Phyre²

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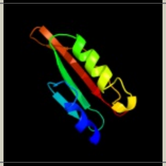
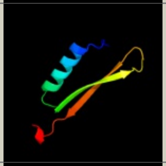
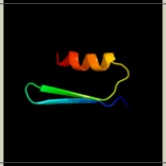
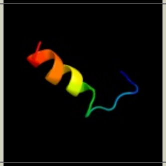
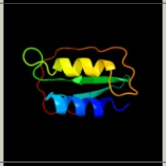
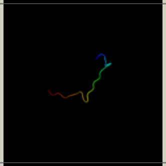
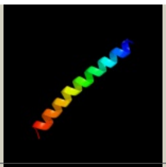
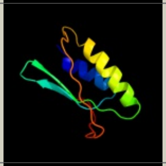
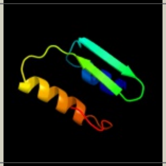
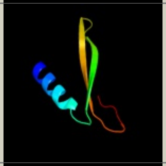
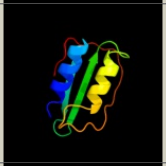
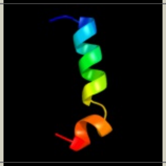
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rjzA_	Alignment		96.9	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pilo protein; **PDBTitle:** crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
2	c2w7vB_	Alignment		61.4	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**general secretion pathway protein l; **PDBTitle:** periplasmic domain of epsl from vibrio parahaemolyticus
3	c3mc8A_	Alignment		49.0	6	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**alr2269 protein; **PDBTitle:** potra1-3 of the periplasmic domain of omp85 from anabaena
4	c2x8xX_	Alignment		27.2	13	**PDB header:**chaperone **Chain:** X: **PDB Molecule:**tlr1789 protein; **PDBTitle:** structure of the n-terminal domain of omp85 from the2 thermophilic cyanobacterium thermosynechococcus elongatus
5	c2kgsA_	Alignment		26.3	29	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** solution structure of the amino-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
6	c2j8pA_	Alignment		23.3	26	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 64 kda subunit; **PDBTitle:** nmr structure of c-terminal domain of human cstf-64
7	d1w2ia_	Alignment		23.0	14	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
8	c1uv7A_	Alignment		22.8	10	**PDB header:**transport **Chain:** A: **PDB Molecule:**general secretion pathway protein m; **PDBTitle:** periplasmic domain of epsm from vibrio cholerae
9	d1uv7a_	Alignment		22.8	10	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**General secretion pathway protein M, EpsM **Family:**General secretion pathway protein M, EpsM
10	c2kxyA_	Alignment		19.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of sur18c from streptococcus thermophilus.2 northeast structural genomics consortium target sur18c
11	c3og5A_	Alignment		17.3	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**outer membrane protein assembly complex, yaet protein; **PDBTitle:** crystal structure of bama potra45 tandem

12	c3hd7A_	Alignment		16.0	12	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
13	c3br8A_	Alignment		14.7	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** crystal structure of acylphosphatase from bacillus subtilis
14	c3ibwA_	Alignment		14.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
15	c3qq5A_	Alignment		13.4	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**small gtp-binding protein; **PDBTitle:** crystal structure of the [fefe]-hydrogenase maturation protein hydf
16	c3k2kA_	Alignment		13.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative carboxypeptidase; **PDBTitle:** crystal structure of putative carboxypeptidase (yp_103406.1) from2 burkholderia mallei atcc 23344 at 2.49 a resolution
17	d1ulra_	Alignment		13.0	15	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
18	d1gnwa1	Alignment		11.8	9	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
19	d2enda_	Alignment		11.0	7	**Fold:**T4 endonuclease V **Superfamily:**T4 endonuclease V **Family:**T4 endonuclease V
20	c2hsmA_	Alignment		10.9	18	**PDB header:**ligase/rna binding protein **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase, cytoplasmic; **PDBTitle:** structural basis of yeast aminoacyl-trna synthetase complex2 formation revealed by crystal structures of two binary sub-3 complexes
21	d1pmta1	Alignment	not modelled	10.8	13	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
22	d2awna1	Alignment	not modelled	10.4	63	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
23	c1qcrD_	Alignment	not modelled	10.1	11	**PDB header:** **PDB COMPND:**
24	c2x3dC_	Alignment	not modelled	9.6	11	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**sso6206; **PDBTitle:** crystal structure of sso6206 from sulfolobus solfataricus p2
25	c3lygA_	Alignment	not modelled	9.5	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of ntf2-like protein of unknown function2 (yp_270605.1) from colwellia psychrerythraea 34h at 1.61 a resolution
26	d3bzfa1	Alignment	not modelled	8.9	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
27	d1vm0a_	Alignment	not modelled	8.8	12	**Fold:**IF3-like **Superfamily:**AlbA-like **Family:**Hypothetical protein At2g34160
28	d1dx4a_	Alignment	not modelled	8.2	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
						PDB header:hydrolase/toxin

29	c1f8uA_	Alignment	not modelled	8.0	11	**Chain:** A: **PDB Molecule:**acetylcholinesterase; **PDBTitle:** crystal structure of mutant e202q of human acetylcholinesterase2 complexed with green mamba venom peptide fasciculin-ii
30	d1f8ua_	Alignment	not modelled	8.0	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
31	c1p84D_	Alignment	not modelled	7.9	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
32	d2ha2a1	Alignment	not modelled	7.6	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
33	d1rl2a1	Alignment	not modelled	7.5	18	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**C-terminal domain of ribosomal protein L2
34	c3ipfA_	Alignment	not modelled	7.4	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q251q8_deshy protein from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr8c.
35	d1qo3a1	Alignment	not modelled	7.4	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
36	c2l5gB_	Alignment	not modelled	7.4	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative uncharacterized protein ncor2; **PDBTitle:** co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
37	d1ea5a_	Alignment	not modelled	7.3	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
38	d2cyya2	Alignment	not modelled	7.3	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
39	c2akrA_	Alignment	not modelled	7.3	19	**PDB header:**immune system **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd1d1; **PDBTitle:** structural basis of sulfatide presentation by mouse cd1d
40	d1onqa1	Alignment	not modelled	7.2	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
41	c2l26A_	Alignment	not modelled	7.1	29	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** rv0899 from mycobacterium tuberculosis contains two separated domains
42	c2jsxA_	Alignment	not modelled	6.9	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein napd; **PDBTitle:** solution structure of the e. coli tat proofreading2 chaperone protein napd
43	c1xz0A_	Alignment	not modelled	6.8	19	**PDB header:**immune system **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd1a; **PDBTitle:** crystal structure of cd1a in complex with a synthetic mycobactin2 lipopeptide
44	d1f6ga_	Alignment	not modelled	6.8	7	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
45	c3af5A_	Alignment	not modelled	6.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404; **PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
46	c1cpbA_	Alignment	not modelled	6.6	13	**PDB header:**hydrolase (c-terminal peptidase) **Chain:** A: **PDB Molecule:**carboxypeptidase b; **PDBTitle:** structure of carboxypeptidase b at 2.8 angstroms resolution
47	d2raqa1	Alignment	not modelled	6.5	15	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
48	d1n2aa1	Alignment	not modelled	6.5	5	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
49	c1kdxB_	Alignment	not modelled	6.4	28	**PDB header:**transcription regulation complex **Chain:** B: **PDB Molecule:**creb; **PDBTitle:** kix domain of mouse cbp (creb binding protein) in complex2 with phosphorylated kinase inducible domain (pkid) of rat3 creb (cyclic amp response element binding protein), nmr 174 structures
50	d1j5ya2	Alignment	not modelled	6.3	8	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain
51	d2cqla1	Alignment	not modelled	6.1	39	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
52	d2axtj1	Alignment	not modelled	6.1	18	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein J, PsbJ **Family:**PsbJ-like
53	c2uvaI_	Alignment	not modelled	6.1	22	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400

54	d1k4ya_	Alignment	not modelled	6.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
55	c3l2nA_	Alignment	not modelled	6.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m14, carboxypeptidase a; **PDBTitle:** crystal structure of putative carboxypeptidase a (yp_562911.1) from2 shewanella denitrificans os-217 at 2.39 a resolution
56	d3bpda1	Alignment	not modelled	6.0	11	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
57	c1qysA_	Alignment	not modelled	5.8	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
58	d1p0ia_	Alignment	not modelled	5.7	8	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
59	c2e0gA_	Alignment	not modelled	5.7	32	**PDB header:**replication **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** dnaa n-terminal domain
60	c2pm8A_	Alignment	not modelled	5.6	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cholinesterase; **PDBTitle:** crystal structure of recombinant full length human2 butyrylcholinesterase
61	c1gzpA_	Alignment	not modelled	5.6	15	**PDB header:**glycoprotein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd1b; **PDBTitle:** cd1b in complex with gm2 ganglioside
62	c2qczA_	Alignment	not modelled	5.5	10	**PDB header:**membrane protein, protein transport **Chain:** A: **PDB Molecule:**outer membrane protein assembly factor yaet; **PDBTitle:** structure of n-terminal domain of e. coli yaet
63	d1rl6a1	Alignment	not modelled	5.5	33	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
64	c2uz8A_	Alignment	not modelled	5.5	0	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**eukaryotic translation elongation factor 1 **PDBTitle:** the crystal structure of p18, human translation elongation2 factor 1 epsilon 1
65	c1cd1C_	Alignment	not modelled	5.5	16	**PDB header:**cd1 **Chain:** C: **PDB Molecule:**cd1; **PDBTitle:** cd1(mouse) antigen presenting molecule
66	c2xr1B_	Alignment	not modelled	5.4	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
67	d1qe3a_	Alignment	not modelled	5.4	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
68	c1gnwA_	Alignment	not modelled	5.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** structure of glutathione s-transferase
69	d2vjva1	Alignment	not modelled	5.4	3	**Fold:**Ferredoxin-like **Superfamily:**Transposase IS200-like **Family:**Transposase IS200-like
70	c2vhgB_	Alignment	not modelled	5.3	3	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**transposase orfa; **PDBTitle:** crystal structure of the ishp608 transposase in complex2 with right end 31-mer dna
71	d2zjre2	Alignment	not modelled	5.3	28	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
72	c1t7wA_	Alignment	not modelled	5.3	14	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**zinc-alpha-2-glycoprotein; **PDBTitle:** zn-alpha-2-glycoprotein; cho-zag peg 400
73	c2kncA_	Alignment	not modelled	5.2	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
74	c2ogsA_	Alignment	not modelled	5.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thermostable carboxylesterase est50; **PDBTitle:** crystal structure of the geobacillus stearothermophilus2 carboxylesterase est55 at ph 6.2
75	c2gv1A_	Alignment	not modelled	5.2	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** nmr solution structure of the acylphosphatase from2 eschaerichia coli
76	c3efcA_	Alignment	not modelled	5.1	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein assembly factor yaet; **PDBTitle:** crystal structure of yaet periplasmic domain
77	c2zxxA_	Alignment	not modelled	5.1	13	**PDB header:**cell cycle/replication **Chain:** A: **PDB Molecule:**geminin; **PDBTitle:** crystal structure of cdt1/geminin complex
78	c4a1eE_	Alignment	not modelled	5.1	11	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**60s ribosomal protein l9; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
79	d1f6wa_	Alignment	not modelled	5.0	5	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like