	VAL_A_13_N	-4.221	1.285	0.774	-3.797	2.482	1.154	1.33	73.34	70.49
13	2jsa-8	VAL_A_13_C	LYS_A_14_N	-5.848	3.779	0.986	-5.516	4.359	-0.158	1.32	149.71	60.21
14	2jsa-8	LYS_A_14_C	LYS_A_15_N	-7.589	3.683	-1.24	-7.132	2.448	-1.098	1.32	83.85	-69.69
15	2jsa-8	LYS_A_15_C	TYR_A_16_N	-8.752	1.111	0.129	-8.009	1.304	1.209	1.33	35.40	14.56
16	2jsa-8	TYR_A_16_C	GLU_A_17_N	-9.514	2.313	2.871	-8.93	3.497	2.98	1.32	85.28	63.75
17	2jsa-8	GLU_A_17_C	GLY_A_18_N	-10.963	4.743	2.424	-10.802	4.332	1.175	1.32	160.54	-68.61
18	2jsa-8	GLY_A_18_C	SER_A_19_N	-12.277	2.903	-0.178	-12.445	2.054	0.826	1.33	40.76	-101.19
19	2jsa-8	SER_A_19_C	ALA_A_20_N	-14.275	0.434	0.888	-14.708	1.001	2.005	1.33	32.57	127.37
20	2jsa-8	ALA_A_20_C	ASP_A_21_N	-16.376	-0.598	2.767	-15.305	-1.375	2.83	1.32	87.27	-35.96
21	2jsa-8	ASP_A_21_C	LYS_A_22_N	-14.639	-3.088	4.426	-13.856	-2.105	4.845	1.32	71.56	51.46
22	2jsa-8	LYS_A_22_C	ASP_A_23_N	-12.42	-3.643	6.067	-11.933	-4.054	4.906	1.32	151.24	-40.16
23	2jsa-8	ASP_A_23_C	ALA_A_24_N	-9.869	-5.178	4.274	-8.926	-5.56	5.122	1.32	50.19	-22.05
24	2jsa-8	ALA_A_24_C	ASN_A_25_N	-7.163	-6.523	3.749	-8.149	-7.353	3.443	1.32	103.36	-139.91
25	2jsa-8	ASN_A_25_C	VAL_A_26_N	-8.272	-7.908	1.077	-9.396	-7.213	0.978	1.33	94.28	148.27
26	2jsa-8	VAL_A_26_C	ILE_A_27_N	-9.114	-5.326	-0.533	-8.399	-4.883	0.49	1.32	39.43	31.78
27	2jsa-8	ILE_A_27_C	LYS_A_28_N	-6.257	-3.898	-0.112	-5.58	-4.818	0.56	1.33	59.53	-53.65
28	2jsa-8	LYS_A_28_C	LYS_A_29_N	-4.241	-5.807	-1.215	-5.327	-6.51	-1.499	1.32	102.38	-147.08
29	2jsa-8	LYS_A_29_C	ASP_A_30_N	-5.664	-6.105	-3.874	-6.614	-5.213	-3.632	1.33	79.48	136.80
30	2jsa-8	ASP_A_30_C	PHE_A_31_N	-5.591	-3.466	-4.982	-4.807	-3.117	-3.973	1.32	40.38	24.00
31	2jsa-8	PHE_A_31_C	ASP_A_32_N	-2.736	-3.183	-5.295	-2.532	-4.473	-5.076	1.32	80.48	-81.01
32	2jsa-8	ASP_A_32_C	ALA_A_33_N	-2.443	-5.176	-7.404	-3.709	-4.785	-7.394	1.33	89.57	162.84
33	2jsa-8	ALA_A_33_C	GLU_A_34_N	-3.959	-3.399	-9.378	-4.021	-2.268	-8.69	1.33	58.73	93.14
34	2jsa-8	GLU_A_34_C	CYS_A_35_N	-2.067	-0.86	-9.127	-1.417	-1.978	-8.84	1.32	77.49	-59.83
35	2jsa-8	CYS_A_35_C	LYS_A_36_N	0.633	-2.879	-9.754	-0.016	-4.013	-9.969	1.32	99.34	-119.78
36	2jsa-8	LYS_A_36_C	LYS_A_37_N	0.376	-4.316	-12.352	-0.823	-3.871	-12.701	1.33	105.26	159.64
37	2jsa-8	LYS_A_37_C	LEU_A_38_N	-0.321	-1.881	-14.01	-0.282	-1.25	-12.845	1.33	28.49	86.46
38	2jsa-8	LEU_A_38_C	PHE_A_39_N	1.84	-0.088	-13.107	2.524	-0.992	-12.421	1.33	58.82	-52.89
39	2jsa-8	PHE_A_39_C	HIS_A_40_N	4.19	-2.69	-13.041	3.509	-3.139	-14.086	1.33	142.03	-146.60
40	2jsa-8	HIS_A_40_C	THR_A_41_N	5.055	-4.719	-15.114	5.357	-3.943	-16.144	1.32	141.05	68.74
41	2jsa-8	THR_A_41_C	ILE_A_42_N	7.777	-3.902	-15.759	7.581	-2.974	-14.834	1.32	45.72	101.93
42	2jsa-8	ILE_A_42_C	PRO_A_43_N	9.152	-4.08	-13.341	10.486	-4.061	-13.073	1.36	78.64	0.82
43	2jsa-8	PRO_A_43_C	PHE_A_44_N	10.853	-5.583	-11.177	10.969	-4.563	-10.34	1.32	50.81	83.51
44	2jsa-8	PHE_A_44_C	GLY_A_45_N	9.376	-4.04	-8.541	8.46	-4.016	-9.498	1.32	136.24	178.50
45	2jsa-8	GLY_A_45_C	THR_A_46_N	6.175	-4.404	-8.676	5.694	-5.295	-9.53	1.32	130.15	-118.36
46	2jsa-8	THR_A_46_C	ARG_A_47_N	5.339	-7.143	-7.961	6.644	-7.351	-8.041	1.32	93.46	-9.06
47	2jsa-8	ARG_A_47_C	GLU_A_48_N	7.191	-7.465	-5.656	7.461	-6.169	-5.627	1.32	88.75	78.23
48	2jsa-8	GLU_A_48_C	CYS_A_49_N	5.895	-5.27	-3.974	5.043	-5.098	-4.974	1.32	139.00	168.59
49	2jsa-8	CYS_A_49_C	ASP_A_50_N	3.172	-6.079	-3.797	3.274	-7.298	-4.308	1.33	112.67	-85.22
50	2jsa-8	ASP_A_50_C	HIS_A_51_N	3.648	-8.476	-2.212	4.825	-7.867	-2.238	1.33	91.12	27.36
51	2jsa-8	HIS_A_51_C	TYR_A_52_N	5.281	-6.563	-0.229	4.184	-5.938	-0.631	1.33	107.66	150.33
52	2jsa-8	TYR_A_52_C	VAL_A_53_N	2.356	-5.01	0.727	1.453	-5.6	-0.042	1.32	125.49	-146.84
53	2jsa-8	VAL_A_53_C	ASN_A_54_N	0.253	-6.769	1.722	1.394	-7.431	1.836	1.32	85.06	-30.12
54	2jsa-8	ASN_A_54_C	SER_A_55_N	3.063	-8.017	3.508	3.294	-6.764	3.872	1.33	74.06	79.55
55	2jsa-8	SER_A_55_C	LYS_A_56_N	4.526	-4.921	4.903	3.846	-4.084	4.133	1.33	125.53	129.09
56	2jsa-8	LYS_A_56_C	VAL_A_57_N	2.215	-2.324	4.541	1.389	-3.359	4.573	1.32	88.62	-128.59
57	2jsa-8	VAL_A_57_C	ASP_A_58_N	-0.533	-3.279	6.064	-0.047	-4.312	6.737	1.33	59.48	-64.80
58	2jsa-8	ASP_A_58_C	PRO_A_59_N	-0.198	-3.261	8.927	0.979	-2.625	8.684	1.36	100.29	28.38
59	2jsa-8	PRO_A_59_C	ILE_A_60_N	0.526	-0.212	8.817	0.664	-0.01	7.514	1.33	169.37	55.66
60	2jsa-8	ILE_A_60_C	ILE_A_61_N	-1.488	1.107	7.315	-2.172	-0.006	7.091	1.33	99.73	-121.57
61	2jsa-8	ILE_A_61_C	HIS_A_62_N	-3.69	0.115	8.988	-2.582	-0.102	9.682	1.33	58.42	-11.08
62	2jsa-8	HIS_A_62_C	GLU_A_63_N	-2.777	1.558	11.456	-1.968	2.402	10.834	1.32	118.01	46.21
63	2jsa-8	GLU_A_63_C	LEU_A_64_N	-3.496	4.314	10.794	-4.02	3.916	9.644	1.32	150.22	-142.78
64	2jsa-8	LEU_A_64_C	GLU_A_65_N	-6.355	3.774	10.312	-6.097	2.554	10.763	1.33	70.12	-78.06
65	2jsa-8	GLU_A_65_C	GLY_A_66_N	-7.039	2.81	13.009	-5.876	3.109	13.568	1.32	65.04	14.42
66	2jsa-8	GLY_A_66_C	GLY_A_67_N	-6.505	5.281	14.533	-6.209	5.879	13.387	1.33	149.79	63.67
67	2jsa-8	GLY_A_67_C	THR_A_68_N	-5.743	8.108	12.463	-4.931	7.564	11.568	1.33	132.48	-33.82
68	2jsa-8	THR_A_68_C	ALA_A_69_N	-4.193	8.559	9.454	-3.946	9.778	8.998	1.32	110.13	78.55
69	2jsa-8	ALA_A_69_C	PRO_A_70_N	-3.405	9.175	6.703	-3.829	9.127	5.412	1.36	161.71	-173.54
70	2jsa-8	PRO_A_70_C	LYS_A_71_N	-1.825	8.858	4.013	-1.618	10.112	4.387	1.32	73.60	80.63
71	2jsa-8	LYS_A_71_C	ASP_A_72_N	0.551	10.784	5.263	-0.047	10.581	6.427	1.32	28.48	-161.25
72	2jsa-8	ASP_A_72_C	VAL_A_73_N	1.382	9.172	7.804	0.735	8.173	7.223	1.32	116.02	-122.93
73	2jsa-8	VAL_A_73_C	CYS_A_74_N	2.551	6.738	6.471	2.498	7.284	5.265	1.32	155.54	95.54
74	2jsa-8	CYS_A_74_C	THR_A_75_N	4.65	8.326	4.909	5.121	8.096	6.126	1.33	23.30	-26.03
75	2jsa-8	THR_A_75_C	LYS_A_76_N	6.459	8.501	8.138	5.437	8.214	8.933	1.33	53.17	-164.31
76	2jsa-8	LYS_A_76_C	LEU_A_77_N	6.463	6.429	10.231	6.062	5.558	9.316	1.33	133.66	-114.72
77	2jsa-8	LEU_A_77_C	ASN_A_78_N	7.799	4.409	8.058	8.4	5.588	7.994	1.32	92.77	62.99
78	2jsa-8	ASN_A_78_C	GLU_A_79_N	9.009	5.243	5.664	7.706	5.258	5.426	1.32	100.35	179.34
79	2jsa-8	GLU_A_79_C	CYS_A_80_N	7.317	5.726	3.054	8.007	6.815	3.361	1.33	76.61	57.64
80	2jsa-8	CYS_A_80_C	PRO_A_81_N	9.366	8.756	2.88	10.274	9.118	1.935	1.36	134.03	21.74
1	2jsa-9	ARG_A_1_C	SER_A_2_N	12.882	2.023	-2.079	12.587	3.144	-2.721	1.33	118.98	104.74
2	2jsa-9	SER_A_2_C	ALA_A_3_N	12.181	5.545	-2.923	10.919	5.283	-3.231	1.33	103.44	-168.27
3	2jsa-9	ALA_A_3_C	LEU_A_4_N	8.803	5.581	-4.395	8.934	4.579	-5.252	1.32	130.30	-82.55
4	2jsa-9	LEU_A_4_C	SER_A_5_N	7.032	3.227	-4.561	7.763	3.056	-3.47	1.32	34.53	-13.17
5	2jsa-9	SER_A_5_C	CYS_A_6_N	6.198	3.442	-1.633	6.537	4.721	-1.715	1.33	93.55	75.16
6	2jsa-9	CYS_A_6_C	GLN_A_7_N	4.32	5.679	-1.832	4.341	5.816	-3.15	1.33	174.00	81.29
7	2jsa-9	GLN_A_7_C	MET_A_8_N	2.255	4.579	-3.484	2.888	3.416	-3.431	1.33	87.71	-61.44
8	2jsa-9	MET_A_8_C	CYS_A_9_N	1.375	2.442	-1.756	1.95	3.223	-0.855	1.32	47.11	53.64
9	2jsa-9	CYS_A_9_C	GLU_A_10_N	-0.043	4.224	0.08	-0.02	5.022	-0.977	1.32	142.94	88.35

11	2jsa-9	LEU_A_11_C	VAL_A_12_N	-3.269	1.797	-2.132	-2.586	1.333	-1.095	1.33	38.53	-34.19
12	2jsa-9	VAL_A_12_C	VAL_A_13_N	-4.29	1.395	0.642	-3.856	2.565	1.086	1.32	70.41	69.65
13	2jsa-9	VAL_A_13_C	LYS_A_14_N	-5.932	3.818	0.866	-5.605	4.362	-0.298	1.33	151.40	58.99
14	2jsa-9	LYS_A_14_C	LYS_A_15_N	-7.658	3.609	-1.365	-7.176	2.388	-1.185	1.32	82.19	-68.46
15	2jsa-9	LYS_A_15_C	TYR_A_16_N	-8.818	1.091	0.058	-8.109	1.324	1.153	1.33	34.28	18.19
16	2jsa-9	TYR_A_16_C	GLU_A_17_N	-9.616	2.444	2.742	-8.981	3.603	2.843	1.33	85.63	61.28
17	2jsa-9	GLU_A_17_C	GLY_A_18_N	-11.009	4.86	2.296	-10.91	4.413	1.053	1.32	159.78	-77.51
18	2jsa-9	GLY_A_18_C	SER_A_19_N	-12.418	2.942	-0.215	-12.364	2.065	0.777	1.33	41.53	-86.48
19	2jsa-9	SER_A_19_C	ALA_A_20_N	-14.179	0.485	0.346	-14.941	1.039	1.277	1.32	45.34	143.98
20	2jsa-9	ALA_A_20_C	ASP_A_21_N	-16.845	-0.366	1.844	-15.879	-1.247	2.062	1.33	80.53	-42.37
21	2jsa-9	ASP_A_21_C	LYS_A_22_N	-15.468	-2.634	4.018	-14.354	-1.924	4.126	1.33	85.33	32.51
22	2jsa-9	LYS_A_22_C	ASP_A_23_N	-13.008	-3.316	5.599	-12.163	-3.739	4.672	1.32	134.45	-26.59
23	2jsa-9	ASP_A_23_C	ALA_A_24_N	-10.106	-4.964	4.233	-9.157	-5.192	5.129	1.32	47.45	-13.51
24	2jsa-9	ALA_A_24_C	ASN_A_25_N	-7.464	-6.243	3.731	-8.442	-7.121	3.56	1.33	97.41	-138.08
25	2jsa-9	ASN_A_25_C	VAL_A_26_N	-8.587	-7.701	1.201	-9.617	-6.874	1.099	1.32	94.42	141.24
26	2jsa-9	VAL_A_26_C	ILE_A_27_N	-9.136	-5.076	-0.469	-8.363	-4.689	0.535	1.32	40.73	26.59
27	2jsa-9	ILE_A_27_C	LYS_A_28_N	-6.115	-3.993	-0.082	-5.449	-4.765	0.764	1.32	50.32	-49.22
28	2jsa-9	LYS_A_28_C	LYS_A_29_N	-4.167	-5.91	-0.959	-5.255	-6.618	-1.221	1.32	101.41	-146.95
29	2jsa-9	LYS_A_29_C	ASP_A_30_N	-5.639	-6.224	-3.592	-6.654	-5.397	-3.38	1.33	80.80	140.83
30	2jsa-9	ASP_A_30_C	PHE_A_31_N	-5.676	-3.681	-4.804	-4.887	-3.241	-3.834	1.33	42.96	29.15
31	2jsa-9	PHE_A_31_C	ASP_A_32_N	-2.877	-3.33	-5.248	-2.513	-4.568	-4.947	1.33	76.87	-73.62
32	2jsa-9	ASP_A_32_C	ALA_A_33_N	-2.454	-5.255	-7.281	-3.772	-5.114	-7.259	1.33	89.05	173.89
33	2jsa-9	ALA_A_33_C	GLU_A_34_N	-4.05	-3.732	-9.243	-4.135	-2.599	-8.562	1.32	59.06	94.29
34	2jsa-9	GLU_A_34_C	CYS_A_35_N	-2.224	-1.107	-8.9	-1.502	-2.209	-8.753	1.33	83.63	-56.77
35	2jsa-9	CYS_A_35_C	LYS_A_36_N	0.644	-2.888	-9.636	0.27	-4.148	-9.798	1.32	97.03	-106.53
36	2jsa-9	LYS_A_36_C	LYS_A_37_N	0.484	-4.427	-12.206	-0.748	-3.946	-12.294	1.33	93.81	158.67
37	2jsa-9	LYS_A_37_C	LEU_A_38_N	-0.647	-1.998	-13.749	-0.61	-1.235	-12.666	1.33	35.20	87.22
38	2jsa-9	LEU_A_38_C	PHE_A_39_N	1.45	0.037	-12.91	2.101	-0.636	-11.972	1.33	44.95	-45.95
39	2jsa-9	PHE_A_39_C	HIS_A_40_N	3.937	-2.01	-12.859	3.041	-2.384	-13.761	1.33	132.89	-157.34
40	2jsa-9	HIS_A_40_C	THR_A_41_N	4.568	-3.311	-15.421	4.981	-2.054	-15.483	1.32	92.68	71.81
41	2jsa-9	THR_A_41_C	ILE_A_42_N	7.408	-1.78	-15.287	7.333	-1.038	-14.191	1.33	34.23	95.77
42	2jsa-9	ILE_A_42_C	PRO_A_43_N	9.151	-2.36	-13.261	10.505	-2.277	-13.159	1.36	85.70	3.51
43	2jsa-9	PRO_A_43_C	PHE_A_44_N	11.242	-4.222	-11.847	10.463	-5.294	-11.86	1.33	90.56	-126.01
44	2jsa-9	PHE_A_44_C	GLY_A_45_N	9.353	-5.411	-9.669	8.93	-4.211	-10.038	1.32	106.17	109.42
45	2jsa-9	GLY_A_45_C	THR_A_46_N	6.903	-4.309	-8.65	6.366	-5.139	-9.532	1.32	131.74	-122.90
46	2jsa-9	THR_A_46_C	ARG_A_47_N	5.643	-6.82	-7.903	6.848	-7.372	-7.921	1.33	90.78	-24.61
47	2jsa-9	ARG_A_47_C	GLU_A_48_N	7.191	-7.358	-5.496	7.466	-6.067	-5.6	1.32	94.51	77.97
48	2jsa-9	GLU_A_48_C	CYS_A_49_N	5.911	-4.943	-4.078	5.079	-4.872	-5.107	1.33	140.94	175.12
49	2jsa-9	CYS_A_49_C	ASP_A_50_N	3.126	-5.726	-3.965	3.304	-6.97	-4.385	1.32	108.48	-81.86
50	2jsa-9	ASP_A_50_C	HIS_A_51_N	3.554	-8.083	-2.235	4.754	-7.52	-2.234	1.33	89.96	25.13
51	2jsa-9	HIS_A_51_C	TYR_A_52_N	5.064	-6.242	-0.181	4.076	-5.54	-0.718	1.33	113.90	144.61
52	2jsa-9	TYR_A_52_C	VAL_A_53_N	2.193	-4.725	0.636	1.493	-5.679	0.039	1.33	116.77	-126.27
53	2jsa-9	VAL_A_53_C	ASN_A_54_N	0.427	-7.257	1.555	1.538	-7.175	2.272	1.32	57.23	4.22
54	2jsa-9	ASN_A_54_C	SER_A_55_N	3.193	-7.829	3.932	3.282	-6.571	4.339	1.33	72.11	85.95
55	2jsa-9	SER_A_55_C	LYS_A_56_N	4.419	-4.558	5.13	3.765	-3.939	4.158	1.33	137.19	136.57
56	2jsa-9	LYS_A_56_C	VAL_A_57_N	2.15	-2.122	4.259	1.312	-3.148	4.223	1.33	91.56	-129.24
57	2jsa-9	VAL_A_57_C	ASP_A_58_N	-0.573	-3.172	5.761	-0.108	-4.277	6.326	1.33	64.77	-67.18
58	2jsa-9	ASP_A_58_C	PRO_A_59_N	-0.158	-3.427	8.605	1.028	-2.803	8.37	1.36	99.95	27.75
59	2jsa-9	PRO_A_59_C	ILE_A_60_N	0.66	-0.402	8.751	0.741	-0.087	7.465	1.33	165.81	75.58
60	2jsa-9	ILE_A_60_C	ILE_A_61_N	-1.377	1.111	7.483	-2.112	0.046	7.198	1.33	102.42	-124.61
61	2jsa-9	ILE_A_61_C	HIS_A_62_N	-3.522	0.009	9.181	-2.386	-0.318	9.782	1.33	63.05	-16.06
62	2jsa-9	HIS_A_62_C	GLU_A_63_N	-2.428	1.136	11.738	-2.003	2.074	10.903	1.33	129.04	65.63
63	2jsa-9	GLU_A_63_C	LEU_A_64_N	-3.483	4.024	10.94	-3.863	3.898	9.677	1.32	162.41	-161.66
64	2jsa-9	LEU_A_64_C	GLU_A_65_N	-6.246	3.801	10.157	-6.138	2.506	10.415	1.32	78.77	-85.23
65	2jsa-9	GLU_A_65_C	GLY_A_66_N	-7.063	2.436	12.681	-5.859	2.775	13.117	1.32	70.78	15.73
66	2jsa-9	GLY_A_66_C	GLY_A_67_N	-6.346	4.732	14.523	-6.451	5.379	13.372	1.32	150.34	99.22
67	2jsa-9	GLY_A_67_C	THR_A_68_N	-6.156	7.69	12.583	-4.986	7.201	12.199	1.32	106.85	-22.68
68	2jsa-9	THR_A_68_C	ALA_A_69_N	-4.508	8.344	10.085	-3.97	9.42	9.531	1.32	114.73	63.43
69	2jsa-9	ALA_A_69_C	PRO_A_70_N	-3.471	9.094	7.172	-3.93	9.123	5.893	1.36	160.22	176.38
70	2jsa-9	PRO_A_70_C	LYS_A_71_N	-1.96	9.256	4.428	-1.779	10.383	5.102	1.33	59.44	80.88
71	2jsa-9	LYS_A_71_C	ASP_A_72_N	0.319	11.197	6.028	-0.144	10.559	7.093	1.33	36.51	-125.97
72	2jsa-9	ASP_A_72_C	VAL_A_73_N	1.312	9.057	8.338	0.59	8.08	7.811	1.32	113.45	-126.46
73	2jsa-9	VAL_A_73_C	CYS_A_74_N	2.397	6.675	6.987	2.339	7.217	5.78	1.32	155.70	96.11
74	2jsa-9	CYS_A_74_C	THR_A_75_N	4.438	8.36	5.408	5.042	8.116	6.562	1.33	29.44	-22.00
75	2jsa-9	THR_A_75_C	LYS_A_76_N	6.414	8.613	8.53	5.471	8.054	9.274	1.32	55.84	-149.34
76	2jsa-9	LYS_A_76_C	LEU_A_77_N	6.536	6.243	10.501	6.037	5.371	9.64	1.32	130.60	-119.78
77	2jsa-9	LEU_A_77_C	ASN_A_78_N	7.753	4.208	8.365	8.152	5.447	8.12	1.32	100.66	72.15
78	2jsa-9	ASN_A_78_C	GLU_A_79_N	8.832	4.996	5.828	7.546	5.007	5.507	1.33	104.01	179.51
79	2jsa-9	GLU_A_79_C	CYS_A_80_N	6.55	5.398	3.304	7.471	6.219	2.82	1.33	111.42	41.71
80	2jsa-9	CYS_A_80_C	PRO_A_81_N	8.39	8.036	1.516	9.359	7.309	0.899	1.36	116.99	-36.88
1	2jsa-10	ARG_A_1_C	SER_A_2_N	14.79	3.756	0.449	13.59	4.266	0.68	1.32	79.95	156.97
2	2jsa-10	SER_A_2_C	ALA_A_3_N	13.051	5.283	-1.475	11.816	5.134	-1.93	1.32	110.09	-173.12
3	2jsa-10	ALA_A_3_C	LEU_A_4_N	10.067	5.114	-3.622	9.602	4.445	-4.668	1.33	142.08	-124.80
4	2jsa-10	LEU_A_4_C	SER_A_5_N	7.344	3.87	-3.969	8.02	3.197	-3.049	1.33	46.04	-44.87
5	2jsa-10	SER_A_5_C	CYS_A_6_N	6.257	3.433	-1.373	6.551	4.725	-1.386	1.33	90.56	77.18
6	2jsa-10	CYS_A_6_C	GLN_A_7_N	4.295	5.569	-1.606	4.348	5.861	-2.898	1.33	167.06	79.71
7	2jsa-10	GLN_A_7_C	MET_A_8_N	2.337	4.542	-3.355	3.007	3.399	-3.344	1.32	89.52	-59.62
8	2jsa-10	MET_A_8_C	CYS_A_9_N	1.467	2.316	-1.763	1.948	3.132	-0.838	1.32	45.68	59.48
9	2jsa-10	CYS_A_9_C	GLU_A_10_N	-0.111	4.055	0.032	-0.035	4.977	-0.917	1.33	135.73	85.29
10	2jsa-10	GLU_A_10_C	LEU_A_11_N	-2.149	4.757	-2.13	-1.663	3.547	-2.359	1.32	99.96	-68.12
11	2jsa-10	LEU_A_11_C	VAL_A_12_N	-3.194	1.677	-2.077	-2.512	1.358	-0.987	1.32	34.63	-25.07
12	2jsa-10	VAL_A_12_C	VAL_A_13_N	-4.117	1.363	0.842	-3.719	2.589	1.147	1.32	76.69	72.01
13	2jsa-10	VAL_A_13_C	LYS_A_14_N	-5.811	3.828	1.058	-5.556	4.43	-0.096	1.33	150.47	67.04
14	2jsa-10	LYS_A_14_C	LYS_A_15_N	-7.62	3.648	-1.121	-7.081	2.441	-1.024	1.33	85.80	-65.94
15	2jsa-10	LYS_A_15_C	TYR_A_16_N	-8.58	0.983	0.221	-7.858	1.304	1.285	1.33	36.60	23.97
16	2jsa-10	TYR_A_16_C	GLU_A_17_N	-9.362	2.22	3.002	-8.817	3.414	3.18	1.32	82.28	65.47
17	2jsa-10	GLU_A_17_C	GLY_A_18_N	-10.677	4.831	2.453	-10.437	4.247	1.288	1.33	151.54	-67.66
18	2jsa-10	GLY_A_18_C	SER_A_19_N	-11.871	3.063	-0.319	-11.979	2.134	0.621	1.33	44.86	-96.63
19	2jsa-10	SER_A_19_C	ALA_A_20_N	-13.996	0.798	0.281	-14.574	1.256	1.381	1.32	33.84	141.61
20	2jsa-10	ALA_A_20_C	ASP_A_21_N	-16.542	-0.053	1.964	-15.629	-1.012	2.018	1.33	87.66	-46.41
21	2jsa-10	ASP_A_21_C	LYS_A_22_N	-15.362	-2.631	3.815	-14.323	-1.87	4.124	1.32	76.51	36.22
22	2jsa-10	LYS_A_22_C	ASP_A_23_N	-13.112	-3.452	5.522	-12.173					

24	2jsa-10	ALA_A_24_C	ASN_A_25_N	-7.475	-6.244	3.739	-8.43	-7.141	3.54	1.33	98.64	-136.79
25	2jsa-10	ASN_A_25_C	VAL_A_26_N	-8.484	-7.67	1.166	-9.652	-7.074	0.976	1.32	98.24	152.97
26	2jsa-10	VAL_A_26_C	ILE_A_27_N	-9.187	-5.237	-0.55	-8.433	-4.859	0.472	1.33	39.53	26.63
27	2jsa-10	ILE_A_27_C	LYS_A_28_N	-6.234	-4.045	-0.18	-5.493	-4.811	0.606	1.32	53.59	-45.95
28	2jsa-10	LYS_A_28_C	LYS_A_29_N	-4.253	-5.873	-1.2	-5.341	-6.594	-1.424	1.32	99.74	-146.47
29	2jsa-10	LYS_A_29_C	ASP_A_30_N	-5.762	-6.187	-3.786	-6.633	-5.236	-3.478	1.33	76.57	132.49
30	2jsa-10	ASP_A_30_C	PHE_A_31_N	-5.618	-3.553	-4.914	-4.782	-3.162	-3.964	1.32	44.17	25.07
31	2jsa-10	PHE_A_31_C	ASP_A_32_N	-2.814	-3.333	-5.427	-2.598	-4.618	-5.181	1.33	79.31	-80.46
32	2jsa-10	ASP_A_32_C	ALA_A_33_N	-2.62	-5.261	-7.529	-3.895	-4.903	-7.48	1.33	87.88	164.32
33	2jsa-10	ALA_A_33_C	GLU_A_34_N	-4.107	-3.428	-9.403	-4.195	-2.303	-8.707	1.33	58.33	94.47
34	2jsa-10	GLU_A_34_C	CYS_A_35_N	-2.207	-0.91	-9.029	-1.554	-2.057	-8.901	1.33	84.46	-60.35
35	2jsa-10	CYS_A_35_C	LYS_A_36_N	0.522	-2.922	-9.788	-0.061	-4.091	-10.011	1.33	99.69	-116.51
36	2jsa-10	LYS_A_36_C	LYS_A_37_N	0.294	-4.338	-12.405	-0.815	-3.631	-12.572	1.33	97.24	147.48
37	2jsa-10	LYS_A_37_C	LEU_A_38_N	-0.391	-1.588	-13.826	-0.376	-0.97	-12.655	1.32	27.83	88.61
38	2jsa-10	LEU_A_38_C	PHE_A_39_N	1.758	0.199	-12.73	2.399	-0.516	-11.816	1.33	46.41	-48.12
39	2jsa-10	PHE_A_39_C	HIS_A_40_N	4.156	-1.975	-12.727	3.248	-2.292	-13.639	1.33	133.48	-160.75
40	2jsa-10	HIS_A_40_C	THR_A_41_N	4.763	-3.356	-15.226	4.974	-2.21	-15.857	1.33	118.44	79.57
41	2jsa-10	THR_A_41_C	ILE_A_42_N	7.418	-2.196	-15.688	7.34	-1.617	-14.498	1.33	26.15	97.67
42	2jsa-10	ILE_A_42_C	PRO_A_43_N	8.906	-3.192	-13.502	10.247	-3.344	-13.339	1.36	83.11	-6.47
43	2jsa-10	PRO_A_43_C	PHE_A_44_N	10.574	-5.345	-11.948	10.913	-4.636	-10.882	1.32	36.40	64.45
44	2jsa-10	PHE_A_44_C	GLY_A_45_N	9.539	-4.451	-8.85	8.558	-4.074	-9.657	1.33	127.52	158.98
45	2jsa-10	GLY_A_45_C	THR_A_46_N	6.341	-4.396	-8.645	5.967	-5.302	-9.536	1.32	132.27	-112.43
46	2jsa-10	THR_A_46_C	ARG_A_47_N	5.471	-7.169	-8.03	6.751	-7.507	-8.078	1.32	92.08	-14.79
47	2jsa-10	ARG_A_47_C	GLU_A_48_N	7.239	-7.603	-5.681	7.502	-6.305	-5.709	1.32	91.21	78.55
48	2jsa-10	GLU_A_48_C	CYS_A_49_N	5.977	-5.281	-4.091	5.107	-5.286	-5.09	1.32	138.95	-179.67
49	2jsa-10	CYS_A_49_C	ASP_A_50_N	3.227	-6.129	-3.825	3.273	-7.386	-4.243	1.33	108.38	-87.90
50	2jsa-10	ASP_A_50_C	HIS_A_51_N	3.692	-8.441	-2.091	4.887	-7.881	-2.211	1.33	95.20	25.11
51	2jsa-10	HIS_A_51_C	TYR_A_52_N	5.402	-6.559	-0.229	4.367	-5.865	-0.682	1.33	109.98	146.16
52	2jsa-10	TYR_A_52_C	VAL_A_53_N	2.509	-4.922	0.622	1.617	-5.439	-0.208	1.32	128.84	-149.90
53	2jsa-10	VAL_A_53_C	ASN_A_54_N	0.305	-6.581	1.493	1.436	-7.245	1.679	1.32	81.93	-30.42
54	2jsa-10	ASN_A_54_C	SER_A_55_N	3.025	-7.892	3.405	3.219	-6.727	4.002	1.32	63.18	80.55
55	2jsa-10	SER_A_55_C	LYS_A_56_N	4.525	-4.917	4.998	3.82	-4.11	4.22	1.32	125.98	131.14
56	2jsa-10	LYS_A_56_C	VAL_A_57_N	2.282	-2.25	4.531	1.403	-3.233	4.398	1.33	95.76	-131.80
57	2jsa-10	VAL_A_57_C	ASP_A_58_N	-0.569	-3.229	5.824	-0.121	-4.335	6.401	1.33	64.19	-67.95
58	2jsa-10	ASP_A_58_C	PRO_A_59_N	-0.281	-3.55	8.698	0.934	-2.957	8.557	1.36	95.95	26.02
59	2jsa-10	PRO_A_59_C	ILE_A_60_N	0.613	-0.557	8.984	0.81	-0.193	7.725	1.33	161.80	61.58
60	2jsa-10	ILE_A_60_C	ILE_A_61_N	-1.279	1.051	7.607	-1.981	-0.029	7.294	1.33	103.66	-123.02
61	2jsa-10	ILE_A_61_C	HIS_A_62_N	-3.556	-0.056	9.148	-2.489	-0.416	9.845	1.32	58.24	-18.64
62	2jsa-10	HIS_A_62_C	GLU_A_63_N	-2.676	1.041	11.791	-1.896	1.933	11.199	1.32	116.55	48.83
63	2jsa-10	GLU_A_63_C	LEU_A_64_N	-3.355	3.897	11.311	-3.826	3.687	10.09	1.33	157.10	-155.97
64	2jsa-10	LEU_A_64_C	GLU_A_65_N	-6.191	3.572	10.651	-5.946	2.334	11.054	1.32	72.29	-78.81
65	2jsa-10	GLU_A_65_C	GLY_A_66_N	-6.891	2.349	13.312	-5.806	3.048	13.61	1.32	77.00	32.79
66	2jsa-10	GLY_A_66_C	GLY_A_67_N	-6.346	5.152	14.763	-6.413	5.648	13.537	1.32	157.79	97.69
67	2jsa-10	GLY_A_67_C	THR_A_68_N	-6.028	7.857	12.53	-4.877	7.29	12.2	1.32	104.42	-26.23
68	2jsa-10	THR_A_68_C	ALA_A_69_N	-4.299	8.277	10.033	-3.979	9.467	9.545	1.33	111.60	74.95
69	2jsa-10	ALA_A_69_C	PRO_A_70_N	-3.521	9.0	7.201	-3.996	8.986	5.927	1.36	159.54	-178.31
70	2jsa-10	PRO_A_70_C	LYS_A_71_N	-2.042	8.936	4.436	-1.993	10.232	4.708	1.33	78.16	87.83
71	2jsa-10	LYS_A_71_C	ASP_A_72_N	0.1	11.152	5.545	-0.281	10.476	6.619	1.32	35.85	-119.41
72	2jsa-10	ASP_A_72_C	VAL_A_73_N	1.239	9.163	7.993	0.593	8.114	7.509	1.32	111.45	-121.63
73	2jsa-10	VAL_A_73_C	CYS_A_74_N	2.456	6.735	6.766	2.393	7.346	5.592	1.32	152.38	95.89
74	2jsa-10	CYS_A_74_C	THR_A_75_N	4.482	8.495	5.18	5.049	8.284	6.358	1.32	27.18	-20.41
75	2jsa-10	THR_A_75_C	LYS_A_76_N	6.365	8.839	8.349	5.394	8.899	9.248	1.32	47.26	176.46
76	2jsa-10	LYS_A_76_C	LEU_A_77_N	6.101	7.077	10.697	5.533	6.266	9.815	1.33	131.69	-125.01
77	2jsa-10	LEU_A_77_C	ASN_A_78_N	7.302	4.709	9.212	7.858	5.833	8.785	1.32	108.80	63.68
78	2jsa-10	ASN_A_78_C	GLU_A_79_N	9.207	5.122	6.888	8.068	5.191	6.215	1.32	120.53	176.53
79	2jsa-10	GLU_A_79_C	CYS_A_80_N	8.231	5.551	3.799	7.2	6.283	3.404	1.32	107.35	144.63
80	2jsa-10	CYS_A_80_C	PRO_A_81_N	8.328	8.342	2.825	9.205	8.779	1.881	1.36	133.93	26.49
1	2jsa-11	ARG_A_1_C	SER_A_2_N	12.734	2.179	-1.501	13.017	2.959	-2.534	1.32	141.23	70.06
2	2jsa-11	SER_A_2_C	ALA_A_3_N	12.737	5.369	-2.836	11.445	5.078	-2.82	1.32	89.31	-167.31
3	2jsa-11	ALA_A_3_C	LEU_A_4_N	9.138	5.324	-3.552	9.243	4.263	-4.339	1.33	126.43	-84.35
4	2jsa-11	LEU_A_4_C	SER_A_5_N	7.205	3.265	-3.462	7.82	2.686	-2.441	1.33	39.60	-43.27
5	2jsa-11	SER_A_5_C	CYS_A_6_N	6.16	3.569	-0.88	6.615	4.776	-1.18	1.32	103.09	69.35
6	2jsa-11	CYS_A_6_C	GLN_A_7_N	4.461	5.78	-1.627	4.495	5.862	-2.949	1.32	176.16	67.48
7	2jsa-11	GLN_A_7_C	MET_A_8_N	2.48	4.505	-3.249	3.167	3.378	-3.141	1.32	85.32	-58.63
8	2jsa-11	MET_A_8_C	CYS_A_9_N	1.666	2.411	-1.452	2.239	3.144	-0.51	1.32	44.64	51.98
9	2jsa-11	CYS_A_9_C	GLU_A_10_N	0.242	4.199	0.354	0.31	4.947	-0.737	1.32	145.46	84.81
10	2jsa-11	GLU_A_10_C	LEU_A_11_N	-1.771	4.793	-2.016	-1.332	3.556	-2.196	1.32	97.81	-70.46
11	2jsa-11	LEU_A_11_C	VAL_A_12_N	-2.981	1.778	-1.985	-2.367	1.369	-0.885	1.32	33.85	-33.67
12	2jsa-11	VAL_A_12_C	VAL_A_13_N	-4.163	1.456	0.755	-3.835	2.727	0.937	1.33	82.11	75.53
13	2jsa-11	VAL_A_13_C	LYS_A_14_N	-5.944	3.884	0.57	-5.608	4.357	-0.622	1.33	154.05	54.61
14	2jsa-11	LYS_A_14_C	LYS_A_15_N	-7.562	3.415	-1.726	-7.004	2.242	-1.466	1.32	78.68	-64.56
15	2jsa-11	LYS_A_15_C	TYR_A_16_N	-8.549	0.852	-0.201	-7.872	1.183	0.888	1.32	34.68	26.06
16	2jsa-11	TYR_A_16_C	GLU_A_17_N	-9.476	2.21	2.443	-8.94	3.416	2.555	1.32	85.15	66.04
17	2jsa-11	GLU_A_17_C	GLY_A_18_N	-11.006	4.544	1.879	-10.773	4.167	0.63	1.33	160.46	-58.28
18	2jsa-11	GLY_A_18_C	SER_A_19_N	-12.065	2.637	-0.796	-12.107	1.741	0.179	1.32	42.61	-92.68
19	2jsa-11	SER_A_19_C	ALA_A_20_N	-13.789	0.042	-0.329	-14.596	0.518	0.608	1.33	45.00	149.47
20	2jsa-11	ALA_A_20_C	ASP_A_21_N	-16.389	-1.044	1.123	-16.026	-1.218	2.385	1.32	17.69	-25.61
21	2jsa-11	ASP_A_21_C	LYS_A_22_N	-15.421	-2.552	4.328	-14.275	-1.892	4.254	1.32	93.20	29.94
22	2jsa-11	LYS_A_22_C	ASP_A_23_N	-12.8	-3.302	5.581	-12.105	-3.795	4.566	1.33	139.99	-35.35
23	2jsa-11	ASP_A_23_C	ALA_A_24_N	-10.094	-5.086	4.109	-9.158	-5.112	5.047	1.33	44.95	-1.59
24	2jsa-11	ALA_A_24_C	ASN_A_25_N	-7.455	-6.169	3.667	-8.371	-7.124	3.587	1.33	93.46	-133.81
25	2jsa-11	ASN_A_25_C	VAL_A_26_N	-8.469	-7.717	1.229	-9.628	-7.098	1.049	1.33	97.80	151.89
26	2jsa-11	VAL_A_26_C	ILE_A_27_N	-9.156	-5.318	-0.542	-8.401	-4.904	0.465	1.32	40.53	28.74
27	2jsa-11	ILE_A_27_C	LYS_A_28_N	-6.17	-4.164	-0.164	-5.418	-4.777	0.74	1.33	47.02	-39.19
28	2jsa-11	LYS_A_28_C	LYS_A_29_N	-4.1	-5.889	-0.978	-5.169	-6.626	-1.237	1.32	101.28	-145.42
29	2jsa-11	LYS_A_29_C	ASP_A_30_N	-5.569	-6.261	-3.61	-6.463	-5.331	-3.306	1.33	76.74	133.87
30	2jsa-11	ASP_A_30_C	PHE_A_31_N	-5.515	-3.594	-4.723	-4.693	-3.219	-3.755	1.32	43.03	24.52
31	2jsa-11	PHE_A_31_C	ASP_A_32_N	-2.665	-3.309	-5.143	-2.528	-4.611	-4.931	1.33	80.80	-83.99
32	2jsa-11	ASP_A_32_C	ALA_A_33_N	-2.451	-5.297	-7.265	-3.721	-4.92	-7.262	1.32	89.87	163.47
33	2jsa-11	ALA_A_33_C	GLU_A_34_N	-3.887	-3.515	-9.242	-4.234	-2.342	-8.732	1.33	67.37	106.48
34	2jsa-11	GLU_A_34_C	CYS_A_35_N	-2.259	-1.144	-9.54	-1.597	-1.916	-8.693	1.32	50.21	-49.39
35	2jsa-11	CYS_A_35										

37	2jsa-11	LYS_A_37_C	LEU_A_38_N	-0.921	-0.943	-13.784	-0.726	-0.225	-12.687	1.33	34.15	74.81
38	2jsa-11	LEU_A_38_C	PHE_A_39_N	1.581	0.547	-12.64	1.871	-0.329	-11.69	1.32	44.17	-71.68
39	2jsa-11	PHE_A_39_C	HIS_A_40_N	3.565	-1.901	-12.53	2.645	-2.095	-13.464	1.33	134.81	-168.09
40	2jsa-11	HIS_A_40_C	THR_A_41_N	4.105	-2.787	-15.291	4.178	-1.555	-15.774	1.33	111.37	86.61
41	2jsa-11	THR_A_41_C	ILE_A_42_N	6.619	-1.353	-15.753	6.455	-1.505	-14.448	1.32	9.72	-137.17
42	2jsa-11	ILE_A_42_C	PRO_A_43_N	8.012	-3.2	-13.66	9.355	-3.416	-13.644	1.36	89.33	-9.14
43	2jsa-11	PRO_A_43_C	PHE_A_44_N	9.728	-5.498	-12.39	10.433	-5.003	-11.383	1.33	40.54	35.07
44	2jsa-11	PHE_A_44_C	GLY_A_45_N	9.194	-5.039	-9.259	8.394	-4.228	-9.934	1.32	120.65	134.61
45	2jsa-11	GLY_A_45_C	THR_A_46_N	6.273	-4.689	-8.779	5.534	-5.278	-9.709	1.33	134.54	-141.44
46	2jsa-11	THR_A_46_C	ARG_A_47_N	5.141	-7.213	-8.258	6.449	-7.417	-8.318	1.33	92.60	-8.86
47	2jsa-11	ARG_A_47_C	GLU_A_48_N	7.049	-7.607	-5.953	7.425	-6.337	-5.904	1.33	87.88	73.51
48	2jsa-11	GLU_A_48_C	CYS_A_49_N	5.965	-5.367	-4.195	5.064	-5.353	-5.166	1.32	137.14	179.11
49	2jsa-11	CYS_A_49_C	ASP_A_50_N	3.226	-6.162	-3.819	3.186	-7.42	-4.236	1.33	108.33	-91.82
50	2jsa-11	ASP_A_50_C	HIS_A_51_N	3.696	-8.473	-2.102	4.883	-7.914	-2.285	1.32	97.94	25.22
51	2jsa-11	HIS_A_51_C	TYR_A_52_N	5.528	-6.603	-0.334	4.472	-5.902	-0.719	1.32	106.90	146.42
52	2jsa-11	TYR_A_52_C	VAL_A_53_N	2.703	-4.934	0.688	1.761	-5.442	-0.092	1.32	126.08	-151.66
53	2jsa-11	VAL_A_53_C	ASN_A_54_N	0.525	-6.596	1.658	1.671	-7.251	1.787	1.33	84.42	-29.75
54	2jsa-11	ASN_A_54_C	SER_A_55_N	3.319	-7.907	3.451	3.49	-6.772	4.113	1.33	60.03	81.43
55	2jsa-11	SER_A_55_C	LYS_A_56_N	4.802	-4.944	5.068	4.021	-4.162	4.337	1.33	123.48	134.96
56	2jsa-11	LYS_A_56_C	VAL_A_57_N	2.47	-2.311	4.632	1.599	-3.309	4.629	1.32	90.13	-131.11
57	2jsa-11	VAL_A_57_C	ASP_A_58_N	-0.335	-3.189	6.101	0.041	-4.294	6.726	1.32	61.83	-71.21
58	2jsa-11	ASP_A_58_C	PRO_A_59_N	-0.066	-3.323	8.954	1.144	-2.744	8.728	1.36	99.56	25.57
59	2jsa-11	PRO_A_59_C	ILE_A_60_N	0.83	-0.317	8.971	0.97	-0.067	7.677	1.33	167.51	60.75
60	2jsa-11	ILE_A_60_C	ILE_A_61_N	-1.118	1.174	7.541	-1.867	0.118	7.257	1.33	102.37	-125.35
61	2jsa-11	ILE_A_61_C	HIS_A_62_N	-3.369	0.209	9.17	-2.26	-0.074	9.837	1.32	59.77	-14.32
62	2jsa-11	HIS_A_62_C	GLU_A_63_N	-2.393	1.48	11.711	-1.96	2.375	10.836	1.32	131.35	64.18
63	2jsa-11	GLU_A_63_C	LEU_A_64_N	-3.467	4.304	10.753	-3.825	4.123	9.491	1.32	162.37	-153.18
64	2jsa-11	LEU_A_64_C	GLU_A_65_N	-6.213	4.007	9.944	-6.067	2.737	10.289	1.32	74.90	-83.44
65	2jsa-11	GLU_A_65_C	GLY_A_66_N	-6.975	2.714	12.563	-5.786	3.168	12.932	1.33	73.83	20.90
66	2jsa-11	GLY_A_66_C	GLY_A_67_N	-6.264	5.164	14.287	-6.171	5.878	13.175	1.32	147.08	82.58
67	2jsa-11	GLY_A_67_C	THR_A_68_N	-5.909	8.125	12.211	-4.683	7.686	11.963	1.33	100.78	-19.70
68	2jsa-11	THR_A_68_C	ALA_A_69_N	-4.319	8.634	9.734	-3.879	9.704	9.087	1.33	119.22	67.65
69	2jsa-11	ALA_A_69_C	PRO_A_70_N	-3.536	9.133	6.746	-4.009	9.143	5.471	1.36	159.64	178.79
70	2jsa-11	PRO_A_70_C	LYS_A_71_N	-2.054	9.033	3.983	-1.909	10.294	4.367	1.33	73.17	83.44
71	2jsa-11	LYS_A_71_C	ASP_A_72_N	0.126	11.271	5.274	-0.204	10.514	6.311	1.33	38.53	-113.55
72	2jsa-11	ASP_A_72_C	VAL_A_73_N	1.042	9.237	7.966	0.745	8.26	7.121	1.33	129.61	-106.91
73	2jsa-11	VAL_A_73_C	CYS_A_74_N	2.561	6.686	6.741	2.737	7.273	5.566	1.33	152.46	73.31
74	2jsa-11	CYS_A_74_C	THR_A_75_N	5.049	7.983	5.599	4.582	8.706	6.605	1.32	40.55	122.86
75	2jsa-11	THR_A_75_C	LYS_A_76_N	5.533	9.021	8.841	4.528	8.236	9.201	1.33	74.24	-142.01
76	2jsa-11	LYS_A_76_C	LEU_A_77_N	5.593	6.662	10.72	5.452	5.534	10.037	1.33	121.00	-97.13
77	2jsa-11	LEU_A_77_C	ASN_A_78_N	7.553	4.756	9.085	7.804	6.037	8.86	1.32	99.78	78.91
78	2jsa-11	ASN_A_78_C	GLU_A_79_N	8.805	5.492	6.71	7.616	4.99	6.413	1.32	102.96	-157.11
79	2jsa-11	GLU_A_79_C	CYS_A_80_N	8.069	4.659	4.03	7.44	5.713	3.535	1.32	111.96	120.83
80	2jsa-11	CYS_A_80_C	PRO_A_81_N	9.407	6.676	2.51	10.245	5.89	1.781	1.36	122.40	-43.17
1	2jsa-12	ARG_A_1_C	SER_A_2_N	11.306	5.35	-1.22	11.49	6.66	-1.288	1.32	92.94	82.00
2	2jsa-12	SER_A_2_C	ALA_A_3_N	10.278	7.427	-3.267	9.502	6.435	-3.678	1.32	108.07	-128.03
3	2jsa-12	ALA_A_3_C	LEU_A_4_N	8.178	5.145	-5.261	8.499	3.938	-4.816	1.33	70.39	-75.11
4	2jsa-12	LEU_A_4_C	SER_A_5_N	6.882	2.629	-3.554	7.702	2.34	-2.554	1.33	41.00	-19.41
5	2jsa-12	SER_A_5_C	CYS_A_6_N	6.252	3.26	-0.815	6.584	4.452	-1.288	1.32	110.92	74.44
6	2jsa-12	CYS_A_6_C	GLN_A_7_N	4.441	5.486	-1.723	4.487	5.726	-3.025	1.32	169.37	79.15
7	2jsa-12	GLN_A_7_C	MET_A_8_N	2.44	4.438	-3.409	3.09	3.285	-3.334	1.33	86.76	-60.59
8	2jsa-12	MET_A_8_C	CYS_A_9_N	1.556	2.303	-1.683	2.116	3.069	-0.759	1.32	45.76	53.83
9	2jsa-12	CYS_A_9_C	GLU_A_10_N	0.106	4.079	0.131	0.15	4.849	-0.946	1.32	144.39	86.73
10	2jsa-12	GLU_A_10_C	LEU_A_11_N	-1.96	4.646	-2.17	-1.483	3.43	-2.392	1.32	99.65	-68.58
11	2jsa-12	LEU_A_11_C	VAL_A_12_N	-3.09	1.622	-2.122	-2.436	1.234	-1.037	1.32	35.03	-30.68
12	2jsa-12	VAL_A_12_C	VAL_A_13_N	-4.151	1.313	0.688	-3.721	2.493	1.109	1.32	71.47	69.98
13	2jsa-12	VAL_A_13_C	LYS_A_14_N	-5.764	3.788	0.848	-5.397	4.36	-0.29	1.33	149.15	57.32
14	2jsa-12	LYS_A_14_C	LYS_A_15_N	-7.415	3.648	-1.45	-6.934	2.419	-1.329	1.33	84.76	-68.63
15	2jsa-12	LYS_A_15_C	TYR_A_16_N	-8.618	1.083	-0.189	-7.948	1.287	0.937	1.33	31.88	16.93
16	2jsa-12	TYR_A_16_C	GLU_A_17_N	-9.438	2.391	2.551	-8.74	3.478	2.849	1.33	77.01	57.29
17	2jsa-12	GLU_A_17_C	GLY_A_18_N	-10.661	4.901	2.317	-10.522	4.55	1.048	1.32	163.43	-68.40
18	2jsa-12	GLY_A_18_C	SER_A_19_N	-11.986	3.298	-0.482	-12.205	2.338	0.405	1.33	47.99	-102.85
19	2jsa-12	SER_A_19_C	ALA_A_20_N	-14.07	0.838	-0.087	-14.728	1.318	0.959	1.33	37.91	143.89
20	2jsa-12	ALA_A_20_C	ASP_A_21_N	-16.583	-0.13	1.578	-15.59	-0.998	1.709	1.33	84.33	-41.16
21	2jsa-12	ASP_A_21_C	LYS_A_22_N	-15.122	-2.503	3.563	-14.118	-1.665	3.774	1.32	80.83	39.85
22	2jsa-12	LYS_A_22_C	ASP_A_23_N	-12.869	-3.137	5.256	-11.976	-3.582	4.384	1.33	131.15	-26.49
23	2jsa-12	ASP_A_23_C	ALA_A_24_N	-9.985	-4.922	3.978	-9.066	-5.22	4.884	1.32	46.84	-17.97
24	2jsa-12	ALA_A_24_C	ASN_A_25_N	-7.407	-6.41	3.561	-8.438	-7.223	3.378	1.33	97.93	-141.74
25	2jsa-12	ASN_A_25_C	VAL_A_26_N	-8.595	-7.894	1.045	-9.678	-7.148	0.88	1.33	97.15	145.44
26	2jsa-12	VAL_A_26_C	ILE_A_27_N	-9.186	-5.406	-0.746	-8.487	-4.932	0.276	1.33	39.57	34.14
27	2jsa-12	ILE_A_27_C	LYS_A_28_N	-6.229	-4.223	-0.294	-5.511	-4.777	0.673	1.33	43.16	-37.65
28	2jsa-12	LYS_A_28_C	LYS_A_29_N	-4.108	-5.921	-0.955	-5.115	-6.741	-1.219	1.33	101.49	-140.84
29	2jsa-12	LYS_A_29_C	ASP_A_30_N	-5.382	-6.426	-3.617	-6.385	-5.578	-3.445	1.32	82.54	139.79
30	2jsa-12	ASP_A_30_C	PHE_A_31_N	-5.379	-3.884	-4.873	-4.656	-3.372	-3.888	1.32	41.97	35.30
31	2jsa-12	PHE_A_31_C	ASP_A_32_N	-2.582	-3.461	-5.205	-2.406	-4.75	-4.953	1.33	79.04	-82.22
32	2jsa-12	ASP_A_32_C	ALA_A_33_N	-2.207	-5.43	-7.28	-3.527	-5.486	-7.376	1.32	94.16	-177.57
33	2jsa-12	ALA_A_33_C	GLU_A_34_N	-3.735	-4.044	-9.325	-4.071	-2.937	-8.679	1.33	60.82	106.88
34	2jsa-12	GLU_A_34_C	CYS_A_35_N	-2.241	-1.628	-9.646	-1.396	-2.21	-8.808	1.32	50.76	-34.56
35	2jsa-12	CYS_A_35_C	LYS_A_36_N	0.194	-2.964	-10.466	-0.578	-4.022	-10.663	1.32	98.55	-126.12
36	2jsa-12	LYS_A_36_C	LYS_A_37_N	-1.225	-3.969	-13.008	-1.727	-2.805	-12.622	1.33	73.06	113.33
37	2jsa-12	LYS_A_37_C	LEU_A_38_N	-1.522	-0.752	-13.911	-0.955	-0.153	-12.874	1.33	38.50	46.57
38	2jsa-12	LEU_A_38_C	PHE_A_39_N	1.38	0.528	-12.976	1.665	-0.241	-11.935	1.33	38.23	-69.66
39	2jsa-12	PHE_A_39_C	HIS_A_40_N	3.222	-2.058	-12.5	2.306	-2.321	-13.421	1.33	134.02	-163.98
40	2jsa-12	HIS_A_40_C	THR_A_41_N	3.639	-3.48	-15.1	3.713	-2.446	-15.924	1.32	128.48	85.91
41	2jsa-12	THR_A_41_C	ILE_A_42_N	6.158	-2.534	-16.057	6.181	-2.091	-14.808	1.33	19.55	87.03
42	2jsa-12	ILE_A_42_C	PRO_A_43_N	7.478	-3.741	-13.576	8.742	-4.243	-13.608	1.36	91.35	-21.66
43	2jsa-12	PRO_A_43_C	PHE_A_44_N	8.928	-5.831	-11.741	9.961	-5.361	-11.059	1.32	59.00	24.46
44	2jsa-12	PHE_A_44_C	GLY_A_45_N	8.833	-4.784	-8.952	8.227	-3.878	-9.706	1.33	124.67	123.78
45	2jsa-12	GLY_A_45_C	THR_A_46_N	5.999	-4.077	-8.687	5.704	-5.089	-9.49	1.33	127.30	-106.25
46	2jsa-12	THR_A_46_C	ARG_A_47_N	5.216	-6.987	-8.02	6.485	-7.347	-8.146	1.33	95.46	-15.84
47	2jsa-12	ARG_A_47_C	GLU_A_48_N	7.161	-7.539	-5.8	7.555	-6.275	-5.817	1.32	90.74	72.69
48	2jsa-12											

50	2jsa-12	ASP_A_50_C	HIS_A_51_N	3.813	-8.395	-2.548	4.999	-7.818	-2.423	1.32	84.59	25.94
51	2jsa-12	HIS_A_51_C	TYR_A_52_N	5.546	-6.8	-0.276	4.6	-5.96	-0.669	1.32	107.26	138.40
52	2jsa-12	TYR_A_52_C	VAL_A_53_N	2.949	-4.999	0.878	2.027	-5.685	0.217	1.33	119.91	-143.35
53	2jsa-12	VAL_A_53_C	ASN_A_54_N	0.841	-7.178	1.729	1.825	-7.124	2.615	1.33	48.04	3.14
54	2jsa-12	ASN_A_54_C	SER_A_55_N	3.251	-7.876	4.437	3.239	-6.658	4.959	1.33	66.80	90.56
55	2jsa-12	SER_A_55_C	LYS_A_56_N	4.276	-4.68	5.95	3.753	-4.044	4.911	1.33	141.60	129.43
56	2jsa-12	LYS_A_56_C	VAL_A_57_N	2.178	-2.193	4.785	1.327	-3.205	4.702	1.32	93.59	-130.06
57	2jsa-12	VAL_A_57_C	ASP_A_58_N	-0.751	-3.148	5.966	-0.327	-4.198	6.655	1.33	58.68	-68.01
58	2jsa-12	ASP_A_58_C	PRO_A_59_N	-0.616	-3.287	8.893	0.619	-2.725	8.793	1.36	94.22	24.47
59	2jsa-12	PRO_A_59_C	ILE_A_60_N	0.325	-0.3	9.078	0.488	-0.078	7.781	1.33	168.01	53.71
60	2jsa-12	ILE_A_60_C	ILE_A_61_N	-1.558	1.218	7.544	-2.25	0.09	7.481	1.32	92.73	-121.53
61	2jsa-12	ILE_A_61_C	HIS_A_62_N	-3.808	0.18	9.349	-2.713	-0.096	10.042	1.32	58.46	-14.15
62	2jsa-12	HIS_A_62_C	GLU_A_63_N	-2.794	1.443	11.931	-2.292	2.316	11.07	1.32	130.53	60.10
63	2jsa-12	GLU_A_63_C	LEU_A_64_N	-3.674	4.337	11.017	-4.115	4.071	9.795	1.33	157.15	-148.90
64	2jsa-12	LEU_A_64_C	GLU_A_65_N	-6.506	4.026	10.241	-6.367	2.757	10.593	1.32	74.58	-83.75
65	2jsa-12	GLU_A_65_C	GLY_A_66_N	-7.247	2.653	12.875	-6.063	3.149	13.205	1.33	75.58	22.73
66	2jsa-12	GLY_A_66_C	GLY_A_67_N	-6.435	5.101	14.654	-6.332	5.857	13.57	1.33	144.86	82.24
67	2jsa-12	GLY_A_67_C	THR_A_68_N	-6.003	8.123	12.674	-4.793	7.658	12.4	1.32	101.94	-21.02
68	2jsa-12	THR_A_68_C	ALA_A_69_N	-4.415	8.581	10.163	-3.952	9.629	9.499	1.32	120.09	66.16
69	2jsa-12	ALA_A_69_C	PRO_A_70_N	-3.521	9.111	7.16	-3.975	9.09	5.878	1.36	160.48	-177.35
70	2jsa-12	PRO_A_70_C	LYS_A_71_N	-1.995	9.137	4.42	-1.976	10.417	4.76	1.32	75.13	89.15
71	2jsa-12	LYS_A_71_C	ASP_A_72_N	0.062	11.404	5.651	-0.226	10.591	6.657	1.33	40.61	-109.51
72	2jsa-12	ASP_A_72_C	VAL_A_73_N	1.265	9.272	8.054	0.564	8.213	7.68	1.32	106.41	-123.50
73	2jsa-12	VAL_A_73_C	CYS_A_74_N	2.437	6.808	7.014	2.399	7.329	5.796	1.33	156.79	94.17
74	2jsa-12	CYS_A_74_C	THR_A_75_N	4.454	8.526	5.353	4.828	8.539	6.623	1.32	16.42	1.99
75	2jsa-12	THR_A_75_C	LYS_A_76_N	6.41	9.138	8.395	5.638	8.724	9.39	1.33	41.36	-151.80
76	2jsa-12	LYS_A_76_C	LEU_A_77_N	6.692	6.807	10.456	5.904	6.046	9.71	1.33	124.25	-136.00
77	2jsa-12	LEU_A_77_C	ASN_A_78_N	7.493	4.583	8.589	7.927	5.751	8.135	1.33	110.02	69.62
78	2jsa-12	ASN_A_78_C	GLU_A_79_N	8.867	5.074	5.994	7.628	5.143	5.531	1.32	110.46	176.81
79	2jsa-12	GLU_A_79_C	CYS_A_80_N	6.728	5.483	3.279	7.643	6.306	2.788	1.33	111.75	41.97
80	2jsa-12	CYS_A_80_C	PRO_A_81_N	8.499	8.235	1.608	8.985	8.804	2.744	1.36	33.37	49.50
1	2jsa-13	ARG_A_1_C	SER_A_2_N	13.65	4.065	1.72	13.91	4.657	0.565	1.32	150.76	66.29
2	2jsa-13	SER_A_2_C	ALA_A_3_N	12.848	5.364	-1.519	11.616	5.12	-1.942	1.33	108.61	-168.80
3	2jsa-13	ALA_A_3_C	LEU_A_4_N	9.834	4.708	-3.547	9.484	3.965	-4.587	1.33	141.70	-115.22
4	2jsa-13	LEU_A_4_C	SER_A_5_N	7.396	3.103	-3.684	8.212	2.547	-2.8	1.33	48.16	-34.27
5	2jsa-13	SER_A_5_C	CYS_A_6_N	6.651	2.822	-0.938	6.96	4.11	-0.917	1.32	89.09	76.51
6	2jsa-13	CYS_A_6_C	GLN_A_7_N	4.745	5.062	-1.103	4.839	5.432	-2.372	1.33	163.26	75.75
7	2jsa-13	GLN_A_7_C	MET_A_8_N	2.77	4.254	-2.944	3.4	3.091	-2.867	1.32	86.67	-61.56
8	2jsa-13	MET_A_8_C	CYS_A_9_N	1.785	2.011	-1.36	2.345	2.648	-0.342	1.33	39.80	48.68
9	2jsa-13	CYS_A_9_C	GLU_A_10_N	0.36	3.674	0.583	0.48	4.524	-0.427	1.33	139.64	81.96
10	2jsa-13	GLU_A_10_C	LEU_A_11_N	-1.607	4.561	-1.705	-1.181	3.358	-2.061	1.32	105.59	-70.50
11	2jsa-13	LEU_A_11_C	VAL_A_12_N	-2.872	1.61	-1.984	-2.254	1.108	-0.924	1.33	36.91	-39.09
12	2jsa-13	VAL_A_12_C	VAL_A_13_N	-3.994	1.088	0.776	-3.542	2.231	1.271	1.33	68.06	68.42
13	2jsa-13	VAL_A_13_C	LYS_A_14_N	-5.566	3.572	1.109	-5.194	4.195	-0.001	1.33	146.83	59.16
14	2jsa-13	LYS_A_14_C	LYS_A_15_N	-7.254	3.608	-1.155	-6.829	2.359	-1.047	1.32	85.32	-71.21
15	2jsa-13	LYS_A_15_C	TYR_A_16_N	-8.503	1.009	0.092	-7.777	1.132	1.193	1.32	33.77	9.62
16	2jsa-13	TYR_A_16_C	GLU_A_17_N	-9.281	2.114	2.872	-8.659	3.27	3.054	1.33	82.11	61.72
17	2jsa-13	GLU_A_17_C	GLY_A_18_N	-10.627	4.619	2.508	-10.441	4.273	1.242	1.33	162.76	-61.74
18	2jsa-13	GLY_A_18_C	SER_A_19_N	-12.036	2.974	-0.104	-12.069	2.099	0.891	1.33	41.35	-92.16
19	2jsa-13	SER_A_19_C	ALA_A_20_N	-14.053	0.673	0.86	-14.494	1.092	2.037	1.32	27.33	136.47
20	2jsa-13	ALA_A_20_C	ASP_A_21_N	-16.329	-0.325	2.777	-15.362	-1.23	2.739	1.32	91.64	-43.10
21	2jsa-13	ASP_A_21_C	LYS_A_22_N	-14.871	-2.923	4.416	-13.927	-2.053	4.746	1.33	75.58	42.66
22	2jsa-13	LYS_A_22_C	ASP_A_23_N	-12.568	-3.642	5.991	-11.833	-3.974	4.94	1.32	142.50	-24.31
23	2jsa-13	ASP_A_23_C	ALA_A_24_N	-9.819	-5.154	4.252	-8.834	-5.459	5.083	1.32	51.13	-17.20
24	2jsa-13	ALA_A_24_C	ASN_A_25_N	-7.156	-6.485	3.649	-8.153	-7.334	3.45	1.32	98.64	-139.58
25	2jsa-13	ASN_A_25_C	VAL_A_26_N	-8.328	-7.943	1.1	-9.469	-7.281	0.975	1.33	95.41	149.88
26	2jsa-13	VAL_A_26_C	ILE_A_27_N	-9.081	-5.495	-0.631	-8.363	-5.02	0.377	1.33	40.50	33.49
27	2jsa-13	ILE_A_27_C	LYS_A_28_N	-6.178	-4.227	-0.344	-5.362	-4.806	0.525	1.33	49.02	-35.36
28	2jsa-13	LYS_A_28_C	LYS_A_29_N	-4.101	-5.895	-1.249	-5.192	-6.612	-1.473	1.32	99.74	-146.69
29	2jsa-13	LYS_A_29_C	ASP_A_30_N	-5.59	-6.257	-3.847	-6.454	-5.293	-3.565	1.32	77.71	131.87
30	2jsa-13	ASP_A_30_C	PHE_A_31_N	-5.433	-3.551	-4.923	-4.644	-3.217	-3.911	1.33	40.25	22.94
31	2jsa-13	PHE_A_31_C	ASP_A_32_N	-2.595	-3.24	-5.27	-2.399	-4.54	-5.108	1.32	82.98	-81.43
32	2jsa-13	ASP_A_32_C	ALA_A_33_N	-2.38	-5.188	-7.453	-3.665	-4.873	-7.388	1.32	87.19	166.23
33	2jsa-13	ALA_A_33_C	GLU_A_34_N	-3.974	-3.487	-9.364	-4.312	-2.323	-8.828	1.33	66.14	106.19
34	2jsa-13	GLU_A_34_C	CYS_A_35_N	-2.409	-1.051	-9.699	-1.692	-1.759	-8.838	1.33	49.49	-44.64
35	2jsa-13	CYS_A_35_C	LYS_A_36_N	0.098	-2.597	-10.231	-0.454	-3.797	-10.332	1.32	94.37	-114.70
36	2jsa-13	LYS_A_36_C	LYS_A_37_N	-0.477	-3.825	-12.765	-1.188	-2.721	-12.588	1.33	82.32	122.78
37	2jsa-13	LYS_A_37_C	LEU_A_38_N	-0.586	-0.636	-13.69	-0.78	0.2	-12.681	1.32	40.38	103.06
38	2jsa-13	LEU_A_38_C	PHE_A_39_N	1.509	1.016	-12.546	1.847	0.067	-11.685	1.33	49.48	-70.40
39	2jsa-13	PHE_A_39_C	HIS_A_40_N	3.484	-1.543	-12.563	2.862	-1.439	-13.728	1.32	151.57	170.51
40	2jsa-13	HIS_A_40_C	THR_A_41_N	4.179	-2.074	-15.679	5.384	-2.169	-15.138	1.32	65.89	-4.51
41	2jsa-13	THR_A_41_C	ILE_A_42_N	7.774	-1.66	-14.965	7.511	-1.019	-13.835	1.33	31.51	112.31
42	2jsa-13	ILE_A_42_C	PRO_A_43_N	9.448	-2.015	-12.748	10.77	-1.755	-12.561	1.36	82.10	11.13
43	2jsa-13	PRO_A_43_C	PHE_A_44_N	11.638	-3.511	-11.076	10.452	-3.426	-10.491	1.33	63.80	175.90
44	2jsa-13	PHE_A_44_C	GLY_A_45_N	8.959	-3.44	-8.538	7.943	-3.237	-9.364	1.33	128.56	168.70
45	2jsa-13	GLY_A_45_C	THR_A_46_N	5.689	-3.802	-8.56	5.332	-4.552	-9.593	1.33	141.20	-115.45
46	2jsa-13	THR_A_46_C	ARG_A_47_N	4.953	-6.697	-8.472	6.275	-6.799	-8.465	1.33	89.70	-4.41
47	2jsa-13	ARG_A_47_C	GLU_A_48_N	6.871	-7.298	-6.143	7.554	-6.197	-5.864	1.33	77.85	58.19
48	2jsa-13	GLU_A_48_C	CYS_A_49_N	6.144	-5.474	-3.998	5.225	-5.293	-4.934	1.32	134.98	168.86
49	2jsa-13	CYS_A_49_C	ASP_A_50_N	3.342	-6.38	-3.874	3.525	-7.505	-4.549	1.32	120.63	-80.76
50	2jsa-13	ASP_A_50_C	HIS_A_51_N	3.811	-9.001	-2.651	4.867	-8.23	-2.436	1.33	80.66	36.13
51	2jsa-13	HIS_A_51_C	TYR_A_52_N	5.303	-7.131	-0.305	4.35	-6.331	-0.76	1.32	110.09	139.99
52	2jsa-13	TYR_A_52_C	VAL_A_53_N	2.599	-5.392	0.688	1.629	-5.838	-0.095	1.32	126.26	-155.31
53	2jsa-13	VAL_A_53_C	ASN_A_54_N	0.426	-6.968	1.692	1.401	-7.864	1.664	1.32	91.21	-42.58
54	2jsa-13	ASN_A_54_C	SER_A_55_N	2.88	-8.287	3.549	3.094	-6.981	3.529	1.32	90.87	80.69
55	2jsa-13	SER_A_55_C	LYS_A_56_N	4.173	-4.872	4.134	3.684	-4.28	5.213	1.32	35.44	129.56
56	2jsa-13	LYS_A_56_C	VAL_A_57_N	2.101	-2.438	5.062	1.27	-3.451	4.868	1.32	98.42	-129.36
57	2jsa-13	VAL_A_57_C	ASP_A_58_N	-0.906	-3.429	5.956	-0.281	-4.176	6.855	1.33	47.29	-50.08
58	2jsa-13	ASP_A_58_C	PRO_A_59_N	-0.713	-3.234	9.057	0.509	-2.64	8.998	1.36	92.49	25.92
59	2jsa-13	PRO_A_59_C	ILE_A_60_N	0.138	-0.221	9.24	0.369	0.005	7.955	1.33	165.88	44.37
60	2jsa-13	ILE_A_60_C	ILE_A_61_N	-1.469	1.265	7.645	-2.377	0.137	7.535	1.33	94.76	-121.34
61	2jsa-13	ILE_A_61_C	HIS_A_62_N</									

63	2jsa-13	GLU_A_63_C	LEU_A_64_N	-3.76	4.563	10.871	-4.421	4.223	9.774	1.33	145.88	-152.78
64	2jsa-13	LEU_A_64_C	GLU_A_65_N	-6.758	4.222	10.452	-6.477	3.017	10.925	1.32	69.08	-76.87
65	2jsa-13	GLU_A_65_C	GLY_A_66_N	-7.369	3.084	13.204	-6.189	3.55	13.588	1.33	73.16	21.55
66	2jsa-13	GLY_A_66_C	GLY_A_67_N	-6.586	5.69	14.732	-6.118	6.39	13.71	1.32	140.51	56.23
67	2jsa-13	GLY_A_67_C	THR_A_68_N	-5.48	8.551	12.723	-4.906	7.901	11.723	1.32	139.07	-48.55
68	2jsa-13	THR_A_68_C	ALA_A_69_N	-4.303	8.587	9.449	-4.398	9.807	8.94	1.33	112.59	94.45
69	2jsa-13	ALA_A_69_C	PRO_A_70_N	-3.917	9.153	6.646	-4.394	8.982	5.384	1.36	158.12	-160.28
70	2jsa-13	PRO_A_70_C	LYS_A_71_N	-2.446	8.952	3.883	-2.485	10.264	4.067	1.33	82.02	91.70
71	2jsa-13	LYS_A_71_C	ASP_A_72_N	-0.443	11.376	4.786	-0.657	10.632	5.861	1.32	35.76	-106.05
72	2jsa-13	ASP_A_72_C	VAL_A_73_N	0.958	9.479	7.269	0.294	8.365	7.002	1.32	101.63	-120.80
73	2jsa-13	VAL_A_73_C	CYS_A_74_N	2.256	7.046	6.429	2.197	7.403	5.155	1.32	164.14	99.38
74	2jsa-13	CYS_A_74_C	THR_A_75_N	4.203	8.675	4.702	4.831	8.606	5.867	1.33	28.47	-6.27
75	2jsa-13	THR_A_75_C	LYS_A_76_N	6.233	9.382	7.72	5.344	9.205	8.686	1.32	43.18	-168.74
76	2jsa-13	LYS_A_76_C	LEU_A_77_N	6.247	7.434	10.091	5.689	6.629	9.198	1.33	132.36	-124.73
77	2jsa-13	LEU_A_77_C	ASN_A_78_N	7.452	5.089	8.532	8.015	6.231	8.164	1.33	106.12	63.76
78	2jsa-13	ASN_A_78_C	GLU_A_79_N	9.329	5.483	6.257	8.144	5.399	5.672	1.32	116.22	-175.95
79	2jsa-13	GLU_A_79_C	CYS_A_80_N	7.953	5.689	3.249	7.942	6.965	3.603	1.32	74.49	90.49
80	2jsa-13	CYS_A_80_C	PRO_A_81_N	8.699	9.217	3.147	9.554	9.795	2.262	1.36	130.61	34.06
1	2jsa-14	ARG_A_1_C	SER_A_2_N	12.372	5.284	-3.37	11.953	5.964	-4.427	1.32	142.92	121.64
2	2jsa-14	SER_A_2_C	ALA_A_3_N	10.391	7.819	-4.736	9.477	6.88	-4.54	1.32	81.49	-134.23
3	2jsa-14	ALA_A_3_C	LEU_A_4_N	7.26	5.877	-4.494	7.649	4.771	-5.11	1.32	117.72	-70.62
4	2jsa-14	LEU_A_4_C	SER_A_5_N	6.573	3.403	-3.409	7.543	3.683	-2.55	1.33	49.61	16.10
5	2jsa-14	SER_A_5_C	CYS_A_6_N	6.032	4.382	-0.76	6.07	5.685	-0.997	1.32	100.30	88.33
6	2jsa-14	CYS_A_6_C	GLN_A_7_N	3.745	6.05	-1.554	3.871	6.253	-2.858	1.33	169.62	58.17
7	2jsa-14	GLN_A_7_C	MET_A_8_N	2.133	4.581	-3.276	2.909	3.51	-3.195	1.33	86.50	-54.07
8	2jsa-14	MET_A_8_C	CYS_A_9_N	1.526	2.426	-1.476	2.064	3.19	-0.537	1.32	44.86	54.85
9	2jsa-14	CYS_A_9_C	GLU_A_10_N	0.046	4.159	0.376	0.089	4.958	-0.68	1.32	142.85	86.92
10	2jsa-14	GLU_A_10_C	LEU_A_11_N	-2.011	4.784	-1.927	-1.534	3.572	-2.169	1.32	100.53	-68.52
11	2jsa-14	LEU_A_11_C	VAL_A_12_N	-3.123	1.74	-1.971	-2.494	1.389	-0.859	1.32	32.93	-29.16
12	2jsa-14	VAL_A_12_C	VAL_A_13_N	-4.197	1.408	0.88	-3.763	2.578	1.326	1.33	70.33	69.65
13	2jsa-14	VAL_A_13_C	LYS_A_14_N	-5.806	3.885	1.129	-5.449	4.478	-0.001	1.33	148.51	58.95
14	2jsa-14	LYS_A_14_C	LYS_A_15_N	-7.487	3.81	-1.15	-7.017	2.575	-1.057	1.32	85.97	-69.16
15	2jsa-14	LYS_A_15_C	TYR_A_16_N	-8.689	1.22	0.077	-8.003	1.406	1.195	1.32	32.45	15.17
16	2jsa-14	TYR_A_16_C	GLU_A_17_N	-9.547	2.427	2.814	-8.924	3.581	3.008	1.33	81.59	61.64
17	2jsa-14	GLU_A_17_C	GLY_A_18_N	-10.955	4.847	2.491	-10.83	4.455	1.232	1.32	161.90	-72.31
18	2jsa-14	GLY_A_18_C	SER_A_19_N	-12.265	3.047	-0.183	-12.323	2.11	0.752	1.32	45.12	-93.54
19	2jsa-14	SER_A_19_C	ALA_A_20_N	-14.099	0.522	0.206	-14.857	0.902	1.225	1.33	39.76	153.37
20	2jsa-14	ALA_A_20_C	ASP_A_21_N	-16.694	-0.655	1.575	-15.679	-1.494	1.722	1.33	83.63	-39.58
21	2jsa-14	ASP_A_21_C	LYS_A_22_N	-15.245	-3.143	3.459	-14.47	-2.164	3.905	1.33	70.34	51.63
22	2jsa-14	LYS_A_22_C	ASP_A_23_N	-13.183	-3.679	5.309	-12.153	-3.924	4.512	1.33	126.97	-13.38
23	2jsa-14	ASP_A_23_C	ALA_A_24_N	-10.04	-5.041	4.056	-9.121	-5.182	5.001	1.33	44.53	-8.72
24	2jsa-14	ALA_A_24_C	ASN_A_25_N	-7.302	-6.112	3.681	-8.192	-7.075	3.494	1.32	98.12	-132.74
25	2jsa-14	ASN_A_25_C	VAL_A_26_N	-8.21	-7.664	1.132	-9.27	-6.879	1.002	1.33	95.63	143.48
26	2jsa-14	VAL_A_26_C	ILE_A_27_N	-8.869	-5.043	-0.544	-8.116	-4.636	0.468	1.33	40.22	28.39
27	2jsa-14	ILE_A_27_C	LYS_A_28_N	-5.909	-3.777	-0.085	-5.322	-4.742	0.607	1.32	58.51	-58.69
28	2jsa-14	LYS_A_28_C	LYS_A_29_N	-3.984	-5.877	-1.079	-5.113	-6.501	-1.383	1.33	103.26	-151.07
29	2jsa-14	LYS_A_29_C	ASP_A_30_N	-5.454	-6.184	-3.772	-6.375	-5.261	-3.54	1.32	79.91	134.94
30	2jsa-14	ASP_A_30_C	PHE_A_31_N	-5.361	-3.531	-4.919	-4.617	-3.115	-3.905	1.32	40.05	29.21
31	2jsa-14	PHE_A_31_C	ASP_A_32_N	-2.451	-3.254	-5.06	-2.498	-4.565	-4.872	1.33	81.84	-92.05
32	2jsa-14	ASP_A_32_C	ALA_A_33_N	-2.182	-5.42	-7.129	-3.474	-5.16	-7.275	1.33	96.32	168.62
33	2jsa-14	ALA_A_33_C	GLU_A_34_N	-3.531	-3.861	-9.332	-3.987	-2.696	-8.895	1.33	70.75	111.38
34	2jsa-14	GLU_A_34_C	CYS_A_35_N	-2.032	-1.423	-9.636	-1.37	-1.918	-8.6	1.33	38.59	-36.79
35	2jsa-14	CYS_A_35_C	LYS_A_36_N	0.549	-2.797	-9.782	0.049	-4.023	-9.835	1.33	92.29	-112.19
36	2jsa-14	LYS_A_36_C	LYS_A_37_N	0.004	-4.308	-12.251	-0.66	-3.164	-12.16	1.33	86.06	120.13
37	2jsa-14	LYS_A_37_C	LEU_A_38_N	-0.141	-1.309	-13.647	-0.267	-0.256	-12.853	1.32	53.18	96.82
38	2jsa-14	LEU_A_38_C	PHE_A_39_N	2.041	0.509	-12.804	2.272	-0.207	-11.713	1.33	34.59	-72.12
39	2jsa-14	PHE_A_39_C	HIS_A_40_N	3.934	-1.98	-12.086	3.396	-2.119	-13.289	1.33	155.21	-165.51
40	2jsa-14	HIS_A_40_C	THR_A_41_N	4.874	-3.154	-14.93	5.057	-1.937	-15.421	1.33	111.75	81.45
41	2jsa-14	THR_A_41_C	ILE_A_42_N	7.502	-1.794	-15.453	7.369	-1.662	-14.141	1.33	8.13	135.22
42	2jsa-14	ILE_A_42_C	PRO_A_43_N	9.083	-3.207	-13.368	10.441	-3.284	-13.36	1.36	89.66	-3.25
43	2jsa-14	PRO_A_43_C	PHE_A_44_N	11.031	-5.336	-12.139	10.364	-4.719	-11.174	1.33	43.28	137.23
44	2jsa-14	PHE_A_44_C	GLY_A_45_N	8.964	-4.784	-9.154	8.073	-4.206	-9.946	1.32	126.71	147.03
45	2jsa-14	GLY_A_45_C	THR_A_46_N	5.934	-4.739	-8.856	5.572	-5.66	-9.736	1.32	131.65	-111.46
46	2jsa-14	THR_A_46_C	ARG_A_47_N	5.299	-7.517	-8.162	6.621	-7.579	-8.14	1.32	89.05	-2.69
47	2jsa-14	ARG_A_47_C	GLU_A_48_N	7.098	-7.538	-5.739	7.307	-6.23	-5.774	1.33	91.51	80.92
48	2jsa-14	GLU_A_48_C	CYS_A_49_N	5.649	-5.299	-4.232	4.816	-5.462	-5.25	1.33	140.18	-168.93
49	2jsa-14	CYS_A_49_C	ASP_A_50_N	2.985	-6.349	-3.943	3.358	-7.607	-4.134	1.33	98.28	-73.48
50	2jsa-14	ASP_A_50_C	HIS_A_51_N	3.983	-8.48	-1.951	5.051	-7.724	-2.163	1.33	99.20	35.29
51	2jsa-14	HIS_A_51_C	TYR_A_52_N	5.584	-6.291	-0.265	4.426	-5.752	-0.616	1.32	105.37	155.04
52	2jsa-14	TYR_A_52_C	VAL_A_53_N	2.584	-4.972	0.812	1.746	-5.718	0.106	1.33	122.18	-138.32
53	2jsa-14	VAL_A_53_C	ASN_A_54_N	0.686	-7.362	1.553	1.671	-7.246	2.432	1.33	48.45	6.72
54	2jsa-14	ASN_A_54_C	SER_A_55_N	3.235	-7.961	4.154	3.221	-6.745	4.681	1.33	66.57	90.66
55	2jsa-14	SER_A_55_C	LYS_A_56_N	4.325	-4.73	5.514	3.692	-4.149	4.505	1.33	139.58	137.45
56	2jsa-14	LYS_A_56_C	VAL_A_57_N	2.128	-2.285	4.439	1.262	-3.285	4.371	1.32	92.94	-130.89
57	2jsa-14	VAL_A_57_C	ASP_A_58_N	-0.703	-3.24	5.805	-0.318	-4.363	6.393	1.32	63.65	-71.08
58	2jsa-14	ASP_A_58_C	PRO_A_59_N	-0.455	-3.502	8.665	0.768	-2.932	8.498	1.36	97.06	24.99
59	2jsa-14	PRO_A_59_C	ILE_A_60_N	0.483	-0.515	8.849	0.658	-0.205	7.573	1.32	164.41	60.55
60	2jsa-14	ILE_A_60_C	ILE_A_61_N	-1.392	1.103	7.493	-2.156	0.049	7.242	1.33	100.91	-125.94
61	2jsa-14	ILE_A_61_C	HIS_A_62_N	-3.637	0.204	9.167	-2.555	-0.165	9.838	1.33	59.59	-18.83
62	2jsa-14	HIS_A_62_C	GLU_A_63_N	-2.604	1.425	11.685	-2.139	2.285	10.789	1.33	132.50	61.60
63	2jsa-14	GLU_A_63_C	LEU_A_64_N	-3.592	4.255	10.816	-4.147	3.914	9.662	1.33	150.56	-148.43
64	2jsa-14	LEU_A_64_C	GLU_A_65_N	-6.473	3.85	10.375	-6.219	2.638	10.845	1.32	69.22	-78.16
65	2jsa-14	GLU_A_65_C	GLY_A_66_N	-6.905	2.755	13.193	-5.72	3.317	13.383	1.33	81.76	25.37
66	2jsa-14	GLY_A_66_C	GLY_A_67_N	-6.044	5.434	14.589	-5.964	6.067	13.428	1.32	151.21	82.80
67	2jsa-14	GLY_A_67_C	THR_A_68_N	-5.629	8.248	12.345	-4.429	7.741	12.098	1.33	100.74	-22.90
68	2jsa-14	THR_A_68_C	ALA_A_69_N	-4.053	8.587	9.83	-3.766	9.732	9.229	1.32	116.98	75.93
69	2jsa-14	ALA_A_69_C	PRO_A_70_N	-3.473	9.141	6.886	-3.99	9.117	5.628	1.36	157.64	-177.34
70	2jsa-14	PRO_A_70_C	LYS_A_71_N	-2.086	9.009	4.076	-2.011	10.31	4.312	1.32	79.74	86.70
71	2jsa-14	LYS_A_71_C	ASP_A_72_N	0.114	11.223	5.069	-0.17	10.469	6.121	1.33	37.45	-110.64
72	2jsa-14	ASP_A_72_C	VAL_A_73_N	1.34	9.141	7.492	0.61	8.098	7.125	1.32	106.08	-124.99
73	2jsa-14	VAL_A_73_C	CYS_A_74_N	2.412	6.623	6.42	2.386	7.232	5.243	1.33	152.62	92.44
74	2											

76	2jsa-14	LYS_A_76_C	LEU_A_77_N	5.953	5.893	10.203	5.525	5.308	9.094	1.32	146.83	-126.19
77	2jsa-14	LEU_A_77_C	ASN_A_78_N	7.131	3.705	8.213	7.912	4.775	8.239	1.32	88.88	53.87
78	2jsa-14	ASN_A_78_C	GLU_A_79_N	9.173	4.161	6.251	8.032	4.378	5.613	1.33	118.78	169.23
79	2jsa-14	GLU_A_79_C	CYS_A_80_N	8.439	4.845	3.245	7.881	6.046	3.201	1.33	91.90	114.92
80	2jsa-14	CYS_A_80_C	PRO_A_81_N	9.888	7.125	2.39	10.516	7.712	1.336	1.36	140.80	43.07
1	2jsa-15	ARG_A_1_C	SER_A_2_N	12.135	3.253	2.072	12.646	3.69	0.929	1.33	149.53	40.54
2	2jsa-15	SER_A_2_C	ALA_A_3_N	12.522	5.196	-0.992	11.362	4.94	-1.578	1.32	116.26	-167.55
3	2jsa-15	ALA_A_3_C	LEU_A_4_N	9.742	4.895	-3.394	9.492	4.183	-4.483	1.32	145.28	-109.35
4	2jsa-15	LEU_A_4_C	SER_A_5_N	7.288	3.382	-3.831	7.981	2.801	-2.862	1.33	43.02	-39.98
5	2jsa-15	SER_A_5_C	CYS_A_6_N	6.269	3.141	-1.152	6.711	4.364	-0.901	1.32	79.08	70.13
6	2jsa-15	CYS_A_6_C	GLN_A_7_N	4.535	5.385	-1.163	4.698	5.486	-2.475	1.33	171.68	31.78
7	2jsa-15	GLN_A_7_C	MET_A_8_N	2.621	4.332	-3.064	3.202	3.142	-3.045	1.32	89.18	-63.98
8	2jsa-15	MET_A_8_C	CYS_A_9_N	1.577	2.113	-1.513	2.157	2.78	-0.526	1.32	41.85	48.99
9	2jsa-15	CYS_A_9_C	GLU_A_10_N	0.193	3.825	0.422	0.292	4.66	-0.603	1.33	140.64	83.24
10	2jsa-15	GLU_A_10_C	LEU_A_11_N	-1.816	4.674	-1.847	-1.407	3.454	-2.163	1.32	103.80	-71.47
11	2jsa-15	LEU_A_11_C	VAL_A_12_N	-3.077	1.688	-2.029	-2.454	1.28	-0.934	1.32	34.22	-33.22
12	2jsa-15	VAL_A_12_C	VAL_A_13_N	-4.136	1.279	0.824	-3.775	2.536	1.032	1.32	80.96	73.98
13	2jsa-15	VAL_A_13_C	LYS_A_14_N	-5.86	3.785	0.907	-5.589	4.332	-0.269	1.33	152.57	63.64
14	2jsa-15	LYS_A_14_C	LYS_A_15_N	-7.626	3.529	-1.332	-7.07	2.329	-1.253	1.32	86.58	-65.14
15	2jsa-15	LYS_A_15_C	TYR_A_16_N	-8.603	0.868	-0.053	-7.885	1.097	1.037	1.33	34.66	17.69
16	2jsa-15	TYR_A_16_C	GLU_A_17_N	-9.351	2.069	2.756	-8.714	3.198	3.027	1.32	78.19	60.57
17	2jsa-15	GLU_A_17_C	GLY_A_18_N	-10.752	4.495	2.633	-10.665	4.168	1.352	1.32	165.20	-75.10
18	2jsa-15	GLY_A_18_C	SER_A_19_N	-12.197	2.823	-0.023	-12.366	1.908	0.922	1.33	44.56	-100.46
19	2jsa-15	SER_A_19_C	ALA_A_20_N	-14.237	0.378	0.564	-14.864	0.842	1.635	1.32	36.07	143.50
20	2jsa-15	ALA_A_20_C	ASP_A_21_N	-16.69	-0.62	2.308	-15.7	-1.5	2.35	1.33	88.18	-41.63
21	2jsa-15	ASP_A_21_C	LYS_A_22_N	-15.088	-3.05	4.122	-14.185	-2.111	4.359	1.32	79.69	46.12
22	2jsa-15	LYS_A_22_C	ASP_A_23_N	-12.788	-3.6	5.683	-12.012	-4.015	4.693	1.32	138.37	-28.14
23	2jsa-15	ASP_A_23_C	ALA_A_24_N	-9.983	-5.272	4.216	-9.065	-5.487	5.146	1.32	45.39	-13.18
24	2jsa-15	ALA_A_24_C	ASN_A_25_N	-7.343	-6.506	3.762	-8.296	-7.406	3.577	1.32	98.03	-136.64
25	2jsa-15	ASN_A_25_C	VAL_A_26_N	-8.442	-7.926	1.204	-9.659	-7.424	1.049	1.33	96.72	157.58
26	2jsa-15	VAL_A_26_C	ILE_A_27_N	-9.329	-5.565	-0.485	-8.588	-5.135	0.526	1.33	40.28	30.13
27	2jsa-15	ILE_A_27_C	LYS_A_28_N	-6.413	-4.237	-0.094	-5.717	-5.068	0.669	1.33	54.86	-50.05
28	2jsa-15	LYS_A_28_C	LYS_A_29_N	-4.362	-5.961	-1.144	-5.404	-6.703	-1.488	1.32	105.05	-144.55
29	2jsa-15	LYS_A_29_C	ASP_A_30_N	-5.779	-6.094	-3.813	-6.748	-5.26	-3.466	1.32	74.81	139.28
30	2jsa-15	ASP_A_30_C	PHE_A_31_N	-5.814	-3.419	-4.755	-4.957	-3.138	-3.783	1.33	42.86	18.15
31	2jsa-15	PHE_A_31_C	ASP_A_32_N	-2.991	-3.114	-5.26	-2.631	-4.376	-5.082	1.32	82.28	-74.08
32	2jsa-15	ASP_A_32_C	ALA_A_33_N	-2.647	-4.854	-7.468	-3.971	-4.82	-7.411	1.33	87.54	178.53
33	2jsa-15	ALA_A_33_C	GLU_A_34_N	-4.212	-3.362	-9.344	-4.274	-2.223	-8.671	1.32	59.46	93.12
34	2jsa-15	GLU_A_34_C	CYS_A_35_N	-2.268	-0.88	-9.081	-1.663	-2.011	-8.745	1.33	75.32	-61.86
35	2jsa-15	CYS_A_35_C	LYS_A_36_N	0.412	-2.642	-9.814	0.07	-3.893	-10.089	1.33	101.97	-105.29
36	2jsa-15	LYS_A_36_C	LYS_A_37_N	0.193	-3.805	-12.517	-0.954	-3.146	-12.426	1.33	86.06	150.12
37	2jsa-15	LYS_A_37_C	LEU_A_38_N	-0.741	-1.024	-13.598	-0.788	-0.32	-12.476	1.33	32.16	93.82
38	2jsa-15	LEU_A_38_C	PHE_A_39_N	1.356	0.822	-12.63	1.974	-0.019	-11.814	1.32	51.98	-53.69
39	2jsa-15	PHE_A_39_C	HIS_A_40_N	3.677	-1.403	-12.922	2.793	-1.522	-13.902	1.33	137.69	-172.33
40	2jsa-15	HIS_A_40_C	THR_A_41_N	4.282	-2.415	-15.614	4.861	-1.231	-15.477	1.33	84.07	63.94
41	2jsa-15	THR_A_41_C	ILE_A_42_N	7.127	-0.401	-15.05	7.572	-1.289	-14.173	1.33	48.56	-63.38
42	2jsa-15	ILE_A_42_C	PRO_A_43_N	9.4	-2.098	-12.786	10.696	-1.787	-12.517	1.36	78.59	13.49
43	2jsa-15	PRO_A_43_C	PHE_A_44_N	11.446	-3.317	-10.745	10.909	-4.526	-10.646	1.33	85.72	-113.95
44	2jsa-15	PHE_A_44_C	GLY_A_45_N	9.395	-4.526	-8.709	8.834	-3.541	-9.394	1.32	121.14	119.66
45	2jsa-15	GLY_A_45_C	THR_A_46_N	6.564	-3.899	-8.518	6.164	-4.692	-9.501	1.32	137.90	-116.77
46	2jsa-15	THR_A_46_C	ARG_A_47_N	5.614	-6.695	-8.201	6.915	-6.944	-8.193	1.32	89.65	-10.83
47	2jsa-15	ARG_A_47_C	GLU_A_48_N	7.307	-7.324	-5.806	7.585	-6.037	-5.652	1.33	83.33	77.81
48	2jsa-15	GLU_A_48_C	CYS_A_49_N	5.974	-5.283	-3.969	5.139	-5.115	-4.984	1.33	140.00	168.62
49	2jsa-15	CYS_A_49_C	ASP_A_50_N	3.266	-6.135	-3.845	3.381	-7.349	-4.362	1.32	112.98	-84.59
50	2jsa-15	ASP_A_50_C	HIS_A_51_N	3.764	-8.543	-2.277	4.955	-7.964	-2.311	1.32	91.47	25.93
51	2jsa-15	HIS_A_51_C	TYR_A_52_N	5.405	-6.69	-0.282	4.294	-6.076	-0.662	1.33	106.67	151.07
52	2jsa-15	TYR_A_52_C	VAL_A_53_N	2.462	-5.197	0.721	1.62	-5.926	0.001	1.33	122.88	-139.11
53	2jsa-15	VAL_A_53_C	ASN_A_54_N	0.429	-7.516	1.406	1.343	-7.43	2.362	1.33	43.84	5.38
54	2jsa-15	ASN_A_54_C	SER_A_55_N	2.784	-8.219	4.157	2.832	-6.981	4.626	1.32	69.27	87.78
55	2jsa-15	SER_A_55_C	LYS_A_56_N	3.89	-5.023	5.637	3.398	-4.36	4.601	1.32	141.45	126.58
56	2jsa-15	LYS_A_56_C	VAL_A_57_N	1.826	-2.503	4.544	0.974	-3.506	4.399	1.32	96.29	-130.35
57	2jsa-15	VAL_A_57_C	ASP_A_58_N	-1.091	-3.501	5.687	-0.373	-4.245	6.516	1.33	51.28	-46.02
58	2jsa-15	ASP_A_58_C	PRO_A_59_N	-0.63	-3.335	8.758	0.593	-2.751	8.645	1.36	94.77	25.53
59	2jsa-15	PRO_A_59_C	ILE_A_60_N	0.255	-0.331	8.913	0.401	-0.118	7.613	1.33	168.76	55.57
60	2jsa-15	ILE_A_60_C	ILE_A_61_N	-1.659	1.162	7.414	-2.368	0.046	7.322	1.33	93.98	-122.43
61	2jsa-15	ILE_A_61_C	HIS_A_62_N	-3.884	0.255	9.215	-2.817	-0.089	9.92	1.32	57.84	-17.87
62	2jsa-15	HIS_A_62_C	GLU_A_63_N	-2.644	1.568	11.7	-2.205	2.327	10.707	1.32	138.56	59.96
63	2jsa-15	GLU_A_63_C	LEU_A_64_N	-3.357	4.488	10.72	-3.969	4.283	9.563	1.32	150.85	-161.48
64	2jsa-15	LEU_A_64_C	GLU_A_65_N	-6.301	4.396	10.249	-6.327	3.079	10.402	1.33	83.37	-91.13
65	2jsa-15	GLU_A_65_C	GLY_A_66_N	-7.061	2.941	12.734	-5.822	3.318	13.013	1.32	77.84	16.92
66	2jsa-15	GLY_A_66_C	GLY_A_67_N	-5.957	5.242	14.537	-5.777	6.047	13.5	1.33	141.50	77.40
67	2jsa-15	GLY_A_67_C	THR_A_68_N	-5.375	8.29	12.577	-4.219	7.76	12.203	1.33	106.39	-24.63
68	2jsa-15	THR_A_68_C	ALA_A_69_N	-4.054	8.716	9.953	-3.46	9.595	9.159	1.33	126.81	55.95
69	2jsa-15	ALA_A_69_C	PRO_A_70_N	-3.317	9.132	6.774	-3.946	9.12	5.568	1.36	152.45	-178.91
70	2jsa-15	PRO_A_70_C	LYS_A_71_N	-2.191	9.147	3.846	-1.857	10.26	4.483	1.33	61.27	73.30
71	2jsa-15	LYS_A_71_C	ASP_A_72_N	0.275	11.214	5.166	0.012	10.492	6.245	1.32	35.46	-110.01
72	2jsa-15	ASP_A_72_C	VAL_A_73_N	1.529	9.151	7.593	0.949	8.166	6.924	1.32	120.34	-120.49
73	2jsa-15	VAL_A_73_C	CYS_A_74_N	2.803	6.716	6.306	2.842	7.262	5.099	1.33	155.61	85.91
74	2jsa-15	CYS_A_74_C	THR_A_75_N	4.911	8.456	4.725	5.111	8.58	6.03	1.33	10.22	31.80
75	2jsa-15	THR_A_75_C	LYS_A_76_N	6.394	9.341	7.972	5.44	9.122	8.865	1.32	47.62	-167.07
76	2jsa-15	LYS_A_76_C	LEU_A_77_N	6.425	7.411	10.29	6.025	6.567	9.349	1.33	135.21	-115.36
77	2jsa-15	LEU_A_77_C	ASN_A_78_N	7.822	5.231	8.399	8.342	6.428	8.176	1.32	99.70	66.52
78	2jsa-15	ASN_A_78_C	GLU_A_79_N	9.339	5.866	6.03	8.076	5.669	5.68	1.33	105.31	-171.13
79	2jsa-15	GLU_A_79_C	CYS_A_80_N	7.632	6.009	3.296	8.57	6.944	3.288	1.32	90.35	44.91
80	2jsa-15	CYS_A_80_C	PRO_A_81_N	9.772	8.906	2.542	10.513	9.239	1.452	1.36	143.30	24.20

Table 2. A reversible spherical geometric conversion of Caenopore-5 backbone peptide bond coordinate matrix to three independent vectors of ρ , θ and ϕ [1–3].

1. Ethical statement

No ethical approval is required.

2. Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the author used OpenAI's ChatGPT in order to improve the readability of the manuscript, and to make it as concise and short as possible. After using this tool, the author reviewed and edited the content as needed and takes full responsibility for the content of the publication.

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