Phyre^2

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Description	P0AAN9
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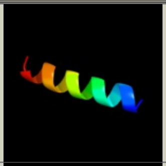
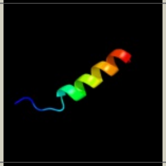
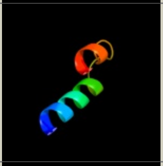
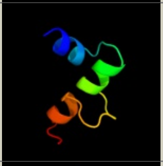
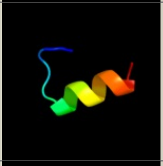
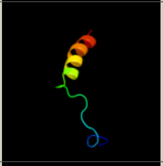
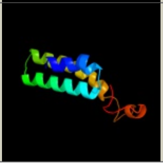
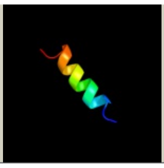
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zxaB_	Alignment		30.3	56	**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
2	c1t3jA_	Alignment		20.6	31	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mitofusin 1; **PDBTitle:** mitofusin domain hr2 v686m/i708m mutant
3	d1r2aa_	Alignment		18.9	40	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
4	c2b8iA_	Alignment		17.7	40	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**pas factor; **PDBTitle:** crystal structure and functional studies reveal that pas2 factor from vibrio vulnificus is a novel member of the3 saposin-fold family
5	d2hwna1	Alignment		16.3	42	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
6	c2qshA_	Alignment		12.2	23	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**dna repair protein rad4; **PDBTitle:** crystal structure of rad4-rad23 bound to a mismatch dna
7	c1p9iA_	Alignment		9.2	56	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cortexillin i/gcn4 hybrid peptide; **PDBTitle:** coiled-coil x-ray structure at 1.17 a resolution
8	d1v2za_	Alignment		8.5	31	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
9	d1r8ja1	Alignment		7.3	31	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
10	d1o0la_	Alignment		6.5	37	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
11	c3cqcB_	Alignment		6.2	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**nuclear pore complex protein nup133; **PDBTitle:** nucleoporin nup107/nup133 interaction complex

12	c1pehA_	Alignment		6.1	58	**PDB header:**nucleotidyltransferase **Chain:** A: **PDB Molecule:**pepnh1; **PDBTitle:** nmr structure of the membrane-binding domain of ctp2 phosphocholine cytidylyltransferase, 10 structures

13	d1y14b2	 Alignment		5.5	35	**Fold:**Dodecin subunit-like **Superfamily:**N-terminal, heterodimerisation domain of RBP7 (RpoE) **Family:**N-terminal, heterodimerisation domain of RBP7 (RpoE)