Phyre^2

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Description	P31468
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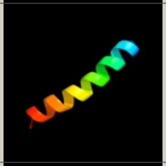
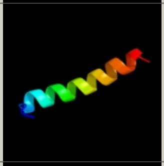
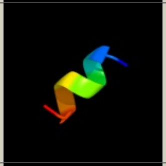
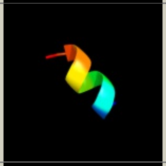
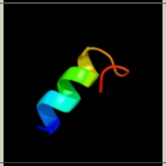
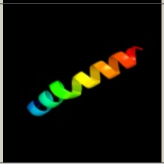
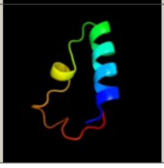
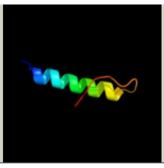
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jb0m_	Alignment		22.1	55	**Fold:**Single transmembrane helix **Superfamily:**Subunit XII of photosystem I reaction centre, PsaM **Family:**Subunit XII of photosystem I reaction centre, PsaM
2	c1jb0M_	Alignment		22.1	55	**PDB header:**photosynthesis **Chain:** M: **PDB Molecule:**photosystem 1 reaction centre subunit xii; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
3	d1jssa_	Alignment		11.0	22	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**STAR domain
4	c1jssB_	Alignment		11.0	22	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**cholesterol-regulated start protein 4; **PDBTitle:** crystal structure of the mus musculus cholesterol-regulated2 start protein 4 (stard4).
5	c1p0lA_	Alignment		9.9	33	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution gln to trp modification in sds-d252 micelles
6	c2l35B_	Alignment		8.5	36	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12-nkg2c transmembrane heterotrimer
7	c1p0oA_	Alignment		8.5	33	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution of trp for gln and asp at position2 17 and 19 modification in sds-d25 micelles
8	c2jd3B_	Alignment		8.3	31	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**stbb protein; **PDBTitle:** parr from plasmid pb171
9	c2l34B_	Alignment		7.9	38	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12 transmembrane homodimer
10	c2l34A_	Alignment		7.9	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12 transmembrane homodimer
11	d1ln1a_	Alignment		6.3	18	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**STAR domain

12	c2zt9E_	Alignment		5.5	45	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
13	d1t0aa_	Alignment		5.5	27	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like

14	c3dbyN_	Alignment		5.4	19	**PDB header:**structural genomics, unknown function **Chain:** N: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein from bacillus cereus2 g9241 (csap target)