Phyre^2

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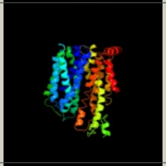
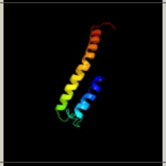
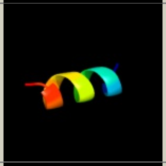
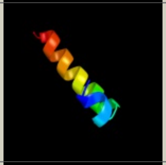
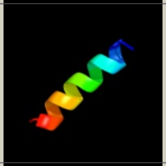
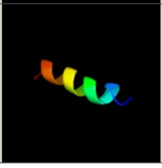
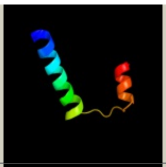
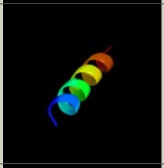
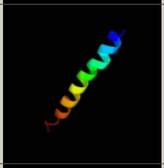
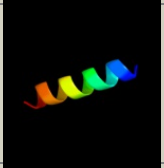
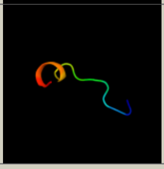
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	Alignment		100.0	11	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
2	d1pv7a_	Alignment		100.0	14	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
3	c2gfpA_	Alignment		99.9	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
4	c3o7pA_	Alignment		99.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
5	c2xutC_	Alignment		99.9	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**proton/peptide symporter family protein; **PDBTitle:** crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
6	c3qnqD_	Alignment		60.1	14	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
7	c1m46B_	Alignment		17.4	25	**PDB header:**cell cycle protein **Chain:** B: **PDB Molecule:**iq4 motif from myo2p, a class v myosin; **PDBTitle:** crystal structure of mlc1p bound to iq4 of myo2p, a class v2 myosin
8	c2kncB_	Alignment		15.7	14	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
9	c2rdcA_	Alignment		13.6	15	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative lipid binding protein (gsu0061) from2 geobacter sulfurreducens pca at 1.80 a resolution
10	c1l4aE_	Alignment		13.4	24	**PDB header:**endocytosis/exocytosis **Chain:** E: **PDB Molecule:**synaphin a; **PDBTitle:** x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
11	c1by0A_	Alignment		10.8	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen

12	c3d9sB_	Alignment		9.8	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin-5; **PDBTitle:** human aquaporin 5 (aqp5) - high resolution x-ray structure
13	d1sb0a_	Alignment		9.0	27	**Fold:**Kix domain of CBP (creb binding protein) **Superfamily:**Kix domain of CBP (creb binding protein) **Family:**Kix domain of CBP (creb binding protein)
14	d2p0ma1	Alignment		8.9	24	**Fold:**Lipoxigenase **Superfamily:**Lipoxigenase **Family:**Animal lipoxigenases
15	d2b5ua2	Alignment		7.9	14	**Fold:**Cloacin translocation domain **Superfamily:**Cloacin translocation domain **Family:**Cloacin translocation domain
16	c2rddB_	Alignment		7.6	10	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
17	c3d3lB_	Alignment		6.8	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arachidonate 12-lipoxygenase, 12s-type; **PDBTitle:** the 2.6 a crystal structure of the lipoxygenase domain of2 human arachidonate 12-lipoxygenase, 12s-type (casp target)
18	c2fnqB_	Alignment		6.4	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**allene oxide synthase-lipoxygenase protein; **PDBTitle:** insights from the x-ray crystal structure of coral 8r-2 lipoxygenase: calcium activation via a c2-like domain and3 a structural basis of product chirality
19	c1c94B_	Alignment		6.3	12	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**retro-gcn4 leucine zipper; **PDBTitle:** reversing the sequence of the gcn4 leucine zipper does not2 affect its fold.
20	c2kjeB_	Alignment		6.2	36	**PDB header:**transcription **Chain:** B: **PDB Molecule:**early e1a 32 kda protein; **PDBTitle:** nmr structure of cbp taz2 and adenoviral e1a complex
21	c2p0mB_	Alignment	not modelled	6.2	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arachidonate 15-lipoxygenase; **PDBTitle:** revised structure of rabbit reticulocyte 15s-lipoxygenase
22	c2oarA_	Alignment	not modelled	6.2	6	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
23	d1ymga1	Alignment	not modelled	6.2	8	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
24	c1ymgA_	Alignment	not modelled	6.2	8	**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
25	c3o8yA_	Alignment	not modelled	6.1	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arachidonate 5-lipoxygenase; **PDBTitle:** stable-5-lipoxygenase
26	c3mkuA_	Alignment	not modelled	5.7	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
27	d1j4na_	Alignment	not modelled	5.7	9	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
28	c1a92B_	Alignment	not modelled	5.6	13	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**delta antigen; **PDBTitle:** oligomerization domain of hepatitis delta antigen
						PDB header:membrane protein

29	c2w8aC_	Alignment	not modelled	5.4	8	**Chain:** C: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
30	c2hjmB_	Alignment	not modelled	5.4	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pf1176; **PDBTitle:** crystal structure of a singleton protein pf1176 from p. furiosus
31	c2kmfA_	Alignment	not modelled	5.3	25	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii 11 kda protein; **PDBTitle:** solution structure of psb27 from cyanobacterial photosystem2 ii
32	c3r4hD_	Alignment	not modelled	5.3	28	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**coiled coil helix cc-tet-phi22; **PDBTitle:** crystal structure of the 4-helix coiled coil cc-tet-phi22
33	c3r4hE_	Alignment	not modelled	5.0	28	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**coiled coil helix cc-tet-phi22; **PDBTitle:** crystal structure of the 4-helix coiled coil cc-tet-phi22