Phyre^2

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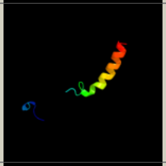
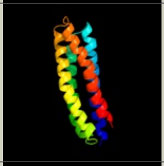
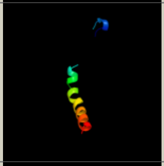
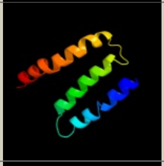
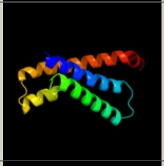
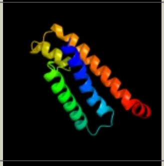
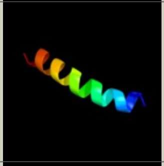
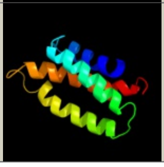
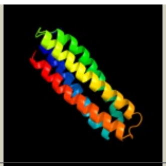
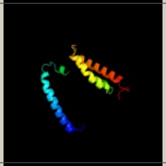
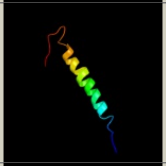
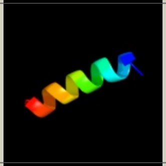
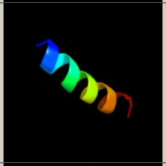
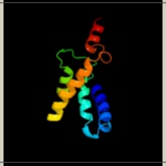
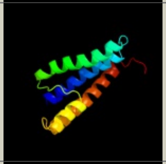
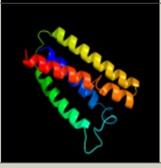
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rwta_	Alignment		19.6	22	**Fold:**Chlorophyll a-b binding protein **Superfamily:**Chlorophyll a-b binding protein **Family:**Chlorophyll a-b binding protein
2	c1oy8A_	Alignment		16.2	18	**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	d3cx5h1	Alignment		13.1	12	**Fold:**Single transmembrane helix **Superfamily:**Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
4	d2b0ha1	Alignment		12.7	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**VBS domain
5	c3cwbT_	Alignment		9.2	42	**PDB header:**oxidoreductase **Chain:** T: **PDB Molecule:**mitochondrial ubiquinol-cytochrome c reductase ubiquinone- **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
6	c3k07A_	Alignment		9.0	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
7	d2r6gf1	Alignment		8.6	8	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
8	d1fx8a_	Alignment		8.2	15	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
9	c1ldaA_	Alignment		8.2	15	**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
10	c2yzwA_	Alignment		8.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosylglycohydrolase; **PDBTitle:** adp-ribosylglycohydrolase-related protein complex
11	d1iwga8	Alignment		7.9	17	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain

12	c2kvpA_	Alignment		7.7	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the talin vbs3 domain, 1815-1973
13	c2xq2A_	Alignment		7.5	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
14	c2wse4_	Alignment		7.1	23	**PDB header:**photosynthesis **Chain:** 4: **PDB Molecule:**chlorophyll a-b binding protein p4, **PDBTitle:** improved model of plant photosystem i
15	c2wocA_	Alignment		6.8	28	**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
16	c3hfwA_	Alignment		6.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein adp-ribosylarginine hydrolase; **PDBTitle:** crystal structure of human adp-ribosylhydrolase 1 (harh1)
17	c3g9dB_	Alignment		6.7	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dinitrogenase reductase activacting **PDBTitle:** crystal structure glycohydrolase
18	c2ht2B_	Alignment		6.7	21	**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
19	d1j4na_	Alignment		6.7	9	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
20	c3oq3A_	Alignment		6.2	15	**PDB header:**cytokine/viral protein **Chain:** A: **PDB Molecule:**interferon alpha-5; **PDBTitle:** structural basis of type-i interferon sequestration by a poxvirus2 decoy receptor
21	d1otsa_	Alignment	not modelled	6.1	16	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
22	d2nwwa1	Alignment	not modelled	5.6	13	**Fold:**Proton glutamate symport protein **Superfamily:**Proton glutamate symport protein **Family:**Proton glutamate symport protein
23	c3kyiA_	Alignment	not modelled	5.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative histidine protein kinase; **PDBTitle:** crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
24	c1rkcA_	Alignment	not modelled	5.4	11	**PDB header:**cell adhesion, structural protein **Chain:** A: **PDB Molecule:**vinculin; **PDBTitle:** human vinculin head (1-258) in complex with talin's2 vinculin binding site 3 (residues 1944-1969)
25	c1iijA_	Alignment	not modelled	5.3	37	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**erbb-2 receptor protein-tyrosine kinase; **PDBTitle:** solution structure of the neu/erbb-2 membrane spanning2 segment
26	d1st6a3	Alignment	not modelled	5.3	9	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin