Phyre^2

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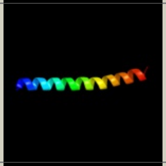
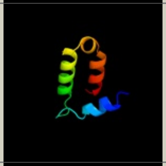
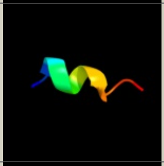
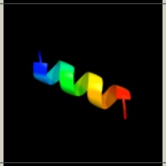
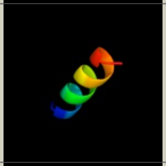
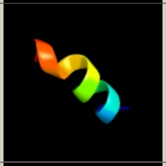
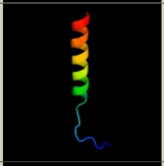
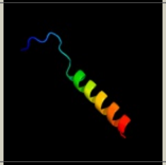
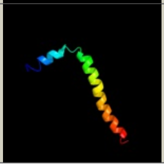
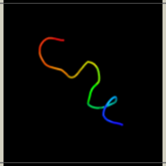
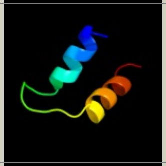
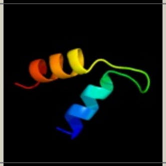
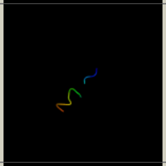
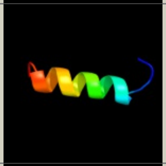
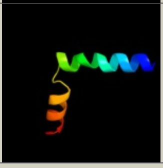
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kvlA_	Alignment		23.2	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major outer capsid protein vp7; **PDBTitle:** nmr structure of the c-terminal domain of vp7
2	c3hd7A_	Alignment		17.8	8	**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
3	c1ciiA_	Alignment		13.5	18	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
4	d1k8rb_	Alignment		9.5	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
5	d2hgca1	Alignment		9.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**YjcQ-like
6	c2hgcA_	Alignment		9.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**yjcq protein; **PDBTitle:** solution nmr structure of the yjcq protein from bacillus2 subtilis. northeast structural genomics target sr346.
7	d1k8ke_	Alignment		8.7	8	**Fold:**Arp2/3 complex 21 kDa subunit ARPC3 **Superfamily:**Arp2/3 complex 21 kDa subunit ARPC3 **Family:**Arp2/3 complex 21 kDa subunit ARPC3
8	c1rh5C_	Alignment		8.6	17	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**secbeta; **PDBTitle:** the structure of a protein conducting channel
9	d1rh5c_	Alignment		8.6	17	**Fold:**Single transmembrane helix **Superfamily:**Sec-beta subunit **Family:**Sec-beta subunit
10	c3go5A_	Alignment		8.2	0	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**multidomain protein with s1 rna-binding domains; **PDBTitle:** crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
11	d1pf4a2	Alignment		8.2	5	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region

12	c1m45B_	Alignment		8.2	6	**PDB header:**cell cycle protein **Chain:** B: **PDB Molecule:**iq2 motif from myo2p, a class v myosin; **PDBTitle:** crystal structure of mlc1p bound to iq2 of myo2p, a class v2 myosin
13	c1q2iA_	Alignment		7.7	0	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**pnc27; **PDBTitle:** nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
14	c1unhD_	Alignment		7.4	71	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**cyclin-dependent kinase 5 activator 1; **PDBTitle:** structural mechanism for the inhibition of cdk5-p25 by2 roscovitine, aloisine and indirubin.
15	d1unld_	Alignment		7.4	71	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
16	c1kq8A_	Alignment		7.3	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 3 forkhead homolog 1; **PDBTitle:** solution structure of winged helix protein hfh-1
17	d1kq8a_	Alignment		7.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
18	c3jqoV_	Alignment		7.0	11	**PDB header:**transport protein **Chain:** V: **PDB Molecule:**traf protein; **PDBTitle:** crystal structure of the outer membrane complex of a type iv2 secretion system
19	c4a1aM_	Alignment		7.0	5	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l5; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
20	c1zp0D_	Alignment		6.9	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**small cytochrome binding protein; **PDBTitle:** crystal structure of mitochondrial respiratory complex ii2 bound with 3-nitropropionate and 2-thenoyltrifluoroacetone
21	d1cg5a_	Alignment	not modelled	6.8	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
22	c3mkuA_	Alignment	not modelled	6.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
23	c1e17A_	Alignment	not modelled	6.4	10	**PDB header:**dna binding domain **Chain:** A: **PDB Molecule:**afx; **PDBTitle:** solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
24	c3co7C_	Alignment	not modelled	6.2	16	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
25	d1myta_	Alignment	not modelled	6.2	19	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
26	d2fx0a2	Alignment	not modelled	6.1	0	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
27	d1hdsa_	Alignment	not modelled	6.1	7	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
28	c2lkeA_	Alignment	not modelled	5.9	30	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-m; **PDBTitle:** structures and interaction analyses of the integrin alpha-m beta-22 cytoplasmic tails

29	c3g73A_	Alignment	not modelled	5.9	10	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**forkhead box protein m1; **PDBTitle:** structure of the foxm1 dna binding
30	c1geaA_	Alignment	not modelled	5.9	25	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**pituitary adenylate cyclase activating **PDBTitle:** receptor-bound conformation of pacap21
31	c2ciuA_	Alignment	not modelled	5.9	0	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**import inner membrane translocase subunit tim21 **PDBTitle:** structure of the ims domain of the mitochondrial import2 protein tim21 from s. cerevisiae
32	c1n2dC_	Alignment	not modelled	5.8	6	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**iq2 and iq3 motifs from myo2p, a class v myosin; **PDBTitle:** ternary complex of mlc1p bound to iq2 and iq3 of myo2p, a2 class v myosin
33	c2lkjA_	Alignment	not modelled	5.6	33	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-m; **PDBTitle:** structures and interaction analyses of the integrin alpha-m beta-22 cytoplasmic tails
34	d2lhba_	Alignment	not modelled	5.6	7	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
35	d1d5va_	Alignment	not modelled	5.6	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
36	c2wwbB_	Alignment	not modelled	5.6	7	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sec61 subunit gamma; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
37	c2rlwA_	Alignment	not modelled	5.6	14	**PDB header:**toxin **Chain:** A: **PDB Molecule:**plnf; **PDBTitle:** three-dimensional structure of the two peptides that2 constitute the two-peptide bacteriocin plantaracin ef
38	c2qq4A_	Alignment	not modelled	5.5	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**iron-sulfur cluster biosynthesis protein iscu; **PDBTitle:** crystal structure of iron-sulfur cluster biosynthesis2 protein iscu (ttha1736) from thermus thermophilus hb8
39	c1yhuW_	Alignment	not modelled	5.5	14	**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.
40	d3bpya1	Alignment	not modelled	5.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
41	d1scta_	Alignment	not modelled	5.5	23	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
42	d2hfha_	Alignment	not modelled	5.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
43	c2zs1D_	Alignment	not modelled	5.4	8	**PDB header:**oxygen storage, oxygen transport **Chain:** D: **PDB Molecule:**extracellular giant hemoglobin major globin subunit b1; **PDBTitle:** structural basis for the heterotropic and homotropic interactions of2 invertebrate giant hemoglobin
44	d1sxja1	Alignment	not modelled	5.4	9	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
45	d1c17m_	Alignment	not modelled	5.4	11	**Fold:**F1F0 ATP synthase subunit A **Superfamily:**F1F0 ATP synthase subunit A **Family:**F1F0 ATP synthase subunit A
46	c1g2cN_	Alignment	not modelled	5.3	13	**PDB header:**viral protein **Chain:** N: **PDB Molecule:**fusion protein (f); **PDBTitle:** human respiratory syncytial virus fusion protein core
47	d2a07f1	Alignment	not modelled	5.3	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
48	c2wukD_	Alignment	not modelled	5.3	17	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
49	c2nq2A_	Alignment	not modelled	5.3	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**hypothetical abc transporter permease protein **PDBTitle:** an inward-facing conformation of a putative metal-chelate2 type abc transporter.
50	d1hbra_	Alignment	not modelled	5.3	0	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
51	c2c0kB_	Alignment	not modelled	5.3	11	**PDB header:**oxygen transport **Chain:** B: **PDB Molecule:**hemoglobin; **PDBTitle:** the structure of hemoglobin from the botfly gasterophilus2 intestinalis
52	c3gztF_	Alignment	not modelled	5.2	28	**PDB header:**virus **Chain:** F: **PDB Molecule:**outer capsid glycoprotein vp7; **PDBTitle:** vp7 recoated rotavirus dlp
53	c3bjqA_	Alignment	not modelled	5.2	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**phage-related protein; **PDBTitle:** crystal structure of a phage-related protein (bb3626) from bordetella2 bronchiseptica rb50 at 2.05 a resolution
						Fold: Globin-like

54	d2gdma_	Alignment	not modelled	5.2	9	**Superfamily:**Globin-like **Family:**Globins
55	c3h8aF_	Alignment	not modelled	5.1	40	**PDB header:**lyase/protein binding **Chain:** F: **PDB Molecule:**rnase e; **PDBTitle:** crystal structure of e. coli enolase bound to its cognate rnase e2 recognition domain