Phyre^2

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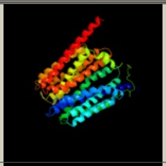
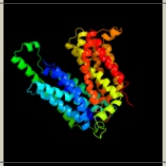
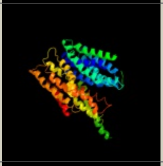
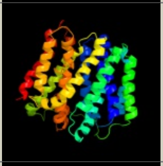
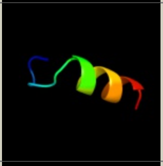
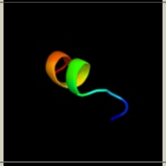
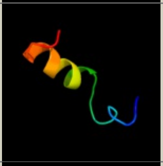
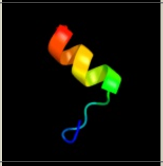
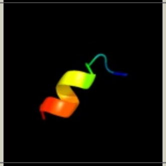
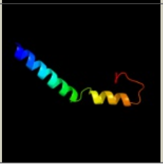
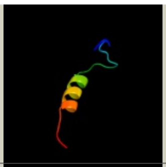
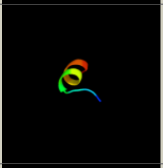
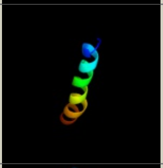
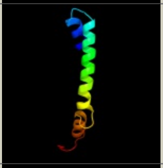
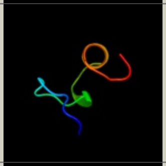
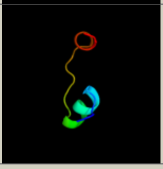
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	Alignment		100.0	13	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
2	c3o7pA_	Alignment		100.0	15	**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	13	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
4	c2xutC_	Alignment		100.0	12	**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.
5	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
6	c3ff5B_	Alignment		35.4	19	**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
7	d1fs1b1	Alignment		26.1	25	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
8	c3mmyF_	Alignment		25.5	27	**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
9	c2w85A_	Alignment		25.4	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisomal membrane anchor protein pex14; **PDBTitle:** structure of pex14 in compex with pex19
10	c3c9pA_	Alignment		21.5	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sp1917; **PDBTitle:** crystal structure of uncharacterized protein sp1917
11	c2wwaA_	Alignment		20.9	15	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**sec sixty-one protein homolog; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome

12	d1wmib1	Alignment		16.7	27	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**RelB-like **Family:**RelB-like
13	d1fs2b1	Alignment		16.1	25	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
14	d2j85a1	Alignment		15.8	25	**Fold:**STIV B116-like **Superfamily:**STIV B116-like **Family:**STIV B116-like
15	c2g9pA_	Alignment		13.7	43	**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	c1by0A_	Alignment		13.7	33	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
17	c3qnqD_	Alignment		12.5	13	**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
18	d1b78a_	Alignment		12.4	12	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
19	d1v7ra_	Alignment		11.9	12	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
20	d1nexa1	Alignment		11.9	16	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
21	c2f9jP_	Alignment	not modelled	11.6	22	**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
22	d2csba1	Alignment	not modelled	11.2	47	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
23	d2ovra1	Alignment	not modelled	10.5	25	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
24	d1ofcx1	Alignment	not modelled	8.0	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
25	c2kncB_	Alignment	not modelled	8.0	8	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
26	d2hkja1	Alignment	not modelled	7.8	21	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Topoisomerase VI-B subunit middle domain
27	c3f46A_	Alignment	not modelled	7.7	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methenyltetrahydromethanopterin hydrogenase; **PDBTitle:** the crystal structure of c176a mutated [fe]-hydrogenase (hmd)2 holoenzyme from methanocaldococcus jannaschii
28	d1k7ka_	Alignment	not modelled	7.6	8	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
						Fold:6-phosphogluconate dehydrogenase C-terminal domain-like

29	d2g5ca1	Alignment	not modelled	7.3	15	**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**TyrA dimerization domain-like
30	d2cara1	Alignment	not modelled	7.3	8	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
31	d1xpja_	Alignment	not modelled	6.3	26	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
32	c3oc5A_	Alignment	not modelled	6.2	32	**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
33	d1e3oc2	Alignment	not modelled	6.1	35	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
34	c1egpA_	Alignment	not modelled	6.1	13	**PDB header:**proteinase inhibitor **Chain:** A: **PDB Molecule:**eglin-c; **PDBTitle:** proteinase inhibitor eglin c with hydrolysed reactive center
35	c2xq2A_	Alignment	not modelled	6.0	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
36	d2a26a1	Alignment	not modelled	6.0	29	**Fold:**Long alpha-hairpin **Superfamily:**Calcyclin-binding protein-like **Family:**Siah interacting protein N terminal domain-like
37	d2a7wa1	Alignment	not modelled	6.0	7	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
38	c2a7wF_	Alignment	not modelled	6.0	7	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**phosphoribosyl-atp pyrophosphatase; **PDBTitle:** crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7
39	c3b9yA_	Alignment	not modelled	6.0	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
40	d1xtda2	Alignment	not modelled	5.8	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
41	d1ni8a_	Alignment	not modelled	5.8	36	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
42	d1ov9a_	Alignment	not modelled	5.7	27	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
43	d1y7oa1	Alignment	not modelled	5.7	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
44	c3ervA_	Alignment	not modelled	5.7	16	**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
45	c3hm5A_	Alignment	not modelled	5.6	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna methyltransferase 1-associated protein 1; **PDBTitle:** sant domain of human dna methyltransferase 1 associated2 protein 1
46	d1v54i_	Alignment	not modelled	5.5	11	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIc **Family:**Mitochondrial cytochrome c oxidase subunit VIc
47	c2p1nD_	Alignment	not modelled	5.4	25	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
48	d1pyya2	Alignment	not modelled	5.3	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
49	d2ipqx1	Alignment	not modelled	5.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**STY4665 C-terminal domain-like
50	c1cirA_	Alignment	not modelled	5.1	20	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**chymotrypsin inhibitor 2; **PDBTitle:** complex of two fragments of ci2 [(1-40)(dot)(41-64)]
51	d1xjsa_	Alignment	not modelled	5.1	7	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
52	d1xeqa1	Alignment	not modelled	5.1	60	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**N-terminal, RNA-binding domain of nonstructural protein NS1
53	c2rddB_	Alignment	not modelled	5.0	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.