Phyre^2

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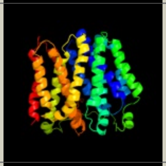
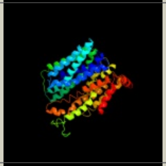
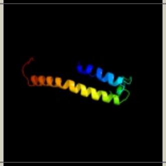
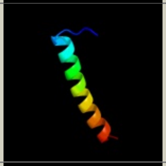
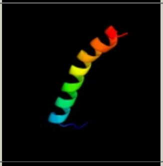
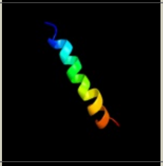
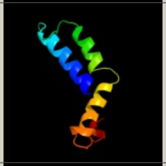
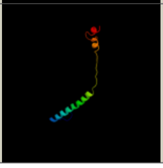
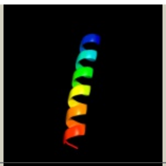
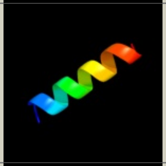
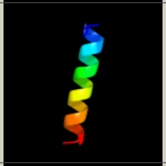
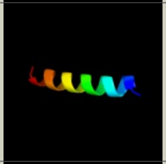
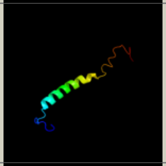
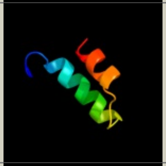
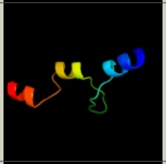
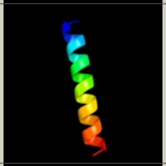
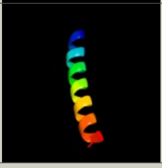
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pv7a_	Alignment		99.9	13	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
2	d1pw4a_	Alignment		99.9	13	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
3	c2gfpA_	Alignment		99.8	14	**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		99.8	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)
5	c2xutC_	Alignment		99.7	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		53.5	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	d2f23a1	Alignment		52.7	10	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
8	d1grja1	Alignment		36.1	24	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
9	c1by0A_	Alignment		28.0	28	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
10	d1ji6a3	Alignment		20.1	14	**Fold:**Toxins' membrane translocation domains **Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain
11	d1f6ga_	Alignment		18.6	13	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels

12	c2q7cC_	Alignment		18.2	22	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**fusion protein between yeast variant gcn4 and **PDBTitle:** crystal structure of iqn17
13	c1m46B_	Alignment		15.6	29	**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
14	d1xmpa_	Alignment		15.6	10	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
15	c1zxaB_	Alignment		13.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cgmp-dependent protein kinase 1, alpha isozyme; **PDBTitle:** solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
16	c2kncA_	Alignment		12.6	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
17	d2ce7a1	Alignment		11.7	13	**Fold:**FtsH protease domain-like **Superfamily:**FtsH protease domain-like **Family:**FtsH protease domain-like
18	d2oara1	Alignment		11.1	18	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
19	c1a92B_	Alignment		10.7	29	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**delta antigen; **PDBTitle:** oligomerization domain of hepatitis delta antigen
20	c2oqqB_	Alignment		10.2	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor hy5; **PDBTitle:** crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
21	c3onoA_	Alignment	not modelled	9.7	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
22	d1u69a_	Alignment	not modelled	9.4	27	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
23	c1ji6A_	Alignment	not modelled	9.2	14	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidial crystal protein cry3bb; **PDBTitle:** crystal structure of the insecticidal bacterial del2 endotoxin cry3bb1 bacillus thuringiensis
24	c3jqhA_	Alignment	not modelled	9.1	24	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**c-type lectin domain family 4 member m; **PDBTitle:** structure of the neck region of the glycan-binding receptor2 dc-signr
25	d1ab4a_	Alignment	not modelled	9.0	13	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
26	c2wl2B_	Alignment	not modelled	8.8	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
27	c3eh0C_	Alignment	not modelled	8.7	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n- **PDBTitle:** crystal structure of lpxd from escherichia coli
28	d1oqwa_	Alignment	not modelled	8.6	13	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin

29	d2pila_	Alignment	not modelled	8.4	11	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
30	c2l5gA_	Alignment	not modelled	8.4	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**g protein pathway suppressor 2; **PDBTitle:** co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
31	c2nuxB_	Alignment	not modelled	8.4	35	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate **PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
32	c2hjmB_	Alignment	not modelled	8.1	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pf1176; **PDBTitle:** crystal structure of a singleton protein pf1176 from p. furiosus
33	c2kwyA_	Alignment	not modelled	7.9	19	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**v-type proton atpase subunit g; **PDBTitle:** structure of g61-101
34	c1l4aE_	Alignment	not modelled	7.8	12	**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
35	c2jo8B_	Alignment	not modelled	7.7	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase 4; **PDBTitle:** solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
36	c2kmfA_	Alignment	not modelled	7.7	20	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii 11 kda protein; **PDBTitle:** solution structure of psb27 from cyanobacterial photosystem2 ii
37	d2h8aa1	Alignment	not modelled	7.7	7	**Fold:**MAPEG domain-like **Superfamily:**MAPEG domain-like **Family:**MAPEG domain
38	c2novD_	Alignment	not modelled	7.6	21	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** breakage-reunion domain of s.pneumoniae topo iv: crystal2 structure of a gram-positive quinolone target
39	c2w8aC_	Alignment	not modelled	7.0	9	**PDB header:**membrane protein **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
40	c3eb7B_	Alignment	not modelled	6.9	18	**PDB header:**toxin **Chain:** B: **PDB Molecule:**insecticidal delta-endotoxin cry8ea1; **PDBTitle:** crystal structure of insecticidal delta-endotoxin cry8ea1 from2 bacillus thuringiensis at 2.2 angstroms resolution
41	c2y6xA_	Alignment	not modelled	6.7	20	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii 11 kd protein; **PDBTitle:** structure of psb27 from thermosynechococcus elongatus
42	c2xzrA_	Alignment	not modelled	6.7	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**immunoglobulin-binding protein eibd; **PDBTitle:** escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
43	d2cqea1	Alignment	not modelled	6.7	11	**Fold:**CCCH zinc finger **Superfamily:**CCCH zinc finger **Family:**CCCH zinc finger
44	d1fx0a1	Alignment	not modelled	6.7	11	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
45	d1ez4a2	Alignment	not modelled	6.6	23	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
46	c1tjlD_	Alignment	not modelled	6.5	0	**PDB header:**transcription **Chain:** D: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** crystal structure of transcription factor dksa from e. coli
47	c3c5yD_	Alignment	not modelled	6.5	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
48	d1i9za_	Alignment	not modelled	6.1	22	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Inositol polyphosphate 5-phosphatase (IPP5)
49	c1zvuA_	Alignment	not modelled	6.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit a; **PDBTitle:** structure of the full-length e. coli parc subunit
50	c3qx3B_	Alignment	not modelled	5.9	18	**PDB header:**isomerase/dna/isomerase inhibitor **Chain:** B: **PDB Molecule:**dna topoisomerase 2-beta; **PDBTitle:** human topoisomerase iibeta in complex with dna and etoposide
51	c2rpaA_	Alignment	not modelled	5.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**katanin p60 atpase-containing subunit a1; **PDBTitle:** the solution structure of n-terminal domain of microtubule severing2 enzyme
52	c3ilwA_	Alignment	not modelled	5.9	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** structure of dna gyrase subunit a n-terminal domain
53	d1h41a2	Alignment	not modelled	5.8	19	**Fold:**Zincin-like **Superfamily:**beta-N-acetylhexosaminidase-like domain **Family:**alpha-D-glucuronidase, N-terminal domain
						Fold: Toxins' membrane translocation domains

54	d1ciya3	Alignment	not modelled	5.7	20	**Superfamily:**delta-Endotoxin (insectocide), N-terminal domain **Family:**delta-Endotoxin (insectocide), N-terminal domain
55	c2inrA_	Alignment	not modelled	5.7	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
56	d2ba0d2	Alignment	not modelled	5.6	15	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
57	c2c5iT_	Alignment	not modelled	5.6	23	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**t-snare affecting a late golgi compartment **PDBTitle:** n-terminal domain of tlg1 complexed with n-terminus of2 vps51 in distorted conformation
58	d2b5ua2	Alignment	not modelled	5.5	17	**Fold:**Cloacin translocation domain **Superfamily:**Cloacin translocation domain **Family:**Cloacin translocation domain
59	d1k1xa1	Alignment	not modelled	5.5	11	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Families 57/38 glycoside transferase middle domain **Family:**4-alpha-glucanotransferase, domain 2
60	c3ifzA_	Alignment	not modelled	5.5	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of the first part of the mycobacterium tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution
61	d1pv0a_	Alignment	not modelled	5.5	22	**Fold:**Long alpha-hairpin **Superfamily:**Sporulation inhibitor Sda **Family:**Sporulation inhibitor Sda
62	d2ia9a1	Alignment	not modelled	5.5	7	**Fold:**SpoVG-like **Superfamily:**SpoVG-like **Family:**SpoVG-like
63	c3d3lB_	Alignment	not modelled	5.4	16	**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)
64	c1jy2O_	Alignment	not modelled	5.4	14	**PDB header:**blood clotting **Chain:** O: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of the central region of bovine2 fibrinogen (e5 fragment) at 1.4 angstroms resolution
65	c1nohB_	Alignment	not modelled	5.3	14	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**head morphogenesis protein; **PDBTitle:** the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
66	c2l16A_	Alignment	not modelled	5.3	15	**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
67	c2zxrA_	Alignment	not modelled	5.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**single-stranded dna specific exonuclease recj; **PDBTitle:** crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8
68	c2kluA_	Alignment	not modelled	5.2	10	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
69	d1rype_	Alignment	not modelled	5.2	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
70	d1bjta_	Alignment	not modelled	5.2	9	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
71	c1bjtA_	Alignment	not modelled	5.2	9	**PDB header:**topoisomerase **Chain:** A: **PDB Molecule:**topoisomerase ii; **PDBTitle:** topoisomerase ii residues 409-1201
72	c2yggA_	Alignment	not modelled	5.2	25	**PDB header:**metal binding protein/transport protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** complex of cambr and cam
73	c2q9qC_	Alignment	not modelled	5.2	7	**PDB header:**replication **Chain:** C: **PDB Molecule:**dna replication complex gins protein psf1; **PDBTitle:** the crystal structure of full length human gins complex
74	c3sokB_	Alignment	not modelled	5.1	17	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
75	c3s2xB_	Alignment	not modelled	5.1	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa synthase subunit alpha; **PDBTitle:** structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
76	d2p0ma1	Alignment	not modelled	5.1	16	**Fold:**Lipoxigenase **Superfamily:**Lipoxigenase **Family:**Animal lipoxigenases
77	d1tsja_	Alignment	not modelled	5.1	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase