Phyre²

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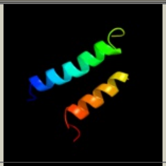
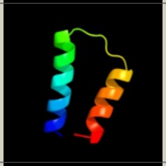
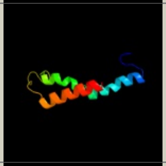
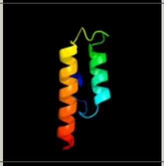
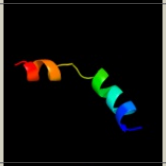
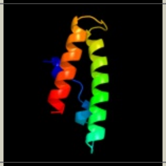
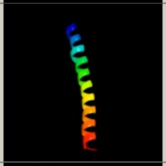
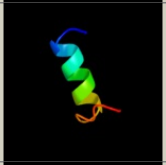
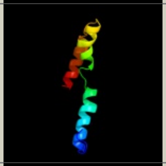
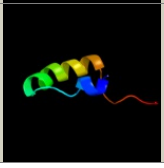
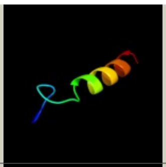
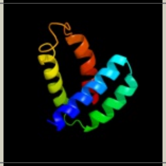
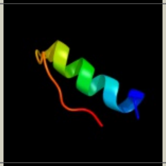
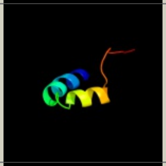
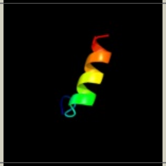
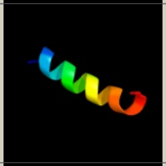
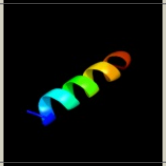
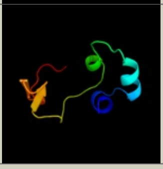
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dmwA_	Alignment		37.4	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**synaptobrevin-like 1 variant; **PDBTitle:** solution structure of the longin domain of synaptobrevin-2 like protein 1
2	c3aqpB_	Alignment		23.9	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
3	d1ljra1	Alignment		21.6	13	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
4	d1iyxa2	Alignment		19.2	24	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
5	c2jttD_	Alignment		17.2	13	**PDB header:**calcium binding protein/antitumor protei **Chain:** D: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** solution structure of calcium loaded s100a6 bound to c-2 terminal siah-1 interacting protein
6	c1zroB_	Alignment		16.6	12	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**erythrocyte binding antigen region ii; **PDBTitle:** crystal structure of eba-175 region ii (rii) crystallized2 in the presence of (alpha)2,3-sialyllactose
7	c3htkB_	Alignment		15.8	13	**PDB header:**recombination/replication/ligase **Chain:** B: **PDB Molecule:**structural maintenance of chromosomes protein 5; **PDBTitle:** crystal structure of mms21 and smc5 complex
8	d1v97a1	Alignment		14.8	20	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
9	d1oaia_	Alignment		13.9	16	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
10	d1axda1	Alignment		13.2	16	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
11	d1hh4e_	Alignment		13.1	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like

12	c1yx5A_	Alignment		12.6	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**26s proteasome non-atpase regulatory subunit 4; **PDBTitle:** solution structure of s5a uim-1/ubiquitin complex
13	c1yhuW_	Alignment		11.2	8	**PDB header:**oxygen storage/transport **Chain:** W: **PDB Molecule:**hemoglobin b1a chain; **PDBTitle:** crystal structure of riftia pachyptila c1 hemoglobin reveals novel2 assembly of 24 subunits.
14	d2i4ra1	Alignment		10.9	35	**Fold:**AtpF-like **Superfamily:**AtpF-like **Family:**AtpF-like
15	d1ds6b_	Alignment		10.9	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
16	c3bd0D_	Alignment		10.8	11	**PDB header:**peptide binding protein **Chain:** D: **PDB Molecule:**protein memo1; **PDBTitle:** crystal structure of memo, form ii
17	d3cx5d2	Alignment		10.3	17	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
18	d1ppjd2	Alignment		10.2	28	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
19	c2j96B_	Alignment		10.0	22	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**phycoerythrocyanin alpha chain; **PDBTitle:** the e-configuration of alfa-phycoerythrocyanin
20	c3c9pA_	Alignment		9.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sp1917; **PDBTitle:** crystal structure of uncharacterized protein sp1917
21	c1l2aD_	Alignment	not modelled	9.7	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
22	d1l1ya_	Alignment	not modelled	9.7	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
23	d1go5a_	Alignment	not modelled	9.7	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
24	d1vmja_	Alignment	not modelled	9.4	23	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
25	d1k3ra2	Alignment	not modelled	9.3	19	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
26	c2kdtA_	Alignment	not modelled	9.3	50	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**neuroendocrine convertase 1; **PDBTitle:** pc1/3 dcsg sorting domain structure in dpc
27	d1t3qa1	Alignment	not modelled	9.1	11	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
28	d2ebfx1	Alignment	not modelled	8.9	18	**Fold:**PMT central region-like **Superfamily:**PMT central region-like **Family:**PMT central region-like
						Fold:S15/NS1 RNA-binding domain

29	d1xeqa1	Alignment	not modelled	8.7	50	**Superfamily:**S15/NS1 RNA-binding domain **Family:**N-terminal, RNA-binding domain of nonstructural protein NS1
30	c2vh3B_	Alignment	not modelled	8.6	29	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**ranasmurfin; **PDBTitle:** ranasmurfin
31	c3r66A_	Alignment	not modelled	8.5	50	**PDB header:**viral protein/antiviral protein **Chain:** A: **PDB Molecule:**non-structural protein 1; **PDBTitle:** crystal structure of human isg15 in complex with ns1 n-terminal region2 from influenza virus b, northeast structural genomics consortium3 target ids hx6481, hr2873, and or2
32	d1t33a1	Alignment	not modelled	8.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
33	c3cloC_	Alignment	not modelled	8.3	14	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
34	c2qr4B_	Alignment	not modelled	8.2	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase m3b, oligoendopeptidase f; **PDBTitle:** crystal structure of oligoendopeptidase-f from enterococcus faecium
35	c2jp7A_	Alignment	not modelled	8.2	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**mrna export factor mex67; **PDBTitle:** nmr structure of the mex67 uba domain
36	d1f1sa1	Alignment	not modelled	8.1	21	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Hyaluronate lyase-like catalytic, N-terminal domain
37	d1s29a_	Alignment	not modelled	8.1	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
38	d1doab_	Alignment	not modelled	8.0	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
39	d1r2za1	Alignment	not modelled	7.9	36	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
40	d1q33a_	Alignment	not modelled	7.9	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
41	c1bm4A_	Alignment	not modelled	7.8	38	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (moloney murine leukemia virus capsid); **PDBTitle:** momlv capsid protein major homology region peptide analog
42	d1vi0a2	Alignment	not modelled	7.6	15	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
43	d1u7ka_	Alignment	not modelled	7.4	20	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
44	d1ee8a1	Alignment	not modelled	7.4	43	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
45	d1j2za_	Alignment	not modelled	7.3	19	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
46	d1g9ga_	Alignment	not modelled	7.2	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
47	c2rrfA_	Alignment	not modelled	7.2	35	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**zinc finger fyve domain-containing protein 21; **PDBTitle:** the solution structure of the c-terminal region of zinc finger fyve2 domain-containing protein 21
48	c1wyoA_	Alignment	not modelled	7.1	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**microtubule-associated protein rp/eb family **PDBTitle:** solution structure of the ch domain of human microtubule-2 associated protein rp/eb family member 3
49	d1utga_	Alignment	not modelled	7.1	18	**Fold:**Uteroglobin-like **Superfamily:**Uteroglobin-like **Family:**Uteroglobin-like
50	d1rm6c1	Alignment	not modelled	7.0	15	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
51	d2cqka1	Alignment	not modelled	7.0	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
52	c2r8uA_	Alignment	not modelled	6.9	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**microtubule-associated protein rp/eb family **PDBTitle:** structure of fragment of human end-binding protein 1 (eb1)2 containing the n-terminal domain at 1.35 a resolution
53	c2p6cB_	Alignment	not modelled	6.8	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**aq_2013 protein; **PDBTitle:** crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
54	d1i3da_	Alignment	not modelled	6.6	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins

55	d1cb8a1	Alignment	not modelled	6.5	12	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Hyaluronate lyase-like catalytic, N-terminal domain
56	c2veqA_	Alignment	not modelled	6.4	40	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** insights into kinetochore-dna interactions from the2 structure of cep3p
57	c1x1jA_	Alignment	not modelled	6.3	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**xanthan lyase; **PDBTitle:** crystal structure of xanthan lyase (n194a) with a substrate.
58	d1w6ta2	Alignment	not modelled	6.1	24	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
59	c3n8bB_	Alignment	not modelled	6.0	13	**PDB header:**nucleic acid binding protein **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
60	c1rm6F_	Alignment	not modelled	6.0	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
61	d1l2la_	Alignment	not modelled	5.9	36	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
62	d1jroa1	Alignment	not modelled	5.9	16	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
63	d2h8aa1	Alignment	not modelled	5.8	15	**Fold:**MAPEG domain-like **Superfamily:**MAPEG domain-like **Family:**MAPEG domain
64	c3zvrA_	Alignment	not modelled	5.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dynamin-1; **PDBTitle:** crystal structure of dynamin
65	d1m22a_	Alignment	not modelled	5.8	25	**Fold:**Amidase signature (AS) enzymes **Superfamily:**Amidase signature (AS) enzymes **Family:**Amidase signature (AS) enzymes
66	d1alla_	Alignment	not modelled	5.7	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
67	d1tw9a1	Alignment	not modelled	5.7	12	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
68	c1cb8A_	Alignment	not modelled	5.6	5	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (chondroitinase ac); **PDBTitle:** chondroitinase ac lyase from flavobacterium heparinum
69	c3nm7D_	Alignment	not modelled	5.6	13	**PDB header:**nucleic acid binding protein **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
70	c2rddB_	Alignment	not modelled	5.5	11	**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.
71	c1q0wA_	Alignment	not modelled	5.5	40	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein **PDBTitle:** solution structure of vps27 amino-terminal uim-ubiquitin2 complex
72	d1n9wa2	Alignment	not modelled	5.4	21	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
73	d1ccda_	Alignment	not modelled	5.4	15	**Fold:**Uteroglobin-like **Superfamily:**Uteroglobin-like **Family:**Uteroglobin-like
74	c3snhA_	Alignment	not modelled	5.3	17	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**dynamin-1; **PDBTitle:** crystal structure of nucleotide-free human dynamin1
75	c1k3rA_	Alignment	not modelled	5.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mt0001; **PDBTitle:** crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
76	d1ffva1	Alignment	not modelled	5.2	9	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
77	d1k1xa1	Alignment	not modelled	5.1	26	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Families 57/38 glycoside transferase middle domain **Family:**4-alpha-glucanotransferase, domain 2
78	c3b9yA_	Alignment	not modelled	5.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein