Phyre^2

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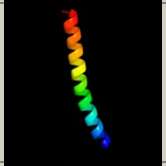
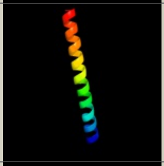
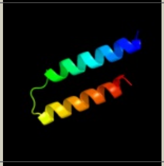
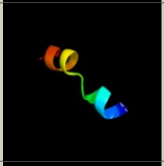
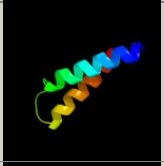
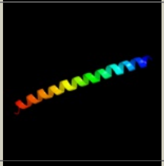
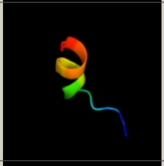
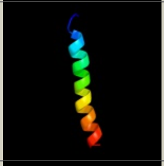
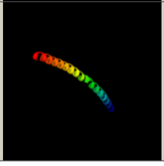
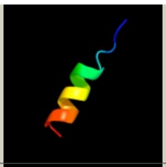
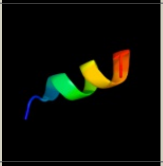
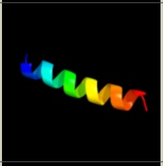
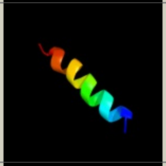
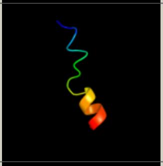
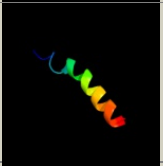
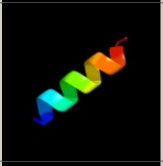
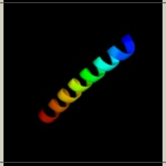
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1n73A_	Alignment		62.8	29	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrin alpha-1 chain; **PDBTitle:** fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
2	c3ghgD_	Alignment		36.0	12	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of human fibrinogen
3	c1m1jA_	Alignment		29.9	24	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
4	c3m9bK_	Alignment		27.9	29	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
5	d1w0ba_	Alignment		25.5	20	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
6	c2c9lZ_	Alignment		22.4	53	**PDB header:**viral protein **Chain:** Z: **PDB Molecule:**bzlf1 trans-activator protein; **PDBTitle:** structure of the epstein-barr virus zebra protein
7	d1z8ua1	Alignment		21.3	20	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
8	c2w6bA_	Alignment		19.4	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 7; **PDBTitle:** crystal structure of the trimeric beta-pix coiled-coil2 domain
9	c1pnbA_	Alignment		17.6	36	**PDB header:**seed storage protein **Chain:** A: **PDB Molecule:**napin bnib; **PDBTitle:** structure of napin bnib, nmr, 10 structures
10	c1hf9B_	Alignment		14.3	19	**PDB header:**atpase inhibitor **Chain:** B: **PDB Molecule:**atpase inhibitor (mitochondrial); **PDBTitle:** c-terminal coiled-coil domain from bovine if1
11	c3kltB_	Alignment		13.0	18	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** crystal structure of a vimentin fragment

12	c1m45B_	Alignment		11.4	13	**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	c2kl5A_	Alignment		11.1	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yutd; **PDBTitle:** solution nmr structure of protein yutd from b.subtilis, northeast2 structural genomics consortium target sr232
14	c2a93B_	Alignment		10.5	29	**PDB header:**leucine zippers **Chain:** B: **PDB Molecule:**c-myc-max heterodimeric leucine zipper; **PDBTitle:** nmr solution structure of the c-myc-max heterodimeric2 leucine zipper, 40 structures
15	d1jb0f_	Alignment		9.7	16	**Fold:**Single transmembrane helix **Superfamily:**Subunit III of photosystem I reaction centre, PsaF **Family:**Subunit III of photosystem I reaction centre, PsaF
16	c2o01F_	Alignment		9.4	11	**PDB header:**photosynthesis **Chain:** F: **PDB Molecule:**photosystem i reaction center subunit iii, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
17	c3h32A_	Alignment		9.0	14	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of d-dimer from human fibrin complexed with gly-his-2 arg-pro-tyr-amide
18	c3gxvD_	Alignment		8.8	40	**PDB header:**hydrolase/replication **Chain:** D: **PDB Molecule:**replicative dna helicase; **PDBTitle:** three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
19	c1go4F_	Alignment		7.8	18	**PDB header:**cell cycle **Chain:** F: **PDB Molecule:**mad1 (mitotic arrest deficient)-like 1; **PDBTitle:** crystal structure of mad1-mad2 reveals a conserved mad22 binding motif in mad1 and cdc20.
20	d1s0pa_	Alignment		7.5	30	**Fold:**N-terminal domain of adenylylcyclase associated protein, CAP **Superfamily:**N-terminal domain of adenylylcyclase associated protein, CAP **Family:**N-terminal domain of adenylylcyclase associated protein, CAP
21	c3n27A_	Alignment	not modelled	6.9	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**fusion glycoprotein f0, linker, fusion glycoprotein f0; **PDBTitle:** molecular basis of the inhibition of henipa viruses
22	c1f8aB_	Alignment	not modelled	6.7	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase nima- **PDBTitle:** structural basis for the phosphoserine-proline recognition2 by group iv ww domains
23	c3gxvC_	Alignment	not modelled	5.8	32	**PDB header:**hydrolase/replication **Chain:** C: **PDB Molecule:**replicative dna helicase; **PDBTitle:** three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
24	c1n2dC_	Alignment	not modelled	5.5	13	**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
25	c2v4hA_	Alignment	not modelled	5.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cc2-lz domain - 1d5 darpin complex