Phyre^2

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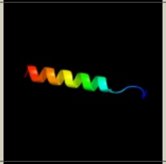
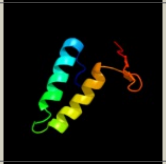
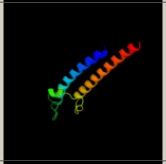
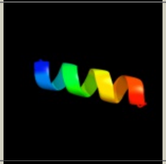
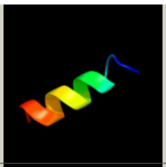
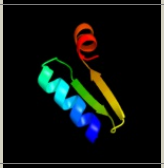
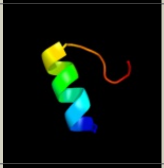
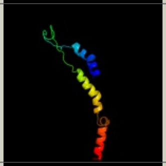
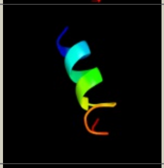
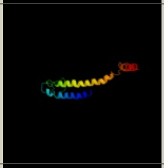
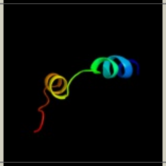
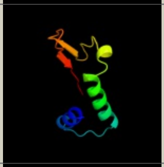
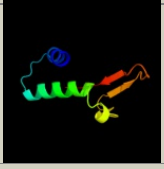
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ejsA_	Alignment		38.2	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**autocrine motility factor receptor, isoform 2; **PDBTitle:** solution structure of ruh-076, a human cue domain
2	c1t3jA_	Alignment		25.2	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mitofusin 1; **PDBTitle:** mitofusin domain hr2 v686m/i708m mutant
3	c3i5qA_	Alignment		19.0	22	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nucleoporin nup170; **PDBTitle:** nup170(aa1253-1502) at 2.2 a, s.cerevisiae
4	d1r3jc_	Alignment		18.8	14	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
5	c3qspB_	Alignment		18.1	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** analysis of a new family of widely distributed metal-independent alpha2 mannosidases provides unique insight into the processing of n-linked3 glycans, streptococcus pneumoniae sp_2144 non-productive substrate4 complex with alpha-1,6-mannobiose
6	c2bg9B_	Alignment		16.8	12	**PDB header:**ion channel/receptor **Chain:** B: **PDB Molecule:**acetylcholine receptor protein, beta chain; **PDBTitle:** refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
7	c2e76E_	Alignment		15.1	40	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
8	d2e74e1	Alignment		15.1	40	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
9	c2e74E_	Alignment		15.1	40	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
10	c1vf5R_	Alignment		15.1	40	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
11	c2e75E_	Alignment		15.1	40	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus

12	c1vf5E_	Alignment		15.1	40	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
13	d1in0a2	Alignment		12.4	15	**Fold:**Ferredoxin-like **Superfamily:**YajQ-like **Family:**YajQ-like
14	d1wf9a1	Alignment		10.5	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
15	d2oara1	Alignment		10.0	9	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
16	c2ba3A_	Alignment		8.9	56	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**nika; **PDBTitle:** nmr structure of nika n-terminal fragment
17	d1f6ga_	Alignment		7.8	14	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
18	c2aorB_	Alignment		7.4	28	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**dna mismatch repair protein muth; **PDBTitle:** crystal structure of muth-hemimethylated dna complex
19	d1cbya_	Alignment		7.4	21	**Fold:**CytB endotoxin-like **Superfamily:**CytB endotoxin-like **Family:**CytB endotoxin-like
20	c1cbyA_	Alignment		7.4	21	**PDB header:**toxin **Chain:** A: **PDB Molecule:**delta-endotoxin cytb; **PDBTitle:** delta-endotoxin
21	c2wh7A_	Alignment	not modelled	7.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-phage associated; **PDBTitle:** the partial structure of a group a streptpcoccal phage-2 encoded tail fibre hyaluronate lyase hylp2
22	c1in0B_	Alignment	not modelled	7.1	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yajq protein; **PDBTitle:** yajq protein (hi1034)
23	c3he5D_	Alignment	not modelled	7.0	23	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**synzip2; **PDBTitle:** heterospecific coiled-coil pair synzip2:synzip1
24	c1y4eA_	Alignment	not modelled	7.0	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** nmr structure of transmembrane segment iv of the nhe12 isoform of the na+/h+ exchanger
25	c1o98A_	Alignment	not modelled	6.9	40	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
26	d1sfsa_	Alignment	not modelled	6.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**1,4-beta-N-acetylmuraminidase
27	c1sfsA_	Alignment	not modelled	6.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** 1.07 a crystal structure of an uncharacterized b.2 stearothermophilus protein
28	c2h09A_	Alignment	not modelled	6.5	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
						PDB header:virus

29	c1iflA_	Alignment	not modelled	6.5	16	**Chain:** A: **PDB Molecule:**inovirus; **PDBTitle:** molecular models and structural comparisons of native and2 mutant class i filamentous bacteriophages ff (fd, f1, m13),3 if1 and ike
30	c2rmgA_	Alignment	not modelled	6.5	27	**PDB header:**hormone **Chain:** A: **PDB Molecule:**urocortin-2; **PDBTitle:** human urocortin 2
31	c2l16A_	Alignment	not modelled	6.2	17	**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
32	c3f1bA_	Alignment	not modelled	6.2	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tetr-like transcriptional regulator; **PDBTitle:** the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1.
33	c2d2cR_	Alignment	not modelled	5.9	43	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**cytochrome b6-f complex subunit vi; **PDBTitle:** crystal structure of cytochrome b6f complex with dbmib from2 m. laminosus
34	c2d2cE_	Alignment	not modelled	5.9	43	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit vi; **PDBTitle:** crystal structure of cytochrome b6f complex with dbmib from2 m. laminosus
35	d2dk5a1	Alignment	not modelled	5.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RPO3F domain-like
36	d1na6a2	Alignment	not modelled	5.7	32	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Type II restriction endonuclease catalytic domain
37	c2oarA_	Alignment	not modelled	5.6	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
38	d1ug2a_	Alignment	not modelled	5.4	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
39	d1tzyb_	Alignment	not modelled	5.3	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
40	d1s4na_	Alignment	not modelled	5.1	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycolipid 2-alpha-mannosyltransferase
41	d1hs7a_	Alignment	not modelled	5.1	28	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
42	d1kyqa2	Alignment	not modelled	5.1	20	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like