Phyre2

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Description	P75719
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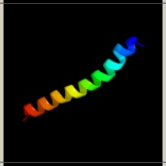
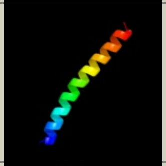
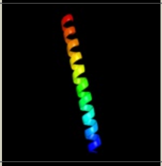
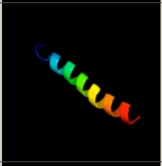
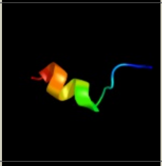
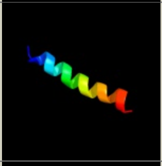
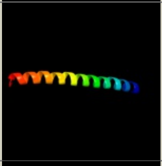
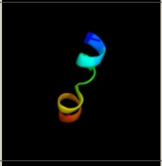
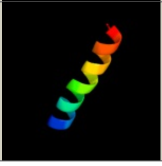
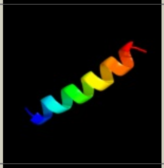
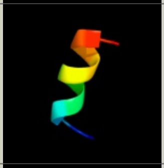
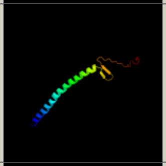
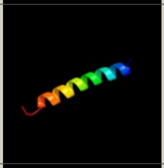
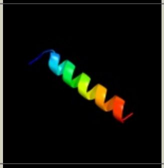
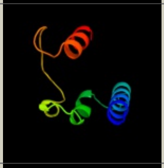
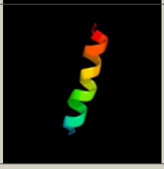
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1n73A_	Alignment		66.6	26	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrin alpha-1 chain; **PDBTitle:** crystal structure of fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
2	c3ghgD_	Alignment		38.5	18	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of human fibrinogen
3	c1m1jA_	Alignment		31.8	26	**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		25.6	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	c1hf9B_	Alignment		20.9	19	**PDB header:**atpase inhibitor **Chain:** B: **PDB Molecule:**atpase inhibitor (mitochondrial); **PDBTitle:** c-terminal coiled-coil domain from bovine if1
6	c1pnbA_	Alignment		14.8	29	**PDB header:**seed storage protein **Chain:** A: **PDB Molecule:**napin bnib; **PDBTitle:** structure of napin bnib, nmr, 10 structures
7	c3dinE_	Alignment		13.1	19	**PDB header:**membrane protein, protein transport **Chain:** E: **PDB Molecule:**preprotein translocase subunit secg; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
8	c2w6bA_	Alignment		11.4	21	**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	c2c9lZ_	Alignment		11.3	53	**PDB header:**viral protein **Chain:** Z: **PDB Molecule:**bzlf1 trans-activator protein; **PDBTitle:** structure of the epstein-barr virus zebra protein
10	c3dl8F_	Alignment		10.7	24	**PDB header:**protein transport **Chain:** F: **PDB Molecule:**protein-export membrane protein secg; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
11	c2l2tA_	Alignment		10.0	43	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain

12	c2kncB_	Alignment		9.7	13	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
13	c2a93B_	Alignment		9.4	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
14	c2kl5A_	Alignment		9.2	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
15	c1cz7C_	Alignment		8.2	10	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**microtubule motor protein ncd; **PDBTitle:** the crystal structure of a minus-end directed microtubule2 motor protein ncd reveals variable dimer conformations
16	c3n27A_	Alignment		7.7	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
17	c1w8xP_	Alignment		7.0	10	**PDB header:**virus **Chain:** P: **PDB Molecule:**protein p16; **PDBTitle:** structural analysis of prd1
18	c1f8aB_	Alignment		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
19	d1s0pa_	Alignment		6.7	40	**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
20	c2akiA_	Alignment		6.5	33	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein-export membrane protein secg; **PDBTitle:** normal mode-based flexible fitted coordinates of a2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
21	d2h9da1	Alignment	not modelled	6.3	8	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Dimeric chorismate mutase
22	c1aa0A_	Alignment	not modelled	6.2	40	**PDB header:**attachment protein **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** fibritin deletion mutant e (bacteriophage t4)
23	c3h32A_	Alignment	not modelled	6.1	23	**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
24	c3mk7F_	Alignment	not modelled	5.8	33	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
25	c3kltB_	Alignment	not modelled	5.6	19	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** crystal structure of a vimentin fragment