# Structural Identification of the Electrostatic Hot Spots for Severe Acute Respiratory Syndrome Coronavirus Spike Protein to Be Complexed with Its Receptor ACE2 and Its Neutralizing Antibodies

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# Supporting Material

## Overall analysis of SARS coronavirus spike protein-related structures

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_31 | NZ | A_GLU_35 | OE1 | 3.992 |
| 2AJF | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.808 |
| 2AJF | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.727 |
| 2AJF | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.080 |
| 2AJF | A_ARG_177 | NH1 | A_GLU_181 | OE2 | 3.241 |
| 2AJF | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.882 |
| 2AJF | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.146 |
| 2AJF | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.420 |
| 2AJF | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 2.794 |
| 2AJF | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.745 |
| 2AJF | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.452 |
| 2AJF | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.763 |
| 2AJF | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.712 |
| 2AJF | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.011 |
| 2AJF | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.673 |
| 2AJF | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.856 |
| 2AJF | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.630 |
| 2AJF | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.271 |
| 2AJF | A_LYS_309 | NZ | A_GLU_312 | OE2 | 3.754 |
| 2AJF | A_LYS_353 | NZ | A_ASP_38 | OD1 | 3.263 |
| 2AJF | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 2.604 |
| 2AJF | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 3.201 |
| 2AJF | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.025 |
| 2AJF | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.882 |
| 2AJF | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 2.606 |
| 2AJF | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.668 |
| 2AJF | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 2.869 |
| 2AJF | A_ARG_393 | NH1 | A_GLU_37 | OE1 | 3.436 |
| 2AJF | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 3.134 |
| 2AJF | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.409 |
| 2AJF | A_HIS_401 | NE2 | A_ASP_382 | OD2 | 3.397 |
| 2AJF | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.685 |
| 2AJF | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.827 |
| 2AJF | A_LYS_458 | NZ | A_GLU_227 | OE1 | 3.613 |
| 2AJF | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.040 |
| 2AJF | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 3.643 |
| 2AJF | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.692 |
| 2AJF | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.567 |
| 2AJF | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.336 |
| 2AJF | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.457 |
| 2AJF | A_HIS_493 | ND1 | A_GLU_166 | OE2 | 3.978 |
| 2AJF | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.395 |
| 2AJF | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.568 |
| 2AJF | A_LYS_534 | NZ | B_ASP_431 | OD1 | 3.656 |
| 2AJF | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.928 |
| 2AJF | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.791 |
| 2AJF | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.920 |
| 2AJF | A_LYS_577 | NZ | A_GLU_571 | OE1 | 3.259 |
| 2AJF | A_LYS_600 | NZ | A_ASP_597 | OD1 | 3.832 |
| 2AJF | A_LYS_600 | NZ | A_ASP_597 | OD2 | 3.177 |
| 2AJF | B_LYS_26 | NZ | B_GLU_22 | OE1 | 3.456 |
| 2AJF | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.258 |
| 2AJF | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.099 |
| 2AJF | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 2.804 |
| 2AJF | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.317 |
| 2AJF | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.392 |
| 2AJF | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.458 |

| 2AJF | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.319 |
|---|---|---|---|---|---|
| 2AJF | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.488 |
| 2AJF | B_ARG_219 | NH2 | B_ASP_201 | OD1 | 3.892 |
| 2AJF | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.087 |
| 2AJF | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.992 |
| 2AJF | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.226 |
| 2AJF | B_ARG_357 | NH2 | B_ASP_355 | OD1 | 2.846 |
| 2AJF | B_ARG_357 | NH2 | B_ASP_355 | OD2 | 2.664 |
| 2AJF | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.307 |
| 2AJF | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.459 |
| 2AJF | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.493 |
| 2AJF | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.992 |
| 2AJF | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.671 |
| 2AJF | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 3.226 |
| 2AJF | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.233 |
| 2AJF | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.525 |
| 2AJF | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.748 |
| 2AJF | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.582 |
| 2AJF | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.890 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.710 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.597 |
| 2AJF | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.035 |
| 2AJF | B_LYS_475 | NZ | B_GLU_479 | OE2 | 3.697 |
| 2AJF | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 2.938 |
| 2AJF | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.429 |
| 2AJF | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.671 |
| 2AJF | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.284 |
| 2AJF | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.981 |
| 2AJF | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.560 |
| 2AJF | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.654 |
| 2AJF | B_LYS_541 | NZ | B_GLU_435 | OE1 | 3.723 |
| 2AJF | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.314 |
| 2AJF | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 2.787 |
| 2AJF | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 2.961 |
| 2AJF | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.004 |
| 2AJF | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.286 |
| 2AJF | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.910 |
| 2AJF | E_ARG_426 | NH1 | A_GLU_329 | OE2 | 3.740 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.855 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 2.946 |
| 2AJF | E_ARG_441 | NH1 | E_ASP_454 | OD1 | 3.531 |
| 2AJF | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.278 |
| 2AJF | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.408 |
| 2AJF | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.735 |
| 2AJF | E_LYS_447 | NZ | E_ASP_407 | OD2 | 3.899 |
| 2AJF | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.268 |
| 2AJF | E_LYS_465 | NZ | E_ASP_463 | OD2 | 3.801 |
| 2AJF | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.014 |
| 2AJF | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.467 |
| 2AJF | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.200 |
| 2AJF | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 2.772 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.890 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.381 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 2.717 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 2.911 |
| 2AJF | F_LYS_439 | NZ | F_ASP_480 | OD1 | 3.696 |
| 2AJF | F_ARG_441 | NH1 | F_ASP_454 | OD1 | 3.900 |
| 2AJF | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.426 |

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|---|---|---|---|---|---|
| 2AJF | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.001 |
| 2AJF | F_ARG_453 | NH2 | F_GLU_341 | OE2 | 3.749 |
| 2AJF | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 3.808 |
| 2DD8 | H_ARG_38 | NH1 | H_ASP_86 | OD1 | 2.908 |
| 2DD8 | H_ARG_38 | NH2 | H_GLU_46 | OE1 | 3.751 |
| 2DD8 | H_ARG_38 | NH2 | H_ASP_86 | OD1 | 3.769 |
| 2DD8 | H_LYS_62 | NZ | H_GLU_46 | OE1 | 3.535 |
| 2DD8 | H_LYS_62 | NZ | H_GLU_46 | OE2 | 3.348 |
| 2DD8 | H_ARG_66 | NH1 | H_ASP_86 | OD1 | 3.583 |
| 2DD8 | H_ARG_66 | NH1 | H_ASP_86 | OD2 | 3.304 |
| 2DD8 | H_ARG_66 | NH2 | H_ASP_86 | OD1 | 2.890 |
| 2DD8 | H_ARG_66 | NH2 | H_ASP_86 | OD2 | 3.740 |
| 2DD8 | H_ARG_94 | NH2 | H_ASP_101 | OD2 | 2.723 |
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE1 | 3.913 |
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE2 | 2.993 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE1 | 2.759 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE2 | 3.226 |
| 2DD8 | H_LYS_210 | NZ | H_GLU_212 | OE1 | 3.571 |
| 2DD8 | H_LYS_210 | NZ | H_GLU_212 | OE2 | 3.616 |
| 2DD8 | L_LYS_31 | NZ | L_ASP_92 | OD1 | 3.038 |
| 2DD8 | L_ARG_61 | NH1 | L_ASP_82 | OD1 | 3.795 |
| 2DD8 | L_ARG_61 | NH1 | L_ASP_82 | OD2 | 2.711 |
| 2DD8 | L_ARG_61 | NH2 | L_ASP_82 | OD1 | 2.938 |
| 2DD8 | L_ARG_61 | NH2 | L_ASP_82 | OD2 | 3.305 |
| 2DD8 | L_LYS_130 | NZ | H_ASP_144 | OD2 | 3.343 |
| 2DD8 | L_LYS_167 | NZ | L_GLU_83 | OE1 | 3.208 |
| 2DD8 | L_ARG_191 | NH1 | L_ASP_152 | OD2 | 3.527 |
| 2DD8 | S_ARG_342 | NH2 | S_ASP_385 | OD1 | 3.426 |
| 2DD8 | S_ARG_342 | NH2 | S_ASP_385 | OD2 | 2.961 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD1 | 3.643 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD2 | 3.461 |
| 2DD8 | S_ARG_395 | NH2 | L_ASP_95A | OD1 | 3.001 |
| 2DD8 | S_ARG_395 | NH2 | S_ASP_392 | OD1 | 3.245 |
| 2DD8 | S_LYS_411 | NZ | S_ASP_407 | OD1 | 2.884 |
| 2DD8 | S_LYS_439 | NZ | S_ASP_480 | OD1 | 3.148 |
| 2DD8 | S_ARG_441 | NH2 | S_ASP_454 | OD1 | 3.375 |
| 2DD8 | S_ARG_444 | NH2 | S_ASP_454 | OD2 | 3.531 |
| 2DD8 | S_LYS_447 | NZ | S_ASP_407 | OD1 | 3.742 |
| 2DD8 | S_ARG_449 | NH1 | S_GLU_452 | OE1 | 3.677 |
| 2DD8 | S_ARG_449 | NH1 | S_GLU_452 | OE2 | 3.337 |
| 2DD8 | S_ARG_449 | NH2 | S_GLU_452 | OE2 | 2.689 |
| 2DD8 | S_ARG_495 | NH2 | S_ASP_429 | OD1 | 3.196 |
| 2DD8 | S_ARG_495 | NH2 | S_ASP_429 | OD2 | 3.755 |
| 2GHV | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.550 |
| 2GHV | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 2.981 |
| 2GHV | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.496 |
| 2GHV | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.534 |
| 2GHV | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.804 |
| 2GHV | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.565 |
| 2GHV | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.040 |
| 2GHV | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.590 |
| 2GHV | C_ARG_342 | NH2 | C_ASP_385 | OD1 | 3.469 |
| 2GHV | C_ARG_342 | NH2 | C_ASP_385 | OD2 | 2.877 |
| 2GHV | C_LYS_343 | NZ | C_GLU_327 | OE1 | 3.965 |
| 2GHV | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.439 |
| 2GHV | C_ARG_444 | NH2 | C_GLU_452 | OE2 | 3.650 |
| 2GHV | C_ARG_444 | NH2 | C_ASP_454 | OD1 | 3.401 |
| 2GHV | C_ARG_449 | NH2 | C_GLU_452 | OE1 | 3.440 |

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|---|---|---|---|---|---|
| 2GHV | C_ARG_449 | NH2 | C_GLU_452 | OE2 | 3.175 |
| 2GHV | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 2.912 |
| 2GHV | C_ARG_495 | NH2 | C_ASP_429 | OD2 | 3.523 |
| 2GHW | A_ARG_342 | NH2 | A_ASP_385 | OD1 | 3.548 |
| 2GHW | A_ARG_342 | NH2 | A_ASP_385 | OD2 | 3.167 |
| 2GHW | A_LYS_439 | NZ | A_ASP_480 | OD2 | 3.192 |
| 2GHW | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.680 |
| 2GHW | A_ARG_444 | NH2 | A_GLU_452 | OE2 | 3.285 |
| 2GHW | A_ARG_444 | NH2 | A_ASP_454 | OD1 | 3.823 |
| 2GHW | A_ARG_449 | NH1 | A_GLU_452 | OE1 | 3.684 |
| 2GHW | A_ARG_449 | NH1 | A_GLU_452 | OE2 | 3.739 |
| 2GHW | A_ARG_449 | NH2 | A_GLU_452 | OE2 | 3.726 |
| 2GHW | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.315 |
| 2GHW | A_ARG_495 | NH2 | A_ASP_429 | OD2 | 3.983 |
| 2GHW | B_HIS_35 | NE2 | B_ASP_99 | OD1 | 3.622 |
| 2GHW | B_ARG_38 | NH1 | B_GLU_89 | OE1 | 3.674 |
| 2GHW | B_ARG_38 | NH1 | B_ASP_90 | OD1 | 3.164 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_46 | OE1 | 3.155 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_46 | OE2 | 3.798 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_89 | OE1 | 3.206 |
| 2GHW | B_ARG_67 | NH1 | B_ASP_90 | OD1 | 3.382 |
| 2GHW | B_ARG_67 | NH1 | B_ASP_90 | OD2 | 2.930 |
| 2GHW | B_ARG_67 | NH2 | B_GLU_89 | OE1 | 3.863 |
| 2GHW | B_ARG_67 | NH2 | B_GLU_89 | OE2 | 3.548 |
| 2GHW | B_ARG_67 | NH2 | B_ASP_90 | OD1 | 3.270 |
| 2GHW | B_ARG_67 | NH2 | B_ASP_90 | OD2 | 3.745 |
| 2GHW | B_LYS_76 | NZ | B_ASP_73 | OD2 | 2.795 |
| 2GHW | B_ARG_98 | NH2 | B_ASP_105 | OD2 | 3.012 |
| 2GHW | B_ARG_156 | NH2 | B_ASP_202 | OD1 | 3.384 |
| 2GHW | B_ARG_156 | NH2 | B_ASP_202 | OD2 | 3.152 |
| 2GHW | B_ARG_162 | NH1 | A_ASP_480 | OD1 | 3.081 |
| 2GHW | B_ARG_193 | NH1 | B_GLU_211 | OE2 | 3.176 |
| 2GHW | B_ARG_193 | NH2 | B_GLU_211 | OE2 | 3.887 |
| 2GHW | B_ARG_193 | NH2 | B_GLU_213 | OE1 | 3.299 |
| 2GHW | B_ARG_193 | NH2 | B_ASP_214 | OD1 | 3.163 |
| 2GHW | B_ARG_193 | NH2 | B_ASP_214 | OD2 | 3.876 |
| 2GHW | B_ARG_223 | NH2 | B_ASP_182 | OD1 | 3.202 |
| 2GHW | B_LYS_235 | NZ | B_GLU_237 | OE2 | 3.402 |
| 2GHW | C_ARG_342 | NH2 | C_ASP_385 | OD1 | 3.626 |
| 2GHW | C_ARG_342 | NH2 | C_ASP_385 | OD2 | 3.156 |
| 2GHW | C_LYS_439 | NZ | C_ASP_480 | OD1 | 3.911 |
| 2GHW | C_LYS_439 | NZ | C_ASP_480 | OD2 | 3.110 |
| 2GHW | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.789 |
| 2GHW | C_ARG_444 | NH2 | C_GLU_452 | OE2 | 3.347 |
| 2GHW | C_ARG_444 | NH2 | C_ASP_454 | OD1 | 3.456 |
| 2GHW | C_ARG_449 | NH1 | C_GLU_452 | OE1 | 3.965 |
| 2GHW | C_ARG_449 | NH1 | C_GLU_452 | OE2 | 3.472 |
| 2GHW | C_ARG_449 | NH2 | C_GLU_452 | OE1 | 3.904 |
| 2GHW | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 3.274 |
| 2GHW | D_HIS_35 | ND1 | D_ASP_99 | OD1 | 3.954 |
| 2GHW | D_HIS_35 | NE2 | D_ASP_99 | OD1 | 3.761 |
| 2GHW | D_ARG_38 | NH1 | D_ASP_90 | OD1 | 3.162 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_46 | OE1 | 3.538 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_46 | OE2 | 3.668 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_89 | OE1 | 3.329 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_89 | OE2 | 2.864 |
| 2GHW | D_LYS_65 | NZ | D_ASP_62 | OD1 | 3.926 |
| 2GHW | D_ARG_67 | NH1 | D_ASP_90 | OD2 | 3.105 |

| 2GHW | D_ARG_67 | NH2 | D_GLU_89 | OE1 | 3.576 |
|---|---|---|---|---|---|
| 2GHW | D_ARG_67 | NH2 | D_ASP_90 | OD1 | 3.163 |
| 2GHW | D_ARG_67 | NH2 | D_ASP_90 | OD2 | 3.377 |
| 2GHW | D_LYS_76 | NZ | D_ASP_73 | OD2 | 3.658 |
| 2GHW | D_ARG_98 | NH2 | D_ASP_105 | OD1 | 3.960 |
| 2GHW | D_ARG_98 | NH2 | D_ASP_105 | OD2 | 3.196 |
| 2GHW | D_ARG_156 | NH1 | D_ASP_202 | OD2 | 3.931 |
| 2GHW | D_ARG_162 | NH2 | C_ASP_480 | OD1 | 3.626 |
| 2GHW | D_ARG_193 | NH1 | D_GLU_211 | OE1 | 3.249 |
| 2GHW | D_ARG_193 | NH1 | D_GLU_211 | OE2 | 3.681 |
| 2GHW | D_ARG_193 | NH2 | D_GLU_211 | OE1 | 3.135 |
| 2GHW | D_ARG_193 | NH2 | D_GLU_213 | OE1 | 3.465 |
| 2GHW | D_ARG_193 | NH2 | D_ASP_214 | OD1 | 3.132 |
| 2GHW | D_ARG_193 | NH2 | D_ASP_214 | OD2 | 3.717 |
| 2GHW | D_ARG_223 | NH2 | D_ASP_182 | OD1 | 3.375 |
| 2GHW | D_LYS_235 | NZ | D_GLU_237 | OE2 | 3.600 |
| 2GHW | D_LYS_239 | NZ | D_GLU_149 | OE1 | 3.290 |
| 2GHW | D_LYS_239 | NZ | D_GLU_149 | OE2 | 3.630 |
| 3BGF | S_ARG_342 | NH2 | S_ASP_385 | OD1 | 3.676 |
| 3BGF | S_ARG_342 | NH2 | S_ASP_385 | OD2 | 3.162 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD1 | 3.504 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD2 | 2.403 |
| 3BGF | S_LYS_439 | NZ | S_ASP_480 | OD1 | 3.797 |
| 3BGF | S_LYS_439 | NZ | A_ASP_480 | OD2 | 3.161 |
| 3BGF | S_ARG_441 | NH2 | S_ASP_454 | OD1 | 2.963 |
| 3BGF | S_ARG_444 | NH2 | S_GLU_452 | OE2 | 3.267 |
| 3BGF | S_ARG_444 | NH2 | S_ASP_454 | OD2 | 3.815 |
| 3BGF | S_LYS_447 | NZ | S_ASP_407 | OD1 | 3.987 |
| 3BGF | S_LYS_447 | NZ | S_ASP_407 | OD2 | 3.876 |
| 3BGF | S_ARG_449 | NH2 | S_GLU_452 | OE1 | 3.535 |
| 3BGF | S_ARG_495 | NH2 | S_ASP_429 | OD1 | 3.362 |
| 3BGF | S_ARG_495 | NH2 | S_ASP_429 | OD2 | 3.615 |
| 3BGF | A_ARG_342 | NH2 | A_ASP_385 | OD1 | 3.423 |
| 3BGF | A_ARG_342 | NH2 | A_ASP_385 | OD2 | 2.961 |
| 3BGF | A_LYS_390 | NZ | A_ASP_393 | OD1 | 3.583 |
| 3BGF | A_LYS_390 | NZ | A_ASP_393 | OD2 | 3.966 |
| 3BGF | A_LYS_439 | NZ | S_ASP_480 | OD2 | 2.520 |
| 3BGF | A_LYS_439 | NZ | A_ASP_480 | OD1 | 3.180 |
| 3BGF | A_ARG_441 | NH2 | A_ASP_454 | OD1 | 3.440 |
| 3BGF | A_ARG_444 | NH2 | A_GLU_452 | OE2 | 3.371 |
| 3BGF | A_ARG_444 | NH2 | A_ASP_454 | OD2 | 3.730 |
| 3BGF | A_LYS_447 | NZ | A_ASP_407 | OD1 | 2.877 |
| 3BGF | A_LYS_447 | NZ | A_ASP_407 | OD2 | 2.805 |
| 3BGF | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.108 |
| 3BGF | A_ARG_495 | NH2 | A_ASP_429 | OD2 | 2.922 |
| 3BGF | L_ARG_24 | NH2 | L_ASP_70 | OD1 | 3.258 |
| 3BGF | L_ARG_24 | NH2 | L_ASP_70 | OD2 | 2.893 |
| 3BGF | L_ARG_46 | NH1 | L_ASP_55 | OD1 | 3.016 |
| 3BGF | L_ARG_46 | NH1 | L_ASP_55 | OD2 | 3.557 |
| 3BGF | L_ARG_61 | NH1 | L_GLU_79 | OE1 | 3.984 |
| 3BGF | L_ARG_61 | NH1 | L_GLU_79 | OE2 | 3.405 |
| 3BGF | L_ARG_61 | NH2 | L_ASP_82 | OD1 | 2.650 |
| 3BGF | L_ARG_61 | NH2 | L_ASP_82 | OD2 | 2.907 |
| 3BGF | L_ARG_66 | NH2 | L_GLU_28 | OE2 | 2.738 |
| 3BGF | L_LYS_149 | NZ | L_GLU_195 | OE1 | 3.683 |
| 3BGF | L_LYS_149 | NZ | L_GLU_195 | OE2 | 3.129 |
| 3BGF | L_HIS_189 | ND1 | L_ASP_151 | OD1 | 2.696 |
| 3BGF | H_ARG_33 | NH1 | H_ASP_56 | OD2 | 3.848 |

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|---|---|---|---|---|---|
| 3BGF | H_HIS_35 | NE2 | H_GLU_95 | OE1 | 2.884 |
| 3BGF | H_LYS_38 | NZ | H_ASP_86 | OD1 | 3.661 |
| 3BGF | H_LYS_62 | NZ | H_GLU_46 | OE1 | 2.635 |
| 3BGF | H_LYS_62 | NZ | H_GLU_46 | OE2 | 3.712 |
| 3BGF | H_LYS_66 | NZ | H_ASP_86 | OD1 | 3.553 |
| 3BGF | H_LYS_66 | NZ | H_ASP_86 | OD2 | 2.671 |
| 3BGF | H_ARG_94 | NH1 | H_ASP_101 | OD1 | 2.347 |
| 3BGF | H_ARG_94 | NH1 | H_ASP_101 | OD2 | 3.381 |
| 3BGF | H_LYS_210 | NZ | L_GLU_123 | OE1 | 3.997 |
| 3BGF | H_LYS_211 | NZ | H_GLU_213 | OE2 | 3.764 |
| 3BGF | C_ARG_24 | NH2 | C_ASP_70 | OD1 | 3.766 |
| 3BGF | C_ARG_46 | NH1 | C_ASP_55 | OD1 | 2.965 |
| 3BGF | C_ARG_61 | NH1 | C_GLU_79 | OE1 | 3.352 |
| 3BGF | C_ARG_61 | NH1 | C_GLU_79 | OE2 | 3.278 |
| 3BGF | C_ARG_61 | NH2 | C_GLU_81 | OE2 | 3.045 |
| 3BGF | C_ARG_61 | NH2 | C_ASP_82 | OD1 | 2.379 |
| 3BGF | C_ARG_61 | NH2 | C_ASP_82 | OD2 | 2.905 |
| 3BGF | C_ARG_66 | NH2 | C_GLU_28 | OE1 | 3.607 |
| 3BGF | C_ARG_66 | NH2 | C_GLU_28 | OE2 | 2.938 |
| 3BGF | C_LYS_142 | NZ | C_GLU_105 | OE1 | 3.341 |
| 3BGF | C_LYS_149 | NZ | C_GLU_195 | OE1 | 3.352 |
| 3BGF | C_LYS_149 | NZ | C_GLU_195 | OE2 | 3.898 |
| 3BGF | C_ARG_155 | NH2 | C_GLU_185 | OE2 | 3.481 |
| 3BGF | C_LYS_199 | NZ | C_ASP_110 | OD2 | 3.825 |
| 3BGF | B_HIS_35 | NE2 | B_GLU_95 | OE1 | 2.642 |
| 3BGF | B_LYS_38 | NZ | B_ASP_86 | OD1 | 3.591 |
| 3BGF | B_LYS_62 | NZ | B_GLU_46 | OE1 | 2.547 |
| 3BGF | B_LYS_62 | NZ | B_GLU_46 | OE2 | 3.280 |
| 3BGF | B_LYS_66 | NZ | B_ASP_86 | OD1 | 3.814 |
| 3BGF | B_LYS_66 | NZ | B_ASP_86 | OD2 | 2.805 |
| 3BGF | B_ARG_94 | NH1 | B_ASP_101 | OD1 | 2.357 |
| 3BGF | B_ARG_94 | NH1 | B_ASP_101 | OD2 | 2.930 |
| 3BGF | B_ARG_100 | NH1 | B_ASP_101 | OD1 | 3.816 |
| 3D0G | A_LYS_26 | NZ | A_GLU_23 | OE1 | 2.776 |
| 3D0G | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.622 |
| 3D0G | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.885 |
| 3D0G | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.369 |
| 3D0G | A_LYS_187 | NZ | A_ASP_509 | OD1 | 3.967 |
| 3D0G | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.239 |
| 3D0G | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.291 |
| 3D0G | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 2.733 |
| 3D0G | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.447 |
| 3D0G | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.737 |
| 3D0G | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.326 |
| 3D0G | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.150 |
| 3D0G | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.034 |
| 3D0G | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.248 |
| 3D0G | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.949 |
| 3D0G | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.812 |
| 3D0G | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.737 |
| 3D0G | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.262 |
| 3D0G | A_LYS_353 | NZ | A_GLU_38 | OE2 | 2.453 |
| 3D0G | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.211 |
| 3D0G | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.562 |
| 3D0G | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.713 |
| 3D0G | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.062 |
| 3D0G | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.290 |
| 3D0G | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.966 |

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|---|---|---|---|---|---|
| 3D0G | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.850 |
| 3D0G | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 2.924 |
| 3D0G | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.555 |
| 3D0G | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.763 |
| 3D0G | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.955 |
| 3D0G | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.595 |
| 3D0G | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.159 |
| 3D0G | A_LYS_465 | NZ | A_GLU_467 | OE1 | 2.701 |
| 3D0G | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.777 |
| 3D0G | A_LYS_476 | NZ | A_GLU_479 | OE1 | 2.526 |
| 3D0G | A_LYS_476 | NZ | A_GLU_479 | OE2 | 3.323 |
| 3D0G | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.955 |
| 3D0G | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.559 |
| 3D0G | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.849 |
| 3D0G | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.410 |
| 3D0G | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.585 |
| 3D0G | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.569 |
| 3D0G | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.965 |
| 3D0G | A_LYS_534 | NZ | A_GLU_549 | OE1 | 3.278 |
| 3D0G | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.979 |
| 3D0G | A_LYS_541 | NZ | A_GLU_435 | OE1 | 2.843 |
| 3D0G | A_LYS_541 | NZ | A_GLU_435 | OE2 | 3.422 |
| 3D0G | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.839 |
| 3D0G | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.548 |
| 3D0G | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.791 |
| 3D0G | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 2.982 |
| 3D0G | B_ARG_177 | NH1 | B_GLU_181 | OE2 | 3.376 |
| 3D0G | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.263 |
| 3D0G | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.324 |
| 3D0G | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.466 |
| 3D0G | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.330 |
| 3D0G | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.128 |
| 3D0G | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.324 |
| 3D0G | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.217 |
| 3D0G | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.383 |
| 3D0G | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.414 |
| 3D0G | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.707 |
| 3D0G | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.600 |
| 3D0G | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.077 |
| 3D0G | B_LYS_309 | NZ | B_GLU_312 | OE2 | 3.968 |
| 3D0G | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.363 |
| 3D0G | B_LYS_353 | NZ | B_GLU_38 | OE2 | 3.062 |
| 3D0G | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.623 |
| 3D0G | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.770 |
| 3D0G | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.697 |
| 3D0G | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.864 |
| 3D0G | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.467 |
| 3D0G | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.478 |
| 3D0G | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.097 |
| 3D0G | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 2.744 |
| 3D0G | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.625 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.856 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.820 |
| 3D0G | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.654 |
| 3D0G | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.787 |
| 3D0G | B_LYS_465 | NZ | B_GLU_467 | OE2 | 3.564 |
| 3D0G | B_LYS_475 | NZ | B_GLU_479 | OE2 | 3.791 |
| 3D0G | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 2.475 |

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|---|---|---|---|---|---|
| 3D0G | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.483 |
| 3D0G | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.939 |
| 3D0G | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.187 |
| 3D0G | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.890 |
| 3D0G | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.723 |
| 3D0G | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.789 |
| 3D0G | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.550 |
| 3D0G | B_LYS_541 | NZ | B_GLU_430 | OE2 | 2.944 |
| 3D0G | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.837 |
| 3D0G | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 2.994 |
| 3D0G | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.222 |
| 3D0G | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.591 |
| 3D0G | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.325 |
| 3D0G | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.203 |
| 3D0G | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.859 |
| 3D0G | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.789 |
| 3D0G | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.460 |
| 3D0G | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.067 |
| 3D0G | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.649 |
| 3D0G | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.432 |
| 3D0G | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 2.983 |
| 3D0G | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.908 |
| 3D0G | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.831 |
| 3D0G | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.314 |
| 3D0G | F_ARG_444 | NH1 | F_GLU_452 | OE2 | 3.743 |
| 3D0G | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.573 |
| 3D0G | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.447 |
| 3D0G | F_LYS_465 | NZ | F_ASP_463 | OD1 | 3.077 |
| 3D0G | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.771 |
| 3D0G | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.277 |
| 3D0H | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.654 |
| 3D0H | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.191 |
| 3D0H | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.636 |
| 3D0H | A_ARG_177 | NH1 | A_GLU_181 | OE1 | 3.849 |
| 3D0H | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.600 |
| 3D0H | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.269 |
| 3D0H | A_LYS_187 | NZ | A_ASP_509 | OD1 | 3.949 |
| 3D0H | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.246 |
| 3D0H | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.322 |
| 3D0H | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.787 |
| 3D0H | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.750 |
| 3D0H | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.495 |
| 3D0H | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.408 |
| 3D0H | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.748 |
| 3D0H | A_LYS_288 | NZ | A_ASP_431 | OD1 | 2.502 |
| 3D0H | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.500 |
| 3D0H | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.942 |
| 3D0H | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.050 |
| 3D0H | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.130 |
| 3D0H | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.006 |
| 3D0H | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.624 |
| 3D0H | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.643 |
| 3D0H | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.324 |
| 3D0H | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 2.663 |
| 3D0H | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.758 |
| 3D0H | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.834 |
| 3D0H | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.253 |
| 3D0H | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.415 |

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|---|---|---|---|---|---|
| 3D0H | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.751 |
| 3D0H | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.376 |
| 3D0H | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.176 |
| 3D0H | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.144 |
| 3D0H | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.261 |
| 3D0H | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.974 |
| 3D0H | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.676 |
| 3D0H | A_LYS_476 | NZ | A_GLU_479 | OE2 | 2.624 |
| 3D0H | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.621 |
| 3D0H | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.471 |
| 3D0H | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.377 |
| 3D0H | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.625 |
| 3D0H | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.765 |
| 3D0H | A_ARG_514 | NH1 | A_GLU_398 | OE1 | 3.428 |
| 3D0H | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.126 |
| 3D0H | A_ARG_518 | NH1 | A_GLU_406 | OE1 | 3.615 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_402 | OE2 | 3.679 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_406 | OE1 | 3.756 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_406 | OE2 | 3.850 |
| 3D0H | A_LYS_534 | NZ | A_GLU_549 | OE2 | 3.173 |
| 3D0H | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.471 |
| 3D0H | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.695 |
| 3D0H | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.854 |
| 3D0H | A_LYS_541 | NZ | A_GLU_435 | OE2 | 3.545 |
| 3D0H | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.272 |
| 3D0H | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.185 |
| 3D0H | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.413 |
| 3D0H | B_ARG_177 | NH1 | B_GLU_181 | OE1 | 3.536 |
| 3D0H | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.392 |
| 3D0H | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.303 |
| 3D0H | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.884 |
| 3D0H | B_ARG_204 | NH1 | B_ASP_198 | OD2 | 3.995 |
| 3D0H | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.825 |
| 3D0H | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.543 |
| 3D0H | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.592 |
| 3D0H | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.819 |
| 3D0H | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.119 |
| 3D0H | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.307 |
| 3D0H | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.891 |
| 3D0H | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.446 |
| 3D0H | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.471 |
| 3D0H | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.557 |
| 3D0H | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.699 |
| 3D0H | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.313 |
| 3D0H | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.675 |
| 3D0H | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.061 |
| 3D0H | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.799 |
| 3D0H | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.437 |
| 3D0H | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.549 |
| 3D0H | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.248 |
| 3D0H | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.405 |
| 3D0H | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.407 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.231 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.198 |
| 3D0H | B_LYS_419 | NZ | B_GLU_430 | OE1 | 3.848 |
| 3D0H | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.001 |
| 3D0H | B_LYS_470 | NZ | B_GLU_181 | OE1 | 2.767 |
| 3D0H | B_LYS_470 | NZ | B_GLU_181 | OE2 | 3.182 |

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|---|---|---|---|---|---|
| 3D0H | B_LYS_476 | NZ | B_GLU_479 | OE1 | 3.337 |
| 3D0H | B_ARG_482 | NH1 | B_GLU_489 | OE1 | 2.732 |
| 3D0H | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.824 |
| 3D0H | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.932 |
| 3D0H | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.877 |
| 3D0H | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.140 |
| 3D0H | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.598 |
| 3D0H | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.836 |
| 3D0H | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.895 |
| 3D0H | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.835 |
| 3D0H | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.851 |
| 3D0H | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.940 |
| 3D0H | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.656 |
| 3D0H | B_LYS_541 | NZ | B_GLU_430 | OE2 | 3.335 |
| 3D0H | B_ARG_582 | NH2 | B_GLU_232 | OE2 | 3.592 |
| 3D0H | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.363 |
| 3D0H | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.221 |
| 3D0H | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.317 |
| 3D0H | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.987 |
| 3D0H | E_LYS_411 | NZ | E_ASP_407 | OD1 | 3.493 |
| 3D0H | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.079 |
| 3D0H | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.678 |
| 3D0H | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.103 |
| 3D0H | E_ARG_453 | NH2 | E_GLU_341 | OE1 | 2.602 |
| 3D0H | E_LYS_479 | NZ | A_GLU_35 | OE1 | 3.397 |
| 3D0H | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.894 |
| 3D0H | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.818 |
| 3D0H | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.718 |
| 3D0H | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.147 |
| 3D0H | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.643 |
| 3D0H | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.793 |
| 3D0H | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.380 |
| 3D0H | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.753 |
| 3D0H | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.628 |
| 3D0H | F_ARG_453 | NH2 | F_GLU_341 | OE1 | 3.737 |
| 3D0H | F_LYS_479 | NZ | B_GLU_35 | OE1 | 3.369 |
| 3D0H | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.824 |
| 3D0H | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.863 |
| 3D0I | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.187 |
| 3D0I | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.852 |
| 3D0I | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.156 |
| 3D0I | A_ARG_177 | NH1 | A_GLU_181 | OE2 | 3.919 |
| 3D0I | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.627 |
| 3D0I | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 2.844 |
| 3D0I | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.851 |
| 3D0I | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.393 |
| 3D0I | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.767 |
| 3D0I | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.602 |
| 3D0I | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.226 |
| 3D0I | A_LYS_234 | NZ | A_GLU_231 | OE2 | 2.886 |
| 3D0I | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.237 |
| 3D0I | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.963 |
| 3D0I | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.134 |
| 3D0I | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.185 |
| 3D0I | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.199 |
| 3D0I | A_LYS_353 | NZ | A_GLU_38 | OE2 | 2.940 |
| 3D0I | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.456 |
| 3D0I | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.694 |

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|---|---|---|---|---|---|
| 3D0I | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.884 |
| 3D0I | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.205 |
| 3D0I | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.038 |
| 3D0I | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.181 |
| 3D0I | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.296 |
| 3D0I | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.690 |
| 3D0I | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.095 |
| 3D0I | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.805 |
| 3D0I | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.364 |
| 3D0I | A_LYS_465 | NZ | A_GLU_197 | OE2 | 3.918 |
| 3D0I | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.269 |
| 3D0I | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.529 |
| 3D0I | A_LYS_476 | NZ | A_GLU_479 | OE2 | 2.537 |
| 3D0I | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.768 |
| 3D0I | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.673 |
| 3D0I | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.974 |
| 3D0I | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.367 |
| 3D0I | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.596 |
| 3D0I | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.716 |
| 3D0I | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 2.781 |
| 3D0I | A_ARG_518 | NH1 | A_GLU_406 | OE1 | 3.545 |
| 3D0I | A_ARG_518 | NH2 | A_GLU_402 | OE2 | 3.220 |
| 3D0I | A_LYS_534 | NZ | A_GLU_549 | OE1 | 3.582 |
| 3D0I | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.978 |
| 3D0I | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.081 |
| 3D0I | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.768 |
| 3D0I | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.991 |
| 3D0I | B_LYS_112 | NZ | B_GLU_189 | OE1 | 2.946 |
| 3D0I | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.482 |
| 3D0I | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.999 |
| 3D0I | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.084 |
| 3D0I | B_ARG_177 | NH1 | B_GLU_181 | OE2 | 3.586 |
| 3D0I | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.500 |
| 3D0I | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.650 |
| 3D0I | B_LYS_187 | NZ | B_ASP_509 | OD1 | 3.839 |
| 3D0I | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.086 |
| 3D0I | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.369 |
| 3D0I | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.495 |
| 3D0I | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.713 |
| 3D0I | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.122 |
| 3D0I | B_LYS_234 | NZ | B_GLU_231 | OE2 | 2.885 |
| 3D0I | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.153 |
| 3D0I | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.676 |
| 3D0I | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.386 |
| 3D0I | B_LYS_313 | NZ | B_GLU_310 | OE2 | 2.999 |
| 3D0I | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.427 |
| 3D0I | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.805 |
| 3D0I | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.438 |
| 3D0I | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.611 |
| 3D0I | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.052 |
| 3D0I | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.803 |
| 3D0I | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.598 |
| 3D0I | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.612 |
| 3D0I | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.112 |
| 3D0I | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.000 |
| 3D0I | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.643 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.355 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.779 |

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|---|---|---|---|---|---|
| 3D0I | B_LYS_419 | NZ | B_GLU_430 | OE1 | 3.547 |
| 3D0I | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.212 |
| 3D0I | B_LYS_470 | NZ | B_GLU_181 | OE1 | 2.879 |
| 3D0I | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.791 |
| 3D0I | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.688 |
| 3D0I | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.914 |
| 3D0I | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.135 |
| 3D0I | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.741 |
| 3D0I | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.923 |
| 3D0I | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.844 |
| 3D0I | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.950 |
| 3D0I | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.992 |
| 3D0I | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.725 |
| 3D0I | B_ARG_582 | NH2 | B_GLU_232 | OE2 | 3.204 |
| 3D0I | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 3.693 |
| 3D0I | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.921 |
| 3D0I | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.555 |
| 3D0I | E_LYS_343 | NZ | E_GLU_327 | OE1 | 2.907 |
| 3D0I | E_LYS_411 | NZ | E_ASP_407 | OD1 | 3.525 |
| 3D0I | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.085 |
| 3D0I | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.247 |
| 3D0I | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.400 |
| 3D0I | E_ARG_453 | NH2 | E_GLU_341 | OE1 | 3.930 |
| 3D0I | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.544 |
| 3D0I | E_LYS_465 | NZ | E_ASP_463 | OD2 | 3.638 |
| 3D0I | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 3.324 |
| 3D0I | E_ARG_479 | NH2 | A_GLU_35 | OE1 | 2.730 |
| 3D0I | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.896 |
| 3D0I | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.932 |
| 3D0I | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.615 |
| 3D0I | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.912 |
| 3D0I | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.980 |
| 3D0I | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.584 |
| 3D0I | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.274 |
| 3D0I | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.530 |
| 3D0I | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.856 |
| 3D0I | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.256 |
| 3D0I | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.236 |
| 3D0I | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.810 |
| 3D0I | F_ARG_453 | NH2 | F_GLU_341 | OE1 | 3.930 |
| 3D0I | F_LYS_465 | NZ | F_ASP_463 | OD2 | 3.412 |
| 3D0I | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 3.405 |
| 3D0I | F_ARG_479 | NH2 | B_GLU_35 | OE1 | 2.961 |
| 3D0I | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.707 |
| 3D0I | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.911 |
| 3SCI | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.333 |
| 3SCI | A_LYS_26 | NZ | A_GLU_23 | OE2 | 3.691 |
| 3SCI | A_HIS_34 | ND1 | A_GLU_37 | OE1 | 3.955 |
| 3SCI | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.520 |
| 3SCI | A_ARG_115 | NH1 | A_GLU_182 | OE1 | 3.485 |
| 3SCI | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 2.973 |
| 3SCI | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.161 |
| 3SCI | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 2.813 |
| 3SCI | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.700 |
| 3SCI | A_ARG_204 | NH2 | A_ASP_198 | OD1 | 3.614 |
| 3SCI | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.484 |
| 3SCI | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.586 |
| 3SCI | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.677 |

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|---|---|---|---|---|---|
| 3SCI | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.059 |
| 3SCI | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.792 |
| 3SCI | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.667 |
| 3SCI | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.649 |
| 3SCI | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.796 |
| 3SCI | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.140 |
| 3SCI | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.555 |
| 3SCI | A_LYS_353 | NZ | A_ASP_38 | OD1 | 3.354 |
| 3SCI | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.324 |
| 3SCI | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 3.867 |
| 3SCI | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.812 |
| 3SCI | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.743 |
| 3SCI | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.027 |
| 3SCI | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.766 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.865 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.741 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 3.842 |
| 3SCI | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 2.993 |
| 3SCI | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.829 |
| 3SCI | A_ARG_393 | NH2 | A_GLU_37 | OE2 | 3.668 |
| 3SCI | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.295 |
| 3SCI | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.686 |
| 3SCI | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.398 |
| 3SCI | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.642 |
| 3SCI | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.133 |
| 3SCI | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.703 |
| 3SCI | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.668 |
| 3SCI | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.756 |
| 3SCI | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.875 |
| 3SCI | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.021 |
| 3SCI | A_HIS_493 | NE2 | A_GLU_166 | OE2 | 3.968 |
| 3SCI | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.898 |
| 3SCI | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.867 |
| 3SCI | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.392 |
| 3SCI | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.358 |
| 3SCI | A_LYS_541 | NZ | A_GLU_430 | OE1 | 3.694 |
| 3SCI | A_LYS_541 | NZ | A_GLU_430 | OE2 | 2.736 |
| 3SCI | A_ARG_582 | NH1 | A_GLU_232 | OE2 | 2.598 |
| 3SCI | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.897 |
| 3SCI | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.718 |
| 3SCI | B_LYS_31 | NZ | B_GLU_35 | OE1 | 3.358 |
| 3SCI | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.974 |
| 3SCI | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.826 |
| 3SCI | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.773 |
| 3SCI | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.548 |
| 3SCI | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.424 |
| 3SCI | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.759 |
| 3SCI | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.703 |
| 3SCI | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.718 |
| 3SCI | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.668 |
| 3SCI | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.689 |
| 3SCI | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.452 |
| 3SCI | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.808 |
| 3SCI | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.168 |
| 3SCI | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.626 |
| 3SCI | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.016 |
| 3SCI | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.303 |
| 3SCI | B_LYS_353 | NZ | B_ASP_38 | OD1 | 3.714 |

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|---|---|---|---|---|---|
| 3SCI | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 2.648 |
| 3SCI | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.568 |
| 3SCI | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.133 |
| 3SCI | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.131 |
| 3SCI | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.146 |
| 3SCI | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.955 |
| 3SCI | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.800 |
| 3SCI | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.582 |
| 3SCI | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 2.767 |
| 3SCI | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.951 |
| 3SCI | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.149 |
| 3SCI | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.545 |
| 3SCI | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.930 |
| 3SCI | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.967 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.520 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.936 |
| 3SCI | B_LYS_458 | NZ | B_GLU_227 | OE2 | 2.656 |
| 3SCI | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.610 |
| 3SCI | B_LYS_465 | NZ | B_GLU_197 | OE2 | 3.379 |
| 3SCI | B_LYS_470 | NZ | B_GLU_181 | OE1 | 3.845 |
| 3SCI | B_LYS_475 | NZ | B_GLU_479 | OE1 | 3.195 |
| 3SCI | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.712 |
| 3SCI | B_ARG_482 | NH1 | B_GLU_489 | OE1 | 3.858 |
| 3SCI | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.969 |
| 3SCI | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.242 |
| 3SCI | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.362 |
| 3SCI | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.799 |
| 3SCI | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.907 |
| 3SCI | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.879 |
| 3SCI | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.740 |
| 3SCI | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.299 |
| 3SCI | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.013 |
| 3SCI | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 3.819 |
| 3SCI | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 3.000 |
| 3SCI | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.193 |
| 3SCI | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.289 |
| 3SCI | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.257 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.110 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.923 |
| 3SCI | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.829 |
| 3SCI | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.668 |
| 3SCI | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 2.901 |
| 3SCI | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.835 |
| 3SCI | E_LYS_447 | NZ | E_ASP_407 | OD2 | 3.979 |
| 3SCI | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.520 |
| 3SCI | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.789 |
| 3SCI | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.688 |
| 3SCI | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.355 |
| 3SCI | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.898 |
| 3SCI | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.783 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.044 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.878 |
| 3SCI | F_LYS_439 | NZ | F_ASP_480 | OD2 | 3.783 |
| 3SCI | F_ARG_441 | NH1 | F_ASP_454 | OD1 | 3.554 |
| 3SCI | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.709 |
| 3SCI | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.691 |
| 3SCI | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 2.977 |
| 3SCI | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.984 |

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|---|---|---|---|---|---|
| 3SCI | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.981 |
| 3SCJ | A_LYS_26 | NZ | A_GLU_23 | OE2 | 3.680 |
| 3SCJ | A_HIS_34 | NE2 | A_ASP_30 | OD1 | 3.716 |
| 3SCJ | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.606 |
| 3SCJ | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.626 |
| 3SCJ | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.662 |
| 3SCJ | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.729 |
| 3SCJ | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.233 |
| 3SCJ | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.854 |
| 3SCJ | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.710 |
| 3SCJ | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.688 |
| 3SCJ | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.693 |
| 3SCJ | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.281 |
| 3SCJ | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.594 |
| 3SCJ | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.711 |
| 3SCJ | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.920 |
| 3SCJ | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.833 |
| 3SCJ | A_LYS_309 | NZ | A_GLU_312 | OE1 | 2.769 |
| 3SCJ | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.597 |
| 3SCJ | A_LYS_353 | NZ | A_ASP_38 | OD1 | 2.877 |
| 3SCJ | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.017 |
| 3SCJ | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.039 |
| 3SCJ | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.858 |
| 3SCJ | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.602 |
| 3SCJ | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.774 |
| 3SCJ | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.008 |
| 3SCJ | A_ARG_393 | NH1 | A_GLU_37 | OE1 | 3.540 |
| 3SCJ | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 3.136 |
| 3SCJ | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.154 |
| 3SCJ | A_ARG_393 | NH2 | A_GLU_37 | OE2 | 3.984 |
| 3SCJ | A_HIS_401 | NE2 | A_ASP_382 | OD2 | 3.168 |
| 3SCJ | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.019 |
| 3SCJ | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.770 |
| 3SCJ | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.761 |
| 3SCJ | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 2.363 |
| 3SCJ | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.678 |
| 3SCJ | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.819 |
| 3SCJ | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.256 |
| 3SCJ | A_LYS_476 | NZ | A_GLU_479 | OE2 | 3.692 |
| 3SCJ | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.323 |
| 3SCJ | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.886 |
| 3SCJ | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.898 |
| 3SCJ | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.065 |
| 3SCJ | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.951 |
| 3SCJ | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.730 |
| 3SCJ | A_ARG_514 | NH2 | A_GLU_398 | OE2 | 3.456 |
| 3SCJ | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.682 |
| 3SCJ | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.913 |
| 3SCJ | A_LYS_577 | NZ | A_GLU_571 | OE1 | 3.432 |
| 3SCJ | A_ARG_582 | NH1 | A_GLU_232 | OE2 | 3.625 |
| 3SCJ | A_LYS_600 | NZ | A_ASP_597 | OD2 | 3.672 |
| 3SCJ | B_LYS_26 | NZ | B_GLU_22 | OE1 | 3.695 |
| 3SCJ | B_LYS_26 | NZ | B_GLU_23 | OE2 | 3.612 |
| 3SCJ | B_LYS_31 | NZ | B_GLU_35 | OE2 | 3.882 |
| 3SCJ | B_HIS_34 | NE2 | B_ASP_30 | OD1 | 3.848 |
| 3SCJ | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.760 |
| 3SCJ | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.993 |
| 3SCJ | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.931 |

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|---|---|---|---|---|---|
| 3SCJ | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 2.746 |
| 3SCJ | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.552 |
| 3SCJ | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.425 |
| 3SCJ | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.488 |
| 3SCJ | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.786 |
| 3SCJ | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.813 |
| 3SCJ | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.381 |
| 3SCJ | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.724 |
| 3SCJ | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.841 |
| 3SCJ | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.087 |
| 3SCJ | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.785 |
| 3SCJ | B_LYS_309 | NZ | B_GLU_312 | OE1 | 2.771 |
| 3SCJ | B_LYS_309 | NZ | B_GLU_312 | OE2 | 3.982 |
| 3SCJ | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.681 |
| 3SCJ | B_LYS_353 | NZ | B_ASP_38 | OD1 | 2.726 |
| 3SCJ | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 2.798 |
| 3SCJ | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.923 |
| 3SCJ | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.731 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_375 | OE2 | 3.983 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.277 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.223 |
| 3SCJ | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.838 |
| 3SCJ | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.709 |
| 3SCJ | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.616 |
| 3SCJ | B_ARG_393 | NH1 | B_GLU_37 | OE1 | 3.412 |
| 3SCJ | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 2.868 |
| 3SCJ | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.040 |
| 3SCJ | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.888 |
| 3SCJ | B_HIS_401 | NE2 | B_ASP_382 | OD2 | 2.952 |
| 3SCJ | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.890 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.617 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.574 |
| 3SCJ | B_LYS_458 | NZ | B_GLU_227 | OE2 | 2.602 |
| 3SCJ | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.815 |
| 3SCJ | B_LYS_465 | NZ | B_GLU_197 | OE2 | 3.351 |
| 3SCJ | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.513 |
| 3SCJ | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.255 |
| 3SCJ | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.169 |
| 3SCJ | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.053 |
| 3SCJ | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.734 |
| 3SCJ | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.171 |
| 3SCJ | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.883 |
| 3SCJ | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.159 |
| 3SCJ | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.270 |
| 3SCJ | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 2.624 |
| 3SCJ | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 2.893 |
| 3SCJ | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.243 |
| 3SCJ | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.607 |
| 3SCJ | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.703 |
| 3SCJ | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.526 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.206 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.277 |
| 3SCJ | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 2.926 |
| 3SCJ | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.893 |
| 3SCJ | E_ARG_479 | NH2 | A_ASP_38 | OD2 | 2.575 |
| 3SCJ | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.820 |
| 3SCJ | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.638 |
| 3SCJ | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 2.917 |

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|---|---|---|---|---|---|
| 3SCJ | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.247 |
| 3SCJ | F_LYS_390 | NZ | F_ASP_393 | OD2 | 3.787 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.547 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.819 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 3.913 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 3.505 |
| 3SCJ | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 2.956 |
| 3SCJ | F_LYS_465 | NZ | F_ASP_463 | OD2 | 3.932 |
| 3SCJ | F_ARG_479 | NH2 | B_ASP_38 | OD2 | 2.718 |
| 3SCJ | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.902 |
| 3SCJ | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.690 |
| 3SCK | A_LYS_26 | NZ | A_GLU_22 | OE2 | 3.783 |
| 3SCK | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.738 |
| 3SCK | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.145 |
| 3SCK | A_LYS_112 | NZ | A_GLU_189 | OE2 | 2.624 |
| 3SCK | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.180 |
| 3SCK | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.905 |
| 3SCK | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.207 |
| 3SCK | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.048 |
| 3SCK | A_ARG_204 | NH2 | A_ASP_198 | OD1 | 3.950 |
| 3SCK | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.586 |
| 3SCK | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.162 |
| 3SCK | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 2.535 |
| 3SCK | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.847 |
| 3SCK | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.343 |
| 3SCK | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.624 |
| 3SCK | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.046 |
| 3SCK | A_LYS_288 | NZ | A_GLU_433 | OE2 | 3.653 |
| 3SCK | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.804 |
| 3SCK | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.263 |
| 3SCK | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.272 |
| 3SCK | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.265 |
| 3SCK | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.121 |
| 3SCK | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.285 |
| 3SCK | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.719 |
| 3SCK | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.223 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_375 | OE1 | 3.653 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.848 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.409 |
| 3SCK | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.833 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.518 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.694 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 3.988 |
| 3SCK | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 2.944 |
| 3SCK | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.268 |
| 3SCK | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.397 |
| 3SCK | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.716 |
| 3SCK | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 3.705 |
| 3SCK | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.038 |
| 3SCK | A_LYS_465 | NZ | A_GLU_197 | OE2 | 3.131 |
| 3SCK | A_LYS_465 | NZ | A_ASP_198 | OD1 | 3.632 |
| 3SCK | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.825 |
| 3SCK | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.693 |
| 3SCK | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.807 |
| 3SCK | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.942 |
| 3SCK | A_HIS_493 | ND1 | A_GLU_166 | OE2 | 3.454 |
| 3SCK | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.435 |
| 3SCK | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.109 |

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| 3SCK | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.751 |
| 3SCK | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.712 |
| 3SCK | A_LYS_541 | NZ | A_GLU_430 | OE2 | 2.691 |
| 3SCK | A_ARG_582 | NH2 | A_GLU_527 | OE1 | 3.214 |
| 3SCK | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.690 |
| 3SCK | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.836 |
| 3SCK | B_LYS_112 | NZ | B_GLU_189 | OE1 | 2.980 |
| 3SCK | B_LYS_112 | NZ | B_GLU_189 | OE2 | 2.757 |
| 3SCK | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.458 |
| 3SCK | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.403 |
| 3SCK | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.746 |
| 3SCK | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.553 |
| 3SCK | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.885 |
| 3SCK | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.682 |
| 3SCK | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.457 |
| 3SCK | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 2.655 |
| 3SCK | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.845 |
| 3SCK | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.278 |
| 3SCK | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.790 |
| 3SCK | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.658 |
| 3SCK | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.747 |
| 3SCK | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.334 |
| 3SCK | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.682 |
| 3SCK | B_LYS_353 | NZ | B_GLU_38 | OE1 | 2.931 |
| 3SCK | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.932 |
| 3SCK | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.088 |
| 3SCK | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.516 |
| 3SCK | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.908 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_375 | OE1 | 3.559 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.398 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 2.956 |
| 3SCK | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.773 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.390 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.299 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_402 | OE2 | 3.828 |
| 3SCK | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 2.702 |
| 3SCK | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.177 |
| 3SCK | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.806 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.939 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.692 |
| 3SCK | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.897 |
| 3SCK | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.129 |
| 3SCK | B_LYS_476 | NZ | B_GLU_479 | OE1 | 2.732 |
| 3SCK | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.669 |
| 3SCK | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.445 |
| 3SCK | B_HIS_493 | ND1 | B_GLU_166 | OE2 | 3.573 |
| 3SCK | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.077 |
| 3SCK | B_HIS_493 | NE2 | B_GLU_166 | OE2 | 3.607 |
| 3SCK | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.737 |
| 3SCK | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.936 |
| 3SCK | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.744 |
| 3SCK | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.632 |
| 3SCK | B_HIS_535 | ND1 | B_GLU_536 | OE1 | 3.467 |
| 3SCK | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 2.753 |
| 3SCK | B_LYS_577 | NZ | B_GLU_571 | OE2 | 3.718 |
| 3SCK | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.321 |
| 3SCK | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.081 |
| 3SCK | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.896 |

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|---|---|---|---|---|---|
| 3SCK | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.985 |
| 3SCK | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.591 |
| 3SCK | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.861 |
| 3SCK | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.076 |
| 3SCK | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.663 |
| 3SCK | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 2.498 |
| 3SCK | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.603 |
| 3SCK | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.263 |
| 3SCK | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.676 |
| 3SCK | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.322 |
| 3SCK | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.370 |
| 3SCK | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.702 |
| 3SCK | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.226 |
| 3SCK | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.187 |
| 3SCK | F_LYS_447 | NZ | F_ASP_407 | OD1 | 3.771 |
| 3SCK | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 2.750 |
| 3SCK | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.668 |
| 3SCK | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.427 |
| 3SCL | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.408 |
| 3SCL | A_LYS_112 | NZ | A_GLU_189 | OE2 | 2.764 |
| 3SCL | A_ARG_115 | NH1 | A_GLU_182 | OE1 | 3.915 |
| 3SCL | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 2.759 |
| 3SCL | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.407 |
| 3SCL | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.290 |
| 3SCL | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.750 |
| 3SCL | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.751 |
| 3SCL | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.854 |
| 3SCL | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.253 |
| 3SCL | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.220 |
| 3SCL | A_ARG_219 | NH2 | A_ASP_201 | OD1 | 3.810 |
| 3SCL | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 2.818 |
| 3SCL | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.556 |
| 3SCL | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.191 |
| 3SCL | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.310 |
| 3SCL | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.328 |
| 3SCL | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.467 |
| 3SCL | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.111 |
| 3SCL | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.461 |
| 3SCL | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.043 |
| 3SCL | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.365 |
| 3SCL | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.733 |
| 3SCL | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.626 |
| 3SCL | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.593 |
| 3SCL | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.408 |
| 3SCL | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.962 |
| 3SCL | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.936 |
| 3SCL | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.998 |
| 3SCL | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.267 |
| 3SCL | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.834 |
| 3SCL | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.060 |
| 3SCL | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.685 |
| 3SCL | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.352 |
| 3SCL | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.158 |
| 3SCL | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.210 |
| 3SCL | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.758 |
| 3SCL | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.716 |
| 3SCL | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 2.872 |
| 3SCL | A_HIS_493 | NE2 | A_GLU_166 | OE2 | 3.834 |

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|---|---|---|---|---|---|
| 3SCL | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.559 |
| 3SCL | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.746 |
| 3SCL | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.042 |
| 3SCL | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.897 |
| 3SCL | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.223 |
| 3SCL | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.963 |
| 3SCL | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.301 |
| 3SCL | B_LYS_187 | NZ | B_ASP_509 | OD2 | 2.965 |
| 3SCL | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.847 |
| 3SCL | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.720 |
| 3SCL | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.715 |
| 3SCL | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.640 |
| 3SCL | B_ARG_219 | NH2 | B_ASP_201 | OD1 | 3.401 |
| 3SCL | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 2.726 |
| 3SCL | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.673 |
| 3SCL | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.548 |
| 3SCL | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.355 |
| 3SCL | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.412 |
| 3SCL | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.658 |
| 3SCL | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.480 |
| 3SCL | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.437 |
| 3SCL | B_LYS_353 | NZ | B_GLU_38 | OE2 | 3.301 |
| 3SCL | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.138 |
| 3SCL | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.046 |
| 3SCL | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.045 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_375 | OE1 | 3.783 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.382 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.256 |
| 3SCL | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.495 |
| 3SCL | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 3.016 |
| 3SCL | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.349 |
| 3SCL | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 2.818 |
| 3SCL | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.784 |
| 3SCL | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.918 |
| 3SCL | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.400 |
| 3SCL | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.623 |
| 3SCL | B_LYS_465 | NZ | B_GLU_467 | OE2 | 2.784 |
| 3SCL | B_LYS_475 | NZ | B_GLU_479 | OE1 | 3.474 |
| 3SCL | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.893 |
| 3SCL | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.520 |
| 3SCL | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.908 |
| 3SCL | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.122 |
| 3SCL | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.707 |
| 3SCL | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.417 |
| 3SCL | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 2.954 |
| 3SCL | B_ARG_518 | NH1 | B_GLU_406 | OE2 | 3.512 |
| 3SCL | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.414 |
| 3SCL | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.367 |
| 3SCL | B_LYS_541 | NZ | B_GLU_430 | OE1 | 3.842 |
| 3SCL | B_LYS_541 | NZ | B_GLU_430 | OE2 | 2.913 |
| 3SCL | B_LYS_562 | NZ | B_ASP_206 | OD1 | 3.640 |
| 3SCL | B_LYS_562 | NZ | B_ASP_206 | OD2 | 3.837 |
| 3SCL | B_LYS_577 | NZ | B_GLU_571 | OE2 | 3.749 |
| 3SCL | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.057 |
| 3SCL | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.532 |
| 3SCL | E_LYS_344 | NZ | E_GLU_502 | OE2 | 3.992 |
| 3SCL | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.916 |
| 3SCL | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.143 |

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|---|---|---|---|---|---|
| 3SCL | E_ARG_441 | NH1 | E_ASP_454 | OD1 | 3.923 |
| 3SCL | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.742 |
| 3SCL | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.601 |
| 3SCL | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.448 |
| 3SCL | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.287 |
| 3SCL | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.682 |
| 3SCL | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.651 |
| 3SCL | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 2.956 |
| 3SCL | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.322 |
| 3SCL | F_LYS_439 | NZ | F_ASP_480 | OD1 | 2.927 |
| 3SCL | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.224 |
| 3SCL | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.909 |
| 3SCL | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.945 |
| 3SCL | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.790 |
| 5X4S | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 2.290 |
| 5X4S | A_ARG_38 | NH1 | A_GLU_184 | OE1 | 3.171 |
| 5X4S | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 3.034 |
| 5X4S | A_ARG_48 | NH1 | A_ASP_44 | OD1 | 2.727 |
| 5X4S | A_ARG_48 | NH1 | A_ASP_44 | OD2 | 3.371 |
| 5X4S | A_ARG_48 | NH2 | A_ASP_44 | OD1 | 3.601 |
| 5X4S | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 2.675 |
| 5X4S | A_LYS_175 | NZ | A_ASP_171 | OD1 | 3.389 |
| 5X4S | A_LYS_175 | NZ | A_ASP_171 | OD2 | 3.027 |
| 5X4S | A_LYS_188 | NZ | A_ASP_57 | OD1 | 3.514 |
| 5X4S | A_LYS_190 | NZ | A_ASP_191 | OD2 | 3.979 |
| 5X58 | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 3.231 |
| 5X58 | A_ARG_38 | NH1 | A_GLU_184 | OE1 | 3.772 |
| 5X58 | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 2.356 |
| 5X58 | A_ARG_48 | NH1 | A_ASP_44 | OD1 | 3.022 |
| 5X58 | A_ARG_48 | NH1 | A_ASP_44 | OD2 | 3.566 |
| 5X58 | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 3.303 |
| 5X58 | A_LYS_188 | NZ | A_ASP_57 | OD1 | 3.617 |
| 5X58 | A_LYS_188 | NZ | A_ASP_57 | OD2 | 3.069 |
| 5X58 | A_LYS_221 | NZ | C_GLU_502 | OE2 | 3.266 |
| 5X58 | A_LYS_297 | NZ | A_ASP_649 | OD1 | 2.479 |
| 5X58 | A_LYS_297 | NZ | A_ASP_649 | OD2 | 3.392 |
| 5X58 | A_LYS_343 | NZ | A_GLU_327 | OE1 | 3.311 |
| 5X58 | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.205 |
| 5X58 | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.550 |
| 5X58 | A_LYS_514 | NZ | A_ASP_376 | OD1 | 3.288 |
| 5X58 | A_LYS_543 | NZ | A_ASP_560 | OD2 | 2.441 |
| 5X58 | A_ARG_620 | NH1 | A_ASP_277 | OD2 | 3.189 |
| 5X58 | A_ARG_797 | NH1 | A_ASP_850 | OD1 | 3.465 |
| 5X58 | A_LYS_836 | NZ | C_ASP_554 | OD2 | 3.822 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.482 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 3.202 |
| 5X58 | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.575 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.983 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.964 |
| 5X58 | A_ARG_1001 | NH2 | A_GLU_755 | OE1 | 3.437 |
| 5X58 | A_ARG_1001 | NH2 | A_GLU_755 | OE2 | 3.596 |
| 5X58 | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.486 |
| 5X58 | A_LYS_1010 | NZ | A_GLU_707 | OE1 | 3.690 |
| 5X58 | A_LYS_1010 | NZ | A_GLU_707 | OE2 | 3.427 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE1 | 3.011 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE2 | 3.438 |
| 5X58 | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.538 |
| 5X58 | A_HIS_1046 | NE2 | A_GLU_707 | OE1 | 2.723 |

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|---|---|---|---|---|---|
| 5X58 | B_HIS_33 | ND1 | B_ASP_208 | OD1 | 3.230 |
| 5X58 | B_ARG_38 | NH1 | B_GLU_184 | OE1 | 3.772 |
| 5X58 | B_ARG_38 | NH1 | B_GLU_184 | OE2 | 2.356 |
| 5X58 | B_ARG_48 | NH1 | B_ASP_44 | OD1 | 3.022 |
| 5X58 | B_ARG_48 | NH1 | B_ASP_44 | OD2 | 3.565 |
| 5X58 | B_ARG_48 | NH2 | B_ASP_44 | OD2 | 3.302 |
| 5X58 | B_LYS_188 | NZ | B_ASP_57 | OD1 | 3.617 |
| 5X58 | B_LYS_188 | NZ | B_ASP_57 | OD2 | 3.068 |
| 5X58 | B_LYS_221 | NZ | A_GLU_502 | OE2 | 3.264 |
| 5X58 | B_LYS_297 | NZ | B_ASP_649 | OD1 | 2.478 |
| 5X58 | B_LYS_297 | NZ | B_ASP_649 | OD2 | 3.391 |
| 5X58 | B_LYS_343 | NZ | B_GLU_327 | OE1 | 3.310 |
| 5X58 | B_ARG_441 | NH2 | B_ASP_454 | OD2 | 3.205 |
| 5X58 | B_ARG_495 | NH2 | B_ASP_429 | OD1 | 3.551 |
| 5X58 | B_LYS_514 | NZ | B_ASP_376 | OD1 | 3.288 |
| 5X58 | B_LYS_543 | NZ | B_ASP_560 | OD2 | 2.442 |
| 5X58 | B_ARG_620 | NH1 | B_ASP_277 | OD2 | 3.189 |
| 5X58 | B_ARG_797 | NH1 | B_ASP_850 | OD1 | 3.464 |
| 5X58 | B_LYS_836 | NZ | A_ASP_554 | OD2 | 3.822 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD1 | 3.484 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD2 | 3.202 |
| 5X58 | B_ARG_977 | NH2 | C_ASP_976 | OD2 | 3.576 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.983 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.963 |
| 5X58 | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.485 |
| 5X58 | B_ARG_1001 | NH2 | B_GLU_755 | OE1 | 3.436 |
| 5X58 | B_ARG_1001 | NH2 | B_GLU_755 | OE2 | 3.597 |
| 5X58 | B_LYS_1010 | NZ | B_GLU_707 | OE1 | 3.691 |
| 5X58 | B_LYS_1010 | NZ | B_GLU_707 | OE2 | 3.427 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.011 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 3.438 |
| 5X58 | B_ARG_1021 | NH2 | C_GLU_1013 | OE2 | 3.540 |
| 5X58 | B_HIS_1046 | NE2 | B_GLU_707 | OE1 | 2.724 |
| 5X58 | C_HIS_33 | ND1 | C_ASP_208 | OD1 | 3.232 |
| 5X58 | C_ARG_38 | NH1 | C_GLU_184 | OE1 | 3.772 |
| 5X58 | C_ARG_38 | NH1 | C_GLU_184 | OE2 | 2.356 |
| 5X58 | C_ARG_48 | NH1 | C_ASP_44 | OD1 | 3.022 |
| 5X58 | C_ARG_48 | NH1 | C_ASP_44 | OD2 | 3.565 |
| 5X58 | C_ARG_48 | NH2 | C_ASP_44 | OD2 | 3.303 |
| 5X58 | C_LYS_188 | NZ | C_ASP_57 | OD1 | 3.616 |
| 5X58 | C_LYS_188 | NZ | C_ASP_57 | OD2 | 3.068 |
| 5X58 | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.265 |
| 5X58 | C_LYS_297 | NZ | C_ASP_649 | OD1 | 2.478 |
| 5X58 | C_LYS_297 | NZ | C_ASP_649 | OD2 | 3.393 |
| 5X58 | C_LYS_343 | NZ | C_GLU_327 | OE1 | 3.310 |
| 5X58 | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.205 |
| 5X58 | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 3.550 |
| 5X58 | C_LYS_514 | NZ | C_ASP_376 | OD1 | 3.288 |
| 5X58 | C_LYS_543 | NZ | C_ASP_560 | OD2 | 2.441 |
| 5X58 | C_ARG_620 | NH1 | C_ASP_277 | OD2 | 3.189 |
| 5X58 | C_ARG_797 | NH1 | C_ASP_850 | OD1 | 3.464 |
| 5X58 | C_LYS_836 | NZ | B_ASP_554 | OD2 | 3.825 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD1 | 3.484 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD2 | 3.202 |
| 5X58 | C_ARG_977 | NH2 | A_ASP_976 | OD2 | 3.575 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.985 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.966 |
| 5X58 | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.487 |

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|---|---|---|---|---|---|
| 5X58 | C_ARG_1001 | NH2 | C_GLU_755 | OE1 | 3.436 |
| 5X58 | C_ARG_1001 | NH2 | C_GLU_755 | OE2 | 3.596 |
| 5X58 | C_LYS_1010 | NZ | C_GLU_707 | OE1 | 3.690 |
| 5X58 | C_LYS_1010 | NZ | C_GLU_707 | OE2 | 3.427 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.011 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 3.438 |
| 5X58 | C_ARG_1021 | NH2 | A_GLU_1013 | OE2 | 3.539 |
| 5X58 | C_HIS_1046 | NE2 | C_GLU_707 | OE1 | 2.724 |
| 5X5B | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 3.598 |
| 5X5B | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 2.409 |
| 5X5B | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 3.936 |
| 5X5B | A_HIS_74 | ND1 | A_ASP_24 | OD2 | 3.604 |
| 5X5B | A_LYS_297 | NZ | A_ASP_649 | OD1 | 2.492 |
| 5X5B | A_LYS_297 | NZ | A_ASP_649 | OD2 | 3.385 |
| 5X5B | A_LYS_343 | NZ | A_GLU_327 | OE1 | 3.311 |
| 5X5B | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.205 |
| 5X5B | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.551 |
| 5X5B | A_LYS_543 | NZ | A_ASP_560 | OD2 | 3.771 |
| 5X5B | A_ARG_553 | NH1 | A_ASP_557 | OD1 | 3.914 |
| 5X5B | A_LYS_566 | NZ | A_ASP_351 | OD1 | 3.661 |
| 5X5B | A_ARG_620 | NH1 | A_ASP_277 | OD2 | 3.104 |
| 5X5B | A_LYS_793 | NZ | A_ASP_802 | OD2 | 3.746 |
| 5X5B | A_ARG_797 | NH1 | A_ASP_850 | OD1 | 3.600 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.912 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 2.504 |
| 5X5B | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.789 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.909 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.948 |
| 5X5B | A_ARG_1001 | NH2 | A_GLU_755 | OE1 | 3.427 |
| 5X5B | A_ARG_1001 | NH2 | A_GLU_755 | OE2 | 3.433 |
| 5X5B | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.377 |
| 5X5B | A_LYS_1010 | NZ | A_GLU_707 | OE1 | 3.733 |
| 5X5B | A_LYS_1010 | NZ | A_GLU_707 | OE2 | 3.301 |
| 5X5B | A_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.722 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.472 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.057 |
| 5X5B | A_HIS_1046 | NE2 | A_GLU_707 | OE1 | 2.555 |
| 5X5B | A_ARG_1073 | NH1 | B_ASP_1100 | OD2 | 3.995 |
| 5X5B | B_HIS_33 | ND1 | B_ASP_208 | OD1 | 2.655 |
| 5X5B | B_ARG_38 | NH1 | B_GLU_184 | OE2 | 2.521 |
| 5X5B | B_ARG_48 | NH2 | B_ASP_44 | OD2 | 3.973 |
| 5X5B | B_LYS_188 | NZ | B_ASP_57 | OD2 | 3.359 |
| 5X5B | B_LYS_297 | NZ | B_ASP_649 | OD1 | 3.108 |
| 5X5B | B_LYS_297 | NZ | B_ASP_649 | OD2 | 3.662 |
| 5X5B | B_ARG_315 | NH2 | B_ASP_376 | OD1 | 3.790 |
| 5X5B | B_ARG_444 | NH1 | B_ASP_454 | OD2 | 2.941 |
| 5X5B | B_ARG_495 | NH2 | B_ASP_429 | OD1 | 2.664 |
| 5X5B | B_ARG_495 | NH2 | B_ASP_429 | OD2 | 3.309 |
| 5X5B | B_LYS_514 | NZ | B_ASP_376 | OD1 | 3.351 |
| 5X5B | B_LYS_543 | NZ | B_ASP_560 | OD2 | 2.696 |
| 5X5B | B_LYS_543 | NZ | B_ASP_572 | OD2 | 3.842 |
| 5X5B | B_ARG_553 | NH1 | B_ASP_557 | OD1 | 3.071 |
| 5X5B | B_ARG_620 | NH1 | B_ASP_277 | OD1 | 3.439 |
| 5X5B | B_ARG_620 | NH1 | B_ASP_277 | OD2 | 2.450 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.930 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.999 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE1 | 3.970 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.150 |

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|---|---|---|---|---|---|
| 5X5B | B_ARG_1001 | NH2 | B_GLU_755 | OE1 | 3.472 |
| 5X5B | B_ARG_1001 | NH2 | B_GLU_755 | OE2 | 3.342 |
| 5X5B | B_LYS_1010 | NZ | B_GLU_707 | OE1 | 3.708 |
| 5X5B | B_LYS_1010 | NZ | B_GLU_707 | OE2 | 3.314 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.450 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 2.311 |
| 5X5B | B_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.517 |
| 5X5B | B_HIS_1046 | NE2 | B_GLU_707 | OE1 | 2.640 |
| 5X5B | C_HIS_33 | ND1 | C_ASP_208 | OD1 | 2.654 |
| 5X5B | C_ARG_38 | NH1 | C_GLU_184 | OE2 | 2.521 |
| 5X5B | C_ARG_48 | NH2 | C_ASP_44 | OD2 | 3.973 |
| 5X5B | C_LYS_188 | NZ | C_ASP_57 | OD2 | 3.359 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE1 | 3.851 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.225 |
| 5X5B | C_LYS_297 | NZ | C_ASP_649 | OD1 | 3.109 |
| 5X5B | C_LYS_297 | NZ | C_ASP_649 | OD2 | 3.663 |
| 5X5B | C_ARG_315 | NH2 | C_ASP_376 | OD1 | 3.790 |
| 5X5B | C_ARG_444 | NH1 | C_ASP_454 | OD2 | 2.942 |
| 5X5B | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 2.664 |
| 5X5B | C_ARG_495 | NH2 | C_ASP_429 | OD2 | 3.308 |
| 5X5B | C_LYS_514 | NZ | C_ASP_376 | OD1 | 3.351 |
| 5X5B | C_LYS_543 | NZ | C_ASP_560 | OD2 | 2.696 |
| 5X5B | C_LYS_543 | NZ | C_ASP_572 | OD2 | 3.841 |
| 5X5B | C_ARG_553 | NH1 | C_ASP_557 | OD1 | 3.070 |
| 5X5B | C_ARG_620 | NH1 | C_ASP_277 | OD1 | 3.439 |
| 5X5B | C_ARG_620 | NH1 | C_ASP_277 | OD2 | 2.450 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.907 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.931 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE1 | 3.965 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.203 |
| 5X5B | C_ARG_1001 | NH2 | C_GLU_755 | OE1 | 3.472 |
| 5X5B | C_ARG_1001 | NH2 | C_GLU_755 | OE2 | 3.341 |
| 5X5B | C_LYS_1010 | NZ | C_GLU_707 | OE1 | 3.708 |
| 5X5B | C_LYS_1010 | NZ | C_GLU_707 | OE2 | 3.314 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.273 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 2.370 |
| 5X5B | C_ARG_1021 | NH2 | C_GLU_1013 | OE1 | 3.517 |
| 5X5B | C_HIS_1046 | NE2 | C_GLU_707 | OE1 | 2.640 |
| 5X5B | C_ARG_1073 | NH1 | A_ASP_1100 | OD2 | 3.761 |

Table 1: Salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| Number of salt bridges | Residue A | Residue B |
|---|---|---|
| 52 | ARG495 | ASP429 |
| 49 | ARG342 | ASP385 |
| 36 | ARG441 | ASP454 |
| 33 | ARG482 | GLU489 |
| 32 | HIS493 | GLU166 |
| 32 | ARG219 | GLU208 |
| 31 | ARG357 | ASP355 |
| 31 | HIS374 | GLU402 |
| 31 | HIS417 | ASP543 |
| 29 | ARG177 | GLU495 |
| 27 | HIS493 | ASP499 |
| 26 | HIS378 | GLU402 |
| 23 | LYS112 | GLU189 |
| 23 | LYS234 | GLU231 |
| 23 | ARG444 | GLU452 |
| 22 | ARG426 | GLU329 |
| 21 | ARG115 | GLU182 |
| 20 | ARG393 | GLU37 |
| 20 | ARG1001 | GLU999 |
| 19 | LYS187 | ASP509 |
| 19 | LYS353 | GLU38 |
| 19 | LYS309 | GLU312 |
| 19 | ARG219 | ASP201 |
| 19 | LYS288 | ASP431 |
| 19 | ARG460 | GLU457 |
| 18 | ARG1021 | GLU1013 |
| 16 | HIS401 | ASP382 |
| 16 | HIS374 | GLU406 |
| 16 | ARG48 | ASP44 |
| 16 | HIS540 | GLU435 |
| 15 | LYS419 | GLU536 |
| 15 | ARG444 | ASP454 |
| 14 | ARG306 | GLU310 |
| 14 | ARG518 | GLU406 |
| 14 | ARG204 | ASP198 |
| 14 | LYS343 | GLU327 |
| 14 | LYS458 | GLU227 |
| 12 | LYS1010 | GLU707 |
| 12 | ARG977 | ASP976 |
| 12 | LYS297 | ASP649 |
| 12 | ARG449 | GLU452 |
| 12 | ARG1001 | GLU755 |
| 12 | LYS447 | ASP407 |
| 12 | LYS541 | GLU435 |
| 11 | LYS439 | ASP480 |
| 11 | ARG38 | GLU184 |
| 11 | ARG514 | GLU398 |
| 11 | ARG453 | GLU341 |
| 10 | LYS26 | GLU23 |
| 10 | HIS378 | GLU375 |
| 10 | LYS476 | GLU479 |
| 10 | LYS470 | GLU181 |
| 10 | LYS288 | GLU433 |
| 10 | LYS313 | GLU310 |
| 10 | ARG582 | GLU232 |
| 10 | LYS541 | GLU430 |
| 10 | LYS390 | ASP393 |

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|---|---|---|
| 9 | LYS188 | ASP57 |
| 9 | ARG204 | ASP201 |
| 8 | ARG61 | ASP82 |
| 8 | ARG620 | ASP277 |
| 7 | HIS33 | ASP208 |
| 7 | ARG67 | ASP90 |
| 7 | LYS475 | GLU479 |
| 6 | LYS62 | GLU46 |
| 6 | LYS26 | GLU22 |
| 6 | ARG479 | GLU35 |
| 6 | ARG177 | GLU181 |
| 6 | HIS1046 | GLU707 |
| 6 | LYS465 | GLU467 |
| 6 | ARG518 | GLU402 |
| 6 | LYS411 | ASP407 |
| 6 | LYS543 | ASP560 |
| 5 | LYS353 | ASP38 |
| 5 | LYS419 | GLU430 |
| 5 | LYS465 | ASP463 |
| 5 | LYS221 | GLU502 |
| 5 | ARG94 | ASP101 |
| 5 | LYS514 | ASP376 |
| 5 | ARG193 | GLU211 |
| 5 | ARG38 | GLU46 |
| 4 | ARG66 | ASP86 |
| 4 | LYS577 | GLU571 |
| 4 | ARG797 | ASP850 |
| 4 | LYS465 | GLU197 |
| 4 | ARG38 | GLU89 |
| 4 | HIS374 | GLU375 |
| 4 | ARG193 | ASP214 |
| 4 | ARG61 | GLU79 |
| 4 | LYS66 | ASP86 |
| 4 | LYS149 | GLU195 |
| 3 | ARG66 | GLU28 |
| 3 | ARG553 | ASP557 |
| 3 | ARG67 | GLU89 |
| 3 | LYS600 | ASP597 |
| 3 | ARG98 | ASP105 |
| 3 | HIS35 | ASP99 |
| 3 | ARG24 | ASP70 |
| 3 | LYS534 | GLU549 |
| 3 | LYS836 | ASP554 |
| 3 | ARG46 | ASP55 |
| 3 | ARG156 | ASP202 |
| 3 | LYS31 | GLU35 |
| 3 | ARG395 | ASP95A |
| 2 | ARG223 | ASP182 |
| 2 | LYS209 | GLU124 |
| 2 | ARG1073 | ASP1100 |
| 2 | LYS235 | GLU237 |
| 2 | LYS479 | GLU35 |
| 2 | HIS35 | GLU95 |
| 2 | ARG315 | ASP376 |
| 2 | LYS175 | ASP171 |
| 2 | LYS38 | ASP86 |
| 2 | ARG162 | ASP480 |
| 2 | ARG38 | ASP90 |

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|---|---|---|
| 2 | ARG479 | ASP38 |
| 2 | ARG38 | ASP86 |
| 2 | LYS210 | GLU212 |
| 2 | LYS129 | GLU212 |
| 2 | LYS562 | ASP206 |
| 2 | LYS543 | ASP572 |
| 2 | LYS239 | GLU149 |
| 2 | HIS34 | ASP30 |
| 2 | ARG426 | ASP56 |
| 2 | ARG193 | GLU213 |
| 2 | LYS76 | ASP73 |
| 1 | HIS189 | ASP151 |
| 1 | ARG155 | GLU185 |
| 1 | ARG61 | GLU81 |
| 1 | LYS793 | ASP802 |
| 1 | HIS34 | GLU37 |
| 1 | LYS465 | ASP198 |
| 1 | LYS210 | GLU123 |
| 1 | LYS211 | GLU213 |
| 1 | ARG33 | ASP56 |
| 1 | LYS534 | ASP431 |
| 1 | ARG395 | ASP392 |
| 1 | LYS199 | ASP110 |
| 1 | LYS130 | ASP144 |
| 1 | LYS65 | ASP62 |
| 1 | LYS190 | ASP191 |
| 1 | LYS142 | GLU105 |
| 1 | HIS74 | ASP24 |
| 1 | ARG191 | ASP152 |
| 1 | HIS535 | GLU536 |
| 1 | LYS31 | ASP92 |
| 1 | LYS167 | GLU83 |
| 1 | LYS566 | ASP351 |
| 1 | ARG582 | GLU527 |
| 1 | ARG100 | ASP101 |
| 1 | LYS344 | GLU502 |

Table 2: Counting of side chain salt bridging networks within the PDB entries.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_534 | NZ | B_ASP_431 | OD1 | 3.656 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.710 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.597 |
| 2AJF | E_ARG_426 | NH1 | A_GLU_329 | OE2 | 3.740 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.855 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 2.946 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.890 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.381 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 2.717 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 2.911 |
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE1 | 3.913 |
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE2 | 2.993 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE1 | 2.759 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE2 | 3.226 |
| 2DD8 | L_LYS_130 | NZ | H_ASP_144 | OD2 | 3.343 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD1 | 3.643 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD2 | 3.461 |
| 2DD8 | S_ARG_395 | NH2 | L_ASP_95A | OD1 | 3.001 |
| 2GHW | B_ARG_162 | NH1 | A_ASP_480 | OD1 | 3.081 |
| 2GHW | D_ARG_162 | NH2 | C_ASP_480 | OD1 | 3.626 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD1 | 3.504 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD2 | 2.403 |
| 3BGF | S_LYS_439 | NZ | A_ASP_480 | OD2 | 3.161 |
| 3BGF | A_LYS_439 | NZ | S_ASP_480 | OD2 | 2.520 |
| 3BGF | H_LYS_210 | NZ | L_GLU_123 | OE1 | 3.997 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.856 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.820 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.231 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.198 |
| 3D0H | E_LYS_479 | NZ | A_GLU_35 | OE1 | 3.397 |
| 3D0H | F_LYS_479 | NZ | B_GLU_35 | OE1 | 3.369 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.355 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.779 |
| 3D0I | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 3.324 |
| 3D0I | E_ARG_479 | NH2 | A_GLU_35 | OE1 | 2.730 |
| 3D0I | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 3.405 |
| 3D0I | F_ARG_479 | NH2 | B_GLU_35 | OE1 | 2.961 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.520 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.936 |
| 3SCI | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.257 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.110 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.923 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.044 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.878 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.617 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.574 |
| 3SCJ | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.526 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.206 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.277 |
| 3SCJ | E_ARG_479 | NH2 | A_ASP_38 | OD2 | 2.575 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.547 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.819 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 3.913 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 3.505 |
| 3SCJ | F_ARG_479 | NH2 | B_ASP_38 | OD2 | 2.718 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.939 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.692 |

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|---|---|---|---|---|---|
| 3SCK | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.591 |
| 3SCK | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 2.498 |
| 3SCK | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 2.750 |
| 3SCL | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.918 |
| 3SCL | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.916 |
| 3SCL | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.143 |
| 5X58 | A_LYS_221 | NZ | C_GLU_502 | OE2 | 3.266 |
| 5X58 | A_LYS_836 | NZ | C_ASP_554 | OD2 | 3.822 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.482 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 3.202 |
| 5X58 | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.575 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.983 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.964 |
| 5X58 | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.486 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE1 | 3.011 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE2 | 3.438 |
| 5X58 | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.538 |
| 5X58 | B_LYS_221 | NZ | A_GLU_502 | OE2 | 3.264 |
| 5X58 | B_LYS_836 | NZ | A_ASP_554 | OD2 | 3.822 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD1 | 3.484 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD2 | 3.202 |
| 5X58 | B_ARG_977 | NH2 | C_ASP_976 | OD2 | 3.576 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.983 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.963 |
| 5X58 | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.485 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.011 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 3.438 |
| 5X58 | B_ARG_1021 | NH2 | C_GLU_1013 | OE2 | 3.540 |
| 5X58 | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.265 |
| 5X58 | C_LYS_836 | NZ | B_ASP_554 | OD2 | 3.825 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD1 | 3.484 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD2 | 3.202 |
| 5X58 | C_ARG_977 | NH2 | A_ASP_976 | OD2 | 3.575 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.985 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.966 |
| 5X58 | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.487 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.011 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 3.438 |
| 5X58 | C_ARG_1021 | NH2 | A_GLU_1013 | OE2 | 3.539 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.912 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 2.504 |
| 5X5B | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.789 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.909 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.948 |
| 5X5B | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.377 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.472 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.057 |
| 5X5B | A_ARG_1073 | NH1 | B_ASP_1100 | OD2 | 3.995 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.930 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.999 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE1 | 3.970 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.150 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.450 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 2.311 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE1 | 3.851 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.225 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.907 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.931 |

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|---|---|---|---|---|---|
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE1 | 3.965 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.203 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.273 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 2.370 |
| 5X5B | C_ARG_1073 | NH1 | A_ASP_1100 | OD2 | 3.761 |

Table 3: Interfacial salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| Number of salt bridges | Residue A | Residue B |
|---|---|---|
| 22 | ARG426 | GLU329 |
| 20 | ARG1001 | GLU999 |
| 15 | ARG1021 | GLU1013 |
| 15 | LYS419 | GLU536 |
| 12 | ARG977 | ASP976 |
| 6 | ARG479 | GLU35 |
| 5 | LYS221 | GLU502 |
| 3 | ARG395 | ASP95A |
| 3 | LYS836 | ASP554 |
| 2 | LYS439 | ASP480 |
| 2 | LYS479 | GLU35 |
| 2 | ARG426 | ASP56 |
| 2 | ARG162 | ASP480 |
| 2 | ARG479 | ASP38 |
| 2 | LYS129 | GLU212 |
| 2 | ARG1073 | ASP1100 |
| 2 | LYS209 | GLU124 |
| 1 | LYS210 | GLU123 |
| 1 | LYS534 | ASP431 |
| 1 | LYS130 | ASP144 |

Table 4: Counting of interfacial side chain salt bridging networks within the PDB entries.

## PDB ID-specific analysis of SARS coronavirus spike protein-related structures

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_31 | NZ | A_GLU_35 | OE1 | 3.992 |
| 2AJF | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.808 |
| 2AJF | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.727 |
| 2AJF | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.080 |
| 2AJF | A_ARG_177 | NH1 | A_GLU_181 | OE2 | 3.241 |
| 2AJF | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.882 |
| 2AJF | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.146 |
| 2AJF | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.420 |
| 2AJF | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 2.794 |
| 2AJF | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.745 |
| 2AJF | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.452 |
| 2AJF | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.763 |
| 2AJF | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.712 |
| 2AJF | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.011 |
| 2AJF | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.673 |
| 2AJF | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.856 |
| 2AJF | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.630 |
| 2AJF | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.271 |
| 2AJF | A_LYS_309 | NZ | A_GLU_312 | OE2 | 3.754 |
| 2AJF | A_LYS_353 | NZ | A_ASP_38 | OD1 | 3.263 |
| 2AJF | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 2.604 |
| 2AJF | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 3.201 |
| 2AJF | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.025 |
| 2AJF | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.882 |
| 2AJF | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 2.606 |
| 2AJF | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.668 |
| 2AJF | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 2.869 |
| 2AJF | A_ARG_393 | NH1 | A_GLU_37 | OE1 | 3.436 |
| 2AJF | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 3.134 |
| 2AJF | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.409 |
| 2AJF | A_HIS_401 | NE2 | A_ASP_382 | OD2 | 3.397 |
| 2AJF | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.685 |
| 2AJF | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.827 |
| 2AJF | A_LYS_458 | NZ | A_GLU_227 | OE1 | 3.613 |
| 2AJF | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.040 |
| 2AJF | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 3.643 |
| 2AJF | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.692 |
| 2AJF | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.567 |
| 2AJF | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.336 |
| 2AJF | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.457 |
| 2AJF | A_HIS_493 | ND1 | A_GLU_166 | OE2 | 3.978 |
| 2AJF | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.395 |
| 2AJF | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.568 |
| 2AJF | A_LYS_534 | NZ | B_ASP_431 | OD1 | 3.656 |
| 2AJF | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.928 |
| 2AJF | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.791 |
| 2AJF | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.920 |
| 2AJF | A_LYS_577 | NZ | A_GLU_571 | OE1 | 3.259 |
| 2AJF | A_LYS_600 | NZ | A_ASP_597 | OD1 | 3.832 |
| 2AJF | A_LYS_600 | NZ | A_ASP_597 | OD2 | 3.177 |
| 2AJF | B_LYS_26 | NZ | B_GLU_22 | OE1 | 3.456 |
| 2AJF | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.258 |
| 2AJF | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.099 |
| 2AJF | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 2.804 |
| 2AJF | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.317 |
| 2AJF | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.392 |
| 2AJF | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.458 |

| 2AJF | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.319 |
|---|---|---|---|---|---|
| 2AJF | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.488 |
| 2AJF | B_ARG_219 | NH2 | B_ASP_201 | OD1 | 3.892 |
| 2AJF | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.087 |
| 2AJF | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.992 |
| 2AJF | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.226 |
| 2AJF | B_ARG_357 | NH2 | B_ASP_355 | OD1 | 2.846 |
| 2AJF | B_ARG_357 | NH2 | B_ASP_355 | OD2 | 2.664 |
| 2AJF | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.307 |
| 2AJF | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.459 |
| 2AJF | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.493 |
| 2AJF | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.992 |
| 2AJF | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.671 |
| 2AJF | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 3.226 |
| 2AJF | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.233 |
| 2AJF | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.525 |
| 2AJF | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.748 |
| 2AJF | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.582 |
| 2AJF | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.890 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.710 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.597 |
| 2AJF | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.035 |
| 2AJF | B_LYS_475 | NZ | B_GLU_479 | OE2 | 3.697 |
| 2AJF | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 2.938 |
| 2AJF | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.429 |
| 2AJF | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.671 |
| 2AJF | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.284 |
| 2AJF | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.981 |
| 2AJF | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.560 |
| 2AJF | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.654 |
| 2AJF | B_LYS_541 | NZ | B_GLU_435 | OE1 | 3.723 |
| 2AJF | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.314 |
| 2AJF | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 2.787 |
| 2AJF | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 2.961 |
| 2AJF | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.004 |
| 2AJF | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.286 |
| 2AJF | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.910 |
| 2AJF | E_ARG_426 | NH1 | A_GLU_329 | OE2 | 3.740 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.855 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 2.946 |
| 2AJF | E_ARG_441 | NH1 | E_ASP_454 | OD1 | 3.531 |
| 2AJF | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.278 |
| 2AJF | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.408 |
| 2AJF | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.735 |
| 2AJF | E_LYS_447 | NZ | E_ASP_407 | OD2 | 3.899 |
| 2AJF | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.268 |
| 2AJF | E_LYS_465 | NZ | E_ASP_463 | OD2 | 3.801 |
| 2AJF | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.014 |
| 2AJF | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.467 |
| 2AJF | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.200 |
| 2AJF | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 2.772 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.890 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.381 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 2.717 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 2.911 |
| 2AJF | F_LYS_439 | NZ | F_ASP_480 | OD1 | 3.696 |
| 2AJF | F_ARG_441 | NH1 | F_ASP_454 | OD1 | 3.900 |
| 2AJF | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.426 |

| | | | | | |
|---|---|---|---|---|---|
| 2AJF | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.001 |
| 2AJF | F_ARG_453 | NH2 | F_GLU_341 | OE2 | 3.749 |
| 2AJF | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 3.808 |

Table 5: 2AJF-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_ARG_38 | NH1 | H_ASP_86 | OD1 | 2.908 |
| 2DD8 | H_ARG_38 | NH2 | H_GLU_46 | OE1 | 3.751 |
| 2DD8 | H_ARG_38 | NH2 | H_ASP_86 | OD1 | 3.769 |
| 2DD8 | H_LYS_62 | NZ | H_GLU_46 | OE1 | 3.535 |
| 2DD8 | H_LYS_62 | NZ | H_GLU_46 | OE2 | 3.348 |
| 2DD8 | H_ARG_66 | NH1 | H_ASP_86 | OD1 | 3.583 |
| 2DD8 | H_ARG_66 | NH1 | H_ASP_86 | OD2 | 3.304 |
| 2DD8 | H_ARG_66 | NH2 | H_ASP_86 | OD1 | 2.890 |
| 2DD8 | H_ARG_66 | NH2 | H_ASP_86 | OD2 | 3.740 |
| 2DD8 | H_ARG_94 | NH2 | H_ASP_101 | OD2 | 2.723 |
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE1 | 3.913 |
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE2 | 2.993 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE1 | 2.759 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE2 | 3.226 |
| 2DD8 | H_LYS_210 | NZ | H_GLU_212 | OE1 | 3.571 |
| 2DD8 | H_LYS_210 | NZ | H_GLU_212 | OE2 | 3.616 |
| 2DD8 | L_LYS_31 | NZ | L_ASP_92 | OD1 | 3.038 |
| 2DD8 | L_ARG_61 | NH1 | L_ASP_82 | OD1 | 3.795 |
| 2DD8 | L_ARG_61 | NH1 | L_ASP_82 | OD2 | 2.711 |
| 2DD8 | L_ARG_61 | NH2 | L_ASP_82 | OD1 | 2.938 |
| 2DD8 | L_ARG_61 | NH2 | L_ASP_82 | OD2 | 3.305 |
| 2DD8 | L_LYS_130 | NZ | H_ASP_144 | OD2 | 3.343 |
| 2DD8 | L_LYS_167 | NZ | L_GLU_83 | OE1 | 3.208 |
| 2DD8 | L_ARG_191 | NH1 | L_ASP_152 | OD2 | 3.527 |
| 2DD8 | S_ARG_342 | NH2 | S_ASP_385 | OD1 | 3.426 |
| 2DD8 | S_ARG_342 | NH2 | S_ASP_385 | OD2 | 2.961 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD1 | 3.643 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD2 | 3.461 |
| 2DD8 | S_ARG_395 | NH2 | L_ASP_95A | OD1 | 3.001 |
| 2DD8 | S_ARG_395 | NH2 | S_ASP_392 | OD1 | 3.245 |
| 2DD8 | S_LYS_411 | NZ | S_ASP_407 | OD1 | 2.884 |
| 2DD8 | S_LYS_439 | NZ | S_ASP_480 | OD1 | 3.148 |
| 2DD8 | S_ARG_441 | NH2 | S_ASP_454 | OD1 | 3.375 |
| 2DD8 | S_ARG_444 | NH2 | S_ASP_454 | OD2 | 3.531 |
| 2DD8 | S_LYS_447 | NZ | S_ASP_407 | OD1 | 3.742 |
| 2DD8 | S_ARG_449 | NH1 | S_GLU_452 | OE1 | 3.677 |
| 2DD8 | S_ARG_449 | NH1 | S_GLU_452 | OE2 | 3.337 |
| 2DD8 | S_ARG_449 | NH2 | S_GLU_452 | OE2 | 2.689 |
| 2DD8 | S_ARG_495 | NH2 | S_ASP_429 | OD1 | 3.196 |
| 2DD8 | S_ARG_495 | NH2 | S_ASP_429 | OD2 | 3.755 |

Table 6: 2DD8-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHV | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.550 |
| 2GHV | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 2.981 |
| 2GHV | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.496 |
| 2GHV | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.534 |
| 2GHV | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.804 |
| 2GHV | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.565 |
| 2GHV | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.040 |
| 2GHV | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.590 |
| 2GHV | C_ARG_342 | NH2 | C_ASP_385 | OD1 | 3.469 |
| 2GHV | C_ARG_342 | NH2 | C_ASP_385 | OD2 | 2.877 |
| 2GHV | C_LYS_343 | NZ | C_GLU_327 | OE1 | 3.965 |
| 2GHV | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.439 |
| 2GHV | C_ARG_444 | NH2 | C_GLU_452 | OE2 | 3.650 |
| 2GHV | C_ARG_444 | NH2 | C_ASP_454 | OD1 | 3.401 |
| 2GHV | C_ARG_449 | NH2 | C_GLU_452 | OE1 | 3.440 |
| 2GHV | C_ARG_449 | NH2 | C_GLU_452 | OE2 | 3.175 |
| 2GHV | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 2.912 |
| 2GHV | C_ARG_495 | NH2 | C_ASP_429 | OD2 | 3.523 |

Table 7: 2GHV-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | A_ARG_342 | NH2 | A_ASP_385 | OD1 | 3.548 |
| 2GHW | A_ARG_342 | NH2 | A_ASP_385 | OD2 | 3.167 |
| 2GHW | A_LYS_439 | NZ | A_ASP_480 | OD2 | 3.192 |
| 2GHW | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.680 |
| 2GHW | A_ARG_444 | NH2 | A_GLU_452 | OE2 | 3.285 |
| 2GHW | A_ARG_444 | NH2 | A_ASP_454 | OD1 | 3.823 |
| 2GHW | A_ARG_449 | NH1 | A_GLU_452 | OE1 | 3.684 |
| 2GHW | A_ARG_449 | NH1 | A_GLU_452 | OE2 | 3.739 |
| 2GHW | A_ARG_449 | NH2 | A_GLU_452 | OE2 | 3.726 |
| 2GHW | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.315 |
| 2GHW | A_ARG_495 | NH2 | A_ASP_429 | OD2 | 3.983 |
| 2GHW | B_HIS_35 | NE2 | B_ASP_99 | OD1 | 3.622 |
| 2GHW | B_ARG_38 | NH1 | B_GLU_89 | OE1 | 3.674 |
| 2GHW | B_ARG_38 | NH1 | B_ASP_90 | OD1 | 3.164 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_46 | OE1 | 3.155 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_46 | OE2 | 3.798 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_89 | OE1 | 3.206 |
| 2GHW | B_ARG_67 | NH1 | B_ASP_90 | OD1 | 3.382 |
| 2GHW | B_ARG_67 | NH1 | B_ASP_90 | OD2 | 2.930 |
| 2GHW | B_ARG_67 | NH2 | B_GLU_89 | OE1 | 3.863 |
| 2GHW | B_ARG_67 | NH2 | B_GLU_89 | OE2 | 3.548 |
| 2GHW | B_ARG_67 | NH2 | B_ASP_90 | OD1 | 3.270 |
| 2GHW | B_ARG_67 | NH2 | B_ASP_90 | OD2 | 3.745 |
| 2GHW | B_LYS_76 | NZ | B_ASP_73 | OD2 | 2.795 |
| 2GHW | B_ARG_98 | NH2 | B_ASP_105 | OD2 | 3.012 |
| 2GHW | B_ARG_156 | NH2 | B_ASP_202 | OD1 | 3.384 |
| 2GHW | B_ARG_156 | NH2 | B_ASP_202 | OD2 | 3.152 |
| 2GHW | B_ARG_162 | NH1 | A_ASP_480 | OD1 | 3.081 |
| 2GHW | B_ARG_193 | NH1 | B_GLU_211 | OE2 | 3.176 |
| 2GHW | B_ARG_193 | NH2 | B_GLU_211 | OE2 | 3.887 |
| 2GHW | B_ARG_193 | NH2 | B_GLU_213 | OE1 | 3.299 |
| 2GHW | B_ARG_193 | NH2 | B_ASP_214 | OD1 | 3.163 |
| 2GHW | B_ARG_193 | NH2 | B_ASP_214 | OD2 | 3.876 |
| 2GHW | B_ARG_223 | NH2 | B_ASP_182 | OD1 | 3.202 |
| 2GHW | B_LYS_235 | NZ | B_GLU_237 | OE2 | 3.402 |
| 2GHW | C_ARG_342 | NH2 | C_ASP_385 | OD1 | 3.626 |
| 2GHW | C_ARG_342 | NH2 | C_ASP_385 | OD2 | 3.156 |
| 2GHW | C_LYS_439 | NZ | C_ASP_480 | OD1 | 3.911 |
| 2GHW | C_LYS_439 | NZ | C_ASP_480 | OD2 | 3.110 |
| 2GHW | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.789 |
| 2GHW | C_ARG_444 | NH2 | C_GLU_452 | OE2 | 3.347 |
| 2GHW | C_ARG_444 | NH2 | C_ASP_454 | OD1 | 3.456 |
| 2GHW | C_ARG_449 | NH1 | C_GLU_452 | OE1 | 3.965 |
| 2GHW | C_ARG_449 | NH1 | C_GLU_452 | OE2 | 3.472 |
| 2GHW | C_ARG_449 | NH2 | C_GLU_452 | OE1 | 3.904 |
| 2GHW | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 3.274 |
| 2GHW | D_HIS_35 | ND1 | D_ASP_99 | OD1 | 3.954 |
| 2GHW | D_HIS_35 | NE2 | D_ASP_99 | OD1 | 3.761 |
| 2GHW | D_ARG_38 | NH1 | D_ASP_90 | OD1 | 3.162 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_46 | OE1 | 3.538 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_46 | OE2 | 3.668 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_89 | OE1 | 3.329 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_89 | OE2 | 2.864 |
| 2GHW | D_LYS_65 | NZ | D_ASP_62 | OD1 | 3.926 |
| 2GHW | D_ARG_67 | NH1 | D_ASP_90 | OD2 | 3.105 |
| 2GHW | D_ARG_67 | NH2 | D_GLU_89 | OE1 | 3.576 |
| 2GHW | D_ARG_67 | NH2 | D_ASP_90 | OD1 | 3.163 |

| | | | | | |
|---|---|---|---|---|---|
| 2GHW | D_ARG_67 | NH2 | D_ASP_90 | OD2 | 3.377 |
| 2GHW | D_LYS_76 | NZ | D_ASP_73 | OD2 | 3.658 |
| 2GHW | D_ARG_98 | NH2 | D_ASP_105 | OD1 | 3.960 |
| 2GHW | D_ARG_98 | NH2 | D_ASP_105 | OD2 | 3.196 |
| 2GHW | D_ARG_156 | NH1 | D_ASP_202 | OD2 | 3.931 |
| 2GHW | D_ARG_162 | NH2 | C_ASP_480 | OD1 | 3.626 |
| 2GHW | D_ARG_193 | NH1 | D_GLU_211 | OE1 | 3.249 |
| 2GHW | D_ARG_193 | NH1 | D_GLU_211 | OE2 | 3.681 |
| 2GHW | D_ARG_193 | NH2 | D_GLU_211 | OE1 | 3.135 |
| 2GHW | D_ARG_193 | NH2 | D_GLU_213 | OE1 | 3.465 |
| 2GHW | D_ARG_193 | NH2 | D_ASP_214 | OD1 | 3.132 |
| 2GHW | D_ARG_193 | NH2 | D_ASP_214 | OD2 | 3.717 |
| 2GHW | D_ARG_223 | NH2 | D_ASP_182 | OD1 | 3.375 |
| 2GHW | D_LYS_235 | NZ | D_GLU_237 | OE2 | 3.600 |
| 2GHW | D_LYS_239 | NZ | D_GLU_149 | OE1 | 3.290 |
| 2GHW | D_LYS_239 | NZ | D_GLU_149 | OE2 | 3.630 |

Table 8: 2GHW-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | S_ARG_342 | NH2 | S_ASP_385 | OD1 | 3.676 |
| 3BGF | S_ARG_342 | NH2 | S_ASP_385 | OD2 | 3.162 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD1 | 3.504 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD2 | 2.403 |
| 3BGF | S_LYS_439 | NZ | S_ASP_480 | OD1 | 3.797 |
| 3BGF | S_LYS_439 | NZ | A_ASP_480 | OD2 | 3.161 |
| 3BGF | S_ARG_441 | NH2 | S_ASP_454 | OD1 | 2.963 |
| 3BGF | S_ARG_444 | NH2 | S_GLU_452 | OE2 | 3.267 |
| 3BGF | S_ARG_444 | NH2 | S_ASP_454 | OD2 | 3.815 |
| 3BGF | S_LYS_447 | NZ | S_ASP_407 | OD1 | 3.987 |
| 3BGF | S_LYS_447 | NZ | S_ASP_407 | OD2 | 3.876 |
| 3BGF | S_ARG_449 | NH2 | S_GLU_452 | OE1 | 3.535 |
| 3BGF | S_ARG_495 | NH2 | S_ASP_429 | OD1 | 3.362 |
| 3BGF | S_ARG_495 | NH2 | S_ASP_429 | OD2 | 3.615 |
| 3BGF | A_ARG_342 | NH2 | A_ASP_385 | OD1 | 3.423 |
| 3BGF | A_ARG_342 | NH2 | A_ASP_385 | OD2 | 2.961 |
| 3BGF | A_LYS_390 | NZ | A_ASP_393 | OD1 | 3.583 |
| 3BGF | A_LYS_390 | NZ | A_ASP_393 | OD2 | 3.966 |
| 3BGF | A_LYS_439 | NZ | S_ASP_480 | OD2 | 2.520 |
| 3BGF | A_LYS_439 | NZ | A_ASP_480 | OD1 | 3.180 |
| 3BGF | A_ARG_441 | NH2 | A_ASP_454 | OD1 | 3.440 |
| 3BGF | A_ARG_444 | NH2 | A_GLU_452 | OE2 | 3.371 |
| 3BGF | A_ARG_444 | NH2 | A_ASP_454 | OD2 | 3.730 |
| 3BGF | A_LYS_447 | NZ | A_ASP_407 | OD1 | 2.877 |
| 3BGF | A_LYS_447 | NZ | A_ASP_407 | OD2 | 2.805 |
| 3BGF | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.108 |
| 3BGF | A_ARG_495 | NH2 | A_ASP_429 | OD2 | 2.922 |
| 3BGF | L_ARG_24 | NH2 | L_ASP_70 | OD1 | 3.258 |
| 3BGF | L_ARG_24 | NH2 | L_ASP_70 | OD2 | 2.893 |
| 3BGF | L_ARG_46 | NH1 | L_ASP_55 | OD1 | 3.016 |
| 3BGF | L_ARG_46 | NH1 | L_ASP_55 | OD2 | 3.557 |
| 3BGF | L_ARG_61 | NH1 | L_GLU_79 | OE1 | 3.984 |
| 3BGF | L_ARG_61 | NH1 | L_GLU_79 | OE2 | 3.405 |
| 3BGF | L_ARG_61 | NH2 | L_ASP_82 | OD1 | 2.650 |
| 3BGF | L_ARG_61 | NH2 | L_ASP_82 | OD2 | 2.907 |
| 3BGF | L_ARG_66 | NH2 | L_GLU_28 | OE2 | 2.738 |
| 3BGF | L_LYS_149 | NZ | L_GLU_195 | OE1 | 3.683 |
| 3BGF | L_LYS_149 | NZ | L_GLU_195 | OE2 | 3.129 |
| 3BGF | L_HIS_189 | ND1 | L_ASP_151 | OD1 | 2.696 |
| 3BGF | H_ARG_33 | NH1 | H_ASP_56 | OD2 | 3.848 |
| 3BGF | H_HIS_35 | NE2 | H_GLU_95 | OE1 | 2.884 |
| 3BGF | H_LYS_38 | NZ | H_ASP_86 | OD1 | 3.661 |
| 3BGF | H_LYS_62 | NZ | H_GLU_46 | OE1 | 2.635 |
| 3BGF | H_LYS_62 | NZ | H_GLU_46 | OE2 | 3.712 |
| 3BGF | H_LYS_66 | NZ | H_ASP_86 | OD1 | 3.553 |
| 3BGF | H_LYS_66 | NZ | H_ASP_86 | OD2 | 2.671 |
| 3BGF | H_ARG_94 | NH1 | H_ASP_101 | OD1 | 2.347 |
| 3BGF | H_ARG_94 | NH1 | H_ASP_101 | OD2 | 3.381 |
| 3BGF | H_LYS_210 | NZ | L_GLU_123 | OE1 | 3.997 |
| 3BGF | H_LYS_211 | NZ | H_GLU_213 | OE2 | 3.764 |
| 3BGF | C_ARG_24 | NH2 | C_ASP_70 | OD1 | 3.766 |
| 3BGF | C_ARG_46 | NH1 | C_ASP_55 | OD1 | 2.965 |
| 3BGF | C_ARG_61 | NH1 | C_GLU_79 | OE1 | 3.352 |
| 3BGF | C_ARG_61 | NH1 | C_GLU_79 | OE2 | 3.278 |
| 3BGF | C_ARG_61 | NH2 | C_GLU_81 | OE2 | 3.045 |
| 3BGF | C_ARG_61 | NH2 | C_ASP_82 | OD1 | 2.379 |
| 3BGF | C_ARG_61 | NH2 | C_ASP_82 | OD2 | 2.905 |

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|---|---|---|---|---|---|
| 3BGF | C_ARG_66 | NH2 | C_GLU_28 | OE1 | 3.607 |
| 3BGF | C_ARG_66 | NH2 | C_GLU_28 | OE2 | 2.938 |
| 3BGF | C_LYS_142 | NZ | C_GLU_105 | OE1 | 3.341 |
| 3BGF | C_LYS_149 | NZ | C_GLU_195 | OE1 | 3.352 |
| 3BGF | C_LYS_149 | NZ | C_GLU_195 | OE2 | 3.898 |
| 3BGF | C_ARG_155 | NH2 | C_GLU_185 | OE2 | 3.481 |
| 3BGF | C_LYS_199 | NZ | C_ASP_110 | OD2 | 3.825 |
| 3BGF | B_HIS_35 | NE2 | B_GLU_95 | OE1 | 2.642 |
| 3BGF | B_LYS_38 | NZ | B_ASP_86 | OD1 | 3.591 |
| 3BGF | B_LYS_62 | NZ | B_GLU_46 | OE1 | 2.547 |
| 3BGF | B_LYS_62 | NZ | B_GLU_46 | OE2 | 3.280 |
| 3BGF | B_LYS_66 | NZ | B_ASP_86 | OD1 | 3.814 |
| 3BGF | B_LYS_66 | NZ | B_ASP_86 | OD2 | 2.805 |
| 3BGF | B_ARG_94 | NH1 | B_ASP_101 | OD1 | 2.357 |
| 3BGF | B_ARG_94 | NH1 | B_ASP_101 | OD2 | 2.930 |
| 3BGF | B_ARG_100 | NH1 | B_ASP_101 | OD1 | 3.816 |

Table 9: 3BGF-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0G | A_LYS_26 | NZ | A_GLU_23 | OE1 | 2.776 |
| 3D0G | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.622 |
| 3D0G | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.885 |
| 3D0G | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.369 |
| 3D0G | A_LYS_187 | NZ | A_ASP_509 | OD1 | 3.967 |
| 3D0G | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.239 |
| 3D0G | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.291 |
| 3D0G | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 2.733 |
| 3D0G | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.447 |
| 3D0G | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.737 |
| 3D0G | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.326 |
| 3D0G | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.150 |
| 3D0G | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.034 |
| 3D0G | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.248 |
| 3D0G | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.949 |
| 3D0G | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.812 |
| 3D0G | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.737 |
| 3D0G | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.262 |
| 3D0G | A_LYS_353 | NZ | A_GLU_38 | OE2 | 2.453 |
| 3D0G | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.211 |
| 3D0G | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.562 |
| 3D0G | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.713 |
| 3D0G | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.062 |
| 3D0G | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.290 |
| 3D0G | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.966 |
| 3D0G | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.850 |
| 3D0G | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 2.924 |
| 3D0G | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.555 |
| 3D0G | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.763 |
| 3D0G | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.955 |
| 3D0G | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.595 |
| 3D0G | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.159 |
| 3D0G | A_LYS_465 | NZ | A_GLU_467 | OE1 | 2.701 |
| 3D0G | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.777 |
| 3D0G | A_LYS_476 | NZ | A_GLU_479 | OE1 | 2.526 |
| 3D0G | A_LYS_476 | NZ | A_GLU_479 | OE2 | 3.323 |
| 3D0G | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.955 |
| 3D0G | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.559 |
| 3D0G | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.849 |
| 3D0G | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.410 |
| 3D0G | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.585 |
| 3D0G | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.569 |
| 3D0G | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.965 |
| 3D0G | A_LYS_534 | NZ | A_GLU_549 | OE1 | 3.278 |
| 3D0G | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.979 |
| 3D0G | A_LYS_541 | NZ | A_GLU_435 | OE1 | 2.843 |
| 3D0G | A_LYS_541 | NZ | A_GLU_435 | OE2 | 3.422 |
| 3D0G | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.839 |
| 3D0G | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.548 |
| 3D0G | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.791 |
| 3D0G | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 2.982 |
| 3D0G | B_ARG_177 | NH1 | B_GLU_181 | OE2 | 3.376 |
| 3D0G | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.263 |
| 3D0G | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.324 |
| 3D0G | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.466 |
| 3D0G | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.330 |
| 3D0G | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.128 |

| 3D0G | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.324 |
|---|---|---|---|---|---|
| 3D0G | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.217 |
| 3D0G | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.383 |
| 3D0G | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.414 |
| 3D0G | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.707 |
| 3D0G | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.600 |
| 3D0G | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.077 |
| 3D0G | B_LYS_309 | NZ | B_GLU_312 | OE2 | 3.968 |
| 3D0G | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.363 |
| 3D0G | B_LYS_353 | NZ | B_GLU_38 | OE2 | 3.062 |
| 3D0G | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.623 |
| 3D0G | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.770 |
| 3D0G | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.697 |
| 3D0G | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.864 |
| 3D0G | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.467 |
| 3D0G | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.478 |
| 3D0G | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.097 |
| 3D0G | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 2.744 |
| 3D0G | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.625 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.856 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.820 |
| 3D0G | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.654 |
| 3D0G | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.787 |
| 3D0G | B_LYS_465 | NZ | B_GLU_467 | OE2 | 3.564 |
| 3D0G | B_LYS_475 | NZ | B_GLU_479 | OE2 | 3.791 |
| 3D0G | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 2.475 |
| 3D0G | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.483 |
| 3D0G | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.939 |
| 3D0G | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.187 |
| 3D0G | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.890 |
| 3D0G | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.723 |
| 3D0G | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.789 |
| 3D0G | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.550 |
| 3D0G | B_LYS_541 | NZ | B_GLU_430 | OE2 | 2.944 |
| 3D0G | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.837 |
| 3D0G | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 2.994 |
| 3D0G | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.222 |
| 3D0G | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.591 |
| 3D0G | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.325 |
| 3D0G | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.203 |
| 3D0G | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.859 |
| 3D0G | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.789 |
| 3D0G | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.460 |
| 3D0G | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.067 |
| 3D0G | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.649 |
| 3D0G | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.432 |
| 3D0G | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 2.983 |
| 3D0G | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.908 |
| 3D0G | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.831 |
| 3D0G | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.314 |
| 3D0G | F_ARG_444 | NH1 | F_GLU_452 | OE2 | 3.743 |
| 3D0G | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.573 |
| 3D0G | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.447 |
| 3D0G | F_LYS_465 | NZ | F_ASP_463 | OD1 | 3.077 |
| 3D0G | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.771 |
| 3D0G | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.277 |

Table 10: 3D0G-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0H | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.654 |
| 3D0H | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.191 |
| 3D0H | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.636 |
| 3D0H | A_ARG_177 | NH1 | A_GLU_181 | OE1 | 3.849 |
| 3D0H | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.600 |
| 3D0H | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.269 |
| 3D0H | A_LYS_187 | NZ | A_ASP_509 | OD1 | 3.949 |
| 3D0H | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.246 |
| 3D0H | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.322 |
| 3D0H | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.787 |
| 3D0H | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.750 |
| 3D0H | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.495 |
| 3D0H | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.408 |
| 3D0H | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.748 |
| 3D0H | A_LYS_288 | NZ | A_ASP_431 | OD1 | 2.502 |
| 3D0H | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.500 |
| 3D0H | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.942 |
| 3D0H | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.050 |
| 3D0H | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.130 |
| 3D0H | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.006 |
| 3D0H | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.624 |
| 3D0H | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.643 |
| 3D0H | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.324 |
| 3D0H | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 2.663 |
| 3D0H | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.758 |
| 3D0H | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.834 |
| 3D0H | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.253 |
| 3D0H | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.415 |
| 3D0H | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.751 |
| 3D0H | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.376 |
| 3D0H | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.176 |
| 3D0H | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.144 |
| 3D0H | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.261 |
| 3D0H | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.974 |
| 3D0H | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.676 |
| 3D0H | A_LYS_476 | NZ | A_GLU_479 | OE2 | 2.624 |
| 3D0H | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.621 |
| 3D0H | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.471 |
| 3D0H | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.377 |
| 3D0H | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.625 |
| 3D0H | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.765 |
| 3D0H | A_ARG_514 | NH1 | A_GLU_398 | OE1 | 3.428 |
| 3D0H | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.126 |
| 3D0H | A_ARG_518 | NH1 | A_GLU_406 | OE1 | 3.615 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_402 | OE2 | 3.679 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_406 | OE1 | 3.756 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_406 | OE2 | 3.850 |
| 3D0H | A_LYS_534 | NZ | A_GLU_549 | OE2 | 3.173 |
| 3D0H | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.471 |
| 3D0H | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.695 |
| 3D0H | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.854 |
| 3D0H | A_LYS_541 | NZ | A_GLU_435 | OE2 | 3.545 |
| 3D0H | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.272 |
| 3D0H | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.185 |
| 3D0H | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.413 |
| 3D0H | B_ARG_177 | NH1 | B_GLU_181 | OE1 | 3.536 |
| 3D0H | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.392 |

| | | | | | |
|---|---|---|---|---|---|
| 3D0H | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.303 |
| 3D0H | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.884 |
| 3D0H | B_ARG_204 | NH1 | B_ASP_198 | OD2 | 3.995 |
| 3D0H | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.825 |
| 3D0H | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.543 |
| 3D0H | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.592 |
| 3D0H | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.819 |
| 3D0H | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.119 |
| 3D0H | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.307 |
| 3D0H | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.891 |
| 3D0H | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.446 |
| 3D0H | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.471 |
| 3D0H | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.557 |
| 3D0H | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.699 |
| 3D0H | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.313 |
| 3D0H | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.675 |
| 3D0H | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.061 |
| 3D0H | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.799 |
| 3D0H | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.437 |
| 3D0H | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.549 |
| 3D0H | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.248 |
| 3D0H | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.405 |
| 3D0H | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.407 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.231 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.198 |
| 3D0H | B_LYS_419 | NZ | B_GLU_430 | OE1 | 3.848 |
| 3D0H | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.001 |
| 3D0H | B_LYS_470 | NZ | B_GLU_181 | OE1 | 2.767 |
| 3D0H | B_LYS_470 | NZ | B_GLU_181 | OE2 | 3.182 |
| 3D0H | B_LYS_476 | NZ | B_GLU_479 | OE1 | 3.337 |
| 3D0H | B_ARG_482 | NH1 | B_GLU_489 | OE1 | 2.732 |
| 3D0H | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.824 |
| 3D0H | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.932 |
| 3D0H | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.877 |
| 3D0H | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.140 |
| 3D0H | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.598 |
| 3D0H | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.836 |
| 3D0H | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.895 |
| 3D0H | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.835 |
| 3D0H | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.851 |
| 3D0H | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.940 |
| 3D0H | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.656 |
| 3D0H | B_LYS_541 | NZ | B_GLU_430 | OE2 | 3.335 |
| 3D0H | B_ARG_582 | NH2 | B_GLU_232 | OE2 | 3.592 |
| 3D0H | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.363 |
| 3D0H | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.221 |
| 3D0H | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.317 |
| 3D0H | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.987 |
| 3D0H | E_LYS_411 | NZ | E_ASP_407 | OD1 | 3.493 |
| 3D0H | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.079 |
| 3D0H | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.678 |
| 3D0H | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.103 |
| 3D0H | E_ARG_453 | NH2 | E_GLU_341 | OE1 | 2.602 |
| 3D0H | E_LYS_479 | NZ | A_GLU_35 | OE1 | 3.397 |
| 3D0H | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.894 |
| 3D0H | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.818 |
| 3D0H | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.718 |
| 3D0H | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.147 |

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|---|---|---|---|---|---|
| 3D0H | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.643 |
| 3D0H | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.793 |
| 3D0H | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.380 |
| 3D0H | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.753 |
| 3D0H | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.628 |
| 3D0H | F_ARG_453 | NH2 | F_GLU_341 | OE1 | 3.737 |
| 3D0H | F_LYS_479 | NZ | B_GLU_35 | OE1 | 3.369 |
| 3D0H | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.824 |
| 3D0H | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.863 |

Table 11: 3D0H-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0I | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.187 |
| 3D0I | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.852 |
| 3D0I | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.156 |
| 3D0I | A_ARG_177 | NH1 | A_GLU_181 | OE2 | 3.919 |
| 3D0I | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.627 |
| 3D0I | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 2.844 |
| 3D0I | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.851 |
| 3D0I | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.393 |
| 3D0I | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.767 |
| 3D0I | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.602 |
| 3D0I | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.226 |
| 3D0I | A_LYS_234 | NZ | A_GLU_231 | OE2 | 2.886 |
| 3D0I | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.237 |
| 3D0I | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.963 |
| 3D0I | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.134 |
| 3D0I | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.185 |
| 3D0I | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.199 |
| 3D0I | A_LYS_353 | NZ | A_GLU_38 | OE2 | 2.940 |
| 3D0I | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.456 |
| 3D0I | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.694 |
| 3D0I | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.884 |
| 3D0I | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.205 |
| 3D0I | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.038 |
| 3D0I | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.181 |
| 3D0I | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.296 |
| 3D0I | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.690 |
| 3D0I | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.095 |
| 3D0I | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.805 |
| 3D0I | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.364 |
| 3D0I | A_LYS_465 | NZ | A_GLU_197 | OE2 | 3.918 |
| 3D0I | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.269 |
| 3D0I | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.529 |
| 3D0I | A_LYS_476 | NZ | A_GLU_479 | OE2 | 2.537 |
| 3D0I | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.768 |
| 3D0I | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.673 |
| 3D0I | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.974 |
| 3D0I | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.367 |
| 3D0I | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.596 |
| 3D0I | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.716 |
| 3D0I | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 2.781 |
| 3D0I | A_ARG_518 | NH1 | A_GLU_406 | OE1 | 3.545 |
| 3D0I | A_ARG_518 | NH2 | A_GLU_402 | OE2 | 3.220 |
| 3D0I | A_LYS_534 | NZ | A_GLU_549 | OE1 | 3.582 |
| 3D0I | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.978 |
| 3D0I | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.081 |
| 3D0I | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.768 |
| 3D0I | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.991 |
| 3D0I | B_LYS_112 | NZ | B_GLU_189 | OE1 | 2.946 |
| 3D0I | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.482 |
| 3D0I | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.999 |
| 3D0I | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.084 |
| 3D0I | B_ARG_177 | NH1 | B_GLU_181 | OE2 | 3.586 |
| 3D0I | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.500 |
| 3D0I | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.650 |
| 3D0I | B_LYS_187 | NZ | B_ASP_509 | OD1 | 3.839 |
| 3D0I | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.086 |
| 3D0I | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.369 |

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|---|---|---|---|---|---|
| 3D0I | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.495 |
| 3D0I | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.713 |
| 3D0I | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.122 |
| 3D0I | B_LYS_234 | NZ | B_GLU_231 | OE2 | 2.885 |
| 3D0I | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.153 |
| 3D0I | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.676 |
| 3D0I | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.386 |
| 3D0I | B_LYS_313 | NZ | B_GLU_310 | OE2 | 2.999 |
| 3D0I | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.427 |
| 3D0I | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.805 |
| 3D0I | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.438 |
| 3D0I | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.611 |
| 3D0I | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.052 |
| 3D0I | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.803 |
| 3D0I | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.598 |
| 3D0I | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.612 |
| 3D0I | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.112 |
| 3D0I | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.000 |
| 3D0I | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.643 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.355 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.779 |
| 3D0I | B_LYS_419 | NZ | B_GLU_430 | OE1 | 3.547 |
| 3D0I | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.212 |
| 3D0I | B_LYS_470 | NZ | B_GLU_181 | OE1 | 2.879 |
| 3D0I | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.791 |
| 3D0I | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.688 |
| 3D0I | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.914 |
| 3D0I | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.135 |
| 3D0I | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.741 |
| 3D0I | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.923 |
| 3D0I | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.844 |
| 3D0I | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.950 |
| 3D0I | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.992 |
| 3D0I | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.725 |
| 3D0I | B_ARG_582 | NH2 | B_GLU_232 | OE2 | 3.204 |
| 3D0I | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 3.693 |
| 3D0I | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.921 |
| 3D0I | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.555 |
| 3D0I | E_LYS_343 | NZ | E_GLU_327 | OE1 | 2.907 |
| 3D0I | E_LYS_411 | NZ | E_ASP_407 | OD1 | 3.525 |
| 3D0I | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.085 |
| 3D0I | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.247 |
| 3D0I | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.400 |
| 3D0I | E_ARG_453 | NH2 | E_GLU_341 | OE1 | 3.930 |
| 3D0I | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.544 |
| 3D0I | E_LYS_465 | NZ | E_ASP_463 | OD2 | 3.638 |
| 3D0I | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 3.324 |
| 3D0I | E_ARG_479 | NH2 | A_GLU_35 | OE1 | 2.730 |
| 3D0I | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.896 |
| 3D0I | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.932 |
| 3D0I | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.615 |
| 3D0I | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.912 |
| 3D0I | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.980 |
| 3D0I | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.584 |
| 3D0I | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.274 |
| 3D0I | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.530 |
| 3D0I | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.856 |
| 3D0I | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.256 |

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|---|---|---|---|---|---|
| 3D0I | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.236 |
| 3D0I | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.810 |
| 3D0I | F_ARG_453 | NH2 | F_GLU_341 | OE1 | 3.930 |
| 3D0I | F_LYS_465 | NZ | F_ASP_463 | OD2 | 3.412 |
| 3D0I | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 3.405 |
| 3D0I | F_ARG_479 | NH2 | B_GLU_35 | OE1 | 2.961 |
| 3D0I | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.707 |
| 3D0I | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.911 |

Table 12: 3D0I-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCI | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.333 |
| 3SCI | A_LYS_26 | NZ | A_GLU_23 | OE2 | 3.691 |
| 3SCI | A_HIS_34 | ND1 | A_GLU_37 | OE1 | 3.955 |
| 3SCI | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.520 |
| 3SCI | A_ARG_115 | NH1 | A_GLU_182 | OE1 | 3.485 |
| 3SCI | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 2.973 |
| 3SCI | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.161 |
| 3SCI | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 2.813 |
| 3SCI | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.700 |
| 3SCI | A_ARG_204 | NH2 | A_ASP_198 | OD1 | 3.614 |
| 3SCI | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.484 |
| 3SCI | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.586 |
| 3SCI | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.677 |
| 3SCI | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.059 |
| 3SCI | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.792 |
| 3SCI | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.667 |
| 3SCI | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.649 |
| 3SCI | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.796 |
| 3SCI | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.140 |
| 3SCI | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.555 |
| 3SCI | A_LYS_353 | NZ | A_ASP_38 | OD1 | 3.354 |
| 3SCI | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.324 |
| 3SCI | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 3.867 |
| 3SCI | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.812 |
| 3SCI | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.743 |
| 3SCI | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.027 |
| 3SCI | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.766 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.865 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.741 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 3.842 |
| 3SCI | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 2.993 |
| 3SCI | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.829 |
| 3SCI | A_ARG_393 | NH2 | A_GLU_37 | OE2 | 3.668 |
| 3SCI | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.295 |
| 3SCI | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.686 |
| 3SCI | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.398 |
| 3SCI | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.642 |
| 3SCI | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.133 |
| 3SCI | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.703 |
| 3SCI | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.668 |
| 3SCI | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.756 |
| 3SCI | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.875 |
| 3SCI | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.021 |
| 3SCI | A_HIS_493 | NE2 | A_GLU_166 | OE2 | 3.968 |
| 3SCI | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.898 |
| 3SCI | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.867 |
| 3SCI | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.392 |
| 3SCI | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.358 |
| 3SCI | A_LYS_541 | NZ | A_GLU_430 | OE1 | 3.694 |
| 3SCI | A_LYS_541 | NZ | A_GLU_430 | OE2 | 2.736 |
| 3SCI | A_ARG_582 | NH1 | A_GLU_232 | OE2 | 2.598 |
| 3SCI | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.897 |
| 3SCI | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.718 |
| 3SCI | B_LYS_31 | NZ | B_GLU_35 | OE1 | 3.358 |
| 3SCI | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.974 |
| 3SCI | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.826 |
| 3SCI | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.773 |

| 3SCI | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.548 |
|---|---|---|---|---|---|
| 3SCI | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.424 |
| 3SCI | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.759 |
| 3SCI | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.703 |
| 3SCI | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.718 |
| 3SCI | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.668 |
| 3SCI | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.689 |
| 3SCI | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.452 |
| 3SCI | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.808 |
| 3SCI | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.168 |
| 3SCI | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.626 |
| 3SCI | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.016 |
| 3SCI | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.303 |
| 3SCI | B_LYS_353 | NZ | B_ASP_38 | OD1 | 3.714 |
| 3SCI | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 2.648 |
| 3SCI | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.568 |
| 3SCI | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.133 |
| 3SCI | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.131 |
| 3SCI | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.146 |
| 3SCI | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.955 |
| 3SCI | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.800 |
| 3SCI | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.582 |
| 3SCI | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 2.767 |
| 3SCI | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.951 |
| 3SCI | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.149 |
| 3SCI | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.545 |
| 3SCI | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.930 |
| 3SCI | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.967 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.520 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.936 |
| 3SCI | B_LYS_458 | NZ | B_GLU_227 | OE2 | 2.656 |
| 3SCI | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.610 |
| 3SCI | B_LYS_465 | NZ | B_GLU_197 | OE2 | 3.379 |
| 3SCI | B_LYS_470 | NZ | B_GLU_181 | OE1 | 3.845 |
| 3SCI | B_LYS_475 | NZ | B_GLU_479 | OE1 | 3.195 |
| 3SCI | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.712 |
| 3SCI | B_ARG_482 | NH1 | B_GLU_489 | OE1 | 3.858 |
| 3SCI | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.969 |
| 3SCI | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.242 |
| 3SCI | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.362 |
| 3SCI | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.799 |
| 3SCI | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.907 |
| 3SCI | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.879 |
| 3SCI | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.740 |
| 3SCI | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.299 |
| 3SCI | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.013 |
| 3SCI | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 3.819 |
| 3SCI | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 3.000 |
| 3SCI | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.193 |
| 3SCI | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.289 |
| 3SCI | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.257 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.110 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.923 |
| 3SCI | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.829 |
| 3SCI | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.668 |
| 3SCI | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 2.901 |
| 3SCI | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.835 |
| 3SCI | E_LYS_447 | NZ | E_ASP_407 | OD2 | 3.979 |

| | | | | | |
|---|---|---|---|---|---|
| 3SCI | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.520 |
| 3SCI | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.789 |
| 3SCI | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.688 |
| 3SCI | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.355 |
| 3SCI | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.898 |
| 3SCI | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.783 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.044 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.878 |
| 3SCI | F_LYS_439 | NZ | F_ASP_480 | OD2 | 3.783 |
| 3SCI | F_ARG_441 | NH1 | F_ASP_454 | OD1 | 3.554 |
| 3SCI | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.709 |
| 3SCI | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.691 |
| 3SCI | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 2.977 |
| 3SCI | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.984 |
| 3SCI | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.981 |

Table 13: 3SCI-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCJ | A_LYS_26 | NZ | A_GLU_23 | OE2 | 3.680 |
| 3SCJ | A_HIS_34 | NE2 | A_ASP_30 | OD1 | 3.716 |
| 3SCJ | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.606 |
| 3SCJ | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.626 |
| 3SCJ | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.662 |
| 3SCJ | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.729 |
| 3SCJ | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.233 |
| 3SCJ | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.854 |
| 3SCJ | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.710 |
| 3SCJ | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.688 |
| 3SCJ | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.693 |
| 3SCJ | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.281 |
| 3SCJ | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.594 |
| 3SCJ | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.711 |
| 3SCJ | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.920 |
| 3SCJ | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.833 |
| 3SCJ | A_LYS_309 | NZ | A_GLU_312 | OE1 | 2.769 |
| 3SCJ | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.597 |
| 3SCJ | A_LYS_353 | NZ | A_ASP_38 | OD1 | 2.877 |
| 3SCJ | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.017 |
| 3SCJ | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.039 |
| 3SCJ | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.858 |
| 3SCJ | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.602 |
| 3SCJ | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.774 |
| 3SCJ | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.008 |
| 3SCJ | A_ARG_393 | NH1 | A_GLU_37 | OE1 | 3.540 |
| 3SCJ | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 3.136 |
| 3SCJ | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.154 |
| 3SCJ | A_ARG_393 | NH2 | A_GLU_37 | OE2 | 3.984 |
| 3SCJ | A_HIS_401 | NE2 | A_ASP_382 | OD2 | 3.168 |
| 3SCJ | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.019 |
| 3SCJ | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.770 |
| 3SCJ | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.761 |
| 3SCJ | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 2.363 |
| 3SCJ | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.678 |
| 3SCJ | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.819 |
| 3SCJ | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.256 |
| 3SCJ | A_LYS_476 | NZ | A_GLU_479 | OE2 | 3.692 |
| 3SCJ | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.323 |
| 3SCJ | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.886 |
| 3SCJ | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.898 |
| 3SCJ | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.065 |
| 3SCJ | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.951 |
| 3SCJ | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.730 |
| 3SCJ | A_ARG_514 | NH2 | A_GLU_398 | OE2 | 3.456 |
| 3SCJ | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.682 |
| 3SCJ | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.913 |
| 3SCJ | A_LYS_577 | NZ | A_GLU_571 | OE1 | 3.432 |
| 3SCJ | A_ARG_582 | NH1 | A_GLU_232 | OE2 | 3.625 |
| 3SCJ | A_LYS_600 | NZ | A_ASP_597 | OD2 | 3.672 |
| 3SCJ | B_LYS_26 | NZ | B_GLU_22 | OE1 | 3.695 |
| 3SCJ | B_LYS_26 | NZ | B_GLU_23 | OE2 | 3.612 |
| 3SCJ | B_LYS_31 | NZ | B_GLU_35 | OE2 | 3.882 |
| 3SCJ | B_HIS_34 | NE2 | B_ASP_30 | OD1 | 3.848 |
| 3SCJ | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.760 |
| 3SCJ | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.993 |
| 3SCJ | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.931 |

| 3SCJ | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 2.746 |
|---|---|---|---|---|---|
| 3SCJ | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.552 |
| 3SCJ | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.425 |
| 3SCJ | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.488 |
| 3SCJ | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.786 |
| 3SCJ | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.813 |
| 3SCJ | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.381 |
| 3SCJ | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.724 |
| 3SCJ | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.841 |
| 3SCJ | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.087 |
| 3SCJ | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.785 |
| 3SCJ | B_LYS_309 | NZ | B_GLU_312 | OE1 | 2.771 |
| 3SCJ | B_LYS_309 | NZ | B_GLU_312 | OE2 | 3.982 |
| 3SCJ | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.681 |
| 3SCJ | B_LYS_353 | NZ | B_ASP_38 | OD1 | 2.726 |
| 3SCJ | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 2.798 |
| 3SCJ | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.923 |
| 3SCJ | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.731 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_375 | OE2 | 3.983 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.277 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.223 |
| 3SCJ | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.838 |
| 3SCJ | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.709 |
| 3SCJ | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.616 |
| 3SCJ | B_ARG_393 | NH1 | B_GLU_37 | OE1 | 3.412 |
| 3SCJ | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 2.868 |
| 3SCJ | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.040 |
| 3SCJ | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.888 |
| 3SCJ | B_HIS_401 | NE2 | B_ASP_382 | OD2 | 2.952 |
| 3SCJ | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.890 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.617 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.574 |
| 3SCJ | B_LYS_458 | NZ | B_GLU_227 | OE2 | 2.602 |
| 3SCJ | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.815 |
| 3SCJ | B_LYS_465 | NZ | B_GLU_197 | OE2 | 3.351 |
| 3SCJ | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.513 |
| 3SCJ | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.255 |
| 3SCJ | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.169 |
| 3SCJ | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.053 |
| 3SCJ | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.734 |
| 3SCJ | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.171 |
| 3SCJ | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.883 |
| 3SCJ | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.159 |
| 3SCJ | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.270 |
| 3SCJ | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 2.624 |
| 3SCJ | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 2.893 |
| 3SCJ | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.243 |
| 3SCJ | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.607 |
| 3SCJ | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.703 |
| 3SCJ | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.526 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.206 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.277 |
| 3SCJ | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 2.926 |
| 3SCJ | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.893 |
| 3SCJ | E_ARG_479 | NH2 | A_ASP_38 | OD2 | 2.575 |
| 3SCJ | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.820 |
| 3SCJ | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.638 |
| 3SCJ | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 2.917 |

| | | | | | |
|---|---|---|---|---|---|
| 3SCJ | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.247 |
| 3SCJ | F_LYS_390 | NZ | F_ASP_393 | OD2 | 3.787 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.547 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.819 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 3.913 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 3.505 |
| 3SCJ | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 2.956 |
| 3SCJ | F_LYS_465 | NZ | F_ASP_463 | OD2 | 3.932 |
| 3SCJ | F_ARG_479 | NH2 | B_ASP_38 | OD2 | 2.718 |
| 3SCJ | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.902 |
| 3SCJ | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.690 |

Table 14: 3SCJ-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCK | A_LYS_26 | NZ | A_GLU_22 | OE2 | 3.783 |
| 3SCK | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.738 |
| 3SCK | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.145 |
| 3SCK | A_LYS_112 | NZ | A_GLU_189 | OE2 | 2.624 |
| 3SCK | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.180 |
| 3SCK | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.905 |
| 3SCK | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.207 |
| 3SCK | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.048 |
| 3SCK | A_ARG_204 | NH2 | A_ASP_198 | OD1 | 3.950 |
| 3SCK | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.586 |
| 3SCK | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.162 |
| 3SCK | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 2.535 |
| 3SCK | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.847 |
| 3SCK | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.343 |
| 3SCK | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.624 |
| 3SCK | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.046 |
| 3SCK | A_LYS_288 | NZ | A_GLU_433 | OE2 | 3.653 |
| 3SCK | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.804 |
| 3SCK | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.263 |
| 3SCK | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.272 |
| 3SCK | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.265 |
| 3SCK | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.121 |
| 3SCK | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.285 |
| 3SCK | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.719 |
| 3SCK | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.223 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_375 | OE1 | 3.653 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.848 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.409 |
| 3SCK | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.833 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.518 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.694 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 3.988 |
| 3SCK | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 2.944 |
| 3SCK | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.268 |
| 3SCK | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.397 |
| 3SCK | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.716 |
| 3SCK | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 3.705 |
| 3SCK | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.038 |
| 3SCK | A_LYS_465 | NZ | A_GLU_197 | OE2 | 3.131 |
| 3SCK | A_LYS_465 | NZ | A_ASP_198 | OD1 | 3.632 |
| 3SCK | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.825 |
| 3SCK | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.693 |
| 3SCK | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.807 |
| 3SCK | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.942 |
| 3SCK | A_HIS_493 | ND1 | A_GLU_166 | OE2 | 3.454 |
| 3SCK | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.435 |
| 3SCK | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.109 |
| 3SCK | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.751 |
| 3SCK | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.712 |
| 3SCK | A_LYS_541 | NZ | A_GLU_430 | OE2 | 2.691 |
| 3SCK | A_ARG_582 | NH2 | A_GLU_527 | OE1 | 3.214 |
| 3SCK | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.690 |
| 3SCK | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.836 |
| 3SCK | B_LYS_112 | NZ | B_GLU_189 | OE1 | 2.980 |
| 3SCK | B_LYS_112 | NZ | B_GLU_189 | OE2 | 2.757 |
| 3SCK | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.458 |
| 3SCK | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.403 |

| 3SCK | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.746 |
|---|---|---|---|---|---|
| 3SCK | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.553 |
| 3SCK | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.885 |
| 3SCK | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.682 |
| 3SCK | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.457 |
| 3SCK | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 2.655 |
| 3SCK | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.845 |
| 3SCK | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.278 |
| 3SCK | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.790 |
| 3SCK | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.658 |
| 3SCK | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.747 |
| 3SCK | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.334 |
| 3SCK | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.682 |
| 3SCK | B_LYS_353 | NZ | B_GLU_38 | OE1 | 2.931 |
| 3SCK | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.932 |
| 3SCK | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.088 |
| 3SCK | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.516 |
| 3SCK | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.908 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_375 | OE1 | 3.559 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.398 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 2.956 |
| 3SCK | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.773 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.390 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.299 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_402 | OE2 | 3.828 |
| 3SCK | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 2.702 |
| 3SCK | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.177 |
| 3SCK | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.806 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.939 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.692 |
| 3SCK | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.897 |
| 3SCK | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.129 |
| 3SCK | B_LYS_476 | NZ | B_GLU_479 | OE1 | 2.732 |
| 3SCK | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.669 |
| 3SCK | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.445 |
| 3SCK | B_HIS_493 | ND1 | B_GLU_166 | OE2 | 3.573 |
| 3SCK | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.077 |
| 3SCK | B_HIS_493 | NE2 | B_GLU_166 | OE2 | 3.607 |
| 3SCK | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.737 |
| 3SCK | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.936 |
| 3SCK | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.744 |
| 3SCK | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.632 |
| 3SCK | B_HIS_535 | ND1 | B_GLU_536 | OE1 | 3.467 |
| 3SCK | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 2.753 |
| 3SCK | B_LYS_577 | NZ | B_GLU_571 | OE2 | 3.718 |
| 3SCK | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.321 |
| 3SCK | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.081 |
| 3SCK | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.896 |
| 3SCK | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.985 |
| 3SCK | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.591 |
| 3SCK | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.861 |
| 3SCK | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.076 |
| 3SCK | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.663 |
| 3SCK | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 2.498 |
| 3SCK | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.603 |
| 3SCK | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.263 |
| 3SCK | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.676 |
| 3SCK | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.322 |

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|---|---|---|---|---|---|
| 3SCK | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.370 |
| 3SCK | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.702 |
| 3SCK | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.226 |
| 3SCK | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.187 |
| 3SCK | F_LYS_447 | NZ | F_ASP_407 | OD1 | 3.771 |
| 3SCK | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 2.750 |
| 3SCK | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.668 |
| 3SCK | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.427 |

Table 15: 3SCK-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCL | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.408 |
| 3SCL | A_LYS_112 | NZ | A_GLU_189 | OE2 | 2.764 |
| 3SCL | A_ARG_115 | NH1 | A_GLU_182 | OE1 | 3.915 |
| 3SCL | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 2.759 |
| 3SCL | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.407 |
| 3SCL | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.290 |
| 3SCL | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.750 |
| 3SCL | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.751 |
| 3SCL | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.854 |
| 3SCL | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.253 |
| 3SCL | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.220 |
| 3SCL | A_ARG_219 | NH2 | A_ASP_201 | OD1 | 3.810 |
| 3SCL | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 2.818 |
| 3SCL | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.556 |
| 3SCL | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.191 |
| 3SCL | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.310 |
| 3SCL | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.328 |
| 3SCL | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.467 |
| 3SCL | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.111 |
| 3SCL | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.461 |
| 3SCL | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.043 |
| 3SCL | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.365 |
| 3SCL | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.733 |
| 3SCL | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.626 |
| 3SCL | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.593 |
| 3SCL | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.408 |
| 3SCL | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.962 |
| 3SCL | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.936 |
| 3SCL | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.998 |
| 3SCL | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.267 |
| 3SCL | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.834 |
| 3SCL | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.060 |
| 3SCL | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.685 |
| 3SCL | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.352 |
| 3SCL | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.158 |
| 3SCL | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.210 |
| 3SCL | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.758 |
| 3SCL | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.716 |
| 3SCL | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 2.872 |
| 3SCL | A_HIS_493 | NE2 | A_GLU_166 | OE2 | 3.834 |
| 3SCL | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.559 |
| 3SCL | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.746 |
| 3SCL | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.042 |
| 3SCL | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.897 |
| 3SCL | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.223 |
| 3SCL | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.963 |
| 3SCL | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.301 |
| 3SCL | B_LYS_187 | NZ | B_ASP_509 | OD2 | 2.965 |
| 3SCL | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.847 |
| 3SCL | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.720 |
| 3SCL | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.715 |
| 3SCL | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.640 |
| 3SCL | B_ARG_219 | NH2 | B_ASP_201 | OD1 | 3.401 |
| 3SCL | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 2.726 |
| 3SCL | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.673 |
| 3SCL | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.548 |
| 3SCL | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.355 |

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|---|---|---|---|---|---|
| 3SCL | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.412 |
| 3SCL | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.658 |
| 3SCL | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.480 |
| 3SCL | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.437 |
| 3SCL | B_LYS_353 | NZ | B_GLU_38 | OE2 | 3.301 |
| 3SCL | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.138 |
| 3SCL | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.046 |
| 3SCL | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.045 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_375 | OE1 | 3.783 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.382 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.256 |
| 3SCL | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.495 |
| 3SCL | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 3.016 |
| 3SCL | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.349 |
| 3SCL | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 2.818 |
| 3SCL | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.784 |
| 3SCL | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.918 |
| 3SCL | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.400 |
| 3SCL | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.623 |
| 3SCL | B_LYS_465 | NZ | B_GLU_467 | OE2 | 2.784 |
| 3SCL | B_LYS_475 | NZ | B_GLU_479 | OE1 | 3.474 |
| 3SCL | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.893 |
| 3SCL | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.520 |
| 3SCL | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.908 |
| 3SCL | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.122 |
| 3SCL | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.707 |
| 3SCL | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.417 |
| 3SCL | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 2.954 |
| 3SCL | B_ARG_518 | NH1 | B_GLU_406 | OE2 | 3.512 |
| 3SCL | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.414 |
| 3SCL | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.367 |
| 3SCL | B_LYS_541 | NZ | B_GLU_430 | OE1 | 3.842 |
| 3SCL | B_LYS_541 | NZ | B_GLU_430 | OE2 | 2.913 |
| 3SCL | B_LYS_562 | NZ | B_ASP_206 | OD1 | 3.640 |
| 3SCL | B_LYS_562 | NZ | B_ASP_206 | OD2 | 3.837 |
| 3SCL | B_LYS_577 | NZ | B_GLU_571 | OE2 | 3.749 |
| 3SCL | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.057 |
| 3SCL | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.532 |
| 3SCL | E_LYS_344 | NZ | E_GLU_502 | OE2 | 3.992 |
| 3SCL | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.916 |
| 3SCL | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.143 |
| 3SCL | E_ARG_441 | NH1 | E_ASP_454 | OD1 | 3.923 |
| 3SCL | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.742 |
| 3SCL | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.601 |
| 3SCL | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.448 |
| 3SCL | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.287 |
| 3SCL | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.682 |
| 3SCL | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.651 |
| 3SCL | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 2.956 |
| 3SCL | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.322 |
| 3SCL | F_LYS_439 | NZ | F_ASP_480 | OD1 | 2.927 |
| 3SCL | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.224 |
| 3SCL | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.909 |
| 3SCL | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.945 |
| 3SCL | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.790 |

Table 16: 3SCL-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X4S | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 2.290 |
| 5X4S | A_ARG_38 | NH1 | A_GLU_184 | OE1 | 3.171 |
| 5X4S | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 3.034 |
| 5X4S | A_ARG_48 | NH1 | A_ASP_44 | OD1 | 2.727 |
| 5X4S | A_ARG_48 | NH1 | A_ASP_44 | OD2 | 3.371 |
| 5X4S | A_ARG_48 | NH2 | A_ASP_44 | OD1 | 3.601 |
| 5X4S | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 2.675 |
| 5X4S | A_LYS_175 | NZ | A_ASP_171 | OD1 | 3.389 |
| 5X4S | A_LYS_175 | NZ | A_ASP_171 | OD2 | 3.027 |
| 5X4S | A_LYS_188 | NZ | A_ASP_57 | OD1 | 3.514 |
| 5X4S | A_LYS_190 | NZ | A_ASP_191 | OD2 | 3.979 |

Table 17: 5X4S-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 3.231 |
| 5X58 | A_ARG_38 | NH1 | A_GLU_184 | OE1 | 3.772 |
| 5X58 | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 2.356 |
| 5X58 | A_ARG_48 | NH1 | A_ASP_44 | OD1 | 3.022 |
| 5X58 | A_ARG_48 | NH1 | A_ASP_44 | OD2 | 3.566 |
| 5X58 | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 3.303 |
| 5X58 | A_LYS_188 | NZ | A_ASP_57 | OD1 | 3.617 |
| 5X58 | A_LYS_188 | NZ | A_ASP_57 | OD2 | 3.069 |
| 5X58 | A_LYS_221 | NZ | C_GLU_502 | OE2 | 3.266 |
| 5X58 | A_LYS_297 | NZ | A_ASP_649 | OD1 | 2.479 |
| 5X58 | A_LYS_297 | NZ | A_ASP_649 | OD2 | 3.392 |
| 5X58 | A_LYS_343 | NZ | A_GLU_327 | OE1 | 3.311 |
| 5X58 | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.205 |
| 5X58 | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.550 |
| 5X58 | A_LYS_514 | NZ | A_ASP_376 | OD1 | 3.288 |
| 5X58 | A_LYS_543 | NZ | A_ASP_560 | OD2 | 2.441 |
| 5X58 | A_ARG_620 | NH1 | A_ASP_277 | OD2 | 3.189 |
| 5X58 | A_ARG_797 | NH1 | A_ASP_850 | OD1 | 3.465 |
| 5X58 | A_LYS_836 | NZ | C_ASP_554 | OD2 | 3.822 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.482 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 3.202 |
| 5X58 | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.575 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.983 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.964 |
| 5X58 | A_ARG_1001 | NH2 | A_GLU_755 | OE1 | 3.437 |
| 5X58 | A_ARG_1001 | NH2 | A_GLU_755 | OE2 | 3.596 |
| 5X58 | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.486 |
| 5X58 | A_LYS_1010 | NZ | A_GLU_707 | OE1 | 3.690 |
| 5X58 | A_LYS_1010 | NZ | A_GLU_707 | OE2 | 3.427 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE1 | 3.011 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE2 | 3.438 |
| 5X58 | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.538 |
| 5X58 | A_HIS_1046 | NE2 | A_GLU_707 | OE1 | 2.723 |
| 5X58 | B_HIS_33 | ND1 | B_ASP_208 | OD1 | 3.230 |
| 5X58 | B_ARG_38 | NH1 | B_GLU_184 | OE1 | 3.772 |
| 5X58 | B_ARG_38 | NH1 | B_GLU_184 | OE2 | 2.356 |
| 5X58 | B_ARG_48 | NH1 | B_ASP_44 | OD1 | 3.022 |
| 5X58 | B_ARG_48 | NH1 | B_ASP_44 | OD2 | 3.565 |
| 5X58 | B_ARG_48 | NH2 | B_ASP_44 | OD2 | 3.302 |
| 5X58 | B_LYS_188 | NZ | B_ASP_57 | OD1 | 3.617 |
| 5X58 | B_LYS_188 | NZ | B_ASP_57 | OD2 | 3.068 |
| 5X58 | B_LYS_221 | NZ | A_GLU_502 | OE2 | 3.264 |
| 5X58 | B_LYS_297 | NZ | B_ASP_649 | OD1 | 2.478 |
| 5X58 | B_LYS_297 | NZ | B_ASP_649 | OD2 | 3.391 |
| 5X58 | B_LYS_343 | NZ | B_GLU_327 | OE1 | 3.310 |
| 5X58 | B_ARG_441 | NH2 | B_ASP_454 | OD2 | 3.205 |
| 5X58 | B_ARG_495 | NH2 | B_ASP_429 | OD1 | 3.551 |
| 5X58 | B_LYS_514 | NZ | B_ASP_376 | OD1 | 3.288 |
| 5X58 | B_LYS_543 | NZ | B_ASP_560 | OD2 | 2.442 |
| 5X58 | B_ARG_620 | NH1 | B_ASP_277 | OD2 | 3.189 |
| 5X58 | B_ARG_797 | NH1 | B_ASP_850 | OD1 | 3.464 |
| 5X58 | B_LYS_836 | NZ | A_ASP_554 | OD2 | 3.822 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD1 | 3.484 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD2 | 3.202 |
| 5X58 | B_ARG_977 | NH2 | C_ASP_976 | OD2 | 3.576 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.983 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.963 |

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|---|---|---|---|---|---|
| 5X58 | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.485 |
| 5X58 | B_ARG_1001 | NH2 | B_GLU_755 | OE1 | 3.436 |
| 5X58 | B_ARG_1001 | NH2 | B_GLU_755 | OE2 | 3.597 |
| 5X58 | B_LYS_1010 | NZ | B_GLU_707 | OE1 | 3.691 |
| 5X58 | B_LYS_1010 | NZ | B_GLU_707 | OE2 | 3.427 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.011 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 3.438 |
| 5X58 | B_ARG_1021 | NH2 | C_GLU_1013 | OE2 | 3.540 |
| 5X58 | B_HIS_1046 | NE2 | B_GLU_707 | OE1 | 2.724 |
| 5X58 | C_HIS_33 | ND1 | C_ASP_208 | OD1 | 3.232 |
| 5X58 | C_ARG_38 | NH1 | C_GLU_184 | OE1 | 3.772 |
| 5X58 | C_ARG_38 | NH1 | C_GLU_184 | OE2 | 2.356 |
| 5X58 | C_ARG_48 | NH1 | C_ASP_44 | OD1 | 3.022 |
| 5X58 | C_ARG_48 | NH1 | C_ASP_44 | OD2 | 3.565 |
| 5X58 | C_ARG_48 | NH2 | C_ASP_44 | OD2 | 3.303 |
| 5X58 | C_LYS_188 | NZ | C_ASP_57 | OD1 | 3.616 |
| 5X58 | C_LYS_188 | NZ | C_ASP_57 | OD2 | 3.068 |
| 5X58 | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.265 |
| 5X58 | C_LYS_297 | NZ | C_ASP_649 | OD1 | 2.478 |
| 5X58 | C_LYS_297 | NZ | C_ASP_649 | OD2 | 3.393 |
| 5X58 | C_LYS_343 | NZ | C_GLU_327 | OE1 | 3.310 |
| 5X58 | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.205 |
| 5X58 | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 3.550 |
| 5X58 | C_LYS_514 | NZ | C_ASP_376 | OD1 | 3.288 |
| 5X58 | C_LYS_543 | NZ | C_ASP_560 | OD2 | 2.441 |
| 5X58 | C_ARG_620 | NH1 | C_ASP_277 | OD2 | 3.189 |
| 5X58 | C_ARG_797 | NH1 | C_ASP_850 | OD1 | 3.464 |
| 5X58 | C_LYS_836 | NZ | B_ASP_554 | OD2 | 3.825 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD1 | 3.484 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD2 | 3.202 |
| 5X58 | C_ARG_977 | NH2 | A_ASP_976 | OD2 | 3.575 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.985 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.966 |
| 5X58 | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.487 |
| 5X58 | C_ARG_1001 | NH2 | C_GLU_755 | OE1 | 3.436 |
| 5X58 | C_ARG_1001 | NH2 | C_GLU_755 | OE2 | 3.596 |
| 5X58 | C_LYS_1010 | NZ | C_GLU_707 | OE1 | 3.690 |
| 5X58 | C_LYS_1010 | NZ | C_GLU_707 | OE2 | 3.427 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.011 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 3.438 |
| 5X58 | C_ARG_1021 | NH2 | A_GLU_1013 | OE2 | 3.539 |
| 5X58 | C_HIS_1046 | NE2 | C_GLU_707 | OE1 | 2.724 |

Table 18: 5X58-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 3.598 |
| 5X5B | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 2.409 |
| 5X5B | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 3.936 |
| 5X5B | A_HIS_74 | ND1 | A_ASP_24 | OD2 | 3.604 |
| 5X5B | A_LYS_297 | NZ | A_ASP_649 | OD1 | 2.492 |
| 5X5B | A_LYS_297 | NZ | A_ASP_649 | OD2 | 3.385 |
| 5X5B | A_LYS_343 | NZ | A_GLU_327 | OE1 | 3.311 |
| 5X5B | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.205 |
| 5X5B | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.551 |
| 5X5B | A_LYS_543 | NZ | A_ASP_560 | OD2 | 3.771 |
| 5X5B | A_ARG_553 | NH1 | A_ASP_557 | OD1 | 3.914 |
| 5X5B | A_LYS_566 | NZ | A_ASP_351 | OD1 | 3.661 |
| 5X5B | A_ARG_620 | NH1 | A_ASP_277 | OD2 | 3.104 |
| 5X5B | A_LYS_793 | NZ | A_ASP_802 | OD2 | 3.746 |
| 5X5B | A_ARG_797 | NH1 | A_ASP_850 | OD1 | 3.600 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.912 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 2.504 |
| 5X5B | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.789 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.909 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.948 |
| 5X5B | A_ARG_1001 | NH2 | A_GLU_755 | OE1 | 3.427 |
| 5X5B | A_ARG_1001 | NH2 | A_GLU_755 | OE2 | 3.433 |
| 5X5B | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.377 |
| 5X5B | A_LYS_1010 | NZ | A_GLU_707 | OE1 | 3.733 |
| 5X5B | A_LYS_1010 | NZ | A_GLU_707 | OE2 | 3.301 |
| 5X5B | A_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.722 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.472 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.057 |
| 5X5B | A_HIS_1046 | NE2 | A_GLU_707 | OE1 | 2.555 |
| 5X5B | A_ARG_1073 | NH1 | B_ASP_1100 | OD2 | 3.995 |
| 5X5B | B_HIS_33 | ND1 | B_ASP_208 | OD1 | 2.655 |
| 5X5B | B_ARG_38 | NH1 | B_GLU_184 | OE2 | 2.521 |
| 5X5B | B_ARG_48 | NH2 | B_ASP_44 | OD2 | 3.973 |
| 5X5B | B_LYS_188 | NZ | B_ASP_57 | OD2 | 3.359 |
| 5X5B | B_LYS_297 | NZ | B_ASP_649 | OD1 | 3.108 |
| 5X5B | B_LYS_297 | NZ | B_ASP_649 | OD2 | 3.662 |
| 5X5B | B_ARG_315 | NH2 | B_ASP_376 | OD1 | 3.790 |
| 5X5B | B_ARG_444 | NH1 | B_ASP_454 | OD2 | 2.941 |
| 5X5B | B_ARG_495 | NH2 | B_ASP_429 | OD1 | 2.664 |
| 5X5B | B_ARG_495 | NH2 | B_ASP_429 | OD2 | 3.309 |
| 5X5B | B_LYS_514 | NZ | B_ASP_376 | OD1 | 3.351 |
| 5X5B | B_LYS_543 | NZ | B_ASP_560 | OD2 | 2.696 |
| 5X5B | B_LYS_543 | NZ | B_ASP_572 | OD2 | 3.842 |
| 5X5B | B_ARG_553 | NH1 | B_ASP_557 | OD1 | 3.071 |
| 5X5B | B_ARG_620 | NH1 | B_ASP_277 | OD1 | 3.439 |
| 5X5B | B_ARG_620 | NH1 | B_ASP_277 | OD2 | 2.450 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.930 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.999 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE1 | 3.970 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.150 |
| 5X5B | B_ARG_1001 | NH2 | B_GLU_755 | OE1 | 3.472 |
| 5X5B | B_ARG_1001 | NH2 | B_GLU_755 | OE2 | 3.342 |
| 5X5B | B_LYS_1010 | NZ | B_GLU_707 | OE1 | 3.708 |
| 5X5B | B_LYS_1010 | NZ | B_GLU_707 | OE2 | 3.314 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.450 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 2.311 |
| 5X5B | B_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.517 |

| 5X5B | B_HIS_1046 | NE2 | B_GLU_707 | OE1 | 2.640 |
|---|---|---|---|---|---|
| 5X5B | C_HIS_33 | ND1 | C_ASP_208 | OD1 | 2.654 |
| 5X5B | C_ARG_38 | NH1 | C_GLU_184 | OE2 | 2.521 |
| 5X5B | C_ARG_48 | NH2 | C_ASP_44 | OD2 | 3.973 |
| 5X5B | C_LYS_188 | NZ | C_ASP_57 | OD2 | 3.359 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE1 | 3.851 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.225 |
| 5X5B | C_LYS_297 | NZ | C_ASP_649 | OD1 | 3.109 |
| 5X5B | C_LYS_297 | NZ | C_ASP_649 | OD2 | 3.663 |
| 5X5B | C_ARG_315 | NH2 | C_ASP_376 | OD1 | 3.790 |
| 5X5B | C_ARG_444 | NH1 | C_ASP_454 | OD2 | 2.942 |
| 5X5B | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 2.664 |
| 5X5B | C_ARG_495 | NH2 | C_ASP_429 | OD2 | 3.308 |
| 5X5B | C_LYS_514 | NZ | C_ASP_376 | OD1 | 3.351 |
| 5X5B | C_LYS_543 | NZ | C_ASP_560 | OD2 | 2.696 |
| 5X5B | C_LYS_543 | NZ | C_ASP_572 | OD2 | 3.841 |
| 5X5B | C_ARG_553 | NH1 | C_ASP_557 | OD1 | 3.070 |
| 5X5B | C_ARG_620 | NH1 | C_ASP_277 | OD1 | 3.439 |
| 5X5B | C_ARG_620 | NH1 | C_ASP_277 | OD2 | 2.450 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.907 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.931 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE1 | 3.965 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.203 |
| 5X5B | C_ARG_1001 | NH2 | C_GLU_755 | OE1 | 3.472 |
| 5X5B | C_ARG_1001 | NH2 | C_GLU_755 | OE2 | 3.341 |
| 5X5B | C_LYS_1010 | NZ | C_GLU_707 | OE1 | 3.708 |
| 5X5B | C_LYS_1010 | NZ | C_GLU_707 | OE2 | 3.314 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.273 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 2.370 |
| 5X5B | C_ARG_1021 | NH2 | C_GLU_1013 | OE1 | 3.517 |
| 5X5B | C_HIS_1046 | NE2 | C_GLU_707 | OE1 | 2.640 |
| 5X5B | C_ARG_1073 | NH1 | A_ASP_1100 | OD2 | 3.761 |

Table 19: 5X5B-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

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| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_534 | NZ | B_ASP_431 | OD1 | 3.656 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.710 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.597 |
| 2AJF | E_ARG_426 | NH1 | A_GLU_329 | OE2 | 3.740 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.855 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 2.946 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.890 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.381 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 2.717 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 2.911 |

Table 20: Interfacial 2AJF-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE1 | 3.913 |
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE2 | 2.993 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE1 | 2.759 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE2 | 3.226 |
| 2DD8 | L_LYS_130 | NZ | H_ASP_144 | OD2 | 3.343 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD1 | 3.643 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD2 | 3.461 |
| 2DD8 | S_ARG_395 | NH2 | L_ASP_95A | OD1 | 3.001 |

Table 21: Interfacial 2DD8-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_162 | NH1 | A_ASP_480 | OD1 | 3.081 |
| 2GHW | D_ARG_162 | NH2 | C_ASP_480 | OD1 | 3.626 |

Table 22: Interfacial 2GHW-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD1 | 3.504 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD2 | 2.403 |
| 3BGF | S_LYS_439 | NZ | A_ASP_480 | OD2 | 3.161 |
| 3BGF | A_LYS_439 | NZ | S_ASP_480 | OD2 | 2.520 |
| 3BGF | H_LYS_210 | NZ | L_GLU_123 | OE1 | 3.997 |

Table 23: Interfacial 3BGF-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.856 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.820 |

Table 24: Interfacial 3D0G-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.231 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.198 |
| 3D0H | E_LYS_479 | NZ | A_GLU_35 | OE1 | 3.397 |
| 3D0H | F_LYS_479 | NZ | B_GLU_35 | OE1 | 3.369 |

Table 25: Interfacial 3D0H-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.355 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.779 |
| 3D0I | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 3.324 |
| 3D0I | E_ARG_479 | NH2 | A_GLU_35 | OE1 | 2.730 |
| 3D0I | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 3.405 |
| 3D0I | F_ARG_479 | NH2 | B_GLU_35 | OE1 | 2.961 |

Table 26: Interfacial 3D0I-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.520 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.936 |
| 3SCI | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.257 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.110 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.923 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.044 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.878 |

Table 27: Interfacial 3SCI-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.617 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.574 |
| 3SCJ | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.526 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.206 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.277 |
| 3SCJ | E_ARG_479 | NH2 | A_ASP_38 | OD2 | 2.575 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.547 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.819 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 3.913 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 3.505 |
| 3SCJ | F_ARG_479 | NH2 | B_ASP_38 | OD2 | 2.718 |

Table 28: Interfacial 3SCJ-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.939 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.692 |
| 3SCK | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.591 |
| 3SCK | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 2.498 |
| 3SCK | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 2.750 |

Table 29: Interfacial 3SCK-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCL | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.918 |
| 3SCL | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.916 |
| 3SCL | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.143 |

Table 30: Interfacial 3SCL-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_221 | NZ | C_GLU_502 | OE2 | 3.266 |
| 5X58 | A_LYS_836 | NZ | C_ASP_554 | OD2 | 3.822 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.482 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 3.202 |
| 5X58 | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.575 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.983 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.964 |
| 5X58 | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.486 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE1 | 3.011 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE2 | 3.438 |
| 5X58 | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.538 |
| 5X58 | B_LYS_221 | NZ | A_GLU_502 | OE2 | 3.264 |
| 5X58 | B_LYS_836 | NZ | A_ASP_554 | OD2 | 3.822 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD1 | 3.484 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD2 | 3.202 |
| 5X58 | B_ARG_977 | NH2 | C_ASP_976 | OD2 | 3.576 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.983 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.963 |
| 5X58 | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.485 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.011 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 3.438 |
| 5X58 | B_ARG_1021 | NH2 | C_GLU_1013 | OE2 | 3.540 |
| 5X58 | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.265 |
| 5X58 | C_LYS_836 | NZ | B_ASP_554 | OD2 | 3.825 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD1 | 3.484 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD2 | 3.202 |
| 5X58 | C_ARG_977 | NH2 | A_ASP_976 | OD2 | 3.575 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.985 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.966 |
| 5X58 | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.487 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.011 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 3.438 |
| 5X58 | C_ARG_1021 | NH2 | A_GLU_1013 | OE2 | 3.539 |

Table 31: Interfacial 5X58-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.912 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 2.504 |
| 5X5B | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.789 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.909 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.948 |
| 5X5B | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.377 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.472 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.057 |
| 5X5B | A_ARG_1073 | NH1 | B_ASP_1100 | OD2 | 3.995 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.930 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.999 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE1 | 3.970 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.150 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.450 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 2.311 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE1 | 3.851 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.225 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.907 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.931 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE1 | 3.965 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.203 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.273 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 2.370 |
| 5X5B | C_ARG_1073 | NH1 | A_ASP_1100 | OD2 | 3.761 |

Table 32: Interfacial 5X5B-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

## Residue-specific analysis of SARS coronavirus spike protein-related structures

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.014 |
| 2AJF | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.467 |
| 2AJF | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 3.808 |
| 2DD8 | S_ARG_495 | NH2 | S_ASP_429 | OD1 | 3.196 |
| 2DD8 | S_ARG_495 | NH2 | S_ASP_429 | OD2 | 3.755 |
| 2GHV | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.040 |
| 2GHV | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.590 |
| 2GHV | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 2.912 |
| 2GHV | C_ARG_495 | NH2 | C_ASP_429 | OD2 | 3.523 |
| 2GHW | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.315 |
| 2GHW | A_ARG_495 | NH2 | A_ASP_429 | OD2 | 3.983 |
| 2GHW | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 3.274 |
| 3BGF | S_ARG_495 | NH2 | S_ASP_429 | OD1 | 3.362 |
| 3BGF | S_ARG_495 | NH2 | S_ASP_429 | OD2 | 3.615 |
| 3BGF | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.108 |
| 3BGF | A_ARG_495 | NH2 | A_ASP_429 | OD2 | 2.922 |
| 3D0G | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.067 |
| 3D0G | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.649 |
| 3D0G | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.771 |
| 3D0G | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.277 |
| 3D0H | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.894 |
| 3D0H | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.818 |
| 3D0H | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.824 |
| 3D0H | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.863 |
| 3D0I | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.896 |
| 3D0I | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.932 |
| 3D0I | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.707 |
| 3D0I | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.911 |
| 3SCI | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.789 |
| 3SCI | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.688 |
| 3SCI | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.984 |
| 3SCI | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.981 |
| 3SCJ | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.820 |
| 3SCJ | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.638 |
| 3SCJ | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.902 |
| 3SCJ | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.690 |
| 3SCK | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.603 |
| 3SCK | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.263 |
| 3SCK | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.668 |
| 3SCK | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.427 |
| 3SCL | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.682 |
| 3SCL | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.651 |
| 3SCL | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.945 |
| 3SCL | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.790 |
| 5X58 | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.550 |
| 5X58 | B_ARG_495 | NH2 | B_ASP_429 | OD1 | 3.551 |
| 5X58 | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 3.550 |
| 5X5B | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.551 |
| 5X5B | B_ARG_495 | NH2 | B_ASP_429 | OD1 | 2.664 |
| 5X5B | B_ARG_495 | NH2 | B_ASP_429 | OD2 | 3.309 |
| 5X5B | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 2.664 |
| 5X5B | C_ARG_495 | NH2 | C_ASP_429 | OD2 | 3.308 |

Table 33: ARG495-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.014 |
| 2AJF | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.467 |
| 2AJF | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 3.808 |
| 2DD8 | S_ARG_495 | NH2 | S_ASP_429 | OD1 | 3.196 |
| 2DD8 | S_ARG_495 | NH2 | S_ASP_429 | OD2 | 3.755 |
| 2GHV | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.040 |
| 2GHV | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.590 |
| 2GHV | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 2.912 |
| 2GHV | C_ARG_495 | NH2 | C_ASP_429 | OD2 | 3.523 |
| 2GHW | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.315 |
| 2GHW | A_ARG_495 | NH2 | A_ASP_429 | OD2 | 3.983 |
| 2GHW | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 3.274 |
| 3BGF | S_ARG_495 | NH2 | S_ASP_429 | OD1 | 3.362 |
| 3BGF | S_ARG_495 | NH2 | S_ASP_429 | OD2 | 3.615 |
| 3BGF | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.108 |
| 3BGF | A_ARG_495 | NH2 | A_ASP_429 | OD2 | 2.922 |
| 3D0G | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 3.067 |
| 3D0G | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.649 |
| 3D0G | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.771 |
| 3D0G | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.277 |
| 3D0H | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.894 |
| 3D0H | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.818 |
| 3D0H | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.824 |
| 3D0H | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.863 |
| 3D0I | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.896 |
| 3D0I | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.932 |
| 3D0I | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.707 |
| 3D0I | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.911 |
| 3SCI | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.789 |
| 3SCI | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.688 |
| 3SCI | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.984 |
| 3SCI | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.981 |
| 3SCJ | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.820 |
| 3SCJ | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.638 |
| 3SCJ | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.902 |
| 3SCJ | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.690 |
| 3SCK | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.603 |
| 3SCK | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.263 |
| 3SCK | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.668 |
| 3SCK | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.427 |
| 3SCL | E_ARG_495 | NH2 | E_ASP_429 | OD1 | 2.682 |
| 3SCL | E_ARG_495 | NH2 | E_ASP_429 | OD2 | 3.651 |
| 3SCL | F_ARG_495 | NH2 | F_ASP_429 | OD1 | 2.945 |
| 3SCL | F_ARG_495 | NH2 | F_ASP_429 | OD2 | 3.790 |
| 5X58 | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.550 |
| 5X58 | B_ARG_495 | NH2 | B_ASP_429 | OD1 | 3.551 |
| 5X58 | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 3.550 |
| 5X5B | A_ARG_495 | NH2 | A_ASP_429 | OD1 | 3.551 |
| 5X5B | B_ARG_495 | NH2 | B_ASP_429 | OD1 | 2.664 |
| 5X5B | B_ARG_495 | NH2 | B_ASP_429 | OD2 | 3.309 |
| 5X5B | C_ARG_495 | NH2 | C_ASP_429 | OD1 | 2.664 |
| 5X5B | C_ARG_495 | NH2 | C_ASP_429 | OD2 | 3.308 |

Table 34: ASP429-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 2.961 |
| 2AJF | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.004 |
| 2AJF | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.200 |
| 2AJF | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 2.772 |
| 2DD8 | S_ARG_342 | NH2 | S_ASP_385 | OD1 | 3.426 |
| 2DD8 | S_ARG_342 | NH2 | S_ASP_385 | OD2 | 2.961 |
| 2GHV | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.550 |
| 2GHV | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 2.981 |
| 2GHV | C_ARG_342 | NH2 | C_ASP_385 | OD1 | 3.469 |
| 2GHV | C_ARG_342 | NH2 | C_ASP_385 | OD2 | 2.877 |
| 2GHW | A_ARG_342 | NH2 | A_ASP_385 | OD1 | 3.548 |
| 2GHW | A_ARG_342 | NH2 | A_ASP_385 | OD2 | 3.167 |
| 2GHW | C_ARG_342 | NH2 | C_ASP_385 | OD1 | 3.626 |
| 2GHW | C_ARG_342 | NH2 | C_ASP_385 | OD2 | 3.156 |
| 3BGF | S_ARG_342 | NH2 | S_ASP_385 | OD1 | 3.676 |
| 3BGF | S_ARG_342 | NH2 | S_ASP_385 | OD2 | 3.162 |
| 3BGF | A_ARG_342 | NH2 | A_ASP_385 | OD1 | 3.423 |
| 3BGF | A_ARG_342 | NH2 | A_ASP_385 | OD2 | 2.961 |
| 3D0G | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.837 |
| 3D0G | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 2.994 |
| 3D0G | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.432 |
| 3D0G | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 2.983 |
| 3D0H | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.363 |
| 3D0H | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.221 |
| 3D0H | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.718 |
| 3D0H | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.147 |
| 3D0I | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 3.693 |
| 3D0I | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.921 |
| 3D0I | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.555 |
| 3D0I | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.615 |
| 3D0I | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.912 |
| 3D0I | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.980 |
| 3D0I | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.584 |
| 3SCI | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 3.000 |
| 3SCI | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.193 |
| 3SCI | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.355 |
| 3SCI | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.898 |
| 3SCJ | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 2.893 |
| 3SCJ | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.243 |
| 3SCJ | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 2.917 |
| 3SCJ | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.247 |
| 3SCK | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.321 |
| 3SCK | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.081 |
| 3SCK | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.676 |
| 3SCK | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.322 |
| 3SCL | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.057 |
| 3SCL | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.532 |
| 3SCL | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 2.956 |
| 3SCL | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.322 |

Table 35: ARG342-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 2.961 |
| 2AJF | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.004 |
| 2AJF | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.200 |
| 2AJF | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 2.772 |
| 2DD8 | S_ARG_342 | NH2 | S_ASP_385 | OD1 | 3.426 |
| 2DD8 | S_ARG_342 | NH2 | S_ASP_385 | OD2 | 2.961 |
| 2GHV | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.550 |
| 2GHV | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 2.981 |
| 2GHV | C_ARG_342 | NH2 | C_ASP_385 | OD1 | 3.469 |
| 2GHV | C_ARG_342 | NH2 | C_ASP_385 | OD2 | 2.877 |
| 2GHW | A_ARG_342 | NH2 | A_ASP_385 | OD1 | 3.548 |
| 2GHW | A_ARG_342 | NH2 | A_ASP_385 | OD2 | 3.167 |
| 2GHW | C_ARG_342 | NH2 | C_ASP_385 | OD1 | 3.626 |
| 2GHW | C_ARG_342 | NH2 | C_ASP_385 | OD2 | 3.156 |
| 3BGF | S_ARG_342 | NH2 | S_ASP_385 | OD1 | 3.676 |
| 3BGF | S_ARG_342 | NH2 | S_ASP_385 | OD2 | 3.162 |
| 3BGF | A_ARG_342 | NH2 | A_ASP_385 | OD1 | 3.423 |
| 3BGF | A_ARG_342 | NH2 | A_ASP_385 | OD2 | 2.961 |
| 3D0G | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.837 |
| 3D0G | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 2.994 |
| 3D0G | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.432 |
| 3D0G | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 2.983 |
| 3D0H | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.363 |
| 3D0H | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.221 |
| 3D0H | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.718 |
| 3D0H | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.147 |
| 3D0I | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 3.693 |
| 3D0I | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.921 |
| 3D0I | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.555 |
| 3D0I | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.615 |
| 3D0I | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.912 |
| 3D0I | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.980 |
| 3D0I | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.584 |
| 3SCI | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 3.000 |
| 3SCI | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.193 |
| 3SCI | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.355 |
| 3SCI | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.898 |
| 3SCJ | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 2.893 |
| 3SCJ | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.243 |
| 3SCJ | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 2.917 |
| 3SCJ | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.247 |
| 3SCK | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.321 |
| 3SCK | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.081 |
| 3SCK | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.676 |
| 3SCK | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.322 |
| 3SCL | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.057 |
| 3SCL | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.532 |
| 3SCL | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 2.956 |
| 3SCL | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.322 |

Table 36: ASP385-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_441 | NH1 | E_ASP_454 | OD1 | 3.531 |
| 2AJF | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.278 |
| 2AJF | F_ARG_441 | NH1 | F_ASP_454 | OD1 | 3.900 |
| 2AJF | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.426 |
| 2DD8 | S_ARG_441 | NH2 | S_ASP_454 | OD1 | 3.375 |
| 2GHV | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.534 |
| 2GHV | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.439 |
| 2GHW | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.680 |
| 2GHW | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.789 |
| 3BGF | S_ARG_441 | NH2 | S_ASP_454 | OD1 | 2.963 |
| 3BGF | A_ARG_441 | NH2 | A_ASP_454 | OD1 | 3.440 |
| 3D0G | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.325 |
| 3D0G | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.831 |
| 3D0G | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.314 |
| 3D0H | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.079 |
| 3D0H | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.793 |
| 3D0H | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.380 |
| 3D0I | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.085 |
| 3D0I | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.856 |
| 3D0I | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.256 |
| 3SCI | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.829 |
| 3SCI | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.668 |
| 3SCI | F_ARG_441 | NH1 | F_ASP_454 | OD1 | 3.554 |
| 3SCI | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.709 |
| 3SCI | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.691 |
| 3SCK | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.861 |
| 3SCK | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.702 |
| 3SCK | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.226 |
| 3SCL | E_ARG_441 | NH1 | E_ASP_454 | OD1 | 3.923 |
| 3SCL | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.742 |
| 3SCL | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.601 |
| 3SCL | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.224 |
| 5X58 | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.205 |
| 5X58 | B_ARG_441 | NH2 | B_ASP_454 | OD2 | 3.205 |
| 5X58 | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.205 |
| 5X5B | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.205 |

Table 37: ARG441-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_441 | NH1 | E_ASP_454 | OD1 | 3.531 |
| 2AJF | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.278 |
| 2AJF | F_ARG_441 | NH1 | F_ASP_454 | OD1 | 3.900 |
| 2AJF | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.426 |
| 2DD8 | S_ARG_441 | NH2 | S_ASP_454 | OD1 | 3.375 |
| 2DD8 | S_ARG_444 | NH2 | S_ASP_454 | OD2 | 3.531 |
| 2GHV | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.534 |
| 2GHV | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.565 |
| 2GHV | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.439 |
| 2GHV | C_ARG_444 | NH2 | C_ASP_454 | OD1 | 3.401 |
| 2GHW | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.680 |
| 2GHW | A_ARG_444 | NH2 | A_ASP_454 | OD1 | 3.823 |
| 2GHW | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.789 |
| 2GHW | C_ARG_444 | NH2 | C_ASP_454 | OD1 | 3.456 |
| 3BGF | S_ARG_441 | NH2 | S_ASP_454 | OD1 | 2.963 |
| 3BGF | S_ARG_444 | NH2 | S_ASP_454 | OD2 | 3.815 |
| 3BGF | A_ARG_441 | NH2 | A_ASP_454 | OD1 | 3.440 |
| 3BGF | A_ARG_444 | NH2 | A_ASP_454 | OD2 | 3.730 |
| 3D0G | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.325 |
| 3D0G | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.859 |
| 3D0G | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.831 |
| 3D0G | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.314 |
| 3D0G | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.447 |
| 3D0H | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.079 |
| 3D0H | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.103 |
| 3D0H | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.793 |
| 3D0H | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.380 |
| 3D0H | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.628 |
| 3D0I | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.085 |
| 3D0I | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.400 |
| 3D0I | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.856 |
| 3D0I | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.256 |
| 3D0I | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.810 |
| 3SCI | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.829 |
| 3SCI | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.668 |
| 3SCI | F_ARG_441 | NH1 | F_ASP_454 | OD1 | 3.554 |
| 3SCI | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.709 |
| 3SCI | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.691 |
| 3SCK | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.861 |
| 3SCK | F_ARG_441 | NH2 | F_ASP_454 | OD1 | 3.702 |
| 3SCK | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.226 |
| 3SCL | E_ARG_441 | NH1 | E_ASP_454 | OD1 | 3.923 |
| 3SCL | E_ARG_441 | NH2 | E_ASP_454 | OD1 | 3.742 |
| 3SCL | E_ARG_441 | NH2 | E_ASP_454 | OD2 | 3.601 |
| 3SCL | F_ARG_441 | NH2 | F_ASP_454 | OD2 | 3.224 |
| 5X58 | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.205 |
| 5X58 | B_ARG_441 | NH2 | B_ASP_454 | OD2 | 3.205 |
| 5X58 | C_ARG_441 | NH2 | C_ASP_454 | OD2 | 3.205 |
| 5X5B | A_ARG_441 | NH2 | A_ASP_454 | OD2 | 3.205 |
| 5X5B | B_ARG_444 | NH1 | B_ASP_454 | OD2 | 2.941 |
| 5X5B | C_ARG_444 | NH1 | C_ASP_454 | OD2 | 2.942 |

Table 38: ASP454-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.336 |
| 2AJF | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.457 |
| 2AJF | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 2.938 |
| 2AJF | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.429 |
| 3D0G | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.955 |
| 3D0G | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.559 |
| 3D0G | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 2.475 |
| 3D0G | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.483 |
| 3D0H | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.621 |
| 3D0H | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.471 |
| 3D0H | B_ARG_482 | NH1 | B_GLU_489 | OE1 | 2.732 |
| 3D0H | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.824 |
| 3D0H | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.932 |
| 3D0I | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.768 |
| 3D0I | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.673 |
| 3D0I | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.791 |
| 3D0I | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.688 |
| 3SCI | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.668 |
| 3SCI | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.756 |
| 3SCI | B_ARG_482 | NH1 | B_GLU_489 | OE1 | 3.858 |
| 3SCI | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.969 |
| 3SCI | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.242 |
| 3SCJ | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.323 |
| 3SCJ | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.886 |
| 3SCJ | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.255 |
| 3SCJ | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.169 |
| 3SCK | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.693 |
| 3SCK | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.807 |
| 3SCK | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.669 |
| 3SCK | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.445 |
| 3SCL | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.210 |
| 3SCL | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.758 |
| 3SCL | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.520 |

Table 39: ARG482-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.336 |
| 2AJF | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.457 |
| 2AJF | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 2.938 |
| 2AJF | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.429 |
| 3D0G | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.955 |
| 3D0G | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.559 |
| 3D0G | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 2.475 |
| 3D0G | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.483 |
| 3D0H | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.621 |
| 3D0H | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.471 |
| 3D0H | B_ARG_482 | NH1 | B_GLU_489 | OE1 | 2.732 |
| 3D0H | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.824 |
| 3D0H | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.932 |
| 3D0I | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.768 |
| 3D0I | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.673 |
| 3D0I | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.791 |
| 3D0I | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.688 |
| 3SCI | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.668 |
| 3SCI | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.756 |
| 3SCI | B_ARG_482 | NH1 | B_GLU_489 | OE1 | 3.858 |
| 3SCI | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.969 |
| 3SCI | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.242 |
| 3SCJ | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.323 |
| 3SCJ | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.886 |
| 3SCJ | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.255 |
| 3SCJ | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.169 |
| 3SCK | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.693 |
| 3SCK | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.807 |
| 3SCK | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.669 |
| 3SCK | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.445 |
| 3SCL | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.210 |
| 3SCL | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.758 |
| 3SCL | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.520 |

Table 40: GLU489-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_493 | ND1 | A_GLU_166 | OE2 | 3.978 |
| 2AJF | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.395 |
| 2AJF | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.568 |
| 2AJF | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.671 |
| 2AJF | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.284 |
| 2AJF | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.981 |
| 3D0G | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.849 |
| 3D0G | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.410 |
| 3D0G | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.585 |
| 3D0G | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.569 |
| 3D0G | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.939 |
| 3D0G | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.187 |
| 3D0G | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.890 |
| 3D0G | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.723 |
| 3D0H | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.377 |
| 3D0H | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.625 |
| 3D0H | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.765 |
| 3D0H | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.877 |
| 3D0H | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.140 |
| 3D0H | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.598 |
| 3D0H | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.836 |
| 3D0I | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.974 |
| 3D0I | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.367 |
| 3D0I | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.596 |
| 3D0I | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.716 |
| 3D0I | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.914 |
| 3D0I | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.135 |
| 3D0I | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.741 |
| 3D0I | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.923 |
| 3SCI | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.875 |
| 3SCI | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.021 |
| 3SCI | A_HIS_493 | NE2 | A_GLU_166 | OE2 | 3.968 |
| 3SCI | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.898 |
| 3SCI | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.867 |
| 3SCI | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.362 |
| 3SCI | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.799 |
| 3SCI | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.907 |
| 3SCJ | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.898 |
| 3SCJ | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.065 |
| 3SCJ | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.951 |
| 3SCJ | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.730 |
| 3SCJ | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.053 |
| 3SCJ | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.734 |
| 3SCK | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.942 |
| 3SCK | A_HIS_493 | ND1 | A_GLU_166 | OE2 | 3.454 |
| 3SCK | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.435 |
| 3SCK | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.109 |
| 3SCK | B_HIS_493 | ND1 | B_GLU_166 | OE2 | 3.573 |
| 3SCK | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.077 |
| 3SCK | B_HIS_493 | NE2 | B_GLU_166 | OE2 | 3.607 |
| 3SCK | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.737 |
| 3SCK | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.936 |
| 3SCL | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.716 |
| 3SCL | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 2.872 |
| 3SCL | A_HIS_493 | NE2 | A_GLU_166 | OE2 | 3.834 |
| 3SCL | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.559 |
| 3SCL | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.908 |

| | | | | | |
|---|---|---|---|---|---|
| 3SCL | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.122 |
| 3SCL | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.707 |

Table 41: HIS493-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_493 | ND1 | A_GLU_166 | OE2 | 3.978 |
| 2AJF | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.395 |
| 2AJF | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.671 |
| 3D0G | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.849 |
| 3D0G | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.410 |
| 3D0G | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.939 |
| 3D0G | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.187 |
| 3D0H | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.377 |
| 3D0H | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.877 |
| 3D0H | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.140 |
| 3D0I | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.974 |
| 3D0I | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.367 |
| 3D0I | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.914 |
| 3D0I | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.135 |
| 3SCI | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.875 |
| 3SCI | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.021 |
| 3SCI | A_HIS_493 | NE2 | A_GLU_166 | OE2 | 3.968 |
| 3SCI | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.362 |
| 3SCJ | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.898 |
| 3SCJ | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.065 |
| 3SCJ | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.053 |
| 3SCK | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.942 |
| 3SCK | A_HIS_493 | ND1 | A_GLU_166 | OE2 | 3.454 |
| 3SCK | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 3.435 |
| 3SCK | B_HIS_493 | ND1 | B_GLU_166 | OE2 | 3.573 |
| 3SCK | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.077 |
| 3SCK | B_HIS_493 | NE2 | B_GLU_166 | OE2 | 3.607 |
| 3SCL | A_HIS_493 | ND1 | A_GLU_166 | OE1 | 3.716 |
| 3SCL | A_HIS_493 | NE2 | A_GLU_166 | OE1 | 2.872 |
| 3SCL | A_HIS_493 | NE2 | A_GLU_166 | OE2 | 3.834 |
| 3SCL | B_HIS_493 | ND1 | B_GLU_166 | OE1 | 3.908 |
| 3SCL | B_HIS_493 | NE2 | B_GLU_166 | OE1 | 3.122 |

Table 42: GLU166-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 2.794 |
| 2AJF | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.745 |
| 2AJF | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.452 |
| 2AJF | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.319 |
| 2AJF | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.488 |
| 2AJF | B_ARG_219 | NH2 | B_ASP_201 | OD1 | 3.892 |
| 2AJF | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.087 |
| 3D0G | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 2.733 |
| 3D0G | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.447 |
| 3D0G | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.737 |
| 3D0G | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.128 |
| 3D0G | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.324 |
| 3D0G | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.217 |
| 3D0H | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.750 |
| 3D0H | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.495 |
| 3D0H | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.408 |
| 3D0H | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.592 |
| 3D0H | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.819 |
| 3D0H | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.119 |
| 3D0I | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.767 |
| 3D0I | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.602 |
| 3D0I | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.226 |
| 3D0I | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.495 |
| 3D0I | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.713 |
| 3D0I | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.122 |
| 3SCI | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.586 |
| 3SCI | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.677 |
| 3SCI | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.059 |
| 3SCI | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.718 |
| 3SCI | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.668 |
| 3SCI | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.689 |
| 3SCJ | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.688 |
| 3SCJ | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.693 |
| 3SCJ | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.281 |
| 3SCJ | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.786 |
| 3SCJ | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.813 |
| 3SCJ | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.381 |
| 3SCK | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.586 |
| 3SCK | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.162 |
| 3SCK | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 2.535 |
| 3SCK | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.682 |
| 3SCK | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.457 |
| 3SCK | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 2.655 |
| 3SCL | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.253 |
| 3SCL | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.220 |
| 3SCL | A_ARG_219 | NH2 | A_ASP_201 | OD1 | 3.810 |
| 3SCL | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 2.818 |
| 3SCL | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.715 |
| 3SCL | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.640 |
| 3SCL | B_ARG_219 | NH2 | B_ASP_201 | OD1 | 3.401 |
| 3SCL | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 2.726 |

Table 43: ARG219-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 2.794 |
| 2AJF | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.745 |
| 2AJF | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.319 |
| 2AJF | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.488 |
| 3D0G | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 2.733 |
| 3D0G | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.447 |
| 3D0G | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.128 |
| 3D0G | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.324 |
| 3D0H | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.750 |
| 3D0H | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.495 |
| 3D0H | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.592 |
| 3D0H | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.819 |
| 3D0I | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.767 |
| 3D0I | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.602 |
| 3D0I | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.495 |
| 3D0I | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.713 |
| 3SCI | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.586 |
| 3SCI | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.677 |
| 3SCI | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.718 |
| 3SCI | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.668 |
| 3SCJ | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.688 |
| 3SCJ | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 2.693 |
| 3SCJ | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.786 |
| 3SCJ | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 2.813 |
| 3SCK | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.586 |
| 3SCK | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.162 |
| 3SCK | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.682 |
| 3SCK | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.457 |
| 3SCL | A_ARG_219 | NH1 | A_GLU_208 | OE1 | 3.253 |
| 3SCL | A_ARG_219 | NH1 | A_GLU_208 | OE2 | 3.220 |
| 3SCL | B_ARG_219 | NH1 | B_GLU_208 | OE1 | 3.715 |
| 3SCL | B_ARG_219 | NH1 | B_GLU_208 | OE2 | 3.640 |

Table 44: GLU208-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 2.604 |
| 2AJF | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 3.201 |
| 2AJF | B_ARG_357 | NH2 | B_ASP_355 | OD1 | 2.846 |
| 2AJF | B_ARG_357 | NH2 | B_ASP_355 | OD2 | 2.664 |
| 3D0G | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.211 |
| 3D0G | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.562 |
| 3D0G | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.623 |
| 3D0G | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.770 |
| 3D0H | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.624 |
| 3D0H | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.643 |
| 3D0H | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.313 |
| 3D0H | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.675 |
| 3D0I | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.456 |
| 3D0I | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.694 |
| 3D0I | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.438 |
| 3D0I | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.611 |
| 3SCI | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.324 |
| 3SCI | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 3.867 |
| 3SCI | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 2.648 |
| 3SCI | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.568 |
| 3SCJ | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.017 |
| 3SCJ | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 2.798 |
| 3SCJ | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.923 |
| 3SCK | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.285 |
| 3SCK | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.719 |
| 3SCK | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.088 |
| 3SCK | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.516 |
| 3SCL | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.365 |
| 3SCL | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.733 |
| 3SCL | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.138 |
| 3SCL | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.046 |

Table 45: ARG357-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 2.604 |
| 2AJF | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 3.201 |
| 2AJF | B_ARG_357 | NH2 | B_ASP_355 | OD1 | 2.846 |
| 2AJF | B_ARG_357 | NH2 | B_ASP_355 | OD2 | 2.664 |
| 3D0G | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.211 |
| 3D0G | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.562 |
| 3D0G | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.623 |
| 3D0G | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.770 |
| 3D0H | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.624 |
| 3D0H | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.643 |
| 3D0H | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.313 |
| 3D0H | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.675 |
| 3D0I | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.456 |
| 3D0I | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.694 |
| 3D0I | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.438 |
| 3D0I | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.611 |
| 3SCI | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.324 |
| 3SCI | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 3.867 |
| 3SCI | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 2.648 |
| 3SCI | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.568 |
| 3SCJ | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.017 |
| 3SCJ | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 2.798 |
| 3SCJ | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.923 |
| 3SCK | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.285 |
| 3SCK | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.719 |
| 3SCK | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.088 |
| 3SCK | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 2.516 |
| 3SCL | A_ARG_357 | NH1 | A_ASP_355 | OD1 | 3.365 |
| 3SCL | A_ARG_357 | NH1 | A_ASP_355 | OD2 | 2.733 |
| 3SCL | B_ARG_357 | NH1 | B_ASP_355 | OD1 | 3.138 |
| 3SCL | B_ARG_357 | NH1 | B_ASP_355 | OD2 | 3.046 |

Table 46: ASP355-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.025 |
| 2AJF | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.882 |
| 2AJF | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 2.606 |
| 2AJF | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.307 |
| 2AJF | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.459 |
| 2AJF | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.493 |
| 3D0G | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.713 |
| 3D0G | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.062 |
| 3D0G | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.290 |
| 3D0G | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.697 |
| 3D0G | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.864 |
| 3D0G | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.467 |
| 3D0H | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.324 |
| 3D0H | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 2.663 |
| 3D0H | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.758 |
| 3D0H | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.061 |
| 3D0H | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.799 |
| 3D0H | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.437 |
| 3D0I | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.884 |
| 3D0I | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.205 |
| 3D0I | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.052 |
| 3D0I | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.803 |
| 3D0I | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.598 |
| 3SCI | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.812 |
| 3SCI | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.743 |
| 3SCI | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.027 |
| 3SCI | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.133 |
| 3SCI | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.131 |
| 3SCI | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.146 |
| 3SCJ | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.039 |
| 3SCJ | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.858 |
| 3SCJ | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.602 |
| 3SCJ | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.731 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_375 | OE2 | 3.983 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.277 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.223 |
| 3SCK | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.223 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_375 | OE1 | 3.653 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.848 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.409 |
| 3SCK | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.908 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_375 | OE1 | 3.559 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.398 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 2.956 |
| 3SCL | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.626 |
| 3SCL | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.593 |
| 3SCL | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.408 |
| 3SCL | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.045 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_375 | OE1 | 3.783 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.382 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.256 |

Table 47: HIS374-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.882 |
| 2AJF | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 2.606 |
| 2AJF | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.668 |
| 2AJF | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 2.869 |
| 2AJF | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.459 |
| 2AJF | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.493 |
| 2AJF | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.671 |
| 2AJF | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.560 |
| 3D0G | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.062 |
| 3D0G | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.290 |
| 3D0G | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.850 |
| 3D0G | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.864 |
| 3D0G | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.467 |
| 3D0G | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.478 |
| 3D0H | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 2.663 |
| 3D0H | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.758 |
| 3D0H | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.834 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_402 | OE2 | 3.679 |
| 3D0H | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.799 |
| 3D0H | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.437 |
| 3D0H | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.549 |
| 3D0H | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.851 |
| 3D0I | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.205 |
| 3D0I | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.038 |
| 3D0I | A_ARG_518 | NH2 | A_GLU_402 | OE2 | 3.220 |
| 3D0I | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 2.803 |
| 3D0I | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.598 |
| 3D0I | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.612 |
| 3SCI | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.743 |
| 3SCI | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.027 |
| 3SCI | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.766 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.741 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 3.842 |
| 3SCI | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.131 |
| 3SCI | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.146 |
| 3SCI | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.955 |
| 3SCI | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.582 |
| 3SCJ | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.858 |
| 3SCJ | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.602 |
| 3SCJ | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.008 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.277 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.223 |
| 3SCJ | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.838 |
| 3SCJ | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.616 |
| 3SCJ | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.883 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.848 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.409 |
| 3SCK | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.833 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.694 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 3.988 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.398 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 2.956 |
| 3SCK | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.773 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.299 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_402 | OE2 | 3.828 |
| 3SCL | A_HIS_374 | NE2 | A_GLU_402 | OE1 | 3.593 |
| 3SCL | A_HIS_374 | NE2 | A_GLU_402 | OE2 | 3.408 |

| | | | | | |
|---|---|---|---|---|---|
| 3SCL | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.962 |
| 3SCL | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.998 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_402 | OE1 | 3.382 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_402 | OE2 | 3.256 |
| 3SCL | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 3.016 |
| 3SCL | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.414 |

Table 48: GLU402-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.685 |
| 2AJF | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.827 |
| 2AJF | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.582 |
| 2AJF | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.890 |
| 3D0G | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.555 |
| 3D0G | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.763 |
| 3D0G | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 2.744 |
| 3D0G | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.625 |
| 3D0H | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.415 |
| 3D0H | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.751 |
| 3D0H | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.405 |
| 3D0H | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.407 |
| 3D0I | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.296 |
| 3D0I | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.690 |
| 3D0I | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.000 |
| 3D0I | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.643 |
| 3SCI | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.686 |
| 3SCI | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.398 |
| 3SCI | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.930 |
| 3SCI | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.967 |
| 3SCJ | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.019 |
| 3SCJ | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.770 |
| 3SCJ | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.890 |
| 3SCK | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.268 |
| 3SCK | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.397 |
| 3SCK | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.177 |
| 3SCK | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.806 |
| 3SCL | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.834 |
| 3SCL | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.060 |
| 3SCL | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 2.818 |
| 3SCL | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.784 |

Table 49: HIS417-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.685 |
| 2AJF | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.827 |
| 2AJF | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.582 |
| 2AJF | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.890 |
| 3D0G | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.555 |
| 3D0G | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.763 |
| 3D0G | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 2.744 |
| 3D0G | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.625 |
| 3D0H | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.415 |
| 3D0H | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.751 |
| 3D0H | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.405 |
| 3D0H | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.407 |
| 3D0I | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.296 |
| 3D0I | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 2.690 |
| 3D0I | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.000 |
| 3D0I | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.643 |
| 3SCI | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.686 |
| 3SCI | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.398 |
| 3SCI | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.930 |
| 3SCI | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.967 |
| 3SCJ | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.019 |
| 3SCJ | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.770 |
| 3SCJ | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 2.890 |
| 3SCK | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.268 |
| 3SCK | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.397 |
| 3SCK | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 3.177 |
| 3SCK | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.806 |
| 3SCL | A_HIS_417 | ND1 | A_ASP_543 | OD1 | 3.834 |
| 3SCL | A_HIS_417 | ND1 | A_ASP_543 | OD2 | 3.060 |
| 3SCL | B_HIS_417 | ND1 | B_ASP_543 | OD1 | 2.818 |
| 3SCL | B_HIS_417 | ND1 | B_ASP_543 | OD2 | 3.784 |

Table 50: ASP543-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_177 | NH1 | A_GLU_181 | OE2 | 3.241 |
| 2AJF | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.882 |
| 2AJF | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 2.804 |
| 2AJF | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.317 |
| 3D0G | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.885 |
| 3D0G | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.369 |
| 3D0G | B_ARG_177 | NH1 | B_GLU_181 | OE2 | 3.376 |
| 3D0G | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.263 |
| 3D0G | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.324 |
| 3D0H | A_ARG_177 | NH1 | A_GLU_181 | OE1 | 3.849 |
| 3D0H | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.600 |
| 3D0H | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.269 |
| 3D0H | B_ARG_177 | NH1 | B_GLU_181 | OE1 | 3.536 |
| 3D0H | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.392 |
| 3D0H | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.303 |
| 3D0I | A_ARG_177 | NH1 | A_GLU_181 | OE2 | 3.919 |
| 3D0I | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.627 |
| 3D0I | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 2.844 |
| 3D0I | B_ARG_177 | NH1 | B_GLU_181 | OE2 | 3.586 |
| 3D0I | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.500 |
| 3D0I | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.650 |
| 3SCI | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.161 |
| 3SCI | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 2.813 |
| 3SCI | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.773 |
| 3SCI | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.548 |
| 3SCJ | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.729 |
| 3SCJ | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.233 |
| 3SCJ | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 2.746 |
| 3SCJ | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.552 |
| 3SCK | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.905 |
| 3SCK | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.207 |
| 3SCK | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.403 |
| 3SCK | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.746 |
| 3SCL | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.407 |
| 3SCL | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.290 |

Table 51: ARG177-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.882 |
| 2AJF | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 2.804 |
| 2AJF | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.317 |
| 3D0G | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.885 |
| 3D0G | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.369 |
| 3D0G | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.263 |
| 3D0G | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.324 |
| 3D0H | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.600 |
| 3D0H | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.269 |
| 3D0H | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.392 |
| 3D0H | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.303 |
| 3D0I | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.627 |
| 3D0I | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 2.844 |
| 3D0I | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.500 |
| 3D0I | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.650 |
| 3SCI | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.161 |
| 3SCI | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 2.813 |
| 3SCI | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.773 |
| 3SCI | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.548 |
| 3SCJ | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.729 |
| 3SCJ | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.233 |
| 3SCJ | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 2.746 |
| 3SCJ | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.552 |
| 3SCK | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 2.905 |
| 3SCK | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.207 |
| 3SCK | B_ARG_177 | NH1 | B_GLU_495 | OE2 | 3.403 |
| 3SCK | B_ARG_177 | NH2 | B_GLU_495 | OE2 | 3.746 |
| 3SCL | A_ARG_177 | NH1 | A_GLU_495 | OE1 | 3.407 |
| 3SCL | A_ARG_177 | NH2 | A_GLU_495 | OE1 | 3.290 |

Table 52: GLU495-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.568 |
| 2AJF | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.284 |
| 2AJF | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.981 |
| 3D0G | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.585 |
| 3D0G | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.569 |
| 3D0G | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.890 |
| 3D0G | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.723 |
| 3D0H | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.625 |
| 3D0H | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.765 |
| 3D0H | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.598 |
| 3D0H | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.836 |
| 3D0I | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.596 |
| 3D0I | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.716 |
| 3D0I | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.741 |
| 3D0I | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.923 |
| 3SCI | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.898 |
| 3SCI | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.867 |
| 3SCI | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.799 |
| 3SCI | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.907 |
| 3SCJ | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.951 |
| 3SCJ | A_HIS_493 | NE2 | A_ASP_499 | OD2 | 3.730 |
| 3SCJ | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.734 |
| 3SCK | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.109 |
| 3SCK | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.737 |
| 3SCK | B_HIS_493 | NE2 | B_ASP_499 | OD2 | 3.936 |
| 3SCL | A_HIS_493 | NE2 | A_ASP_499 | OD1 | 3.559 |
| 3SCL | B_HIS_493 | NE2 | B_ASP_499 | OD1 | 3.707 |

Table 53: ASP499-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.668 |
| 2AJF | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 2.869 |
| 2AJF | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.992 |
| 2AJF | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.671 |
| 3D0G | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.966 |
| 3D0G | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.850 |
| 3D0G | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.478 |
| 3D0H | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.834 |
| 3D0H | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.549 |
| 3D0I | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.038 |
| 3D0I | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.612 |
| 3SCI | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.766 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.865 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.741 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 3.842 |
| 3SCI | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.955 |
| 3SCI | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.800 |
| 3SCI | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.582 |
| 3SCJ | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.774 |
| 3SCJ | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 3.008 |
| 3SCJ | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.838 |
| 3SCJ | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.709 |
| 3SCJ | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.616 |
| 3SCK | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.833 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.518 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.694 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_402 | OE2 | 3.988 |
| 3SCK | B_HIS_378 | ND1 | B_GLU_402 | OE1 | 3.773 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.390 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 2.299 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_402 | OE2 | 3.828 |
| 3SCL | A_HIS_378 | ND1 | A_GLU_402 | OE1 | 3.962 |
| 3SCL | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.936 |
| 3SCL | A_HIS_378 | NE2 | A_GLU_402 | OE1 | 2.998 |
| 3SCL | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.495 |
| 3SCL | B_HIS_378 | NE2 | B_GLU_402 | OE1 | 3.016 |

Table 54: HIS378-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.808 |
| 2AJF | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.727 |
| 3D0G | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.839 |
| 3D0G | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.548 |
| 3D0H | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.191 |
| 3D0H | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.185 |
| 3D0I | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.187 |
| 3D0I | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.852 |
| 3D0I | B_LYS_112 | NZ | B_GLU_189 | OE1 | 2.946 |
| 3D0I | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.482 |
| 3SCI | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.520 |
| 3SCI | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.974 |
| 3SCJ | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.606 |
| 3SCJ | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.626 |
| 3SCJ | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.760 |
| 3SCJ | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.993 |
| 3SCK | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.145 |
| 3SCK | A_LYS_112 | NZ | A_GLU_189 | OE2 | 2.624 |
| 3SCK | B_LYS_112 | NZ | B_GLU_189 | OE1 | 2.980 |
| 3SCK | B_LYS_112 | NZ | B_GLU_189 | OE2 | 2.757 |
| 3SCL | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.408 |
| 3SCL | A_LYS_112 | NZ | A_GLU_189 | OE2 | 2.764 |
| 3SCL | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.963 |

Table 55: LYS112-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.808 |
| 2AJF | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.727 |
| 3D0G | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.839 |
| 3D0G | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.548 |
| 3D0H | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.191 |
| 3D0H | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.185 |
| 3D0I | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.187 |
| 3D0I | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.852 |
| 3D0I | B_LYS_112 | NZ | B_GLU_189 | OE1 | 2.946 |
| 3D0I | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.482 |
| 3SCI | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.520 |
| 3SCI | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.974 |
| 3SCJ | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.606 |
| 3SCJ | A_LYS_112 | NZ | A_GLU_189 | OE2 | 3.626 |
| 3SCJ | B_LYS_112 | NZ | B_GLU_189 | OE1 | 3.760 |
| 3SCJ | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.993 |
| 3SCK | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.145 |
| 3SCK | A_LYS_112 | NZ | A_GLU_189 | OE2 | 2.624 |
| 3SCK | B_LYS_112 | NZ | B_GLU_189 | OE1 | 2.980 |
| 3SCK | B_LYS_112 | NZ | B_GLU_189 | OE2 | 2.757 |
| 3SCL | A_LYS_112 | NZ | A_GLU_189 | OE1 | 3.408 |
| 3SCL | A_LYS_112 | NZ | A_GLU_189 | OE2 | 2.764 |
| 3SCL | B_LYS_112 | NZ | B_GLU_189 | OE2 | 3.963 |

Table 56: GLU189-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.763 |
| 2AJF | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.712 |
| 2AJF | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.992 |
| 3D0G | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.326 |
| 3D0G | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.150 |
| 3D0G | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.383 |
| 3D0H | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.748 |
| 3D0H | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.307 |
| 3D0I | A_LYS_234 | NZ | A_GLU_231 | OE2 | 2.886 |
| 3D0I | B_LYS_234 | NZ | B_GLU_231 | OE2 | 2.885 |
| 3SCI | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.792 |
| 3SCI | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.452 |
| 3SCI | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.808 |
| 3SCJ | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.594 |
| 3SCJ | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.724 |
| 3SCK | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.847 |
| 3SCK | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.343 |
| 3SCK | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.845 |
| 3SCK | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.278 |
| 3SCL | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.556 |
| 3SCL | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.191 |
| 3SCL | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.673 |
| 3SCL | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.548 |

Table 57: LYS234-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.763 |
| 2AJF | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.712 |
| 2AJF | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.992 |
| 3D0G | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.326 |
| 3D0G | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.150 |
| 3D0G | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.383 |
| 3D0H | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.748 |
| 3D0H | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.307 |
| 3D0I | A_LYS_234 | NZ | A_GLU_231 | OE2 | 2.886 |
| 3D0I | B_LYS_234 | NZ | B_GLU_231 | OE2 | 2.885 |
| 3SCI | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.792 |
| 3SCI | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.452 |
| 3SCI | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.808 |
| 3SCJ | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.594 |
| 3SCJ | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.724 |
| 3SCK | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.847 |
| 3SCK | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.343 |
| 3SCK | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.845 |
| 3SCK | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.278 |
| 3SCL | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.556 |
| 3SCL | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.191 |
| 3SCL | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.673 |
| 3SCL | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.548 |

Table 58: GLU231-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.408 |
| 2AJF | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.001 |
| 2DD8 | S_ARG_444 | NH2 | S_ASP_454 | OD2 | 3.531 |
| 2GHV | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.804 |
| 2GHV | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.565 |
| 2GHV | C_ARG_444 | NH2 | C_GLU_452 | OE2 | 3.650 |
| 2GHV | C_ARG_444 | NH2 | C_ASP_454 | OD1 | 3.401 |
| 2GHW | A_ARG_444 | NH2 | A_GLU_452 | OE2 | 3.285 |
| 2GHW | A_ARG_444 | NH2 | A_ASP_454 | OD1 | 3.823 |
| 2GHW | C_ARG_444 | NH2 | C_GLU_452 | OE2 | 3.347 |
| 2GHW | C_ARG_444 | NH2 | C_ASP_454 | OD1 | 3.456 |
| 3BGF | S_ARG_444 | NH2 | S_GLU_452 | OE2 | 3.267 |
| 3BGF | S_ARG_444 | NH2 | S_ASP_454 | OD2 | 3.815 |
| 3BGF | A_ARG_444 | NH2 | A_GLU_452 | OE2 | 3.371 |
| 3BGF | A_ARG_444 | NH2 | A_ASP_454 | OD2 | 3.730 |
| 3D0G | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.203 |
| 3D0G | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.859 |
| 3D0G | F_ARG_444 | NH1 | F_GLU_452 | OE2 | 3.743 |
| 3D0G | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.573 |
| 3D0G | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.447 |
| 3D0H | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.678 |
| 3D0H | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.103 |
| 3D0H | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.753 |
| 3D0H | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.628 |
| 3D0I | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.247 |
| 3D0I | E_ARG_444 | NH2 | E_ASP_454 | OD1 | 3.400 |
| 3D0I | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.236 |
| 3D0I | F_ARG_444 | NH2 | F_ASP_454 | OD1 | 3.810 |
| 3SCI | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 2.901 |
| 3SCI | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 2.977 |
| 3SCJ | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 2.926 |
| 3SCJ | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 2.956 |
| 3SCK | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.076 |
| 3SCK | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.187 |
| 3SCL | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.448 |
| 3SCL | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.909 |
| 5X5B | B_ARG_444 | NH1 | B_ASP_454 | OD2 | 2.941 |
| 5X5B | C_ARG_444 | NH1 | C_ASP_454 | OD2 | 2.942 |

Table 59: ARG444-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.408 |
| 2AJF | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.001 |
| 2DD8 | S_ARG_449 | NH1 | S_GLU_452 | OE1 | 3.677 |
| 2DD8 | S_ARG_449 | NH1 | S_GLU_452 | OE2 | 3.337 |
| 2DD8 | S_ARG_449 | NH2 | S_GLU_452 | OE2 | 2.689 |
| 2GHV | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.804 |
| 2GHV | C_ARG_444 | NH2 | C_GLU_452 | OE2 | 3.650 |
| 2GHV | C_ARG_449 | NH2 | C_GLU_452 | OE1 | 3.440 |
| 2GHV | C_ARG_449 | NH2 | C_GLU_452 | OE2 | 3.175 |
| 2GHW | A_ARG_444 | NH2 | A_GLU_452 | OE2 | 3.285 |
| 2GHW | A_ARG_449 | NH1 | A_GLU_452 | OE1 | 3.684 |
| 2GHW | A_ARG_449 | NH1 | A_GLU_452 | OE2 | 3.739 |
| 2GHW | A_ARG_449 | NH2 | A_GLU_452 | OE2 | 3.726 |
| 2GHW | C_ARG_444 | NH2 | C_GLU_452 | OE2 | 3.347 |
| 2GHW | C_ARG_449 | NH1 | C_GLU_452 | OE1 | 3.965 |
| 2GHW | C_ARG_449 | NH1 | C_GLU_452 | OE2 | 3.472 |
| 2GHW | C_ARG_449 | NH2 | C_GLU_452 | OE1 | 3.904 |
| 3BGF | S_ARG_444 | NH2 | S_GLU_452 | OE2 | 3.267 |
| 3BGF | S_ARG_449 | NH2 | S_GLU_452 | OE1 | 3.535 |
| 3BGF | A_ARG_444 | NH2 | A_GLU_452 | OE2 | 3.371 |
| 3D0G | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.203 |
| 3D0G | F_ARG_444 | NH1 | F_GLU_452 | OE2 | 3.743 |
| 3D0G | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.573 |
| 3D0H | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.678 |
| 3D0H | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.753 |
| 3D0I | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.247 |
| 3D0I | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.236 |
| 3SCI | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 2.901 |
| 3SCI | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 2.977 |
| 3SCJ | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 2.926 |
| 3SCJ | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 2.956 |
| 3SCK | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.076 |
| 3SCK | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.187 |
| 3SCL | E_ARG_444 | NH2 | E_GLU_452 | OE2 | 3.448 |
| 3SCL | F_ARG_444 | NH2 | F_GLU_452 | OE2 | 3.909 |

Table 60: GLU452-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_426 | NH1 | A_GLU_329 | OE2 | 3.740 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.855 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 2.946 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.890 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.381 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 2.717 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 2.911 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD1 | 3.504 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD2 | 2.403 |
| 3SCI | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.257 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.110 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.923 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.044 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.878 |
| 3SCJ | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.526 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.206 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.277 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.547 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.819 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 3.913 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 3.505 |
| 3SCK | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.591 |
| 3SCL | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.916 |
| 3SCL | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.143 |

Table 61: ARG426-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_426 | NH1 | A_GLU_329 | OE2 | 3.740 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.855 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 2.946 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.890 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.381 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 2.717 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 2.911 |
| 3SCI | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.257 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.110 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.923 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.044 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.878 |
| 3SCJ | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.526 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.206 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.277 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.547 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.819 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 3.913 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 3.505 |
| 3SCK | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.591 |
| 3SCL | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.916 |
| 3SCL | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.143 |

Table 62: GLU329-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.080 |
| 2AJF | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.258 |
| 2AJF | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.099 |
| 3D0G | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.622 |
| 3D0G | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.791 |
| 3D0G | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 2.982 |
| 3D0H | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.636 |
| 3D0H | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.413 |
| 3D0I | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.156 |
| 3D0I | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.999 |
| 3D0I | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.084 |
| 3SCI | A_ARG_115 | NH1 | A_GLU_182 | OE1 | 3.485 |
| 3SCI | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 2.973 |
| 3SCI | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.826 |
| 3SCJ | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.662 |
| 3SCJ | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.931 |
| 3SCK | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.180 |
| 3SCK | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.458 |
| 3SCL | A_ARG_115 | NH1 | A_GLU_182 | OE1 | 3.915 |
| 3SCL | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 2.759 |
| 3SCL | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.301 |

Table 63: ARG115-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.080 |
| 2AJF | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.258 |
| 2AJF | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.099 |
| 3D0G | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.622 |
| 3D0G | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.791 |
| 3D0G | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 2.982 |
| 3D0H | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.636 |
| 3D0H | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.413 |
| 3D0I | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.156 |
| 3D0I | B_ARG_115 | NH1 | B_GLU_182 | OE1 | 3.999 |
| 3D0I | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.084 |
| 3SCI | A_ARG_115 | NH1 | A_GLU_182 | OE1 | 3.485 |
| 3SCI | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 2.973 |
| 3SCI | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.826 |
| 3SCJ | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.662 |
| 3SCJ | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.931 |
| 3SCK | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 3.180 |
| 3SCK | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.458 |
| 3SCL | A_ARG_115 | NH1 | A_GLU_182 | OE1 | 3.915 |
| 3SCL | A_ARG_115 | NH1 | A_GLU_182 | OE2 | 2.759 |
| 3SCL | B_ARG_115 | NH1 | B_GLU_182 | OE2 | 3.301 |

Table 64: GLU182-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_393 | NH1 | A_GLU_37 | OE1 | 3.436 |
| 2AJF | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 3.134 |
| 2AJF | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.409 |
| 2AJF | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 3.226 |
| 2AJF | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.233 |
| 2AJF | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.525 |
| 3SCI | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 2.993 |
| 3SCI | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.829 |
| 3SCI | A_ARG_393 | NH2 | A_GLU_37 | OE2 | 3.668 |
| 3SCI | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 2.767 |
| 3SCI | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.951 |
| 3SCI | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.149 |
| 3SCJ | A_ARG_393 | NH1 | A_GLU_37 | OE1 | 3.540 |
| 3SCJ | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 3.136 |
| 3SCJ | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.154 |
| 3SCJ | A_ARG_393 | NH2 | A_GLU_37 | OE2 | 3.984 |
| 3SCJ | B_ARG_393 | NH1 | B_GLU_37 | OE1 | 3.412 |
| 3SCJ | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 2.868 |
| 3SCJ | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.040 |
| 3SCJ | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.888 |

Table 65: ARG393-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_393 | NH1 | A_GLU_37 | OE1 | 3.436 |
| 2AJF | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 3.134 |
| 2AJF | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.409 |
| 2AJF | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.992 |
| 2AJF | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 3.226 |
| 2AJF | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.233 |
| 2AJF | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.525 |
| 3D0G | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.966 |
| 3SCI | A_HIS_34 | ND1 | A_GLU_37 | OE1 | 3.955 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.865 |
| 3SCI | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 2.993 |
| 3SCI | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.829 |
| 3SCI | A_ARG_393 | NH2 | A_GLU_37 | OE2 | 3.668 |
| 3SCI | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.800 |
| 3SCI | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 2.767 |
| 3SCI | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.951 |
| 3SCI | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.149 |
| 3SCJ | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.774 |
| 3SCJ | A_ARG_393 | NH1 | A_GLU_37 | OE1 | 3.540 |
| 3SCJ | A_ARG_393 | NH1 | A_GLU_37 | OE2 | 3.136 |
| 3SCJ | A_ARG_393 | NH2 | A_GLU_37 | OE1 | 3.154 |
| 3SCJ | A_ARG_393 | NH2 | A_GLU_37 | OE2 | 3.984 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_375 | OE2 | 3.983 |
| 3SCJ | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.709 |
| 3SCJ | B_ARG_393 | NH1 | B_GLU_37 | OE1 | 3.412 |
| 3SCJ | B_ARG_393 | NH1 | B_GLU_37 | OE2 | 2.868 |
| 3SCJ | B_ARG_393 | NH2 | B_GLU_37 | OE1 | 3.040 |
| 3SCJ | B_ARG_393 | NH2 | B_GLU_37 | OE2 | 3.888 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_375 | OE1 | 3.653 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.518 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_375 | OE1 | 3.559 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.390 |
| 3SCL | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.936 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_375 | OE1 | 3.783 |
| 3SCL | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.495 |

Table 66: GLU37-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.983 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.964 |
| 5X58 | A_ARG_1001 | NH2 | A_GLU_755 | OE1 | 3.437 |
| 5X58 | A_ARG_1001 | NH2 | A_GLU_755 | OE2 | 3.596 |
| 5X58 | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.486 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.983 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.963 |
| 5X58 | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.485 |
| 5X58 | B_ARG_1001 | NH2 | B_GLU_755 | OE1 | 3.436 |
| 5X58 | B_ARG_1001 | NH2 | B_GLU_755 | OE2 | 3.597 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.985 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.966 |
| 5X58 | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.487 |
| 5X58 | C_ARG_1001 | NH2 | C_GLU_755 | OE1 | 3.436 |
| 5X58 | C_ARG_1001 | NH2 | C_GLU_755 | OE2 | 3.596 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.909 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.948 |
| 5X5B | A_ARG_1001 | NH2 | A_GLU_755 | OE1 | 3.427 |
| 5X5B | A_ARG_1001 | NH2 | A_GLU_755 | OE2 | 3.433 |
| 5X5B | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.377 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.930 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.999 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE1 | 3.970 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.150 |
| 5X5B | B_ARG_1001 | NH2 | B_GLU_755 | OE1 | 3.472 |
| 5X5B | B_ARG_1001 | NH2 | B_GLU_755 | OE2 | 3.342 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.907 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.931 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE1 | 3.965 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.203 |
| 5X5B | C_ARG_1001 | NH2 | C_GLU_755 | OE1 | 3.472 |
| 5X5B | C_ARG_1001 | NH2 | C_GLU_755 | OE2 | 3.341 |

Table 67: ARG1001-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.983 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.964 |
| 5X58 | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.486 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.983 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.963 |
| 5X58 | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.485 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.985 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.966 |
| 5X58 | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.487 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.909 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.948 |
| 5X5B | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.377 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.930 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.999 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE1 | 3.970 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.150 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.907 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.931 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE1 | 3.965 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.203 |

Table 68: GLU999-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.146 |
| 2AJF | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.392 |
| 3D0G | A_LYS_187 | NZ | A_ASP_509 | OD1 | 3.967 |
| 3D0G | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.239 |
| 3D0G | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.466 |
| 3D0H | A_LYS_187 | NZ | A_ASP_509 | OD1 | 3.949 |
| 3D0H | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.246 |
| 3D0H | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.884 |
| 3D0I | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.851 |
| 3D0I | B_LYS_187 | NZ | B_ASP_509 | OD1 | 3.839 |
| 3D0I | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.086 |
| 3SCI | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.700 |
| 3SCI | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.424 |
| 3SCJ | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.854 |
| 3SCJ | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.425 |
| 3SCK | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.048 |
| 3SCK | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.553 |
| 3SCL | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.750 |
| 3SCL | B_LYS_187 | NZ | B_ASP_509 | OD2 | 2.965 |

Table 69: LYS187-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.146 |
| 2AJF | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.392 |
| 3D0G | A_LYS_187 | NZ | A_ASP_509 | OD1 | 3.967 |
| 3D0G | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.239 |
| 3D0G | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.466 |
| 3D0H | A_LYS_187 | NZ | A_ASP_509 | OD1 | 3.949 |
| 3D0H | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.246 |
| 3D0H | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.884 |
| 3D0I | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.851 |
| 3D0I | B_LYS_187 | NZ | B_ASP_509 | OD1 | 3.839 |
| 3D0I | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.086 |
| 3SCI | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.700 |
| 3SCI | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.424 |
| 3SCJ | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.854 |
| 3SCJ | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.425 |
| 3SCK | A_LYS_187 | NZ | A_ASP_509 | OD2 | 3.048 |
| 3SCK | B_LYS_187 | NZ | B_ASP_509 | OD2 | 3.553 |
| 3SCL | A_LYS_187 | NZ | A_ASP_509 | OD2 | 2.750 |
| 3SCL | B_LYS_187 | NZ | B_ASP_509 | OD2 | 2.965 |

Table 70: ASP509-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_353 | NZ | A_ASP_38 | OD1 | 3.263 |
| 3D0G | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.262 |
| 3D0G | A_LYS_353 | NZ | A_GLU_38 | OE2 | 2.453 |
| 3D0G | B_LYS_353 | NZ | B_GLU_38 | OE2 | 3.062 |
| 3D0H | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.130 |
| 3D0H | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.006 |
| 3D0H | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.557 |
| 3D0H | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.699 |
| 3D0I | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.199 |
| 3D0I | A_LYS_353 | NZ | A_GLU_38 | OE2 | 2.940 |
| 3D0I | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.427 |
| 3D0I | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.805 |
| 3SCI | A_LYS_353 | NZ | A_ASP_38 | OD1 | 3.354 |
| 3SCI | B_LYS_353 | NZ | B_ASP_38 | OD1 | 3.714 |
| 3SCJ | A_LYS_353 | NZ | A_ASP_38 | OD1 | 2.877 |
| 3SCJ | B_LYS_353 | NZ | B_ASP_38 | OD1 | 2.726 |
| 3SCK | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.265 |
| 3SCK | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.121 |
| 3SCK | B_LYS_353 | NZ | B_GLU_38 | OE1 | 2.931 |
| 3SCK | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.932 |
| 3SCL | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.461 |
| 3SCL | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.043 |
| 3SCL | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.437 |
| 3SCL | B_LYS_353 | NZ | B_GLU_38 | OE2 | 3.301 |

Table 71: LYS353-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0G | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.262 |
| 3D0G | A_LYS_353 | NZ | A_GLU_38 | OE2 | 2.453 |
| 3D0G | B_LYS_353 | NZ | B_GLU_38 | OE2 | 3.062 |
| 3D0H | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.130 |
| 3D0H | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.006 |
| 3D0H | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.557 |
| 3D0H | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.699 |
| 3D0I | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.199 |
| 3D0I | A_LYS_353 | NZ | A_GLU_38 | OE2 | 2.940 |
| 3D0I | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.427 |
| 3D0I | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.805 |
| 3SCK | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.265 |
| 3SCK | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.121 |
| 3SCK | B_LYS_353 | NZ | B_GLU_38 | OE1 | 2.931 |
| 3SCK | B_LYS_353 | NZ | B_GLU_38 | OE2 | 2.932 |
| 3SCL | A_LYS_353 | NZ | A_GLU_38 | OE1 | 3.461 |
| 3SCL | A_LYS_353 | NZ | A_GLU_38 | OE2 | 3.043 |
| 3SCL | B_LYS_353 | NZ | B_GLU_38 | OE1 | 3.437 |
| 3SCL | B_LYS_353 | NZ | B_GLU_38 | OE2 | 3.301 |

Table 72: GLU38-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.271 |
| 2AJF | A_LYS_309 | NZ | A_GLU_312 | OE2 | 3.754 |
| 2AJF | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.226 |
| 3D0G | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.812 |
| 3D0G | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.077 |
| 3D0G | B_LYS_309 | NZ | B_GLU_312 | OE2 | 3.968 |
| 3D0H | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.050 |
| 3D0H | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.471 |
| 3D0I | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.134 |
| 3D0I | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.386 |
| 3SCI | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.140 |
| 3SCI | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.016 |
| 3SCJ | A_LYS_309 | NZ | A_GLU_312 | OE1 | 2.769 |
| 3SCJ | B_LYS_309 | NZ | B_GLU_312 | OE1 | 2.771 |
| 3SCJ | B_LYS_309 | NZ | B_GLU_312 | OE2 | 3.982 |
| 3SCK | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.263 |
| 3SCK | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.334 |
| 3SCL | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.111 |
| 3SCL | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.480 |

Table 73: LYS309-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.271 |
| 2AJF | A_LYS_309 | NZ | A_GLU_312 | OE2 | 3.754 |
| 2AJF | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.226 |
| 3D0G | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.812 |
| 3D0G | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.077 |
| 3D0G | B_LYS_309 | NZ | B_GLU_312 | OE2 | 3.968 |
| 3D0H | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.050 |
| 3D0H | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.471 |
| 3D0I | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.134 |
| 3D0I | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.386 |
| 3SCI | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.140 |
| 3SCI | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.016 |
| 3SCJ | A_LYS_309 | NZ | A_GLU_312 | OE1 | 2.769 |
| 3SCJ | B_LYS_309 | NZ | B_GLU_312 | OE1 | 2.771 |
| 3SCJ | B_LYS_309 | NZ | B_GLU_312 | OE2 | 3.982 |
| 3SCK | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.263 |
| 3SCK | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.334 |
| 3SCL | A_LYS_309 | NZ | A_GLU_312 | OE1 | 3.111 |
| 3SCL | B_LYS_309 | NZ | B_GLU_312 | OE1 | 3.480 |

Table 74: GLU312-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.420 |
| 2AJF | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.452 |
| 2AJF | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.458 |
| 2AJF | B_ARG_219 | NH2 | B_ASP_201 | OD1 | 3.892 |
| 2AJF | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.087 |
| 3D0G | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.737 |
| 3D0G | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.217 |
| 3D0H | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.787 |
| 3D0H | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.408 |
| 3D0H | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.543 |
| 3D0H | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.119 |
| 3D0I | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.393 |
| 3D0I | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.226 |
| 3D0I | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.369 |
| 3D0I | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.122 |
| 3SCI | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.059 |
| 3SCI | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.689 |
| 3SCJ | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.710 |
| 3SCJ | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 3.281 |
| 3SCJ | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.488 |
| 3SCJ | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 3.381 |
| 3SCK | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 2.535 |
| 3SCK | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 2.655 |
| 3SCL | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.854 |
| 3SCL | A_ARG_219 | NH2 | A_ASP_201 | OD1 | 3.810 |
| 3SCL | A_ARG_219 | NH2 | A_ASP_201 | OD2 | 2.818 |
| 3SCL | B_ARG_219 | NH2 | B_ASP_201 | OD1 | 3.401 |
| 3SCL | B_ARG_219 | NH2 | B_ASP_201 | OD2 | 2.726 |

Table 75: ASP201-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.011 |
| 2AJF | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.673 |
| 2AJF | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.856 |
| 3D0G | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.034 |
| 3D0G | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.248 |
| 3D0G | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.414 |
| 3D0G | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.707 |
| 3D0H | A_LYS_288 | NZ | A_ASP_431 | OD1 | 2.502 |
| 3D0H | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.500 |
| 3D0H | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.891 |
| 3D0I | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.237 |
| 3D0I | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.963 |
| 3D0I | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.153 |
| 3SCI | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.667 |
| 3SCI | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.649 |
| 3SCI | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.168 |
| 3SCJ | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.711 |
| 3SCJ | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.920 |
| 3SCJ | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.841 |
| 3SCJ | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.087 |
| 3SCK | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.624 |
| 3SCK | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.046 |
| 3SCK | A_LYS_288 | NZ | A_GLU_433 | OE2 | 3.653 |
| 3SCK | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.790 |
| 3SCK | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.658 |
| 3SCL | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.310 |
| 3SCL | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.328 |
| 3SCL | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.355 |
| 3SCL | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.412 |

Table 76: LYS288-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.011 |
| 2AJF | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.673 |
| 2AJF | A_LYS_534 | NZ | B_ASP_431 | OD1 | 3.656 |
| 3D0G | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.034 |
| 3D0G | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.248 |
| 3D0G | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.414 |
| 3D0H | A_LYS_288 | NZ | A_ASP_431 | OD1 | 2.502 |
| 3D0H | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.500 |
| 3D0H | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.891 |
| 3D0I | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.237 |
| 3D0I | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.153 |
| 3SCI | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.667 |
| 3SCJ | A_LYS_288 | NZ | A_ASP_431 | OD2 | 2.711 |
| 3SCJ | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.841 |
| 3SCK | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.624 |
| 3SCK | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.046 |
| 3SCK | B_LYS_288 | NZ | B_ASP_431 | OD1 | 2.790 |
| 3SCL | A_LYS_288 | NZ | A_ASP_431 | OD1 | 3.310 |
| 3SCL | A_LYS_288 | NZ | A_ASP_431 | OD2 | 3.328 |
| 3SCL | B_LYS_288 | NZ | B_ASP_431 | OD2 | 3.355 |

Table 77: ASP431-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 3.643 |
| 2AJF | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.692 |
| 2AJF | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.035 |
| 3D0G | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.159 |
| 3D0G | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.787 |
| 3D0H | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.144 |
| 3D0H | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.001 |
| 3D0I | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.364 |
| 3D0I | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.212 |
| 3SCI | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.133 |
| 3SCI | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.610 |
| 3SCJ | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 2.363 |
| 3SCJ | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.678 |
| 3SCJ | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.815 |
| 3SCK | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 3.705 |
| 3SCK | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.038 |
| 3SCK | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.129 |
| 3SCL | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.352 |
| 3SCL | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.623 |

Table 78: ARG460-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 3.643 |
| 2AJF | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.692 |
| 2AJF | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.035 |
| 3D0G | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.159 |
| 3D0G | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.787 |
| 3D0H | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.144 |
| 3D0H | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.001 |
| 3D0I | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.364 |
| 3D0I | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.212 |
| 3SCI | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.133 |
| 3SCI | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.610 |
| 3SCJ | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 2.363 |
| 3SCJ | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.678 |
| 3SCJ | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.815 |
| 3SCK | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 3.705 |
| 3SCK | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.038 |
| 3SCK | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.129 |
| 3SCL | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.352 |
| 3SCL | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.623 |

Table 79: GLU457-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE1 | 3.011 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE2 | 3.438 |
| 5X58 | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.538 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.011 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 3.438 |
| 5X58 | B_ARG_1021 | NH2 | C_GLU_1013 | OE2 | 3.540 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.011 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 3.438 |
| 5X58 | C_ARG_1021 | NH2 | A_GLU_1013 | OE2 | 3.539 |
| 5X5B | A_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.722 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.472 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.057 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.450 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 2.311 |
| 5X5B | B_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.517 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.273 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 2.370 |
| 5X5B | C_ARG_1021 | NH2 | C_GLU_1013 | OE1 | 3.517 |

Table 80: ARG1021-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE1 | 3.011 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE2 | 3.438 |
| 5X58 | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.538 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.011 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 3.438 |
| 5X58 | B_ARG_1021 | NH2 | C_GLU_1013 | OE2 | 3.540 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.011 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 3.438 |
| 5X58 | C_ARG_1021 | NH2 | A_GLU_1013 | OE2 | 3.539 |
| 5X5B | A_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.722 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.472 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.057 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.450 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 2.311 |
| 5X5B | B_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.517 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.273 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 2.370 |
| 5X5B | C_ARG_1021 | NH2 | C_GLU_1013 | OE1 | 3.517 |

Table 81: GLU1013-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_401 | NE2 | A_ASP_382 | OD2 | 3.397 |
| 2AJF | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.748 |
| 3D0G | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 2.924 |
| 3D0G | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.097 |
| 3D0H | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.253 |
| 3D0H | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.248 |
| 3D0I | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.181 |
| 3D0I | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.112 |
| 3SCI | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.295 |
| 3SCI | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.545 |
| 3SCJ | A_HIS_401 | NE2 | A_ASP_382 | OD2 | 3.168 |
| 3SCJ | B_HIS_401 | NE2 | B_ASP_382 | OD2 | 2.952 |
| 3SCK | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 2.944 |
| 3SCK | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 2.702 |
| 3SCL | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.267 |
| 3SCL | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.349 |

Table 82: HIS401-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_401 | NE2 | A_ASP_382 | OD2 | 3.397 |
| 2AJF | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.748 |
| 3D0G | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 2.924 |
| 3D0G | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.097 |
| 3D0H | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.253 |
| 3D0H | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.248 |
| 3D0I | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.181 |
| 3D0I | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.112 |
| 3SCI | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.295 |
| 3SCI | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.545 |
| 3SCJ | A_HIS_401 | NE2 | A_ASP_382 | OD2 | 3.168 |
| 3SCJ | B_HIS_401 | NE2 | B_ASP_382 | OD2 | 2.952 |
| 3SCK | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 2.944 |
| 3SCK | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 2.702 |
| 3SCL | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.267 |
| 3SCL | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.349 |

Table 83: ASP382-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.025 |
| 2AJF | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.307 |
| 3D0G | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.713 |
| 3D0G | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.697 |
| 3D0H | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.324 |
| 3D0H | A_ARG_518 | NH1 | A_GLU_406 | OE1 | 3.615 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_406 | OE1 | 3.756 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_406 | OE2 | 3.850 |
| 3D0H | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.061 |
| 3D0H | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.835 |
| 3D0H | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.940 |
| 3D0I | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.884 |
| 3D0I | A_ARG_518 | NH1 | A_GLU_406 | OE1 | 3.545 |
| 3D0I | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.052 |
| 3D0I | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.950 |
| 3D0I | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.992 |
| 3SCI | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 2.812 |
| 3SCI | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.133 |
| 3SCI | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.879 |
| 3SCI | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.740 |
| 3SCJ | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.039 |
| 3SCJ | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.731 |
| 3SCJ | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.171 |
| 3SCK | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.223 |
| 3SCK | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 2.908 |
| 3SCK | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.632 |
| 3SCL | A_HIS_374 | ND1 | A_GLU_406 | OE2 | 3.626 |
| 3SCL | B_HIS_374 | ND1 | B_GLU_406 | OE2 | 3.045 |
| 3SCL | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 2.954 |
| 3SCL | B_ARG_518 | NH1 | B_GLU_406 | OE2 | 3.512 |

Table 84: GLU406-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.336 |
| 2AJF | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.457 |
| 2AJF | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 2.938 |
| 2AJF | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.429 |
| 3D0G | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.955 |
| 3D0G | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.559 |
| 3D0G | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 2.475 |
| 3D0G | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.483 |
| 3D0H | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.621 |
| 3D0H | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.471 |
| 3D0H | B_ARG_482 | NH1 | B_GLU_489 | OE1 | 2.732 |
| 3D0H | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.824 |
| 3D0H | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.932 |
| 3D0I | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.768 |
| 3D0I | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.673 |
| 3D0I | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.791 |
| 3D0I | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.688 |
| 3SCI | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.668 |
| 3SCI | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.756 |
| 3SCI | B_ARG_482 | NH1 | B_GLU_489 | OE1 | 3.858 |
| 3SCI | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.969 |
| 3SCI | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.242 |
| 3SCJ | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.323 |
| 3SCJ | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.886 |
| 3SCJ | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.255 |
| 3SCJ | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.169 |
| 3SCK | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 2.693 |
| 3SCK | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 3.807 |
| 3SCK | B_ARG_482 | NH1 | B_GLU_489 | OE2 | 3.669 |
| 3SCK | B_ARG_482 | NH2 | B_GLU_489 | OE2 | 3.445 |
| 3SCL | A_ARG_482 | NH2 | A_GLU_489 | OE1 | 3.210 |
| 3SCL | A_ARG_482 | NH2 | A_GLU_489 | OE2 | 2.758 |
| 3SCL | B_ARG_482 | NH2 | B_GLU_489 | OE1 | 3.520 |
| 5X4S | A_ARG_48 | NH1 | A_ASP_44 | OD1 | 2.727 |
| 5X4S | A_ARG_48 | NH1 | A_ASP_44 | OD2 | 3.371 |
| 5X4S | A_ARG_48 | NH2 | A_ASP_44 | OD1 | 3.601 |
| 5X4S | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 2.675 |
| 5X58 | A_ARG_48 | NH1 | A_ASP_44 | OD1 | 3.022 |
| 5X58 | A_ARG_48 | NH1 | A_ASP_44 | OD2 | 3.566 |
| 5X58 | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 3.303 |
| 5X58 | B_ARG_48 | NH1 | B_ASP_44 | OD1 | 3.022 |
| 5X58 | B_ARG_48 | NH1 | B_ASP_44 | OD2 | 3.565 |
| 5X58 | B_ARG_48 | NH2 | B_ASP_44 | OD2 | 3.302 |
| 5X58 | C_ARG_48 | NH1 | C_ASP_44 | OD1 | 3.022 |
| 5X58 | C_ARG_48 | NH1 | C_ASP_44 | OD2 | 3.565 |
| 5X58 | C_ARG_48 | NH2 | C_ASP_44 | OD2 | 3.303 |
| 5X5B | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 3.936 |
| 5X5B | B_ARG_48 | NH2 | B_ASP_44 | OD2 | 3.973 |
| 5X5B | C_ARG_48 | NH2 | C_ASP_44 | OD2 | 3.973 |

Table 85: ARG48-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X4S | A_ARG_48 | NH1 | A_ASP_44 | OD1 | 2.727 |
| 5X4S | A_ARG_48 | NH1 | A_ASP_44 | OD2 | 3.371 |
| 5X4S | A_ARG_48 | NH2 | A_ASP_44 | OD1 | 3.601 |
| 5X4S | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 2.675 |
| 5X58 | A_ARG_48 | NH1 | A_ASP_44 | OD1 | 3.022 |
| 5X58 | A_ARG_48 | NH1 | A_ASP_44 | OD2 | 3.566 |
| 5X58 | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 3.303 |
| 5X58 | B_ARG_48 | NH1 | B_ASP_44 | OD1 | 3.022 |
| 5X58 | B_ARG_48 | NH1 | B_ASP_44 | OD2 | 3.565 |
| 5X58 | B_ARG_48 | NH2 | B_ASP_44 | OD2 | 3.302 |
| 5X58 | C_ARG_48 | NH1 | C_ASP_44 | OD1 | 3.022 |
| 5X58 | C_ARG_48 | NH1 | C_ASP_44 | OD2 | 3.565 |
| 5X58 | C_ARG_48 | NH2 | C_ASP_44 | OD2 | 3.303 |
| 5X5B | A_ARG_48 | NH2 | A_ASP_44 | OD2 | 3.936 |
| 5X5B | B_ARG_48 | NH2 | B_ASP_44 | OD2 | 3.973 |
| 5X5B | C_ARG_48 | NH2 | C_ASP_44 | OD2 | 3.973 |

Table 86: ASP44-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.928 |
| 2AJF | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.654 |
| 3D0G | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.979 |
| 3D0G | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.789 |
| 3D0G | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.550 |
| 3D0H | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.471 |
| 3D0H | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.656 |
| 3D0I | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.978 |
| 3D0I | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.725 |
| 3SCI | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.358 |
| 3SCI | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.299 |
| 3SCJ | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.682 |
| 3SCJ | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.159 |
| 3SCK | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.712 |
| 3SCK | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 2.753 |
| 3SCL | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.367 |

Table 87: HIS540-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.928 |
| 2AJF | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.791 |
| 2AJF | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.920 |
| 2AJF | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.654 |
| 2AJF | B_LYS_541 | NZ | B_GLU_435 | OE1 | 3.723 |
| 3D0G | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.979 |
| 3D0G | A_LYS_541 | NZ | A_GLU_435 | OE1 | 2.843 |
| 3D0G | A_LYS_541 | NZ | A_GLU_435 | OE2 | 3.422 |
| 3D0G | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.789 |
| 3D0G | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.550 |
| 3D0H | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.471 |
| 3D0H | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.854 |
| 3D0H | A_LYS_541 | NZ | A_GLU_435 | OE2 | 3.545 |
| 3D0H | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.656 |
| 3D0I | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 2.978 |
| 3D0I | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.768 |
| 3D0I | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.991 |
| 3D0I | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.725 |
| 3SCI | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.358 |
| 3SCI | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.299 |
| 3SCJ | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.682 |
| 3SCJ | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.913 |
| 3SCJ | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 3.159 |
| 3SCK | A_HIS_540 | NE2 | A_GLU_435 | OE1 | 3.712 |
| 3SCK | B_HIS_540 | NE2 | B_GLU_435 | OE1 | 2.753 |
| 3SCL | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.042 |
| 3SCL | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.897 |
| 3SCL | B_HIS_540 | NE2 | B_GLU_435 | OE2 | 3.367 |

Table 88: GLU435-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.710 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.597 |
| 3D0G | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.955 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.856 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.820 |
| 3D0H | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.376 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.231 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.198 |
| 3D0H | B_LYS_419 | NZ | B_GLU_430 | OE1 | 3.848 |
| 3D0I | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.095 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.355 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.779 |
| 3D0I | B_LYS_419 | NZ | B_GLU_430 | OE1 | 3.547 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.520 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.936 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.617 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.574 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.939 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.692 |
| 3SCL | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.918 |

Table 89: LYS419-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.710 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.597 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.856 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.820 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.231 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.198 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.355 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.779 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.520 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.936 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.617 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.574 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.939 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.692 |
| 3SCK | B_HIS_535 | ND1 | B_GLU_536 | OE1 | 3.467 |
| 3SCL | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.918 |

Table 90: GLU536-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.630 |
| 3D0G | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.949 |
| 3D0G | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.600 |
| 3D0H | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.942 |
| 3D0H | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.446 |
| 3D0I | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.676 |
| 3SCI | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.796 |
| 3SCI | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.626 |
| 3SCJ | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.833 |
| 3SCJ | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.785 |
| 3SCK | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.804 |
| 3SCK | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.747 |
| 3SCL | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.467 |
| 3SCL | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.658 |

Table 91: ARG306-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.630 |
| 3D0G | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.949 |
| 3D0G | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.737 |
| 3D0G | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.600 |
| 3D0G | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.363 |
| 3D0H | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.942 |
| 3D0H | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.446 |
| 3D0I | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.185 |
| 3D0I | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.676 |
| 3D0I | B_LYS_313 | NZ | B_GLU_310 | OE2 | 2.999 |
| 3SCI | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.796 |
| 3SCI | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.555 |
| 3SCI | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.626 |
| 3SCI | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.303 |
| 3SCJ | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.833 |
| 3SCJ | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.597 |
| 3SCJ | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.785 |
| 3SCJ | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.681 |
| 3SCK | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.804 |
| 3SCK | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.272 |
| 3SCK | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.747 |
| 3SCK | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.682 |
| 3SCL | A_ARG_306 | NH2 | A_GLU_310 | OE1 | 3.467 |
| 3SCL | B_ARG_306 | NH2 | B_GLU_310 | OE1 | 3.658 |

Table 92: GLU310-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.560 |
| 3D0H | A_ARG_518 | NH1 | A_GLU_406 | OE1 | 3.615 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_402 | OE2 | 3.679 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_406 | OE1 | 3.756 |
| 3D0H | A_ARG_518 | NH2 | A_GLU_406 | OE2 | 3.850 |
| 3D0H | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.835 |
| 3D0H | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.851 |
| 3D0H | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.940 |
| 3D0I | A_ARG_518 | NH1 | A_GLU_406 | OE1 | 3.545 |
| 3D0I | A_ARG_518 | NH2 | A_GLU_402 | OE2 | 3.220 |
| 3D0I | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.950 |
| 3D0I | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.992 |
| 3SCI | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.879 |
| 3SCI | B_ARG_518 | NH2 | B_GLU_406 | OE1 | 3.740 |
| 3SCJ | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.171 |
| 3SCJ | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.883 |
| 3SCK | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 3.632 |
| 3SCL | B_ARG_518 | NH1 | B_GLU_406 | OE1 | 2.954 |
| 3SCL | B_ARG_518 | NH1 | B_GLU_406 | OE2 | 3.512 |
| 3SCL | B_ARG_518 | NH2 | B_GLU_402 | OE2 | 3.414 |

Table 93: ARG518-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.420 |
| 2AJF | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.458 |
| 3D0G | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.291 |
| 3D0G | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.330 |
| 3D0H | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.322 |
| 3D0H | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.787 |
| 3D0H | B_ARG_204 | NH1 | B_ASP_198 | OD2 | 3.995 |
| 3D0H | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.825 |
| 3D0H | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.543 |
| 3D0I | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.393 |
| 3D0I | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.369 |
| 3SCI | A_ARG_204 | NH2 | A_ASP_198 | OD1 | 3.614 |
| 3SCI | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.484 |
| 3SCI | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.759 |
| 3SCI | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.703 |
| 3SCJ | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.710 |
| 3SCJ | B_ARG_204 | NH2 | B_ASP_201 | OD1 | 3.488 |
| 3SCK | A_ARG_204 | NH2 | A_ASP_198 | OD1 | 3.950 |
| 3SCK | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.885 |
| 3SCL | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.751 |
| 3SCL | A_ARG_204 | NH2 | A_ASP_201 | OD1 | 3.854 |
| 3SCL | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.847 |
| 3SCL | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.720 |

Table 94: ARG204-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0G | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.291 |
| 3D0G | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.330 |
| 3D0H | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.322 |
| 3D0H | B_ARG_204 | NH1 | B_ASP_198 | OD2 | 3.995 |
| 3D0H | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.825 |
| 3SCI | A_ARG_204 | NH2 | A_ASP_198 | OD1 | 3.614 |
| 3SCI | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.484 |
| 3SCI | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.759 |
| 3SCI | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.703 |
| 3SCK | A_ARG_204 | NH2 | A_ASP_198 | OD1 | 3.950 |
| 3SCK | A_LYS_465 | NZ | A_ASP_198 | OD1 | 3.632 |
| 3SCK | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.885 |
| 3SCL | A_ARG_204 | NH2 | A_ASP_198 | OD2 | 3.751 |
| 3SCL | B_ARG_204 | NH2 | B_ASP_198 | OD1 | 3.847 |
| 3SCL | B_ARG_204 | NH2 | B_ASP_198 | OD2 | 3.720 |

Table 95: ASP198-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHV | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.496 |
| 2GHV | C_LYS_343 | NZ | C_GLU_327 | OE1 | 3.965 |
| 3D0G | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.222 |
| 3D0H | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.317 |
| 3D0I | E_LYS_343 | NZ | E_GLU_327 | OE1 | 2.907 |
| 3D0I | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.274 |
| 3SCI | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.289 |
| 3SCI | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.783 |
| 3SCK | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.896 |
| 3SCK | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.370 |
| 5X58 | A_LYS_343 | NZ | A_GLU_327 | OE1 | 3.311 |
| 5X58 | B_LYS_343 | NZ | B_GLU_327 | OE1 | 3.310 |
| 5X58 | C_LYS_343 | NZ | C_GLU_327 | OE1 | 3.310 |
| 5X5B | A_LYS_343 | NZ | A_GLU_327 | OE1 | 3.311 |

Table 96: LYS343-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHV | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.496 |
| 2GHV | C_LYS_343 | NZ | C_GLU_327 | OE1 | 3.965 |
| 3D0G | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.222 |
| 3D0H | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.317 |
| 3D0I | E_LYS_343 | NZ | E_GLU_327 | OE1 | 2.907 |
| 3D0I | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.274 |
| 3SCI | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.289 |
| 3SCI | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.783 |
| 3SCK | E_LYS_343 | NZ | E_GLU_327 | OE1 | 3.896 |
| 3SCK | F_LYS_343 | NZ | F_GLU_327 | OE1 | 3.370 |
| 5X58 | A_LYS_343 | NZ | A_GLU_327 | OE1 | 3.311 |
| 5X58 | B_LYS_343 | NZ | B_GLU_327 | OE1 | 3.310 |
| 5X58 | C_LYS_343 | NZ | C_GLU_327 | OE1 | 3.310 |
| 5X5B | A_LYS_343 | NZ | A_GLU_327 | OE1 | 3.311 |

Table 97: GLU327-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_458 | NZ | A_GLU_227 | OE1 | 3.613 |
| 2AJF | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.040 |
| 3D0G | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.595 |
| 3D0G | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.654 |
| 3D0H | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.176 |
| 3D0I | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.805 |
| 3SCI | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.642 |
| 3SCI | B_LYS_458 | NZ | B_GLU_227 | OE2 | 2.656 |
| 3SCJ | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.761 |
| 3SCJ | B_LYS_458 | NZ | B_GLU_227 | OE2 | 2.602 |
| 3SCK | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.716 |
| 3SCK | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.897 |
| 3SCL | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.685 |
| 3SCL | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.400 |

Table 98: LYS458-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_458 | NZ | A_GLU_227 | OE1 | 3.613 |
| 2AJF | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.040 |
| 3D0G | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.595 |
| 3D0G | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.654 |
| 3D0H | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.176 |
| 3D0I | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.805 |
| 3SCI | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.642 |
| 3SCI | B_LYS_458 | NZ | B_GLU_227 | OE2 | 2.656 |
| 3SCJ | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.761 |
| 3SCJ | B_LYS_458 | NZ | B_GLU_227 | OE2 | 2.602 |
| 3SCK | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.716 |
| 3SCK | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.897 |
| 3SCL | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.685 |
| 3SCL | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.400 |

Table 99: GLU227-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_1010 | NZ | A_GLU_707 | OE1 | 3.690 |
| 5X58 | A_LYS_1010 | NZ | A_GLU_707 | OE2 | 3.427 |
| 5X58 | B_LYS_1010 | NZ | B_GLU_707 | OE1 | 3.691 |
| 5X58 | B_LYS_1010 | NZ | B_GLU_707 | OE2 | 3.427 |
| 5X58 | C_LYS_1010 | NZ | C_GLU_707 | OE1 | 3.690 |
| 5X58 | C_LYS_1010 | NZ | C_GLU_707 | OE2 | 3.427 |
| 5X5B | A_LYS_1010 | NZ | A_GLU_707 | OE1 | 3.733 |
| 5X5B | A_LYS_1010 | NZ | A_GLU_707 | OE2 | 3.301 |
| 5X5B | B_LYS_1010 | NZ | B_GLU_707 | OE1 | 3.708 |
| 5X5B | B_LYS_1010 | NZ | B_GLU_707 | OE2 | 3.314 |
| 5X5B | C_LYS_1010 | NZ | C_GLU_707 | OE1 | 3.708 |
| 5X5B | C_LYS_1010 | NZ | C_GLU_707 | OE2 | 3.314 |

Table 100: LYS1010-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_1010 | NZ | A_GLU_707 | OE1 | 3.690 |
| 5X58 | A_LYS_1010 | NZ | A_GLU_707 | OE2 | 3.427 |
| 5X58 | A_HIS_1046 | NE2 | A_GLU_707 | OE1 | 2.723 |
| 5X58 | B_LYS_1010 | NZ | B_GLU_707 | OE1 | 3.691 |
| 5X58 | B_LYS_1010 | NZ | B_GLU_707 | OE2 | 3.427 |
| 5X58 | B_HIS_1046 | NE2 | B_GLU_707 | OE1 | 2.724 |
| 5X58 | C_LYS_1010 | NZ | C_GLU_707 | OE1 | 3.690 |
| 5X58 | C_LYS_1010 | NZ | C_GLU_707 | OE2 | 3.427 |
| 5X58 | C_HIS_1046 | NE2 | C_GLU_707 | OE1 | 2.724 |
| 5X5B | A_LYS_1010 | NZ | A_GLU_707 | OE1 | 3.733 |
| 5X5B | A_LYS_1010 | NZ | A_GLU_707 | OE2 | 3.301 |
| 5X5B | A_HIS_1046 | NE2 | A_GLU_707 | OE1 | 2.555 |
| 5X5B | B_LYS_1010 | NZ | B_GLU_707 | OE1 | 3.708 |
| 5X5B | B_LYS_1010 | NZ | B_GLU_707 | OE2 | 3.314 |
| 5X5B | B_HIS_1046 | NE2 | B_GLU_707 | OE1 | 2.640 |
| 5X5B | C_LYS_1010 | NZ | C_GLU_707 | OE1 | 3.708 |
| 5X5B | C_LYS_1010 | NZ | C_GLU_707 | OE2 | 3.314 |
| 5X5B | C_HIS_1046 | NE2 | C_GLU_707 | OE1 | 2.640 |

Table 101: GLU707-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.482 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 3.202 |
| 5X58 | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.575 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD1 | 3.484 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD2 | 3.202 |
| 5X58 | B_ARG_977 | NH2 | C_ASP_976 | OD2 | 3.576 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD1 | 3.484 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD2 | 3.202 |
| 5X58 | C_ARG_977 | NH2 | A_ASP_976 | OD2 | 3.575 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.912 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 2.504 |
| 5X5B | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.789 |

Table 102: ARG977-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.482 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 3.202 |
| 5X58 | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.575 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD1 | 3.484 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD2 | 3.202 |
| 5X58 | B_ARG_977 | NH2 | C_ASP_976 | OD2 | 3.576 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD1 | 3.484 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD2 | 3.202 |
| 5X58 | C_ARG_977 | NH2 | A_ASP_976 | OD2 | 3.575 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.912 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 2.504 |
| 5X5B | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.789 |

Table 103: ASP976-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_297 | NZ | A_ASP_649 | OD1 | 2.479 |
| 5X58 | A_LYS_297 | NZ | A_ASP_649 | OD2 | 3.392 |
| 5X58 | B_LYS_297 | NZ | B_ASP_649 | OD1 | 2.478 |
| 5X58 | B_LYS_297 | NZ | B_ASP_649 | OD2 | 3.391 |
| 5X58 | C_LYS_297 | NZ | C_ASP_649 | OD1 | 2.478 |
| 5X58 | C_LYS_297 | NZ | C_ASP_649 | OD2 | 3.393 |
| 5X5B | A_LYS_297 | NZ | A_ASP_649 | OD1 | 2.492 |
| 5X5B | A_LYS_297 | NZ | A_ASP_649 | OD2 | 3.385 |
| 5X5B | B_LYS_297 | NZ | B_ASP_649 | OD1 | 3.108 |
| 5X5B | B_LYS_297 | NZ | B_ASP_649 | OD2 | 3.662 |
| 5X5B | C_LYS_297 | NZ | C_ASP_649 | OD1 | 3.109 |
| 5X5B | C_LYS_297 | NZ | C_ASP_649 | OD2 | 3.663 |

Table 104: LYS297-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_297 | NZ | A_ASP_649 | OD1 | 2.479 |
| 5X58 | A_LYS_297 | NZ | A_ASP_649 | OD2 | 3.392 |
| 5X58 | B_LYS_297 | NZ | B_ASP_649 | OD1 | 2.478 |
| 5X58 | B_LYS_297 | NZ | B_ASP_649 | OD2 | 3.391 |
| 5X58 | C_LYS_297 | NZ | C_ASP_649 | OD1 | 2.478 |
| 5X58 | C_LYS_297 | NZ | C_ASP_649 | OD2 | 3.393 |
| 5X5B | A_LYS_297 | NZ | A_ASP_649 | OD1 | 2.492 |
| 5X5B | A_LYS_297 | NZ | A_ASP_649 | OD2 | 3.385 |
| 5X5B | B_LYS_297 | NZ | B_ASP_649 | OD1 | 3.108 |
| 5X5B | B_LYS_297 | NZ | B_ASP_649 | OD2 | 3.662 |
| 5X5B | C_LYS_297 | NZ | C_ASP_649 | OD1 | 3.109 |
| 5X5B | C_LYS_297 | NZ | C_ASP_649 | OD2 | 3.663 |

Table 105: ASP649-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | S_ARG_449 | NH1 | S_GLU_452 | OE1 | 3.677 |
| 2DD8 | S_ARG_449 | NH1 | S_GLU_452 | OE2 | 3.337 |
| 2DD8 | S_ARG_449 | NH2 | S_GLU_452 | OE2 | 2.689 |
| 2GHV | C_ARG_449 | NH2 | C_GLU_452 | OE1 | 3.440 |
| 2GHV | C_ARG_449 | NH2 | C_GLU_452 | OE2 | 3.175 |
| 2GHW | A_ARG_449 | NH1 | A_GLU_452 | OE1 | 3.684 |
| 2GHW | A_ARG_449 | NH1 | A_GLU_452 | OE2 | 3.739 |
| 2GHW | A_ARG_449 | NH2 | A_GLU_452 | OE2 | 3.726 |
| 2GHW | C_ARG_449 | NH1 | C_GLU_452 | OE1 | 3.965 |
| 2GHW | C_ARG_449 | NH1 | C_GLU_452 | OE2 | 3.472 |
| 2GHW | C_ARG_449 | NH2 | C_GLU_452 | OE1 | 3.904 |
| 3BGF | S_ARG_449 | NH2 | S_GLU_452 | OE1 | 3.535 |

Table 106: ARG449-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_1001 | NH2 | A_GLU_755 | OE1 | 3.437 |
| 5X58 | A_ARG_1001 | NH2 | A_GLU_755 | OE2 | 3.596 |
| 5X58 | B_ARG_1001 | NH2 | B_GLU_755 | OE1 | 3.436 |
| 5X58 | B_ARG_1001 | NH2 | B_GLU_755 | OE2 | 3.597 |
| 5X58 | C_ARG_1001 | NH2 | C_GLU_755 | OE1 | 3.436 |
| 5X58 | C_ARG_1001 | NH2 | C_GLU_755 | OE2 | 3.596 |
| 5X5B | A_ARG_1001 | NH2 | A_GLU_755 | OE1 | 3.427 |
| 5X5B | A_ARG_1001 | NH2 | A_GLU_755 | OE2 | 3.433 |
| 5X5B | B_ARG_1001 | NH2 | B_GLU_755 | OE1 | 3.472 |
| 5X5B | B_ARG_1001 | NH2 | B_GLU_755 | OE2 | 3.342 |
| 5X5B | C_ARG_1001 | NH2 | C_GLU_755 | OE1 | 3.472 |
| 5X5B | C_ARG_1001 | NH2 | C_GLU_755 | OE2 | 3.341 |

Table 107: GLU755-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.735 |
| 2AJF | E_LYS_447 | NZ | E_ASP_407 | OD2 | 3.899 |
| 2DD8 | S_LYS_447 | NZ | S_ASP_407 | OD1 | 3.742 |
| 3BGF | S_LYS_447 | NZ | S_ASP_407 | OD1 | 3.987 |
| 3BGF | S_LYS_447 | NZ | S_ASP_407 | OD2 | 3.876 |
| 3BGF | A_LYS_447 | NZ | A_ASP_407 | OD1 | 2.877 |
| 3BGF | A_LYS_447 | NZ | A_ASP_407 | OD2 | 2.805 |
| 3D0G | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.789 |
| 3SCI | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.835 |
| 3SCI | E_LYS_447 | NZ | E_ASP_407 | OD2 | 3.979 |
| 3SCK | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.663 |
| 3SCK | F_LYS_447 | NZ | F_ASP_407 | OD1 | 3.771 |

Table 108: LYS447-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.735 |
| 2AJF | E_LYS_447 | NZ | E_ASP_407 | OD2 | 3.899 |
| 2DD8 | S_LYS_411 | NZ | S_ASP_407 | OD1 | 2.884 |
| 2DD8 | S_LYS_447 | NZ | S_ASP_407 | OD1 | 3.742 |
| 3BGF | S_LYS_447 | NZ | S_ASP_407 | OD1 | 3.987 |
| 3BGF | S_LYS_447 | NZ | S_ASP_407 | OD2 | 3.876 |
| 3BGF | A_LYS_447 | NZ | A_ASP_407 | OD1 | 2.877 |
| 3BGF | A_LYS_447 | NZ | A_ASP_407 | OD2 | 2.805 |
| 3D0G | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.789 |
| 3D0G | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.908 |
| 3D0H | E_LYS_411 | NZ | E_ASP_407 | OD1 | 3.493 |
| 3D0H | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.643 |
| 3D0I | E_LYS_411 | NZ | E_ASP_407 | OD1 | 3.525 |
| 3D0I | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.530 |
| 3SCI | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.835 |
| 3SCI | E_LYS_447 | NZ | E_ASP_407 | OD2 | 3.979 |
| 3SCK | E_LYS_447 | NZ | E_ASP_407 | OD1 | 3.663 |
| 3SCK | F_LYS_447 | NZ | F_ASP_407 | OD1 | 3.771 |

Table 109: ASP407-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.791 |
| 2AJF | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.920 |
| 2AJF | B_LYS_541 | NZ | B_GLU_435 | OE1 | 3.723 |
| 3D0G | A_LYS_541 | NZ | A_GLU_435 | OE1 | 2.843 |
| 3D0G | A_LYS_541 | NZ | A_GLU_435 | OE2 | 3.422 |
| 3D0G | B_LYS_541 | NZ | B_GLU_430 | OE2 | 2.944 |
| 3D0H | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.695 |
| 3D0H | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.854 |
| 3D0H | A_LYS_541 | NZ | A_GLU_435 | OE2 | 3.545 |
| 3D0H | B_LYS_541 | NZ | B_GLU_430 | OE2 | 3.335 |
| 3D0I | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.081 |
| 3D0I | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.768 |
| 3D0I | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.991 |
| 3SCI | A_LYS_541 | NZ | A_GLU_430 | OE1 | 3.694 |
| 3SCI | A_LYS_541 | NZ | A_GLU_430 | OE2 | 2.736 |
| 3SCJ | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.913 |
| 3SCK | A_LYS_541 | NZ | A_GLU_430 | OE2 | 2.691 |
| 3SCL | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.746 |
| 3SCL | A_LYS_541 | NZ | A_GLU_435 | OE1 | 3.042 |
| 3SCL | A_LYS_541 | NZ | A_GLU_435 | OE2 | 2.897 |
| 3SCL | B_LYS_541 | NZ | B_GLU_430 | OE1 | 3.842 |
| 3SCL | B_LYS_541 | NZ | B_GLU_430 | OE2 | 2.913 |

Table 110: LYS541-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | F_LYS_439 | NZ | F_ASP_480 | OD1 | 3.696 |
| 2DD8 | S_LYS_439 | NZ | S_ASP_480 | OD1 | 3.148 |
| 2GHW | A_LYS_439 | NZ | A_ASP_480 | OD2 | 3.192 |
| 2GHW | C_LYS_439 | NZ | C_ASP_480 | OD1 | 3.911 |
| 2GHW | C_LYS_439 | NZ | C_ASP_480 | OD2 | 3.110 |
| 3BGF | S_LYS_439 | NZ | S_ASP_480 | OD1 | 3.797 |
| 3BGF | S_LYS_439 | NZ | A_ASP_480 | OD2 | 3.161 |
| 3BGF | A_LYS_439 | NZ | S_ASP_480 | OD2 | 2.520 |
| 3BGF | A_LYS_439 | NZ | A_ASP_480 | OD1 | 3.180 |
| 3SCI | F_LYS_439 | NZ | F_ASP_480 | OD2 | 3.783 |
| 3SCL | F_LYS_439 | NZ | F_ASP_480 | OD1 | 2.927 |

Table 111: LYS439-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | F_LYS_439 | NZ | F_ASP_480 | OD1 | 3.696 |
| 2DD8 | S_LYS_439 | NZ | S_ASP_480 | OD1 | 3.148 |
| 2GHW | A_LYS_439 | NZ | A_ASP_480 | OD2 | 3.192 |
| 2GHW | B_ARG_162 | NH1 | A_ASP_480 | OD1 | 3.081 |
| 2GHW | C_LYS_439 | NZ | C_ASP_480 | OD1 | 3.911 |
| 2GHW | C_LYS_439 | NZ | C_ASP_480 | OD2 | 3.110 |
| 2GHW | D_ARG_162 | NH2 | C_ASP_480 | OD1 | 3.626 |
| 3BGF | S_LYS_439 | NZ | S_ASP_480 | OD1 | 3.797 |
| 3BGF | S_LYS_439 | NZ | A_ASP_480 | OD2 | 3.161 |
| 3BGF | A_LYS_439 | NZ | S_ASP_480 | OD2 | 2.520 |
| 3BGF | A_LYS_439 | NZ | A_ASP_480 | OD1 | 3.180 |
| 3SCI | F_LYS_439 | NZ | F_ASP_480 | OD2 | 3.783 |
| 3SCL | F_LYS_439 | NZ | F_ASP_480 | OD1 | 2.927 |

Table 112: ASP480-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_ARG_38 | NH1 | H_ASP_86 | OD1 | 2.908 |
| 2DD8 | H_ARG_38 | NH2 | H_GLU_46 | OE1 | 3.751 |
| 2DD8 | H_ARG_38 | NH2 | H_ASP_86 | OD1 | 3.769 |
| 2GHW | B_ARG_38 | NH1 | B_GLU_89 | OE1 | 3.674 |
| 2GHW | B_ARG_38 | NH1 | B_ASP_90 | OD1 | 3.164 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_46 | OE1 | 3.155 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_46 | OE2 | 3.798 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_89 | OE1 | 3.206 |
| 2GHW | D_ARG_38 | NH1 | D_ASP_90 | OD1 | 3.162 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_46 | OE1 | 3.538 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_46 | OE2 | 3.668 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_89 | OE1 | 3.329 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_89 | OE2 | 2.864 |
| 5X4S | A_ARG_38 | NH1 | A_GLU_184 | OE1 | 3.171 |
| 5X4S | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 3.034 |
| 5X58 | A_ARG_38 | NH1 | A_GLU_184 | OE1 | 3.772 |
| 5X58 | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 2.356 |
| 5X58 | B_ARG_38 | NH1 | B_GLU_184 | OE1 | 3.772 |
| 5X58 | B_ARG_38 | NH1 | B_GLU_184 | OE2 | 2.356 |
| 5X58 | C_ARG_38 | NH1 | C_GLU_184 | OE1 | 3.772 |
| 5X58 | C_ARG_38 | NH1 | C_GLU_184 | OE2 | 2.356 |
| 5X5B | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 2.409 |
| 5X5B | B_ARG_38 | NH1 | B_GLU_184 | OE2 | 2.521 |
| 5X5B | C_ARG_38 | NH1 | C_GLU_184 | OE2 | 2.521 |

Table 113: ARG38-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X4S | A_ARG_38 | NH1 | A_GLU_184 | OE1 | 3.171 |
| 5X4S | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 3.034 |
| 5X58 | A_ARG_38 | NH1 | A_GLU_184 | OE1 | 3.772 |
| 5X58 | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 2.356 |
| 5X58 | B_ARG_38 | NH1 | B_GLU_184 | OE1 | 3.772 |
| 5X58 | B_ARG_38 | NH1 | B_GLU_184 | OE2 | 2.356 |
| 5X58 | C_ARG_38 | NH1 | C_GLU_184 | OE1 | 3.772 |
| 5X58 | C_ARG_38 | NH1 | C_GLU_184 | OE2 | 2.356 |
| 5X5B | A_ARG_38 | NH1 | A_GLU_184 | OE2 | 2.409 |
| 5X5B | B_ARG_38 | NH1 | B_GLU_184 | OE2 | 2.521 |
| 5X5B | C_ARG_38 | NH1 | C_GLU_184 | OE2 | 2.521 |

Table 114: GLU184-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0G | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.965 |
| 3D0H | A_ARG_514 | NH1 | A_GLU_398 | OE1 | 3.428 |
| 3D0H | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.126 |
| 3D0H | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.895 |
| 3D0I | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 2.781 |
| 3D0I | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.844 |
| 3SCI | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.392 |
| 3SCJ | A_ARG_514 | NH2 | A_GLU_398 | OE2 | 3.456 |
| 3SCK | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.751 |
| 3SCK | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.744 |
| 3SCL | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.417 |

Table 115: ARG514-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0G | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.965 |
| 3D0H | A_ARG_514 | NH1 | A_GLU_398 | OE1 | 3.428 |
| 3D0H | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.126 |
| 3D0H | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.895 |
| 3D0I | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 2.781 |
| 3D0I | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.844 |
| 3SCI | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.392 |
| 3SCJ | A_ARG_514 | NH2 | A_GLU_398 | OE2 | 3.456 |
| 3SCK | A_ARG_514 | NH2 | A_GLU_398 | OE1 | 3.751 |
| 3SCK | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.744 |
| 3SCL | B_ARG_514 | NH2 | B_GLU_398 | OE1 | 3.417 |

Table 116: GLU398-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.268 |
| 2AJF | F_ARG_453 | NH2 | F_GLU_341 | OE2 | 3.749 |
| 3D0G | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.460 |
| 3D0H | E_ARG_453 | NH2 | E_GLU_341 | OE1 | 2.602 |
| 3D0H | F_ARG_453 | NH2 | F_GLU_341 | OE1 | 3.737 |
| 3D0I | E_ARG_453 | NH2 | E_GLU_341 | OE1 | 3.930 |
| 3D0I | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.544 |
| 3D0I | F_ARG_453 | NH2 | F_GLU_341 | OE1 | 3.930 |
| 3SCI | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.520 |
| 3SCJ | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.893 |
| 3SCL | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.287 |

Table 117: ARG453-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.268 |
| 2AJF | F_ARG_453 | NH2 | F_GLU_341 | OE2 | 3.749 |
| 3D0G | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.460 |
| 3D0H | E_ARG_453 | NH2 | E_GLU_341 | OE1 | 2.602 |
| 3D0H | F_ARG_453 | NH2 | F_GLU_341 | OE1 | 3.737 |
| 3D0I | E_ARG_453 | NH2 | E_GLU_341 | OE1 | 3.930 |
| 3D0I | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.544 |
| 3D0I | F_ARG_453 | NH2 | F_GLU_341 | OE1 | 3.930 |
| 3SCI | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.520 |
| 3SCJ | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.893 |
| 3SCL | E_ARG_453 | NH2 | E_GLU_341 | OE2 | 3.287 |

Table 118: GLU341-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | B_LYS_26 | NZ | B_GLU_22 | OE1 | 3.456 |
| 3D0G | A_LYS_26 | NZ | A_GLU_23 | OE1 | 2.776 |
| 3D0H | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.654 |
| 3D0H | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.272 |
| 3SCI | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.333 |
| 3SCI | A_LYS_26 | NZ | A_GLU_23 | OE2 | 3.691 |
| 3SCI | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.897 |
| 3SCI | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.718 |
| 3SCJ | A_LYS_26 | NZ | A_GLU_23 | OE2 | 3.680 |
| 3SCJ | B_LYS_26 | NZ | B_GLU_22 | OE1 | 3.695 |
| 3SCJ | B_LYS_26 | NZ | B_GLU_23 | OE2 | 3.612 |
| 3SCK | A_LYS_26 | NZ | A_GLU_22 | OE2 | 3.783 |
| 3SCK | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.738 |
| 3SCK | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.690 |
| 3SCK | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.836 |
| 3SCL | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.223 |

Table 119: LYS26-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.763 |
| 2AJF | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.712 |
| 2AJF | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.992 |
| 2AJF | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.314 |
| 2AJF | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 2.787 |
| 2GHW | B_LYS_235 | NZ | B_GLU_237 | OE2 | 3.402 |
| 2GHW | D_LYS_235 | NZ | D_GLU_237 | OE2 | 3.600 |
| 3D0G | A_LYS_26 | NZ | A_GLU_23 | OE1 | 2.776 |
| 3D0G | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.326 |
| 3D0G | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.150 |
| 3D0G | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.383 |
| 3D0H | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.654 |
| 3D0H | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.748 |
| 3D0H | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.272 |
| 3D0H | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.307 |
| 3D0H | B_ARG_582 | NH2 | B_GLU_232 | OE2 | 3.592 |
| 3D0I | A_LYS_234 | NZ | A_GLU_231 | OE2 | 2.886 |
| 3D0I | B_LYS_234 | NZ | B_GLU_231 | OE2 | 2.885 |
| 3D0I | B_ARG_582 | NH2 | B_GLU_232 | OE2 | 3.204 |
| 3SCI | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.333 |
| 3SCI | A_LYS_26 | NZ | A_GLU_23 | OE2 | 3.691 |
| 3SCI | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.792 |
| 3SCI | A_ARG_582 | NH1 | A_GLU_232 | OE2 | 2.598 |
| 3SCI | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.718 |
| 3SCI | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.452 |
| 3SCI | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.808 |
| 3SCI | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.013 |
| 3SCI | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 3.819 |
| 3SCJ | A_LYS_26 | NZ | A_GLU_23 | OE2 | 3.680 |
| 3SCJ | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.594 |
| 3SCJ | A_ARG_582 | NH1 | A_GLU_232 | OE2 | 3.625 |
| 3SCJ | B_LYS_26 | NZ | B_GLU_23 | OE2 | 3.612 |
| 3SCJ | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.724 |
| 3SCJ | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.270 |
| 3SCJ | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 2.624 |
| 3SCK | A_LYS_26 | NZ | A_GLU_23 | OE1 | 3.738 |
| 3SCK | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.847 |
| 3SCK | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.343 |
| 3SCK | B_LYS_26 | NZ | B_GLU_23 | OE1 | 3.836 |
| 3SCK | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.845 |
| 3SCK | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.278 |
| 3SCL | A_LYS_234 | NZ | A_GLU_231 | OE1 | 3.556 |
| 3SCL | A_LYS_234 | NZ | A_GLU_231 | OE2 | 3.191 |
| 3SCL | B_LYS_234 | NZ | B_GLU_231 | OE1 | 3.673 |
| 3SCL | B_LYS_234 | NZ | B_GLU_231 | OE2 | 3.548 |

Table 120: GLU23-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.992 |
| 3D0G | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.966 |
| 3SCI | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.865 |
| 3SCI | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.800 |
| 3SCJ | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.774 |
| 3SCJ | B_HIS_374 | NE2 | B_GLU_375 | OE2 | 3.983 |
| 3SCJ | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.709 |
| 3SCK | A_HIS_374 | NE2 | A_GLU_375 | OE1 | 3.653 |
| 3SCK | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.518 |
| 3SCK | B_HIS_374 | NE2 | B_GLU_375 | OE1 | 3.559 |
| 3SCK | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.390 |
| 3SCL | A_HIS_378 | NE2 | A_GLU_375 | OE1 | 3.936 |
| 3SCL | B_HIS_374 | NE2 | B_GLU_375 | OE1 | 3.783 |
| 3SCL | B_HIS_378 | NE2 | B_GLU_375 | OE1 | 3.495 |

Table 121: GLU375-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0G | A_LYS_476 | NZ | A_GLU_479 | OE1 | 2.526 |
| 3D0G | A_LYS_476 | NZ | A_GLU_479 | OE2 | 3.323 |
| 3D0H | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.676 |
| 3D0H | A_LYS_476 | NZ | A_GLU_479 | OE2 | 2.624 |
| 3D0H | B_LYS_476 | NZ | B_GLU_479 | OE1 | 3.337 |
| 3D0I | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.529 |
| 3D0I | A_LYS_476 | NZ | A_GLU_479 | OE2 | 2.537 |
| 3SCJ | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.256 |
| 3SCJ | A_LYS_476 | NZ | A_GLU_479 | OE2 | 3.692 |
| 3SCK | B_LYS_476 | NZ | B_GLU_479 | OE1 | 2.732 |

Table 122: LYS476-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | B_LYS_475 | NZ | B_GLU_479 | OE2 | 3.697 |
| 3D0G | A_LYS_476 | NZ | A_GLU_479 | OE1 | 2.526 |
| 3D0G | A_LYS_476 | NZ | A_GLU_479 | OE2 | 3.323 |
| 3D0G | B_LYS_475 | NZ | B_GLU_479 | OE2 | 3.791 |
| 3D0H | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.676 |
| 3D0H | A_LYS_476 | NZ | A_GLU_479 | OE2 | 2.624 |
| 3D0H | B_LYS_476 | NZ | B_GLU_479 | OE1 | 3.337 |
| 3D0I | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.529 |
| 3D0I | A_LYS_476 | NZ | A_GLU_479 | OE2 | 2.537 |
| 3SCI | B_LYS_475 | NZ | B_GLU_479 | OE1 | 3.195 |
| 3SCI | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.712 |
| 3SCJ | A_LYS_476 | NZ | A_GLU_479 | OE1 | 3.256 |
| 3SCJ | A_LYS_476 | NZ | A_GLU_479 | OE2 | 3.692 |
| 3SCJ | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.513 |
| 3SCK | B_LYS_476 | NZ | B_GLU_479 | OE1 | 2.732 |
| 3SCL | B_LYS_475 | NZ | B_GLU_479 | OE1 | 3.474 |
| 3SCL | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.893 |

Table 123: GLU479-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0G | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.777 |
| 3D0H | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.974 |
| 3D0H | B_LYS_470 | NZ | B_GLU_181 | OE1 | 2.767 |
| 3D0H | B_LYS_470 | NZ | B_GLU_181 | OE2 | 3.182 |
| 3D0I | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.269 |
| 3D0I | B_LYS_470 | NZ | B_GLU_181 | OE1 | 2.879 |
| 3SCI | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.703 |
| 3SCI | B_LYS_470 | NZ | B_GLU_181 | OE1 | 3.845 |
| 3SCK | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.825 |
| 3SCL | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.158 |

Table 124: LYS470-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_177 | NH1 | A_GLU_181 | OE2 | 3.241 |
| 3D0G | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.777 |
| 3D0G | B_ARG_177 | NH1 | B_GLU_181 | OE2 | 3.376 |
| 3D0H | A_ARG_177 | NH1 | A_GLU_181 | OE1 | 3.849 |
| 3D0H | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.974 |
| 3D0H | B_ARG_177 | NH1 | B_GLU_181 | OE1 | 3.536 |
| 3D0H | B_LYS_470 | NZ | B_GLU_181 | OE1 | 2.767 |
| 3D0H | B_LYS_470 | NZ | B_GLU_181 | OE2 | 3.182 |
| 3D0I | A_ARG_177 | NH1 | A_GLU_181 | OE2 | 3.919 |
| 3D0I | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.269 |
| 3D0I | B_ARG_177 | NH1 | B_GLU_181 | OE2 | 3.586 |
| 3D0I | B_LYS_470 | NZ | B_GLU_181 | OE1 | 2.879 |
| 3SCI | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.703 |
| 3SCI | B_LYS_470 | NZ | B_GLU_181 | OE1 | 3.845 |
| 3SCK | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.825 |
| 3SCL | A_LYS_470 | NZ | A_GLU_181 | OE1 | 3.158 |

Table 125: GLU181-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.856 |
| 3D0G | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.707 |
| 3D0I | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.963 |
| 3SCI | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.649 |
| 3SCI | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.168 |
| 3SCJ | A_LYS_288 | NZ | A_GLU_433 | OE1 | 3.920 |
| 3SCJ | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.087 |
| 3SCK | A_LYS_288 | NZ | A_GLU_433 | OE2 | 3.653 |
| 3SCK | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.658 |
| 3SCL | B_LYS_288 | NZ | B_GLU_433 | OE1 | 3.412 |

Table 126: GLU433-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0G | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.737 |
| 3D0G | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.363 |
| 3D0I | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.185 |
| 3D0I | B_LYS_313 | NZ | B_GLU_310 | OE2 | 2.999 |
| 3SCI | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.555 |
| 3SCI | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.303 |
| 3SCJ | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.597 |
| 3SCJ | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.681 |
| 3SCK | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.272 |
| 3SCK | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.682 |

Table 127: LYS313-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.314 |
| 2AJF | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 2.787 |
| 3D0H | B_ARG_582 | NH2 | B_GLU_232 | OE2 | 3.592 |
| 3D0I | B_ARG_582 | NH2 | B_GLU_232 | OE2 | 3.204 |
| 3SCI | A_ARG_582 | NH1 | A_GLU_232 | OE2 | 2.598 |
| 3SCI | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.013 |
| 3SCI | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 3.819 |
| 3SCJ | A_ARG_582 | NH1 | A_GLU_232 | OE2 | 3.625 |
| 3SCJ | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.270 |
| 3SCJ | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 2.624 |
| 3SCK | A_ARG_582 | NH2 | A_GLU_527 | OE1 | 3.214 |

Table 128: ARG582-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.314 |
| 2AJF | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 2.787 |
| 3D0H | B_ARG_582 | NH2 | B_GLU_232 | OE2 | 3.592 |
| 3D0I | B_ARG_582 | NH2 | B_GLU_232 | OE2 | 3.204 |
| 3SCI | A_ARG_582 | NH1 | A_GLU_232 | OE2 | 2.598 |
| 3SCI | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.013 |
| 3SCI | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 3.819 |
| 3SCJ | A_ARG_582 | NH1 | A_GLU_232 | OE2 | 3.625 |
| 3SCJ | B_ARG_582 | NH1 | B_GLU_232 | OE1 | 3.270 |
| 3SCJ | B_ARG_582 | NH1 | B_GLU_232 | OE2 | 2.624 |

Table 129: GLU232-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0G | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.955 |
| 3D0G | B_LYS_541 | NZ | B_GLU_430 | OE2 | 2.944 |
| 3D0H | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.376 |
| 3D0H | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.695 |
| 3D0H | B_LYS_419 | NZ | B_GLU_430 | OE1 | 3.848 |
| 3D0H | B_LYS_541 | NZ | B_GLU_430 | OE2 | 3.335 |
| 3D0I | A_LYS_419 | NZ | A_GLU_430 | OE1 | 3.095 |
| 3D0I | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.081 |
| 3D0I | B_LYS_419 | NZ | B_GLU_430 | OE1 | 3.547 |
| 3SCI | A_LYS_541 | NZ | A_GLU_430 | OE1 | 3.694 |
| 3SCI | A_LYS_541 | NZ | A_GLU_430 | OE2 | 2.736 |
| 3SCK | A_LYS_541 | NZ | A_GLU_430 | OE2 | 2.691 |
| 3SCL | A_LYS_541 | NZ | A_GLU_430 | OE2 | 3.746 |
| 3SCL | B_LYS_541 | NZ | B_GLU_430 | OE1 | 3.842 |
| 3SCL | B_LYS_541 | NZ | B_GLU_430 | OE2 | 2.913 |

Table 130: GLU430-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.286 |
| 2AJF | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.910 |
| 3BGF | A_LYS_390 | NZ | A_ASP_393 | OD1 | 3.583 |
| 3BGF | A_LYS_390 | NZ | A_ASP_393 | OD2 | 3.966 |
| 3D0G | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.591 |
| 3D0H | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.987 |
| 3SCJ | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.607 |
| 3SCJ | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.703 |
| 3SCJ | F_LYS_390 | NZ | F_ASP_393 | OD2 | 3.787 |
| 3SCK | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.985 |

Table 131: LYS390-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.286 |
| 2AJF | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.910 |
| 3BGF | A_LYS_390 | NZ | A_ASP_393 | OD1 | 3.583 |
| 3BGF | A_LYS_390 | NZ | A_ASP_393 | OD2 | 3.966 |
| 3D0G | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.591 |
| 3D0H | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.987 |
| 3SCJ | E_LYS_390 | NZ | E_ASP_393 | OD1 | 3.607 |
| 3SCJ | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.703 |
| 3SCJ | F_LYS_390 | NZ | F_ASP_393 | OD2 | 3.787 |
| 3SCK | E_LYS_390 | NZ | E_ASP_393 | OD2 | 3.985 |

Table 132: ASP393-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X4S | A_LYS_188 | NZ | A_ASP_57 | OD1 | 3.514 |
| 5X58 | A_LYS_188 | NZ | A_ASP_57 | OD1 | 3.617 |
| 5X58 | A_LYS_188 | NZ | A_ASP_57 | OD2 | 3.069 |
| 5X58 | B_LYS_188 | NZ | B_ASP_57 | OD1 | 3.617 |
| 5X58 | B_LYS_188 | NZ | B_ASP_57 | OD2 | 3.068 |
| 5X58 | C_LYS_188 | NZ | C_ASP_57 | OD1 | 3.616 |
| 5X58 | C_LYS_188 | NZ | C_ASP_57 | OD2 | 3.068 |
| 5X5B | B_LYS_188 | NZ | B_ASP_57 | OD2 | 3.359 |
| 5X5B | C_LYS_188 | NZ | C_ASP_57 | OD2 | 3.359 |

Table 133: LYS188-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X4S | A_LYS_188 | NZ | A_ASP_57 | OD1 | 3.514 |
| 5X58 | A_LYS_188 | NZ | A_ASP_57 | OD1 | 3.617 |
| 5X58 | A_LYS_188 | NZ | A_ASP_57 | OD2 | 3.069 |
| 5X58 | B_LYS_188 | NZ | B_ASP_57 | OD1 | 3.617 |
| 5X58 | B_LYS_188 | NZ | B_ASP_57 | OD2 | 3.068 |
| 5X58 | C_LYS_188 | NZ | C_ASP_57 | OD1 | 3.616 |
| 5X58 | C_LYS_188 | NZ | C_ASP_57 | OD2 | 3.068 |
| 5X5B | B_LYS_188 | NZ | B_ASP_57 | OD2 | 3.359 |
| 5X5B | B_LYS_543 | NZ | B_ASP_572 | OD2 | 3.842 |
| 5X5B | C_LYS_188 | NZ | C_ASP_57 | OD2 | 3.359 |
| 5X5B | C_LYS_543 | NZ | C_ASP_572 | OD2 | 3.841 |

Table 134: ASP57-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | L_ARG_61 | NH1 | L_ASP_82 | OD1 | 3.795 |
| 2DD8 | L_ARG_61 | NH1 | L_ASP_82 | OD2 | 2.711 |
| 2DD8 | L_ARG_61 | NH2 | L_ASP_82 | OD1 | 2.938 |
| 2DD8 | L_ARG_61 | NH2 | L_ASP_82 | OD2 | 3.305 |
| 3BGF | L_ARG_61 | NH1 | L_GLU_79 | OE1 | 3.984 |
| 3BGF | L_ARG_61 | NH1 | L_GLU_79 | OE2 | 3.405 |
| 3BGF | L_ARG_61 | NH2 | L_ASP_82 | OD1 | 2.650 |
| 3BGF | L_ARG_61 | NH2 | L_ASP_82 | OD2 | 2.907 |
| 3BGF | C_ARG_61 | NH1 | C_GLU_79 | OE1 | 3.352 |
| 3BGF | C_ARG_61 | NH1 | C_GLU_79 | OE2 | 3.278 |
| 3BGF | C_ARG_61 | NH2 | C_GLU_81 | OE2 | 3.045 |
| 3BGF | C_ARG_61 | NH2 | C_ASP_82 | OD1 | 2.379 |
| 3BGF | C_ARG_61 | NH2 | C_ASP_82 | OD2 | 2.905 |

Table 135: ARG61-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | L_ARG_61 | NH1 | L_ASP_82 | OD1 | 3.795 |
| 2DD8 | L_ARG_61 | NH1 | L_ASP_82 | OD2 | 2.711 |
| 2DD8 | L_ARG_61 | NH2 | L_ASP_82 | OD1 | 2.938 |
| 2DD8 | L_ARG_61 | NH2 | L_ASP_82 | OD2 | 3.305 |
| 3BGF | L_ARG_61 | NH2 | L_ASP_82 | OD1 | 2.650 |
| 3BGF | L_ARG_61 | NH2 | L_ASP_82 | OD2 | 2.907 |
| 3BGF | C_ARG_61 | NH2 | C_ASP_82 | OD1 | 2.379 |
| 3BGF | C_ARG_61 | NH2 | C_ASP_82 | OD2 | 2.905 |

Table 136: ASP82-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_620 | NH1 | A_ASP_277 | OD2 | 3.189 |
| 5X58 | B_ARG_620 | NH1 | B_ASP_277 | OD2 | 3.189 |
| 5X58 | C_ARG_620 | NH1 | C_ASP_277 | OD2 | 3.189 |
| 5X5B | A_ARG_620 | NH1 | A_ASP_277 | OD2 | 3.104 |
| 5X5B | B_ARG_620 | NH1 | B_ASP_277 | OD1 | 3.439 |
| 5X5B | B_ARG_620 | NH1 | B_ASP_277 | OD2 | 2.450 |
| 5X5B | C_ARG_620 | NH1 | C_ASP_277 | OD1 | 3.439 |
| 5X5B | C_ARG_620 | NH1 | C_ASP_277 | OD2 | 2.450 |

Table 137: ARG620-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_620 | NH1 | A_ASP_277 | OD2 | 3.189 |
| 5X58 | B_ARG_620 | NH1 | B_ASP_277 | OD2 | 3.189 |
| 5X58 | C_ARG_620 | NH1 | C_ASP_277 | OD2 | 3.189 |
| 5X5B | A_ARG_620 | NH1 | A_ASP_277 | OD2 | 3.104 |
| 5X5B | B_ARG_620 | NH1 | B_ASP_277 | OD1 | 3.439 |
| 5X5B | B_ARG_620 | NH1 | B_ASP_277 | OD2 | 2.450 |
| 5X5B | C_ARG_620 | NH1 | C_ASP_277 | OD1 | 3.439 |
| 5X5B | C_ARG_620 | NH1 | C_ASP_277 | OD2 | 2.450 |

Table 138: ASP277-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X4S | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 2.290 |
| 5X58 | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 3.231 |
| 5X58 | B_HIS_33 | ND1 | B_ASP_208 | OD1 | 3.230 |
| 5X58 | C_HIS_33 | ND1 | C_ASP_208 | OD1 | 3.232 |
| 5X5B | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 3.598 |
| 5X5B | B_HIS_33 | ND1 | B_ASP_208 | OD1 | 2.655 |
| 5X5B | C_HIS_33 | ND1 | C_ASP_208 | OD1 | 2.654 |

Table 139: HIS33-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X4S | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 2.290 |
| 5X58 | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 3.231 |
| 5X58 | B_HIS_33 | ND1 | B_ASP_208 | OD1 | 3.230 |
| 5X58 | C_HIS_33 | ND1 | C_ASP_208 | OD1 | 3.232 |
| 5X5B | A_HIS_33 | ND1 | A_ASP_208 | OD1 | 3.598 |
| 5X5B | B_HIS_33 | ND1 | B_ASP_208 | OD1 | 2.655 |
| 5X5B | C_HIS_33 | ND1 | C_ASP_208 | OD1 | 2.654 |

Table 140: ASP208-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_67 | NH1 | B_ASP_90 | OD1 | 3.382 |
| 2GHW | B_ARG_67 | NH1 | B_ASP_90 | OD2 | 2.930 |
| 2GHW | B_ARG_67 | NH2 | B_GLU_89 | OE1 | 3.863 |
| 2GHW | B_ARG_67 | NH2 | B_GLU_89 | OE2 | 3.548 |
| 2GHW | B_ARG_67 | NH2 | B_ASP_90 | OD1 | 3.270 |
| 2GHW | B_ARG_67 | NH2 | B_ASP_90 | OD2 | 3.745 |
| 2GHW | D_ARG_67 | NH1 | D_ASP_90 | OD2 | 3.105 |
| 2GHW | D_ARG_67 | NH2 | D_GLU_89 | OE1 | 3.576 |
| 2GHW | D_ARG_67 | NH2 | D_ASP_90 | OD1 | 3.163 |
| 2GHW | D_ARG_67 | NH2 | D_ASP_90 | OD2 | 3.377 |

Table 141: ARG67-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_38 | NH1 | B_ASP_90 | OD1 | 3.164 |
| 2GHW | B_ARG_67 | NH1 | B_ASP_90 | OD1 | 3.382 |
| 2GHW | B_ARG_67 | NH1 | B_ASP_90 | OD2 | 2.930 |
| 2GHW | B_ARG_67 | NH2 | B_ASP_90 | OD1 | 3.270 |
| 2GHW | B_ARG_67 | NH2 | B_ASP_90 | OD2 | 3.745 |
| 2GHW | D_ARG_38 | NH1 | D_ASP_90 | OD1 | 3.162 |
| 2GHW | D_ARG_67 | NH1 | D_ASP_90 | OD2 | 3.105 |
| 2GHW | D_ARG_67 | NH2 | D_ASP_90 | OD1 | 3.163 |
| 2GHW | D_ARG_67 | NH2 | D_ASP_90 | OD2 | 3.377 |

Table 142: ASP90-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | B_LYS_475 | NZ | B_GLU_479 | OE2 | 3.697 |
| 3D0G | B_LYS_475 | NZ | B_GLU_479 | OE2 | 3.791 |
| 3SCI | B_LYS_475 | NZ | B_GLU_479 | OE1 | 3.195 |
| 3SCI | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.712 |
| 3SCJ | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.513 |
| 3SCL | B_LYS_475 | NZ | B_GLU_479 | OE1 | 3.474 |
| 3SCL | B_LYS_475 | NZ | B_GLU_479 | OE2 | 2.893 |

Table 143: LYS475-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_LYS_62 | NZ | H_GLU_46 | OE1 | 3.535 |
| 2DD8 | H_LYS_62 | NZ | H_GLU_46 | OE2 | 3.348 |
| 3BGF | H_LYS_62 | NZ | H_GLU_46 | OE1 | 2.635 |
| 3BGF | H_LYS_62 | NZ | H_GLU_46 | OE2 | 3.712 |
| 3BGF | B_LYS_62 | NZ | B_GLU_46 | OE1 | 2.547 |
| 3BGF | B_LYS_62 | NZ | B_GLU_46 | OE2 | 3.280 |

Table 144: LYS62-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.567 |
| 2DD8 | H_ARG_38 | NH2 | H_GLU_46 | OE1 | 3.751 |
| 2DD8 | H_LYS_62 | NZ | H_GLU_46 | OE1 | 3.535 |
| 2DD8 | H_LYS_62 | NZ | H_GLU_46 | OE2 | 3.348 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_46 | OE1 | 3.155 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_46 | OE2 | 3.798 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_46 | OE1 | 3.538 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_46 | OE2 | 3.668 |
| 3BGF | H_LYS_62 | NZ | H_GLU_46 | OE1 | 2.635 |
| 3BGF | H_LYS_62 | NZ | H_GLU_46 | OE2 | 3.712 |
| 3BGF | B_LYS_62 | NZ | B_GLU_46 | OE1 | 2.547 |
| 3BGF | B_LYS_62 | NZ | B_GLU_46 | OE2 | 3.280 |
| 3D0G | A_LYS_465 | NZ | A_GLU_467 | OE1 | 2.701 |
| 3D0G | B_LYS_465 | NZ | B_GLU_467 | OE2 | 3.564 |
| 3D0H | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.261 |
| 3SCJ | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.819 |
| 3SCL | B_LYS_465 | NZ | B_GLU_467 | OE2 | 2.784 |

Table 145: GLU46-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_458 | NZ | A_GLU_227 | OE1 | 3.613 |
| 2AJF | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.040 |
| 2AJF | B_LYS_26 | NZ | B_GLU_22 | OE1 | 3.456 |
| 3D0G | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.595 |
| 3D0G | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.654 |
| 3D0H | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.176 |
| 3D0I | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.805 |
| 3SCI | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.642 |
| 3SCI | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.897 |
| 3SCI | B_LYS_458 | NZ | B_GLU_227 | OE2 | 2.656 |
| 3SCJ | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.761 |
| 3SCJ | B_LYS_26 | NZ | B_GLU_22 | OE1 | 3.695 |
| 3SCJ | B_LYS_458 | NZ | B_GLU_227 | OE2 | 2.602 |
| 3SCK | A_LYS_26 | NZ | A_GLU_22 | OE2 | 3.783 |
| 3SCK | A_LYS_458 | NZ | A_GLU_227 | OE2 | 2.716 |
| 3SCK | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.690 |
| 3SCK | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.897 |
| 3SCL | A_LYS_458 | NZ | A_GLU_227 | OE2 | 3.685 |
| 3SCL | B_LYS_26 | NZ | B_GLU_22 | OE2 | 3.223 |
| 3SCL | B_LYS_458 | NZ | B_GLU_227 | OE2 | 3.400 |

Table 146: GLU22-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0I | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 3.324 |
| 3D0I | E_ARG_479 | NH2 | A_GLU_35 | OE1 | 2.730 |
| 3D0I | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 3.405 |
| 3D0I | F_ARG_479 | NH2 | B_GLU_35 | OE1 | 2.961 |
| 3SCJ | E_ARG_479 | NH2 | A_ASP_38 | OD2 | 2.575 |
| 3SCJ | F_ARG_479 | NH2 | B_ASP_38 | OD2 | 2.718 |
| 3SCK | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 2.498 |
| 3SCK | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 2.750 |

Table 147: ARG479-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_31 | NZ | A_GLU_35 | OE1 | 3.992 |
| 3D0H | E_LYS_479 | NZ | A_GLU_35 | OE1 | 3.397 |
| 3D0H | F_LYS_479 | NZ | B_GLU_35 | OE1 | 3.369 |
| 3D0I | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 3.324 |
| 3D0I | E_ARG_479 | NH2 | A_GLU_35 | OE1 | 2.730 |
| 3D0I | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 3.405 |
| 3D0I | F_ARG_479 | NH2 | B_GLU_35 | OE1 | 2.961 |
| 3SCI | B_LYS_31 | NZ | B_GLU_35 | OE1 | 3.358 |
| 3SCJ | B_LYS_31 | NZ | B_GLU_35 | OE2 | 3.882 |
| 3SCK | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 2.498 |
| 3SCK | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 2.750 |

Table 148: GLU35-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_HIS_1046 | NE2 | A_GLU_707 | OE1 | 2.723 |
| 5X58 | B_HIS_1046 | NE2 | B_GLU_707 | OE1 | 2.724 |
| 5X58 | C_HIS_1046 | NE2 | C_GLU_707 | OE1 | 2.724 |
| 5X5B | A_HIS_1046 | NE2 | A_GLU_707 | OE1 | 2.555 |
| 5X5B | B_HIS_1046 | NE2 | B_GLU_707 | OE1 | 2.640 |
| 5X5B | C_HIS_1046 | NE2 | C_GLU_707 | OE1 | 2.640 |

Table 149: HIS1046-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.567 |
| 2AJF | E_LYS_465 | NZ | E_ASP_463 | OD2 | 3.801 |
| 3D0G | A_LYS_465 | NZ | A_GLU_467 | OE1 | 2.701 |
| 3D0G | B_LYS_465 | NZ | B_GLU_467 | OE2 | 3.564 |
| 3D0G | F_LYS_465 | NZ | F_ASP_463 | OD1 | 3.077 |
| 3D0H | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.261 |
| 3D0I | A_LYS_465 | NZ | A_GLU_197 | OE2 | 3.918 |
| 3D0I | E_LYS_465 | NZ | E_ASP_463 | OD2 | 3.638 |
| 3D0I | F_LYS_465 | NZ | F_ASP_463 | OD2 | 3.412 |
| 3SCI | B_LYS_465 | NZ | B_GLU_197 | OE2 | 3.379 |
| 3SCJ | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.819 |
| 3SCJ | B_LYS_465 | NZ | B_GLU_197 | OE2 | 3.351 |
| 3SCJ | F_LYS_465 | NZ | F_ASP_463 | OD2 | 3.932 |
| 3SCK | A_LYS_465 | NZ | A_GLU_197 | OE2 | 3.131 |
| 3SCK | A_LYS_465 | NZ | A_ASP_198 | OD1 | 3.632 |
| 3SCL | B_LYS_465 | NZ | B_GLU_467 | OE2 | 2.784 |

Table 150: LYS465-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.567 |
| 3D0G | A_LYS_465 | NZ | A_GLU_467 | OE1 | 2.701 |
| 3D0G | B_LYS_465 | NZ | B_GLU_467 | OE2 | 3.564 |
| 3D0H | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.261 |
| 3SCJ | A_LYS_465 | NZ | A_GLU_467 | OE1 | 3.819 |
| 3SCL | B_LYS_465 | NZ | B_GLU_467 | OE2 | 2.784 |

Table 151: GLU467-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | S_LYS_411 | NZ | S_ASP_407 | OD1 | 2.884 |
| 3D0G | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.908 |
| 3D0H | E_LYS_411 | NZ | E_ASP_407 | OD1 | 3.493 |
| 3D0H | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.643 |
| 3D0I | E_LYS_411 | NZ | E_ASP_407 | OD1 | 3.525 |
| 3D0I | F_LYS_411 | NZ | F_ASP_407 | OD1 | 3.530 |

Table 152: LYS411-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_543 | NZ | A_ASP_560 | OD2 | 2.441 |
| 5X58 | B_LYS_543 | NZ | B_ASP_560 | OD2 | 2.442 |
| 5X58 | C_LYS_543 | NZ | C_ASP_560 | OD2 | 2.441 |
| 5X5B | A_LYS_543 | NZ | A_ASP_560 | OD2 | 3.771 |
| 5X5B | B_LYS_543 | NZ | B_ASP_560 | OD2 | 2.696 |
| 5X5B | B_LYS_543 | NZ | B_ASP_572 | OD2 | 3.842 |
| 5X5B | C_LYS_543 | NZ | C_ASP_560 | OD2 | 2.696 |
| 5X5B | C_LYS_543 | NZ | C_ASP_572 | OD2 | 3.841 |

Table 153: LYS543-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_543 | NZ | A_ASP_560 | OD2 | 2.441 |
| 5X58 | B_LYS_543 | NZ | B_ASP_560 | OD2 | 2.442 |
| 5X58 | C_LYS_543 | NZ | C_ASP_560 | OD2 | 2.441 |
| 5X5B | A_LYS_543 | NZ | A_ASP_560 | OD2 | 3.771 |
| 5X5B | B_LYS_543 | NZ | B_ASP_560 | OD2 | 2.696 |
| 5X5B | C_LYS_543 | NZ | C_ASP_560 | OD2 | 2.696 |

Table 154: ASP560-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_353 | NZ | A_ASP_38 | OD1 | 3.263 |
| 2AJF | A_HIS_401 | NE2 | A_ASP_382 | OD2 | 3.397 |
| 2AJF | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.748 |
| 2AJF | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 2.961 |
| 2AJF | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.004 |
| 2AJF | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.200 |
| 2AJF | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 2.772 |
| 2DD8 | S_ARG_342 | NH2 | S_ASP_385 | OD1 | 3.426 |
| 2DD8 | S_ARG_342 | NH2 | S_ASP_385 | OD2 | 2.961 |
| 2GHV | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.550 |
| 2GHV | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 2.981 |
| 2GHV | C_ARG_342 | NH2 | C_ASP_385 | OD1 | 3.469 |
| 2GHV | C_ARG_342 | NH2 | C_ASP_385 | OD2 | 2.877 |
| 2GHW | A_ARG_342 | NH2 | A_ASP_385 | OD1 | 3.548 |
| 2GHW | A_ARG_342 | NH2 | A_ASP_385 | OD2 | 3.167 |
| 2GHW | C_ARG_342 | NH2 | C_ASP_385 | OD1 | 3.626 |
| 2GHW | C_ARG_342 | NH2 | C_ASP_385 | OD2 | 3.156 |
| 3BGF | S_ARG_342 | NH2 | S_ASP_385 | OD1 | 3.676 |
| 3BGF | S_ARG_342 | NH2 | S_ASP_385 | OD2 | 3.162 |
| 3BGF | A_ARG_342 | NH2 | A_ASP_385 | OD1 | 3.423 |
| 3BGF | A_ARG_342 | NH2 | A_ASP_385 | OD2 | 2.961 |
| 3D0G | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 2.924 |
| 3D0G | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.097 |
| 3D0G | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.837 |
| 3D0G | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 2.994 |
| 3D0G | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.432 |
| 3D0G | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 2.983 |
| 3D0H | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.253 |
| 3D0H | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.248 |
| 3D0H | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.363 |
| 3D0H | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.221 |
| 3D0H | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.718 |
| 3D0H | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.147 |
| 3D0I | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.181 |
| 3D0I | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.112 |
| 3D0I | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 3.693 |
| 3D0I | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.921 |
| 3D0I | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.555 |
| 3D0I | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.615 |
| 3D0I | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.912 |
| 3D0I | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.980 |
| 3D0I | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.584 |
| 3SCI | A_LYS_353 | NZ | A_ASP_38 | OD1 | 3.354 |
| 3SCI | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.295 |
| 3SCI | B_LYS_353 | NZ | B_ASP_38 | OD1 | 3.714 |
| 3SCI | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.545 |
| 3SCI | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 3.000 |
| 3SCI | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.193 |
| 3SCI | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 3.355 |
| 3SCI | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.898 |
| 3SCJ | A_LYS_353 | NZ | A_ASP_38 | OD1 | 2.877 |
| 3SCJ | A_HIS_401 | NE2 | A_ASP_382 | OD2 | 3.168 |
| 3SCJ | B_LYS_353 | NZ | B_ASP_38 | OD1 | 2.726 |
| 3SCJ | B_HIS_401 | NE2 | B_ASP_382 | OD2 | 2.952 |
| 3SCJ | E_ARG_342 | NH1 | E_ASP_385 | OD1 | 2.893 |
| 3SCJ | E_ARG_342 | NH1 | E_ASP_385 | OD2 | 3.243 |
| 3SCJ | E_ARG_479 | NH2 | A_ASP_38 | OD2 | 2.575 |

| | | | | | |
|---|---|---|---|---|---|
| 3SCJ | F_ARG_342 | NH1 | F_ASP_385 | OD1 | 2.917 |
| 3SCJ | F_ARG_342 | NH1 | F_ASP_385 | OD2 | 3.247 |
| 3SCJ | F_ARG_479 | NH2 | B_ASP_38 | OD2 | 2.718 |
| 3SCK | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 2.944 |
| 3SCK | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 2.702 |
| 3SCK | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.321 |
| 3SCK | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.081 |
| 3SCK | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 3.676 |
| 3SCK | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.322 |
| 3SCL | A_HIS_401 | NE2 | A_ASP_382 | OD1 | 3.267 |
| 3SCL | B_HIS_401 | NE2 | B_ASP_382 | OD1 | 3.349 |
| 3SCL | E_ARG_342 | NH2 | E_ASP_385 | OD1 | 3.057 |
| 3SCL | E_ARG_342 | NH2 | E_ASP_385 | OD2 | 3.532 |
| 3SCL | F_ARG_342 | NH2 | F_ASP_385 | OD1 | 2.956 |
| 3SCL | F_ARG_342 | NH2 | F_ASP_385 | OD2 | 3.322 |

Table 155: ASP38-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_LYS_465 | NZ | E_ASP_463 | OD2 | 3.801 |
| 3D0G | F_LYS_465 | NZ | F_ASP_463 | OD1 | 3.077 |
| 3D0I | E_LYS_465 | NZ | E_ASP_463 | OD2 | 3.638 |
| 3D0I | F_LYS_465 | NZ | F_ASP_463 | OD2 | 3.412 |
| 3SCJ | F_LYS_465 | NZ | F_ASP_463 | OD2 | 3.932 |

Table 156: ASP463-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_221 | NZ | C_GLU_502 | OE2 | 3.266 |
| 5X58 | B_LYS_221 | NZ | A_GLU_502 | OE2 | 3.264 |
| 5X58 | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.265 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE1 | 3.851 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.225 |

Table 157: LYS221-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCL | E_LYS_344 | NZ | E_GLU_502 | OE2 | 3.992 |
| 5X58 | A_LYS_221 | NZ | C_GLU_502 | OE2 | 3.266 |
| 5X58 | B_LYS_221 | NZ | A_GLU_502 | OE2 | 3.264 |
| 5X58 | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.265 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE1 | 3.851 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.225 |

Table 158: GLU502-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_ARG_94 | NH2 | H_ASP_101 | OD2 | 2.723 |
| 3BGF | H_ARG_94 | NH1 | H_ASP_101 | OD1 | 2.347 |
| 3BGF | H_ARG_94 | NH1 | H_ASP_101 | OD2 | 3.381 |
| 3BGF | B_ARG_94 | NH1 | B_ASP_101 | OD1 | 2.357 |
| 3BGF | B_ARG_94 | NH1 | B_ASP_101 | OD2 | 2.930 |

Table 159: ARG94-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_ARG_94 | NH2 | H_ASP_101 | OD2 | 2.723 |
| 3BGF | H_ARG_94 | NH1 | H_ASP_101 | OD1 | 2.347 |
| 3BGF | H_ARG_94 | NH1 | H_ASP_101 | OD2 | 3.381 |
| 3BGF | B_ARG_94 | NH1 | B_ASP_101 | OD1 | 2.357 |
| 3BGF | B_ARG_94 | NH1 | B_ASP_101 | OD2 | 2.930 |
| 3BGF | B_ARG_100 | NH1 | B_ASP_101 | OD1 | 3.816 |

Table 160: ASP101-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_514 | NZ | A_ASP_376 | OD1 | 3.288 |
| 5X58 | B_LYS_514 | NZ | B_ASP_376 | OD1 | 3.288 |
| 5X58 | C_LYS_514 | NZ | C_ASP_376 | OD1 | 3.288 |
| 5X5B | B_LYS_514 | NZ | B_ASP_376 | OD1 | 3.351 |
| 5X5B | C_LYS_514 | NZ | C_ASP_376 | OD1 | 3.351 |

Table 161: LYS514-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_514 | NZ | A_ASP_376 | OD1 | 3.288 |
| 5X58 | B_LYS_514 | NZ | B_ASP_376 | OD1 | 3.288 |
| 5X58 | C_LYS_514 | NZ | C_ASP_376 | OD1 | 3.288 |
| 5X5B | B_ARG_315 | NH2 | B_ASP_376 | OD1 | 3.790 |
| 5X5B | B_LYS_514 | NZ | B_ASP_376 | OD1 | 3.351 |
| 5X5B | C_ARG_315 | NH2 | C_ASP_376 | OD1 | 3.790 |
| 5X5B | C_LYS_514 | NZ | C_ASP_376 | OD1 | 3.351 |

Table 162: ASP376-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_193 | NH1 | B_GLU_211 | OE2 | 3.176 |
| 2GHW | B_ARG_193 | NH2 | B_GLU_211 | OE2 | 3.887 |
| 2GHW | B_ARG_193 | NH2 | B_GLU_213 | OE1 | 3.299 |
| 2GHW | B_ARG_193 | NH2 | B_ASP_214 | OD1 | 3.163 |
| 2GHW | B_ARG_193 | NH2 | B_ASP_214 | OD2 | 3.876 |
| 2GHW | D_ARG_193 | NH1 | D_GLU_211 | OE1 | 3.249 |
| 2GHW | D_ARG_193 | NH1 | D_GLU_211 | OE2 | 3.681 |
| 2GHW | D_ARG_193 | NH2 | D_GLU_211 | OE1 | 3.135 |
| 2GHW | D_ARG_193 | NH2 | D_GLU_213 | OE1 | 3.465 |
| 2GHW | D_ARG_193 | NH2 | D_ASP_214 | OD1 | 3.132 |
| 2GHW | D_ARG_193 | NH2 | D_ASP_214 | OD2 | 3.717 |

Table 163: ARG193-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_193 | NH1 | B_GLU_211 | OE2 | 3.176 |
| 2GHW | B_ARG_193 | NH2 | B_GLU_211 | OE2 | 3.887 |
| 2GHW | D_ARG_193 | NH1 | D_GLU_211 | OE1 | 3.249 |
| 2GHW | D_ARG_193 | NH1 | D_GLU_211 | OE2 | 3.681 |
| 2GHW | D_ARG_193 | NH2 | D_GLU_211 | OE1 | 3.135 |

Table 164: GLU211-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_ARG_66 | NH1 | H_ASP_86 | OD1 | 3.583 |
| 2DD8 | H_ARG_66 | NH1 | H_ASP_86 | OD2 | 3.304 |
| 2DD8 | H_ARG_66 | NH2 | H_ASP_86 | OD1 | 2.890 |
| 2DD8 | H_ARG_66 | NH2 | H_ASP_86 | OD2 | 3.740 |
| 3BGF | L_ARG_66 | NH2 | L_GLU_28 | OE2 | 2.738 |
| 3BGF | C_ARG_66 | NH2 | C_GLU_28 | OE1 | 3.607 |
| 3BGF | C_ARG_66 | NH2 | C_GLU_28 | OE2 | 2.938 |

Table 165: ARG66-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_ARG_38 | NH1 | H_ASP_86 | OD1 | 2.908 |
| 2DD8 | H_ARG_38 | NH2 | H_ASP_86 | OD1 | 3.769 |
| 2DD8 | H_ARG_66 | NH1 | H_ASP_86 | OD1 | 3.583 |
| 2DD8 | H_ARG_66 | NH1 | H_ASP_86 | OD2 | 3.304 |
| 2DD8 | H_ARG_66 | NH2 | H_ASP_86 | OD1 | 2.890 |
| 2DD8 | H_ARG_66 | NH2 | H_ASP_86 | OD2 | 3.740 |
| 3BGF | H_LYS_38 | NZ | H_ASP_86 | OD1 | 3.661 |
| 3BGF | H_LYS_66 | NZ | H_ASP_86 | OD1 | 3.553 |
| 3BGF | H_LYS_66 | NZ | H_ASP_86 | OD2 | 2.671 |
| 3BGF | B_LYS_38 | NZ | B_ASP_86 | OD1 | 3.591 |
| 3BGF | B_LYS_66 | NZ | B_ASP_86 | OD1 | 3.814 |
| 3BGF | B_LYS_66 | NZ | B_ASP_86 | OD2 | 2.805 |

Table 166: ASP86-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_577 | NZ | A_GLU_571 | OE1 | 3.259 |
| 3SCJ | A_LYS_577 | NZ | A_GLU_571 | OE1 | 3.432 |
| 3SCK | B_LYS_577 | NZ | B_GLU_571 | OE2 | 3.718 |
| 3SCL | B_LYS_577 | NZ | B_GLU_571 | OE2 | 3.749 |

Table 167: LYS577-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_577 | NZ | A_GLU_571 | OE1 | 3.259 |
| 3SCJ | A_LYS_577 | NZ | A_GLU_571 | OE1 | 3.432 |
| 3SCK | B_LYS_577 | NZ | B_GLU_571 | OE2 | 3.718 |
| 3SCL | B_LYS_577 | NZ | B_GLU_571 | OE2 | 3.749 |

Table 168: GLU571-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_797 | NH1 | A_ASP_850 | OD1 | 3.465 |
| 5X58 | B_ARG_797 | NH1 | B_ASP_850 | OD1 | 3.464 |
| 5X58 | C_ARG_797 | NH1 | C_ASP_850 | OD1 | 3.464 |
| 5X5B | A_ARG_797 | NH1 | A_ASP_850 | OD1 | 3.600 |

Table 169: ARG797-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_797 | NH1 | A_ASP_850 | OD1 | 3.465 |
| 5X58 | B_ARG_797 | NH1 | B_ASP_850 | OD1 | 3.464 |
| 5X58 | C_ARG_797 | NH1 | C_ASP_850 | OD1 | 3.464 |
| 5X5B | A_ARG_797 | NH1 | A_ASP_850 | OD1 | 3.600 |

Table 170: ASP850-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0I | A_LYS_465 | NZ | A_GLU_197 | OE2 | 3.918 |
| 3SCI | B_LYS_465 | NZ | B_GLU_197 | OE2 | 3.379 |
| 3SCJ | B_LYS_465 | NZ | B_GLU_197 | OE2 | 3.351 |
| 3SCK | A_LYS_465 | NZ | A_GLU_197 | OE2 | 3.131 |

Table 171: GLU197-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_38 | NH1 | B_GLU_89 | OE1 | 3.674 |
| 2GHW | B_ARG_38 | NH2 | B_GLU_89 | OE1 | 3.206 |
| 2GHW | B_ARG_67 | NH2 | B_GLU_89 | OE1 | 3.863 |
| 2GHW | B_ARG_67 | NH2 | B_GLU_89 | OE2 | 3.548 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_89 | OE1 | 3.329 |
| 2GHW | D_ARG_38 | NH2 | D_GLU_89 | OE2 | 2.864 |
| 2GHW | D_ARG_67 | NH2 | D_GLU_89 | OE1 | 3.576 |

Table 172: GLU89-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_193 | NH2 | B_ASP_214 | OD1 | 3.163 |
| 2GHW | B_ARG_193 | NH2 | B_ASP_214 | OD2 | 3.876 |
| 2GHW | D_ARG_193 | NH2 | D_ASP_214 | OD1 | 3.132 |
| 2GHW | D_ARG_193 | NH2 | D_ASP_214 | OD2 | 3.717 |

Table 173: ASP214-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | L_ARG_61 | NH1 | L_GLU_79 | OE1 | 3.984 |
| 3BGF | L_ARG_61 | NH1 | L_GLU_79 | OE2 | 3.405 |
| 3BGF | C_ARG_61 | NH1 | C_GLU_79 | OE1 | 3.352 |
| 3BGF | C_ARG_61 | NH1 | C_GLU_79 | OE2 | 3.278 |

Table 174: GLU79-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | H_LYS_66 | NZ | H_ASP_86 | OD1 | 3.553 |
| 3BGF | H_LYS_66 | NZ | H_ASP_86 | OD2 | 2.671 |
| 3BGF | B_LYS_66 | NZ | B_ASP_86 | OD1 | 3.814 |
| 3BGF | B_LYS_66 | NZ | B_ASP_86 | OD2 | 2.805 |

Table 175: LYS66-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | L_LYS_149 | NZ | L_GLU_195 | OE1 | 3.683 |
| 3BGF | L_LYS_149 | NZ | L_GLU_195 | OE2 | 3.129 |
| 3BGF | C_LYS_149 | NZ | C_GLU_195 | OE1 | 3.352 |
| 3BGF | C_LYS_149 | NZ | C_GLU_195 | OE2 | 3.898 |

Table 176: LYS149-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | L_LYS_149 | NZ | L_GLU_195 | OE1 | 3.683 |
| 3BGF | L_LYS_149 | NZ | L_GLU_195 | OE2 | 3.129 |
| 3BGF | C_LYS_149 | NZ | C_GLU_195 | OE1 | 3.352 |
| 3BGF | C_LYS_149 | NZ | C_GLU_195 | OE2 | 3.898 |

Table 177: GLU195-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | L_ARG_66 | NH2 | L_GLU_28 | OE2 | 2.738 |
| 3BGF | C_ARG_66 | NH2 | C_GLU_28 | OE1 | 3.607 |
| 3BGF | C_ARG_66 | NH2 | C_GLU_28 | OE2 | 2.938 |

Table 178: GLU28-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_ARG_553 | NH1 | A_ASP_557 | OD1 | 3.914 |
| 5X5B | B_ARG_553 | NH1 | B_ASP_557 | OD1 | 3.071 |
| 5X5B | C_ARG_553 | NH1 | C_ASP_557 | OD1 | 3.070 |

Table 179: ARG553-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_ARG_553 | NH1 | A_ASP_557 | OD1 | 3.914 |
| 5X5B | B_ARG_553 | NH1 | B_ASP_557 | OD1 | 3.071 |
| 5X5B | C_ARG_553 | NH1 | C_ASP_557 | OD1 | 3.070 |

Table 180: ASP557-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_600 | NZ | A_ASP_597 | OD1 | 3.832 |
| 2AJF | A_LYS_600 | NZ | A_ASP_597 | OD2 | 3.177 |
| 3SCJ | A_LYS_600 | NZ | A_ASP_597 | OD2 | 3.672 |

Table 181: LYS600-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_600 | NZ | A_ASP_597 | OD1 | 3.832 |
| 2AJF | A_LYS_600 | NZ | A_ASP_597 | OD2 | 3.177 |
| 3SCJ | A_LYS_600 | NZ | A_ASP_597 | OD2 | 3.672 |

Table 182: ASP597-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_98 | NH2 | B_ASP_105 | OD2 | 3.012 |
| 2GHW | D_ARG_98 | NH2 | D_ASP_105 | OD1 | 3.960 |
| 2GHW | D_ARG_98 | NH2 | D_ASP_105 | OD2 | 3.196 |

Table 183: ARG98-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_98 | NH2 | B_ASP_105 | OD2 | 3.012 |
| 2GHW | D_ARG_98 | NH2 | D_ASP_105 | OD1 | 3.960 |
| 2GHW | D_ARG_98 | NH2 | D_ASP_105 | OD2 | 3.196 |

Table 184: ASP105-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_HIS_35 | NE2 | B_ASP_99 | OD1 | 3.622 |
| 2GHW | D_HIS_35 | ND1 | D_ASP_99 | OD1 | 3.954 |
| 2GHW | D_HIS_35 | NE2 | D_ASP_99 | OD1 | 3.761 |
| 3BGF | H_HIS_35 | NE2 | H_GLU_95 | OE1 | 2.884 |
| 3BGF | B_HIS_35 | NE2 | B_GLU_95 | OE1 | 2.642 |

Table 185: HIS35-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_HIS_35 | NE2 | B_ASP_99 | OD1 | 3.622 |
| 2GHW | D_HIS_35 | ND1 | D_ASP_99 | OD1 | 3.954 |
| 2GHW | D_HIS_35 | NE2 | D_ASP_99 | OD1 | 3.761 |

Table 186: ASP99-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | L_ARG_24 | NH2 | L_ASP_70 | OD1 | 3.258 |
| 3BGF | L_ARG_24 | NH2 | L_ASP_70 | OD2 | 2.893 |
| 3BGF | C_ARG_24 | NH2 | C_ASP_70 | OD1 | 3.766 |

Table 187: ARG24-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | L_ARG_24 | NH2 | L_ASP_70 | OD1 | 3.258 |
| 3BGF | L_ARG_24 | NH2 | L_ASP_70 | OD2 | 2.893 |
| 3BGF | C_ARG_24 | NH2 | C_ASP_70 | OD1 | 3.766 |

Table 188: ASP70-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_534 | NZ | B_ASP_431 | OD1 | 3.656 |
| 3D0G | A_LYS_534 | NZ | A_GLU_549 | OE1 | 3.278 |
| 3D0H | A_LYS_534 | NZ | A_GLU_549 | OE2 | 3.173 |
| 3D0I | A_LYS_534 | NZ | A_GLU_549 | OE1 | 3.582 |

Table 189: LYS534-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0G | A_LYS_534 | NZ | A_GLU_549 | OE1 | 3.278 |
| 3D0H | A_LYS_534 | NZ | A_GLU_549 | OE2 | 3.173 |
| 3D0I | A_LYS_534 | NZ | A_GLU_549 | OE1 | 3.582 |

Table 190: GLU549-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_836 | NZ | C_ASP_554 | OD2 | 3.822 |
| 5X58 | B_LYS_836 | NZ | A_ASP_554 | OD2 | 3.822 |
| 5X58 | C_LYS_836 | NZ | B_ASP_554 | OD2 | 3.825 |

Table 191: LYS836-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_836 | NZ | C_ASP_554 | OD2 | 3.822 |
| 5X58 | B_LYS_836 | NZ | A_ASP_554 | OD2 | 3.822 |
| 5X58 | C_LYS_836 | NZ | B_ASP_554 | OD2 | 3.825 |

Table 192: ASP554-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 3.643 |
| 2AJF | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.692 |
| 2AJF | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.035 |
| 3BGF | L_ARG_46 | NH1 | L_ASP_55 | OD1 | 3.016 |
| 3BGF | L_ARG_46 | NH1 | L_ASP_55 | OD2 | 3.557 |
| 3BGF | C_ARG_46 | NH1 | C_ASP_55 | OD1 | 2.965 |
| 3D0G | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.159 |
| 3D0G | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.787 |
| 3D0H | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.144 |
| 3D0H | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.001 |
| 3D0I | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.364 |
| 3D0I | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.212 |
| 3SCI | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.133 |
| 3SCI | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.610 |
| 3SCJ | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 2.363 |
| 3SCJ | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.678 |
| 3SCJ | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.815 |
| 3SCK | A_ARG_460 | NH1 | A_GLU_457 | OE1 | 3.705 |
| 3SCK | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 3.038 |
| 3SCK | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 3.129 |
| 3SCL | A_ARG_460 | NH1 | A_GLU_457 | OE2 | 2.352 |
| 3SCL | B_ARG_460 | NH1 | B_GLU_457 | OE2 | 2.623 |

Table 193: ARG46-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | L_ARG_46 | NH1 | L_ASP_55 | OD1 | 3.016 |
| 3BGF | L_ARG_46 | NH1 | L_ASP_55 | OD2 | 3.557 |
| 3BGF | C_ARG_46 | NH1 | C_ASP_55 | OD1 | 2.965 |
| 5X58 | A_LYS_836 | NZ | C_ASP_554 | OD2 | 3.822 |
| 5X58 | B_LYS_836 | NZ | A_ASP_554 | OD2 | 3.822 |
| 5X58 | C_LYS_836 | NZ | B_ASP_554 | OD2 | 3.825 |
| 5X5B | A_ARG_553 | NH1 | A_ASP_557 | OD1 | 3.914 |
| 5X5B | B_ARG_553 | NH1 | B_ASP_557 | OD1 | 3.071 |
| 5X5B | C_ARG_553 | NH1 | C_ASP_557 | OD1 | 3.070 |

Table 194: ASP55-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_156 | NH2 | B_ASP_202 | OD1 | 3.384 |
| 2GHW | B_ARG_156 | NH2 | B_ASP_202 | OD2 | 3.152 |
| 2GHW | D_ARG_156 | NH1 | D_ASP_202 | OD2 | 3.931 |

Table 195: ARG156-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_156 | NH2 | B_ASP_202 | OD1 | 3.384 |
| 2GHW | B_ARG_156 | NH2 | B_ASP_202 | OD2 | 3.152 |
| 2GHW | D_ARG_156 | NH1 | D_ASP_202 | OD2 | 3.931 |

Table 196: ASP202-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_31 | NZ | A_GLU_35 | OE1 | 3.992 |
| 2DD8 | L_LYS_31 | NZ | L_ASP_92 | OD1 | 3.038 |
| 3D0G | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.737 |
| 3D0G | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.363 |
| 3D0I | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.185 |
| 3D0I | B_LYS_313 | NZ | B_GLU_310 | OE2 | 2.999 |
| 3SCI | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.555 |
| 3SCI | B_LYS_31 | NZ | B_GLU_35 | OE1 | 3.358 |
| 3SCI | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.303 |
| 3SCJ | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.597 |
| 3SCJ | B_LYS_31 | NZ | B_GLU_35 | OE2 | 3.882 |
| 3SCJ | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.681 |
| 3SCK | A_LYS_313 | NZ | A_GLU_310 | OE2 | 3.272 |
| 3SCK | B_LYS_313 | NZ | B_GLU_310 | OE2 | 3.682 |

Table 197: LYS31-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD1 | 3.643 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD2 | 3.461 |
| 2DD8 | S_ARG_395 | NH2 | L_ASP_95A | OD1 | 3.001 |
| 2DD8 | S_ARG_395 | NH2 | S_ASP_392 | OD1 | 3.245 |

Table 198: ARG395-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD1 | 3.643 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD2 | 3.461 |
| 2DD8 | S_ARG_395 | NH2 | L_ASP_95A | OD1 | 3.001 |

Table 199: ASP95A-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_223 | NH2 | B_ASP_182 | OD1 | 3.202 |
| 2GHW | D_ARG_223 | NH2 | D_ASP_182 | OD1 | 3.375 |

Table 200: ARG223-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_223 | NH2 | B_ASP_182 | OD1 | 3.202 |
| 2GHW | D_ARG_223 | NH2 | D_ASP_182 | OD1 | 3.375 |

Table 201: ASP182-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE1 | 2.759 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE2 | 3.226 |

Table 202: LYS209-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE1 | 2.759 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE2 | 3.226 |

Table 203: GLU124-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_ARG_1073 | NH1 | B_ASP_1100 | OD2 | 3.995 |
| 5X5B | C_ARG_1073 | NH1 | A_ASP_1100 | OD2 | 3.761 |

Table 204: ARG1073-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_ARG_1073 | NH1 | B_ASP_1100 | OD2 | 3.995 |
| 5X5B | C_ARG_1073 | NH1 | A_ASP_1100 | OD2 | 3.761 |

Table 205: ASP1100-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_LYS_235 | NZ | B_GLU_237 | OE2 | 3.402 |
| 2GHW | D_LYS_235 | NZ | D_GLU_237 | OE2 | 3.600 |

Table 206: LYS235-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_LYS_235 | NZ | B_GLU_237 | OE2 | 3.402 |
| 2GHW | D_LYS_235 | NZ | D_GLU_237 | OE2 | 3.600 |

Table 207: GLU237-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0H | E_LYS_479 | NZ | A_GLU_35 | OE1 | 3.397 |
| 3D0H | F_LYS_479 | NZ | B_GLU_35 | OE1 | 3.369 |

Table 208: LYS479-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | H_HIS_35 | NE2 | H_GLU_95 | OE1 | 2.884 |
| 3BGF | B_HIS_35 | NE2 | B_GLU_95 | OE1 | 2.642 |

Table 209: GLU95-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | B_ARG_315 | NH2 | B_ASP_376 | OD1 | 3.790 |
| 5X5B | C_ARG_315 | NH2 | C_ASP_376 | OD1 | 3.790 |

Table 210: ARG315-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X4S | A_LYS_175 | NZ | A_ASP_171 | OD1 | 3.389 |
| 5X4S | A_LYS_175 | NZ | A_ASP_171 | OD2 | 3.027 |

Table 211: LYS175-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X4S | A_LYS_175 | NZ | A_ASP_171 | OD1 | 3.389 |
| 5X4S | A_LYS_175 | NZ | A_ASP_171 | OD2 | 3.027 |

Table 212: ASP171-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | H_LYS_38 | NZ | H_ASP_86 | OD1 | 3.661 |
| 3BGF | B_LYS_38 | NZ | B_ASP_86 | OD1 | 3.591 |

Table 213: LYS38-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_162 | NH1 | A_ASP_480 | OD1 | 3.081 |
| 2GHW | D_ARG_162 | NH2 | C_ASP_480 | OD1 | 3.626 |

Table 214: ARG162-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_LYS_210 | NZ | H_GLU_212 | OE1 | 3.571 |
| 2DD8 | H_LYS_210 | NZ | H_GLU_212 | OE2 | 3.616 |
| 3BGF | H_LYS_210 | NZ | L_GLU_123 | OE1 | 3.997 |

Table 215: LYS210-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE1 | 3.913 |
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE2 | 2.993 |
| 2DD8 | H_LYS_210 | NZ | H_GLU_212 | OE1 | 3.571 |
| 2DD8 | H_LYS_210 | NZ | H_GLU_212 | OE2 | 3.616 |

Table 216: GLU212-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE1 | 3.913 |
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE2 | 2.993 |

Table 217: LYS129-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCL | B_LYS_562 | NZ | B_ASP_206 | OD1 | 3.640 |
| 3SCL | B_LYS_562 | NZ | B_ASP_206 | OD2 | 3.837 |

Table 218: LYS562-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCL | B_LYS_562 | NZ | B_ASP_206 | OD1 | 3.640 |
| 3SCL | B_LYS_562 | NZ | B_ASP_206 | OD2 | 3.837 |

Table 219: ASP206-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | B_LYS_543 | NZ | B_ASP_572 | OD2 | 3.842 |
| 5X5B | C_LYS_543 | NZ | C_ASP_572 | OD2 | 3.841 |

Table 220: ASP572-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | D_LYS_239 | NZ | D_GLU_149 | OE1 | 3.290 |
| 2GHW | D_LYS_239 | NZ | D_GLU_149 | OE2 | 3.630 |

Table 221: LYS239-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | D_LYS_239 | NZ | D_GLU_149 | OE1 | 3.290 |
| 2GHW | D_LYS_239 | NZ | D_GLU_149 | OE2 | 3.630 |

Table 222: GLU149-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCI | A_HIS_34 | ND1 | A_GLU_37 | OE1 | 3.955 |
| 3SCJ | A_HIS_34 | NE2 | A_ASP_30 | OD1 | 3.716 |
| 3SCJ | B_HIS_34 | NE2 | B_ASP_30 | OD1 | 3.848 |

Table 223: HIS34-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCJ | A_HIS_34 | NE2 | A_ASP_30 | OD1 | 3.716 |
| 3SCJ | B_HIS_34 | NE2 | B_ASP_30 | OD1 | 3.848 |

Table 224: ASP30-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD1 | 3.504 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD2 | 2.403 |
| 3BGF | H_ARG_33 | NH1 | H_ASP_56 | OD2 | 3.848 |
| 5X58 | A_LYS_543 | NZ | A_ASP_560 | OD2 | 2.441 |
| 5X58 | B_LYS_543 | NZ | B_ASP_560 | OD2 | 2.442 |
| 5X58 | C_LYS_543 | NZ | C_ASP_560 | OD2 | 2.441 |
| 5X5B | A_LYS_543 | NZ | A_ASP_560 | OD2 | 3.771 |
| 5X5B | B_LYS_543 | NZ | B_ASP_560 | OD2 | 2.696 |
| 5X5B | C_LYS_543 | NZ | C_ASP_560 | OD2 | 2.696 |

Table 225: ASP56-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_193 | NH2 | B_GLU_213 | OE1 | 3.299 |
| 2GHW | D_ARG_193 | NH2 | D_GLU_213 | OE1 | 3.465 |
| 3BGF | H_LYS_211 | NZ | H_GLU_213 | OE2 | 3.764 |

Table 226: GLU213-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_LYS_76 | NZ | B_ASP_73 | OD2 | 2.795 |
| 2GHW | D_LYS_76 | NZ | D_ASP_73 | OD2 | 3.658 |

Table 227: LYS76-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_LYS_76 | NZ | B_ASP_73 | OD2 | 2.795 |
| 2GHW | D_LYS_76 | NZ | D_ASP_73 | OD2 | 3.658 |

Table 228: ASP73-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | L_HIS_189 | ND1 | L_ASP_151 | OD1 | 2.696 |

Table 229: HIS189-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | L_HIS_189 | ND1 | L_ASP_151 | OD1 | 2.696 |

Table 230: ASP151-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | C_ARG_155 | NH2 | C_GLU_185 | OE2 | 3.481 |

Table 231: ARG155-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | C_ARG_155 | NH2 | C_GLU_185 | OE2 | 3.481 |

Table 232: GLU185-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | C_ARG_61 | NH2 | C_GLU_81 | OE2 | 3.045 |

Table 233: GLU81-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_LYS_793 | NZ | A_ASP_802 | OD2 | 3.746 |

Table 234: LYS793-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_LYS_793 | NZ | A_ASP_802 | OD2 | 3.746 |

Table 235: ASP802-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | H_LYS_210 | NZ | L_GLU_123 | OE1 | 3.997 |

Table 236: GLU123-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | H_LYS_211 | NZ | H_GLU_213 | OE2 | 3.764 |

Table 237: LYS211-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | H_ARG_33 | NH1 | H_ASP_56 | OD2 | 3.848 |

Table 238: ARG33-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | S_ARG_395 | NH2 | S_ASP_392 | OD1 | 3.245 |

Table 239: ASP392-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | C_LYS_199 | NZ | C_ASP_110 | OD2 | 3.825 |

Table 240: LYS199-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | C_LYS_199 | NZ | C_ASP_110 | OD2 | 3.825 |
| 5X5B | A_ARG_1073 | NH1 | B_ASP_1100 | OD2 | 3.995 |
| 5X5B | C_ARG_1073 | NH1 | A_ASP_1100 | OD2 | 3.761 |

Table 241: ASP110-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | L_LYS_130 | NZ | H_ASP_144 | OD2 | 3.343 |

Table 242: LYS130-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | L_LYS_130 | NZ | H_ASP_144 | OD2 | 3.343 |

Table 243: ASP144-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | D_LYS_65 | NZ | D_ASP_62 | OD1 | 3.926 |

Table 244: LYS65-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | D_LYS_65 | NZ | D_ASP_62 | OD1 | 3.926 |

Table 245: ASP62-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X4S | A_LYS_190 | NZ | A_ASP_191 | OD2 | 3.979 |

Table 246: LYS190-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X4S | A_LYS_190 | NZ | A_ASP_191 | OD2 | 3.979 |

Table 247: ASP191-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | C_LYS_142 | NZ | C_GLU_105 | OE1 | 3.341 |

Table 248: LYS142-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | C_LYS_142 | NZ | C_GLU_105 | OE1 | 3.341 |

Table 249: GLU105-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_HIS_74 | ND1 | A_ASP_24 | OD2 | 3.604 |

Table 250: HIS74-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_HIS_74 | ND1 | A_ASP_24 | OD2 | 3.604 |

Table 251: ASP24-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | L_ARG_191 | NH1 | L_ASP_152 | OD2 | 3.527 |

Table 252: ARG191-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | L_ARG_191 | NH1 | L_ASP_152 | OD2 | 3.527 |

Table 253: ASP152-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCK | B_HIS_535 | ND1 | B_GLU_536 | OE1 | 3.467 |

Table 254: HIS535-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | L_LYS_31 | NZ | L_ASP_92 | OD1 | 3.038 |

Table 255: ASP92-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | L_LYS_167 | NZ | L_GLU_83 | OE1 | 3.208 |

Table 256: LYS167-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | L_LYS_167 | NZ | L_GLU_83 | OE1 | 3.208 |

Table 257: GLU83-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_LYS_566 | NZ | A_ASP_351 | OD1 | 3.661 |

Table 258: LYS566-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_LYS_566 | NZ | A_ASP_351 | OD1 | 3.661 |

Table 259: ASP351-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCK | A_ARG_582 | NH2 | A_GLU_527 | OE1 | 3.214 |

Table 260: GLU527-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | B_ARG_100 | NH1 | B_ASP_101 | OD1 | 3.816 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.983 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.964 |
| 5X58 | A_ARG_1001 | NH2 | A_GLU_755 | OE1 | 3.437 |
| 5X58 | A_ARG_1001 | NH2 | A_GLU_755 | OE2 | 3.596 |
| 5X58 | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.486 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.983 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.963 |
| 5X58 | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.485 |
| 5X58 | B_ARG_1001 | NH2 | B_GLU_755 | OE1 | 3.436 |
| 5X58 | B_ARG_1001 | NH2 | B_GLU_755 | OE2 | 3.597 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.985 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.966 |
| 5X58 | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.487 |
| 5X58 | C_ARG_1001 | NH2 | C_GLU_755 | OE1 | 3.436 |
| 5X58 | C_ARG_1001 | NH2 | C_GLU_755 | OE2 | 3.596 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.909 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.948 |
| 5X5B | A_ARG_1001 | NH2 | A_GLU_755 | OE1 | 3.427 |
| 5X5B | A_ARG_1001 | NH2 | A_GLU_755 | OE2 | 3.433 |
| 5X5B | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.377 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.930 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.999 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE1 | 3.970 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.150 |
| 5X5B | B_ARG_1001 | NH2 | B_GLU_755 | OE1 | 3.472 |
| 5X5B | B_ARG_1001 | NH2 | B_GLU_755 | OE2 | 3.342 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.907 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.931 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE1 | 3.965 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.203 |
| 5X5B | C_ARG_1001 | NH2 | C_GLU_755 | OE1 | 3.472 |
| 5X5B | C_ARG_1001 | NH2 | C_GLU_755 | OE2 | 3.341 |

Table 261: ARG100-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCL | E_LYS_344 | NZ | E_GLU_502 | OE2 | 3.992 |

Table 262: LYS344-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

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| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_426 | NH1 | A_GLU_329 | OE2 | 3.740 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.855 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 2.946 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.890 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.381 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 2.717 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 2.911 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD1 | 3.504 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD2 | 2.403 |
| 3SCI | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.257 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.110 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.923 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.044 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.878 |
| 3SCJ | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.526 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.206 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.277 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.547 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.819 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 3.913 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 3.505 |
| 3SCK | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.591 |
| 3SCL | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.916 |
| 3SCL | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.143 |

Table 263: Interfacial ARG426-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | E_ARG_426 | NH1 | A_GLU_329 | OE2 | 3.740 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.855 |
| 2AJF | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 2.946 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.890 |
| 2AJF | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.381 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 2.717 |
| 2AJF | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 2.911 |
| 3SCI | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.257 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.110 |
| 3SCI | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.923 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.044 |
| 3SCI | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.878 |
| 3SCJ | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.526 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.206 |
| 3SCJ | E_ARG_426 | NH2 | A_GLU_329 | OE2 | 3.277 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE1 | 3.547 |
| 3SCJ | F_ARG_426 | NH1 | B_GLU_329 | OE2 | 3.819 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE1 | 3.913 |
| 3SCJ | F_ARG_426 | NH2 | B_GLU_329 | OE2 | 3.505 |
| 3SCK | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.591 |
| 3SCL | E_ARG_426 | NH1 | A_GLU_329 | OE1 | 3.916 |
| 3SCL | E_ARG_426 | NH2 | A_GLU_329 | OE1 | 3.143 |

Table 264: Interfacial GLU329-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.983 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.964 |
| 5X58 | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.486 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.983 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.963 |
| 5X58 | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.485 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.985 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.966 |
| 5X58 | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.487 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.909 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.948 |
| 5X5B | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.377 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.930 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.999 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE1 | 3.970 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.150 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.907 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.931 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE1 | 3.965 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.203 |

Table 265: Interfacial ARG1001-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.983 |
| 5X58 | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.964 |
| 5X58 | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.486 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.983 |
| 5X58 | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.963 |
| 5X58 | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.485 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.985 |
| 5X58 | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.966 |
| 5X58 | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.487 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE1 | 3.909 |
| 5X5B | A_ARG_1001 | NH1 | C_GLU_999 | OE2 | 2.948 |
| 5X5B | A_ARG_1001 | NH2 | C_GLU_999 | OE2 | 3.377 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE1 | 3.930 |
| 5X5B | B_ARG_1001 | NH1 | A_GLU_999 | OE2 | 2.999 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE1 | 3.970 |
| 5X5B | B_ARG_1001 | NH2 | A_GLU_999 | OE2 | 3.150 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE1 | 3.907 |
| 5X5B | C_ARG_1001 | NH1 | B_GLU_999 | OE2 | 2.931 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE1 | 3.965 |
| 5X5B | C_ARG_1001 | NH2 | B_GLU_999 | OE2 | 3.203 |

Table 266: Interfacial GLU999-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE1 | 3.011 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE2 | 3.438 |
| 5X58 | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.538 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.011 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 3.438 |
| 5X58 | B_ARG_1021 | NH2 | C_GLU_1013 | OE2 | 3.540 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.011 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 3.438 |
| 5X58 | C_ARG_1021 | NH2 | A_GLU_1013 | OE2 | 3.539 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.472 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.057 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.450 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 2.311 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.273 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 2.370 |

Table 267: Interfacial ARG1021-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE1 | 3.011 |
| 5X58 | A_ARG_1021 | NH1 | B_GLU_1013 | OE2 | 3.438 |
| 5X58 | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.538 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.011 |
| 5X58 | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 3.438 |
| 5X58 | B_ARG_1021 | NH2 | C_GLU_1013 | OE2 | 3.540 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.011 |
| 5X58 | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 3.438 |
| 5X58 | C_ARG_1021 | NH2 | A_GLU_1013 | OE2 | 3.539 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE1 | 3.472 |
| 5X5B | A_ARG_1021 | NH2 | B_GLU_1013 | OE2 | 3.057 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE1 | 3.450 |
| 5X5B | B_ARG_1021 | NH1 | C_GLU_1013 | OE2 | 2.311 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE1 | 3.273 |
| 5X5B | C_ARG_1021 | NH1 | A_GLU_1013 | OE2 | 2.370 |

Table 268: Interfacial GLU1013-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.710 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.597 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.856 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.820 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.231 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.198 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.355 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.779 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.520 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.936 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.617 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.574 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.939 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.692 |
| 3SCL | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.918 |

Table 269: Interfacial LYS419-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.710 |
| 2AJF | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.597 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.856 |
| 3D0G | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.820 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.231 |
| 3D0H | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.198 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.355 |
| 3D0I | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.779 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE1 | 3.520 |
| 3SCI | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.936 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.617 |
| 3SCJ | B_LYS_419 | NZ | A_GLU_536 | OE2 | 3.574 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.939 |
| 3SCK | B_LYS_419 | NZ | A_GLU_536 | OE2 | 2.692 |
| 3SCL | B_LYS_419 | NZ | A_GLU_536 | OE1 | 2.918 |

Table 270: Interfacial GLU536-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.482 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 3.202 |
| 5X58 | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.575 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD1 | 3.484 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD2 | 3.202 |
| 5X58 | B_ARG_977 | NH2 | C_ASP_976 | OD2 | 3.576 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD1 | 3.484 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD2 | 3.202 |
| 5X58 | C_ARG_977 | NH2 | A_ASP_976 | OD2 | 3.575 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.912 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 2.504 |
| 5X5B | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.789 |

Table 271: Interfacial ARG977-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.482 |
| 5X58 | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 3.202 |
| 5X58 | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.575 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD1 | 3.484 |
| 5X58 | B_ARG_977 | NH1 | C_ASP_976 | OD2 | 3.202 |
| 5X58 | B_ARG_977 | NH2 | C_ASP_976 | OD2 | 3.576 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD1 | 3.484 |
| 5X58 | C_ARG_977 | NH1 | A_ASP_976 | OD2 | 3.202 |
| 5X58 | C_ARG_977 | NH2 | A_ASP_976 | OD2 | 3.575 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD1 | 3.912 |
| 5X5B | A_ARG_977 | NH1 | B_ASP_976 | OD2 | 2.504 |
| 5X5B | A_ARG_977 | NH2 | B_ASP_976 | OD2 | 3.789 |

Table 272: Interfacial ASP976-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0I | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 3.324 |
| 3D0I | E_ARG_479 | NH2 | A_GLU_35 | OE1 | 2.730 |
| 3D0I | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 3.405 |
| 3D0I | F_ARG_479 | NH2 | B_GLU_35 | OE1 | 2.961 |
| 3SCJ | E_ARG_479 | NH2 | A_ASP_38 | OD2 | 2.575 |
| 3SCJ | F_ARG_479 | NH2 | B_ASP_38 | OD2 | 2.718 |
| 3SCK | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 2.498 |
| 3SCK | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 2.750 |

Table 273: Interfacial ARG479-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0H | E_LYS_479 | NZ | A_GLU_35 | OE1 | 3.397 |
| 3D0H | F_LYS_479 | NZ | B_GLU_35 | OE1 | 3.369 |
| 3D0I | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 3.324 |
| 3D0I | E_ARG_479 | NH2 | A_GLU_35 | OE1 | 2.730 |
| 3D0I | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 3.405 |
| 3D0I | F_ARG_479 | NH2 | B_GLU_35 | OE1 | 2.961 |
| 3SCK | E_ARG_479 | NH1 | A_GLU_35 | OE1 | 2.498 |
| 3SCK | F_ARG_479 | NH1 | B_GLU_35 | OE1 | 2.750 |

Table 274: Interfacial GLU35-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_221 | NZ | C_GLU_502 | OE2 | 3.266 |
| 5X58 | B_LYS_221 | NZ | A_GLU_502 | OE2 | 3.264 |
| 5X58 | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.265 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE1 | 3.851 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.225 |

Table 275: Interfacial LYS221-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_221 | NZ | C_GLU_502 | OE2 | 3.266 |
| 5X58 | B_LYS_221 | NZ | A_GLU_502 | OE2 | 3.264 |
| 5X58 | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.265 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE1 | 3.851 |
| 5X5B | C_LYS_221 | NZ | B_GLU_502 | OE2 | 3.225 |

Table 276: Interfacial GLU502-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD1 | 3.643 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD2 | 3.461 |
| 2DD8 | S_ARG_395 | NH2 | L_ASP_95A | OD1 | 3.001 |

Table 277: Interfacial ARG395-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD1 | 3.643 |
| 2DD8 | S_ARG_395 | NH1 | L_ASP_95A | OD2 | 3.461 |
| 2DD8 | S_ARG_395 | NH2 | L_ASP_95A | OD1 | 3.001 |

Table 278: Interfacial ASP95A-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_836 | NZ | C_ASP_554 | OD2 | 3.822 |
| 5X58 | B_LYS_836 | NZ | A_ASP_554 | OD2 | 3.822 |
| 5X58 | C_LYS_836 | NZ | B_ASP_554 | OD2 | 3.825 |

Table 279: Interfacial LYS836-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X58 | A_LYS_836 | NZ | C_ASP_554 | OD2 | 3.822 |
| 5X58 | B_LYS_836 | NZ | A_ASP_554 | OD2 | 3.822 |
| 5X58 | C_LYS_836 | NZ | B_ASP_554 | OD2 | 3.825 |

Table 280: Interfacial ASP554-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | S_LYS_439 | NZ | A_ASP_480 | OD2 | 3.161 |
| 3BGF | A_LYS_439 | NZ | S_ASP_480 | OD2 | 2.520 |

Table 281: Interfacial LYS439-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_162 | NH1 | A_ASP_480 | OD1 | 3.081 |
| 2GHW | D_ARG_162 | NH2 | C_ASP_480 | OD1 | 3.626 |
| 3BGF | S_LYS_439 | NZ | A_ASP_480 | OD2 | 3.161 |
| 3BGF | A_LYS_439 | NZ | S_ASP_480 | OD2 | 2.520 |

Table 282: Interfacial ASP480-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3D0H | E_LYS_479 | NZ | A_GLU_35 | OE1 | 3.397 |
| 3D0H | F_LYS_479 | NZ | B_GLU_35 | OE1 | 3.369 |

Table 283: Interfacial LYS479-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD1 | 3.504 |
| 3BGF | S_ARG_426 | NH1 | H_ASP_56 | OD2 | 2.403 |

Table 284: Interfacial ASP56-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2GHW | B_ARG_162 | NH1 | A_ASP_480 | OD1 | 3.081 |
| 2GHW | D_ARG_162 | NH2 | C_ASP_480 | OD1 | 3.626 |

Table 285: Interfacial ARG162-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3SCJ | E_ARG_479 | NH2 | A_ASP_38 | OD2 | 2.575 |
| 3SCJ | F_ARG_479 | NH2 | B_ASP_38 | OD2 | 2.718 |

Table 286: Interfacial ASP38-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE1 | 3.913 |
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE2 | 2.993 |

Table 287: Interfacial LYS129-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE1 | 3.913 |
| 2DD8 | H_LYS_129 | NZ | L_GLU_212 | OE2 | 2.993 |

Table 288: Interfacial GLU212-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_ARG_1073 | NH1 | B_ASP_1100 | OD2 | 3.995 |
| 5X5B | C_ARG_1073 | NH1 | A_ASP_1100 | OD2 | 3.761 |

Table 289: Interfacial ARG1073-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 5X5B | A_ARG_1073 | NH1 | B_ASP_1100 | OD2 | 3.995 |
| 5X5B | C_ARG_1073 | NH1 | A_ASP_1100 | OD2 | 3.761 |

Table 290: Interfacial ASP1100-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE1 | 2.759 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE2 | 3.226 |

Table 291: Interfacial LYS209-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE1 | 2.759 |
| 2DD8 | H_LYS_209 | NZ | L_GLU_124 | OE2 | 3.226 |

Table 292: Interfacial GLU124-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | H_LYS_210 | NZ | L_GLU_123 | OE1 | 3.997 |

Table 293: Interfacial LYS210-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 3BGF | H_LYS_210 | NZ | L_GLU_123 | OE1 | 3.997 |

Table 294: Interfacial GLU123-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_534 | NZ | B_ASP_431 | OD1 | 3.656 |

Table 295: Interfacial LYS534-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2AJF | A_LYS_534 | NZ | B_ASP_431 | OD1 | 3.656 |

Table 296: Interfacial ASP431-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | L_LYS_130 | NZ | H_ASP_144 | OD2 | 3.343 |

Table 297: Interfacial LYS130-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

| PDB ID | Residue A | Atom A | Residue B | Atom B | Distance (Å) |
|---|---|---|---|---|---|
| 2DD8 | L_LYS_130 | NZ | H_ASP_144 | OD2 | 3.343 |

Table 298: Interfacial ASP144-specific salt bridging networks within the PDB entries. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.