

species	Deviation	Log Ratio	Domains	Average	Superfamily
<i>SC</i>	7.72%	4.12	2114	27.5	<u>SrcR-like</u>
	3.79%	1.71	1246	160.8	<u>Ankyrin repeat</u>
	2.47%	0.68	1344	503	<u>Protein kinase-like (PK-like)</u>
	2.30%	3.04	650	26.7	<u>TRAF domain-like</u>
	1.95%	1.38	701	145.9	<u>Fibronectin type III</u>
	1.89%	1.25	710	170.4	<u>EGF/Laminin</u>
	1.80%	3.23	503	13.5	<u>CalX-like</u>
	1.57%	0.68	852	367.8	<u>Immunoglobulin</u>
	1.47%	1.69	482	74.6	<u>Complement control module/SCR domain</u>
	1.37%	2.68	394	23.3	<u>DEATH domain</u>
	0.83%	0.15	1641	911.6	<u>P-loop containing nucleoside triphosphate hydrolases</u>
	0.78%	0.52	516	233.5	<u>RING/U-box</u>
	0.72%	1.5	246	40.9	<u>Kelch motif</u>
	0.66%	0.87	303	92.3	<u>E set domains</u>
	0.59%	2.44	172	10.6	<u>NHL repeat</u>
	0.52%	0.6	305	147.3	<u>Ribonuclease H-like</u>
	-0.57%	-1.23	60	175.2	<u>Family A G protein-coupled receptor-like</u>
	-0.58%	-0.71	148	191	<u>alpha/beta-Hydrolases</u>
	-0.64%	-0.7	166	231.4	<u>RNA-binding domain, RBD</u>
	-0.91%	-0.77	208	288.9	<u>ARM repeat</u>
-2.45%	-1.93	109	625	<u>beta-beta-alpha zinc fingers</u>	
<i>XT</i>	3.52%	0.51	1959	911.6	<u>P-loop containing nucleoside triphosphate hydrolases</u>
	3.50%	3.35	808	27.5	<u>SrcR-like</u>
	3.10%	1.05	1062	266.1	<u>NAD(P)-binding Rossmann-fold domains</u>
	1.79%	1.14	586	160.8	<u>Ankyrin repeat</u>
	1.30%	1.44	377	64.2	<u>PLP-dependent transferases</u>
	1.08%	2.02	275	27.8	<u>ClpP/crotonase</u>
	0.95%	2.13	238	21.1	<u>Alkaline phosphatase-like</u>
	0.79%	0.79	319	103.3	<u>Nucleic acid-binding proteins</u>
	0.72%	1.58	200	29.1	<u>Glutathione synthetase ATP-binding domain-like</u>
	0.69%	1.54	194	28.1	<u>Thiamin diphosphate-binding fold (THDP-binding)</u>
	0.59%	1.25	184	34.7	<u>Nucleotidyl transferase</u>
	0.56%	0.55	294	117.7	<u>FAD/NAD(P)-binding domain</u>
	0.55%	1.86	143	23.3	<u>DEATH domain</u>
	0.52%	0.59	262	145.9	<u>Fibronectin type III</u>
	0.50%	1.2	156	29.8	<u>Class II aaRS and biotin synthetases</u>
	0.50%	1	175	44	<u>Ribosomal protein S5 domain 2-like</u>
	-0.61%	-0.66	143	231.4	<u>RNA-binding domain, RBD</u>

-0.64%	-1.65	32	175.2	<u>Family A G protein-coupled receptor-like</u>
-0.84%	-0.68	189	288.9	<u>ARM repeat</u>
-0.88%	-0.99	114	212.6	<u>MFS general substrate transporter</u>
-0.90%	-0.44	360	503	<u>Protein kinase-like (PK-like)</u>
-2.52%	-2.14	73	625	<u>beta-beta-alpha zinc fingers</u>

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