Phyre^2

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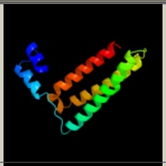
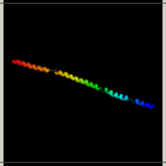
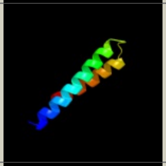
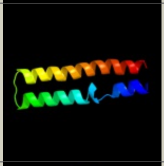
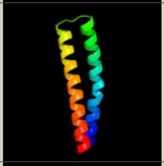
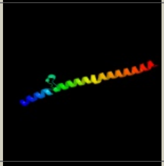
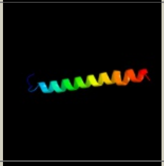
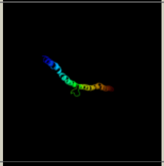
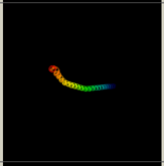
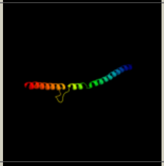
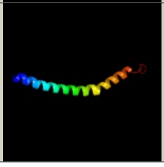
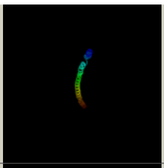
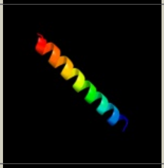
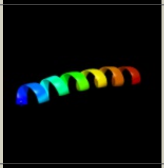
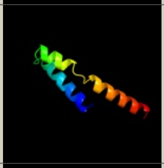
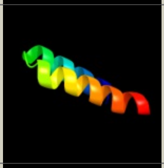
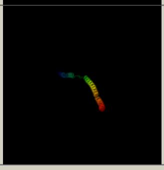
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y4cA_	Alignment		69.4	11	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
2	c3u59C_	Alignment		67.5	18	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
3	d1k4ta1	Alignment		37.6	28	**Fold:**Long alpha-hairpin **Superfamily:**Eukaryotic DNA topoisomerase I, dispensable insert domain **Family:**Eukaryotic DNA topoisomerase I, dispensable insert domain
4	c2k48A_	Alignment		31.1	20	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nucleoprotein; **PDBTitle:** nmr structure of the n-terminal coiled coil domain of the2 andes hantavirus nucleocapsid protein
5	c2ic6B_	Alignment		22.3	23	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**nucleocapsid protein; **PDBTitle:** the coiled-coil domain (residues 1-75) structure of the sin2 nombre virus nucleocapsid protein
6	c1d7mA_	Alignment		19.3	26	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**cortexillin i; **PDBTitle:** coiled-coil dimerization domain from cortexillin i
7	c2khkA_	Alignment		17.9	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**atp synthase subunit b; **PDBTitle:** nmr solution structure of the b30-82 domain of subunit b of2 escherichia coli f1fo atp synthase
8	c3ghgK_	Alignment		17.5	10	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
9	c3ipkA_	Alignment		16.4	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**agi/ii; **PDBTitle:** crystal structure of a3vp1 of agi/ii of streptococcus mutans
10	c3hnwB_	Alignment		15.3	6	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
11	c3errB_	Alignment		14.9	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fusion protein of microtubule binding domain from **PDBTitle:** microtubule binding domain from mouse cytoplasmic dynein as2 a fusion with seryl-trna synthetase

12	c2fxmB_	Alignment		14.0	14	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
13	c2qdqA_	Alignment		9.9	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** crystal structure of the talin dimerisation domain
14	c1zxaB_	Alignment		8.7	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cgmp-dependent protein kinase 1, alpha isozyme; **PDBTitle:** solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
15	d1vp7a_	Alignment		7.2	12	**Fold:**Spectrin repeat-like **Superfamily:**XseB-like **Family:**XseB-like
16	c1r48A_	Alignment		6.8	29	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**proline/betaine transporter; **PDBTitle:** solution structure of the c-terminal cytoplasmic domain2 residues 468-497 of escherichia coli protein prop
17	c2gl2B_	Alignment		6.8	12	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**adhesion a; **PDBTitle:** crystal structure of the tetra muntant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
18	c3l8rA_	Alignment		6.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative pts system, cellobiose-specific iia **PDBTitle:** the crystal structure of ptca from s. mutans
19	c1wcrA_	Alignment		5.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, n, n'-diacetylchitobiose-specific **PDBTitle:** trimeric structure of the enzyme iia from escherichia coli2 phosphotransferase system specific for n,n'-3 diacetylchitobiose
20	c2d3eD_	Alignment		5.5	18	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 **PDBTitle:** crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
21	c1deqD_	Alignment	not modelled	5.4	15	**PDB header:** **PDB COMPND:**
22	c3k1sE_	Alignment	not modelled	5.2	20	**PDB header:**transferase **Chain:** E: **PDB Molecule:**pts system, cellobiose-specific iia component; **PDBTitle:** crystal structure of the pts cellobiose specific enzyme iia2 from bacillus anthracis