Phyre^2

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Description	P32715
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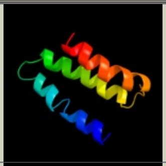
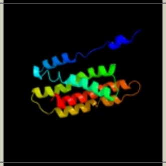
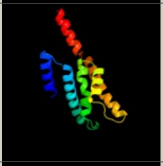
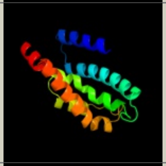
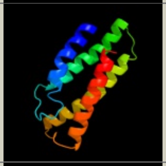
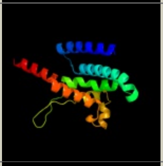
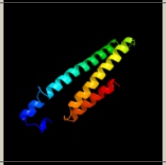
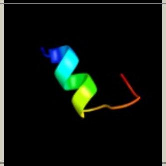
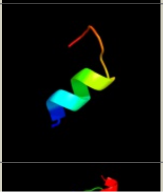
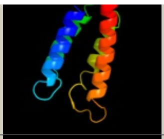
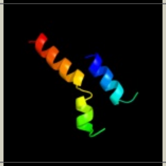
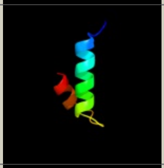
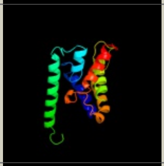
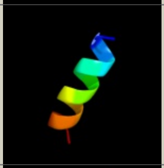
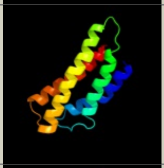
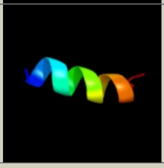
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2r6gf1	Alignment		32.8	10	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
2	c1oy8A_	Alignment		21.7	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
3	c2w2eA_	Alignment		21.0	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin; **PDBTitle:** 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
4	d1kpla_	Alignment		20.0	12	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
5	c3nd0A_	Alignment		19.4	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sll0855 protein; **PDBTitle:** x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
6	c2ht2B_	Alignment		16.1	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
7	d1st6a4	Alignment		13.8	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
8	d1otsa_	Alignment		13.0	17	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
9	d1szia_	Alignment		12.9	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain **Family:**Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
10	c1no1C_	Alignment		11.3	36	**PDB header:**replication **Chain:** C: **PDB Molecule:**replisome organizer; **PDBTitle:** structure of truncated variant of b.subtilis spp1 phage g39p helicase2 loader/inhibitor protein
11	d1no1a_	Alignment		11.3	36	**Fold:**Replisome organizer (g39p helicase loader/inhibitor protein) **Superfamily:**Replisome organizer (g39p helicase loader/inhibitor protein) **Family:**Replisome organizer (g39p helicase loader/inhibitor protein)
						

12	c2ksfA_	Alignment		11.2	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein kdpd; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor kdpd, center for structures of3 membrane proteins (csmp) target 4312c
13	c1bhbA_	Alignment		9.9	12	**PDB header:**photoreceptor **Chain:** A: **PDB Molecule:**bacteriorhodopsin; **PDBTitle:** three-dimensional structure of (1-71) bacterioopsin2 solubilized in methanol-chloroform and sds micelles3 determined by 15n-1h heteronuclear nmr spectroscopy
14	c1b9uA_	Alignment		9.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (atp synthase); **PDBTitle:** membrane domain of the subunit b of the e.coli atp synthase
15	c3su8X_	Alignment		8.5	13	**PDB header:**apoptosis/signaling protein **Chain:** X: **PDB Molecule:**plexin-b1; **PDBTitle:** crystal structure of a truncated intracellular domain of plexin-b1 in2 complex with rac1
16	c2d57A_	Alignment		8.4	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** double layered 2d crystal structure of aquaporin-4 (aqp4m23) at 3.2 a2 resolution by electron crystallography
17	c3g9dB_	Alignment		8.3	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dinitrogenase reductase activacting **PDBTitle:** crystal structure glycohydrolase
18	d1st6a3	Alignment		8.3	10	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
19	c2b5fD_	Alignment		8.3	15	**PDB header:**transport protein,membrane protein **Chain:** D: **PDB Molecule:**aquaporin; **PDBTitle:** crystal structure of the spinach aquaporin sopip2;1 in an2 open conformation to 3.9 resolution
20	c2wocA_	Alignment		8.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosyl-[dinitrogen reductase] glycohydrolase; **PDBTitle:** crystal structure of the dinitrogenase reductase-activating2 glycohydrolase (drag) from rhodospirillum rubrum
21	d2nwwa1	Alignment	not modelled	7.9	20	**Fold:**Proton glutamate symport protein **Superfamily:**Proton glutamate symport protein **Family:**Proton glutamate symport protein
22	c2f2bA_	Alignment	not modelled	7.8	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin aqpm; **PDBTitle:** crystal structure of integral membrane protein aquaporin aqpm at 1.68a2 resolution
23	c2xq2A_	Alignment	not modelled	7.7	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
24	c3hfwA_	Alignment	not modelled	7.5	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein adp-ribosylarginine hydrolase; **PDBTitle:** crystal structure of human adp-ribosylhydrolase 1 (harh1)
25	d1st6a5	Alignment	not modelled	7.4	7	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
26	c3gd8A_	Alignment	not modelled	7.3	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** crystal structure of human aquaporin 4 at 1.8 and its mechanism of2 conductance
27	d2e74d2	Alignment	not modelled	7.3	33	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
28	c2yvxD_	Alignment	not modelled	7.3	10	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
29	d1rc2a_	Alignment	not modelled	7.2	15	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like

30	c3dh4A_	Alignment	not modelled	7.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
31	c2qtyB_	Alignment	not modelled	6.8	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(adp-ribose) glycohydrolase arh3; **PDBTitle:** crystal structure of mouse adp-ribosylhydrolase 3 (marh3)
32	c2yzwA_	Alignment	not modelled	6.7	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosylglycohydrolase; **PDBTitle:** adp-ribosylglycohydrolase-related protein complex
33	c2hjdA_	Alignment	not modelled	6.7	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**quorum-sensing antiactivator; **PDBTitle:** crystal structure of a second quorum sensing antiactivator tram2 from2 a. tumefaciens strain a6
34	d1fx8a_	Alignment	not modelled	6.7	11	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
35	c1ldaA_	Alignment	not modelled	6.7	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycerol uptake facilitator protein; **PDBTitle:** crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
36	c3k3gA_	Alignment	not modelled	6.5	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**urea transporter; **PDBTitle:** crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
37	c3orgB_	Alignment	not modelled	6.5	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cmclc; **PDBTitle:** crystal structure of a eukaryotic clc transporter
38	c3ig3A_	Alignment	not modelled	6.0	29	**PDB header:**signaling protein, membrane protein **Chain:** A: **PDB Molecule:**plxna3 protein; **PDBTitle:** crystal strucure of mouse plexin a3 intracellular domain
39	c2l16A_	Alignment	not modelled	5.9	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**sec-independent protein translocase protein tatad; **PDBTitle:** solution structure of bacillus subtilits tatad protein in dpc micelles
40	c3hm6X_	Alignment	not modelled	5.8	13	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**plexin-b1; **PDBTitle:** crystal structure of the cytoplasmic domain of human plexin b1
41	d1t5ja_	Alignment	not modelled	5.8	31	**Fold:**ADP-ribosylglycohydrolase **Superfamily:**ADP-ribosylglycohydrolase **Family:**ADP-ribosylglycohydrolase
42	d1rfya_	Alignment	not modelled	5.6	15	**Fold:**Long alpha-hairpin **Superfamily:**Transcriptional repressor TraM **Family:**Transcriptional repressor TraM
43	d1rzhh2	Alignment	not modelled	5.3	38	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
44	d1ymga1	Alignment	not modelled	5.2	14	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
45	c1ymgA_	Alignment	not modelled	5.2	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein; **PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution
46	d1v54l_	Alignment	not modelled	5.2	13	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa) **Family:**Mitochondrial cytochrome c oxidase subunit VIIc (aka VIIIa)
47	c2wscL_	Alignment	not modelled	5.2	18	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem i reaction center subunit xi, **PDBTitle:** improved model of plant photosystem i
48	c2fhdA_	Alignment	not modelled	5.0	35	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains
49	c2o01L_	Alignment	not modelled	5.0	18	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem i reaction center subunit xi, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
50	d2axti1	Alignment	not modelled	5.0	8	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like