Phyre^2

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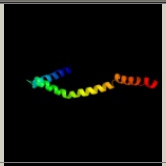
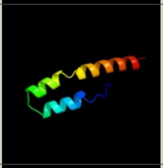
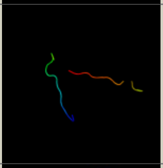
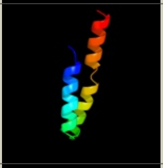
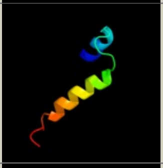
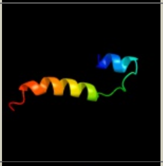
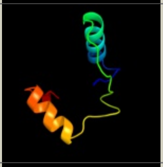
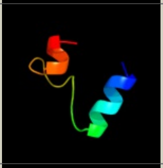
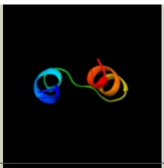
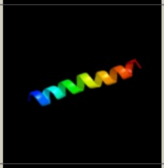
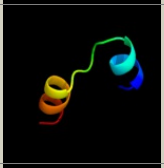
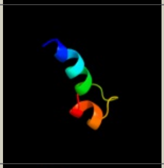
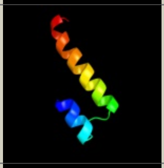
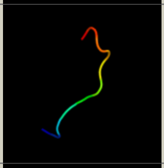
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w8aC_	Alignment		64.8	11	**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
2	d1jkva_	Alignment		22.1	15	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Manganese catalase (T-catalase)
3	d1go5a_	Alignment		19.7	8	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
4	c2qwuB_	Alignment		17.8	35	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**intracellular growth locus, subunit c; **PDBTitle:** crystal structure of f. tularensis pathogenicity island2 protein c
5	d2cwla1	Alignment		16.4	18	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Manganese catalase (T-catalase)
6	d1oaia_	Alignment		16.2	8	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
7	d1joga_	Alignment		15.3	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Family 1 bi-partite nucleotidyltransferase subunit
8	d1wtya_	Alignment		14.7	18	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Family 1 bi-partite nucleotidyltransferase subunit
9	c3gkxB_	Alignment		14.3	2	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative arsc family related protein; **PDBTitle:** crystal structure of putative arsc family related protein from2 bacteroides fragilis
10	c3cuqA_	Alignment		14.2	30	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
11	c2zmeA_	Alignment		13.5	30	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex

12	d2gykb1	Alignment		13.2	23	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
13	d1e8oa_	Alignment		12.9	10	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
14	c2rddB_	Alignment		12.4	8	**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.
15	c2jobA_	Alignment		12.1	30	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
16	c1914A_	Alignment		12.0	23	**PDB header:**alu domain **Chain:** A: **PDB Molecule:**signal recognition particle 9/14 fusion protein; **PDBTitle:** signal recognition particle alu rna binding heterodimer, srp9/14
17	c1zdbA_	Alignment		11.9	25	**PDB header:**igg binding domain **Chain:** A: **PDB Molecule:**mini protein a domain, z38; **PDBTitle:** phage-selected mini protein a domain, z38, nmr, minimized2 mean structure
18	c1wwpA_	Alignment		11.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha0636; **PDBTitle:** crystal structure of ttk003001694 from thermus thermophilus2 hb8
19	d2rh2a1	Alignment		10.6	45	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**R67 dihydrofolate reductase
20	d1qqra_	Alignment		9.0	42	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
21	c3fz4A_	Alignment	not modelled	8.6	2	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** the crystal structure of a possible arsenate reductase from2 streptococcus mutans ua159
22	d1dd4d_	Alignment	not modelled	8.4	27	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
23	d1f6va_	Alignment	not modelled	8.2	20	**Fold:**C-terminal domain of B transposition protein **Superfamily:**C-terminal domain of B transposition protein **Family:**C-terminal domain of B transposition protein
24	c2vqcA_	Alignment	not modelled	7.9	17	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**hypothetical 13.2 kda protein; **PDBTitle:** structure of a dna binding winged-helix protein, f-112,2 from sulfolobus spindle-shaped virus 1.
25	d2vqca1	Alignment	not modelled	7.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**F112-like
26	c3kcvG_	Alignment	not modelled	7.9	13	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**probable formate transporter 1; **PDBTitle:** structure of formate channel
27	d1eexa_	Alignment	not modelled	7.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Diol dehydratase, alpha subunit
28	d1tz7a1	Alignment	not modelled	7.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

29	d2p12a1	Alignment	not modelled	7.5	17	**Fold:**FomD barrel-like **Superfamily:**FomD-like **Family:**FomD-like
30	d2jioa2	Alignment	not modelled	7.4	13	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
31	c3l78A_	Alignment	not modelled	7.3	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
32	d1eswa_	Alignment	not modelled	7.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
33	d1qusa_	Alignment	not modelled	7.1	15	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
34	c3sokB_	Alignment	not modelled	6.9	35	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
35	d2o8ia1	Alignment	not modelled	6.9	21	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
36	d1914a1	Alignment	not modelled	6.7	20	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
37	d1oqwa_	Alignment	not modelled	6.2	41	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
38	c2v5iA_	Alignment	not modelled	6.2	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**salmonella typhimurium db7155 bacteriophage det7 **PDBTitle:** structure of the receptor-binding protein of bacteriophage2 det7: a podoviral tailspike in a myovirus
39	c3klzE_	Alignment	not modelled	6.2	12	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**putative formate transporter 1; **PDBTitle:** pentameric formate channel with formate bound
40	c1svfB_	Alignment	not modelled	6.0	35	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**protein (fusion glycoprotein); **PDBTitle:** paramyxovirus sv5 fusion protein core
41	d1x1na1	Alignment	not modelled	6.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
42	d2fug34	Alignment	not modelled	5.7	40	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
43	c2p7vA_	Alignment	not modelled	5.6	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulator of sigma d; **PDBTitle:** crystal structure of the escherichia coli regulator of sigma 70, rsd,2 in complex with sigma 70 domain 4
44	d2pila_	Alignment	not modelled	5.6	29	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
45	d1pyta_	Alignment	not modelled	5.4	16	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
46	c1bhbA_	Alignment	not modelled	5.3	24	**PDB header:**photoreceptor **Chain:** A: **PDB Molecule:**bacteriorhodopsin; **PDBTitle:** three-dimensional structure of (1-71) bacterioopsin2 solubilized in methanol-chloroform and sds micelles3 determined by 15n-1h heteronuclear nmr spectroscopy
47	c2k85A_	Alignment	not modelled	5.2	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glucocorticoid receptor dna-binding factor 1; **PDBTitle:** p190-a rhogap ff1 domain
48	c3m8eA_	Alignment	not modelled	5.1	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** protein structure of type iii plasmid segregation tubr
49	d2q37a1	Alignment	not modelled	5.1	21	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
50	c2q37A_	Alignment	not modelled	5.1	21	**PDB header:**plant protein, lyase **Chain:** A: **PDB Molecule:**ohcu decarboxylase; **PDBTitle:** crystal structure of ohcu decarboxylase in the presence of2 (s)-allantoin