

Supplementary Table S1. Sequence analysis of all human L-PRX regions (UniProtKB - Q9BXM0-1) using ProtParam¹.

Region	PDZ domain		Basic region		Hydrophobic region		PEVK-rich region		AHNAK-homology region		Acidic region	
Residue range	1-99		100-200		201-430		431-783		784-1097		1098-1461	
Residue count	99		101		230		353		314		364	
Isoelectric point (pI)	5.07		11.23		8.81		5.72		8.95		5.19	
Net charge at pH 7.4 ²	+3.3		+12.8		+1.8		-5.8		+3.9		-9.9	
Aliphatic index	89.7		96.53		100.22		104.33		82.99		72.36	
GRAVY	-0.304		-0.228		+0.202		-0.227		-0.232		-0.456	
Residue type ³	Amount	%	Amount	%	Amount	%	Amount	%	Amount	%	Amount	%
Ala	10	10.1	12	11.9	43	18.7	14	4	38	12.1	39	10.7
Arg	10	10.1	11	10.9	13	5.7	8	2.3	14	4.5	27	7.4
Asn	2	2	1	1	0	0	0	0	0	0	1	0.3
Asp	3	3	3	3	2	0.9	6	1.7	8	2.5	5	1.4
Cys	2	2	0	0	1	0.4	1	0.3	1	0.3	1	0.3
Gln	4	4	2	2	5	2.2	11	3.1	8	2.5	18	4.9
Glu	14	14.1	5	5	20	8.7	52	14.7	33	10.5	46	12.6
Gly	7	7.1	8	7.9	18	7.8	2	0.6	40	12.7	57	15.7
His	0	0	0	0	1	0.4	5	1.4	2	0.6	3	0.8
Ile	4	4	2	2	3	1.3	2	0.6	6	1.9	1	0.3
Leu	11	11.1	11	10.9	25	10.9	42	11.9	31	9.9	32	8.8
Lys	4	4	10	9.9	11	4.8	44	12.5	31	9.9	14	3.8
Met	1	1	1	1	3	1.3	24	6.8	8	2.5	5	1.4
Phe	5	5.1	3	3	5	2.2	0	0	10	3.2	8	2.2
Pro	2	2	12	11.9	34	14.8	72	20.4	28	8.9	29	8
Ser	8	8.1	5	5	10	4.3	7	2	18	5.7	28	7.7
Thr	3	3	2	2	9	3.9	0	0	9	2.9	15	4.1
Trp	0	0	0	0	0	0	0	0	2	0.6	0	0
Tyr	2	2	1	1	0	0	0	0	0	0	2	0.5
Val	7	7.1	12	11.9	27	11.7	63	17.8	27	8.6	33	9.1
Pyl	0	0	0	0	0	0	0	0	0	0	0	0
Sec	0	0	0	0	0	0	0	0	0	0	0	0
Total	99	100	101	100	230	100	353	100	314	100	364	100

¹ Gasteiger, E.; Hoogland, C.; Gattiker, A.; Duvaud, S.; Wilkins, M.R.; Appel, R.D.; Bairoch, A. Protein Identification and Analysis Tools on the ExPASy Server; (In) John M. Walker (ed): The Proteomics Protocols Handbook, Humana Press 2005, 571-607.

² Estimated using Protein Calculator v3.4 (<http://protcalc.sourceforge.net>)

³ Dominant residue types (9% or above) are highlighted for each region: acidic (blue), basic (red) or uncharged (gray).