Phyre^2

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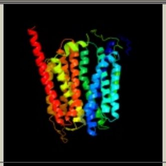
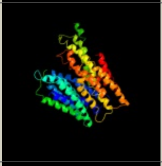
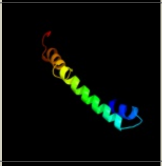
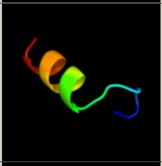
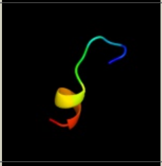
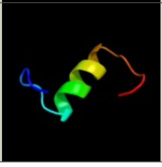
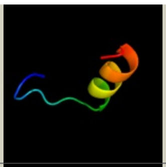
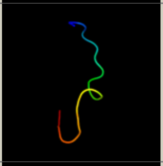
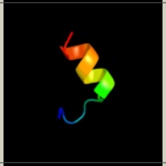
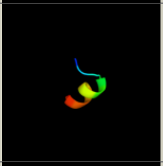
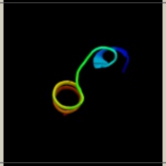
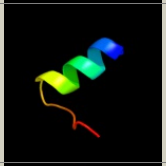
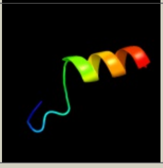
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	Alignment		100.0	15	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
2	c3o7pA_	Alignment		100.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
3	d1pv7a_	Alignment		100.0	12	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
4	c2gfpA_	Alignment		100.0	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
5	c2xutC_	Alignment		100.0	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		30.1	17	**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	c3b9yA_	Alignment		26.4	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
8	c3ff5B_	Alignment		25.7	25	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**peroxisomal biogenesis factor 14; **PDBTitle:** crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
9	d1fs1b1	Alignment		24.8	31	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
10	c3c9pA_	Alignment		19.3	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sp1917; **PDBTitle:** crystal structure of uncharacterized protein sp1917
11	c2w85A_	Alignment		18.6	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisomal membrane anchor protein pex14; **PDBTitle:** structure of pex14 in compex with pex19

12	d2j85a1	Alignment		15.5	20	**Fold:**STIV B116-like **Superfamily:**STIV B116-like **Family:**STIV B116-like
13	c2f9jP_	Alignment		15.4	28	**PDB header:**rna binding protein **Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1; **PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
14	d1ofcx1	Alignment		13.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
15	c2g9pA_	Alignment		12.9	36	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
16	d1fs2b1	Alignment		12.8	33	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
17	c1egpA_	Alignment		12.7	18	**PDB header:**proteinase inhibitor **Chain:** A: **PDB Molecule:**eglin-c; **PDBTitle:** proteinase inhibitor eglin c with hydrolysed reactive center
18	d2csba1	Alignment		12.2	35	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
19	c3hd6A_	Alignment		12.0	9	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
20	c3oc5A_	Alignment		11.6	42	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**toxin coregulated pilus biosynthesis protein f; **PDBTitle:** crystal structure of the vibrio cholerae secreted colonization factor2 tcpf
21	c3ervA_	Alignment	not modelled	11.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative c39-like peptidase; **PDBTitle:** crystal structure of an putative c39-like peptidase from2 bacillus anthracis
22	c3mmyF_	Alignment	not modelled	10.0	23	**PDB header:**nuclear protein **Chain:** F: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1
23	d1nexa1	Alignment	not modelled	9.8	25	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
24	d1u7ga_	Alignment	not modelled	8.8	8	**Fold:**Ammonium transporter **Superfamily:**Ammonium transporter **Family:**Ammonium transporter
25	d2ovra1	Alignment	not modelled	8.2	33	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
26	d1pyya2	Alignment	not modelled	7.9	22	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
27	d2id1a1	Alignment	not modelled	7.6	15	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
28	d2hkja1	Alignment	not modelled	7.1	18	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Topoisomerase VI-B subunit middle domain
						Fold: Lesion bypass DNA polymerase (Y-family), little finger domain

29	d1jx4a1	Alignment	not modelled	7.1	41	**Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
30	d1rp5a2	Alignment	not modelled	6.6	22	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
31	d1nh2d1	Alignment	not modelled	6.5	18	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
32	d1nvpd1	Alignment	not modelled	6.3	12	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
33	c1bzgA_	Alignment	not modelled	5.9	17	**PDB header:**hormone **Chain:** A: **PDB Molecule:**parathyroid hormone-related protein; **PDBTitle:** the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
34	d1ogmx1	Alignment	not modelled	5.8	26	**Fold:**Dextranase, N-terminal domain **Superfamily:**Dextranase, N-terminal domain **Family:**Dextranase, N-terminal domain
35	d1wmib1	Alignment	not modelled	5.8	27	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**RelB-like **Family:**RelB-like
36	d1cwpa_	Alignment	not modelled	5.8	41	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Bromoviridae-like VP
37	c3hm5A_	Alignment	not modelled	5.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna methyltransferase 1-associated protein 1; **PDBTitle:** sant domain of human dna methyltransferase 1 associated2 protein 1
38	d1k25a2	Alignment	not modelled	5.8	22	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
39	d3cx5c2	Alignment	not modelled	5.6	13	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
40	c1cwpB_	Alignment	not modelled	5.4	41	**PDB header:**virus/rna **Chain:** B: **PDB Molecule:**coat protein; **PDBTitle:** structures of the native and swollen forms of cowpea2 chlorotic mottle virus determined by x-ray crystallography3 and cryo-electron microscopy