Phyre^2

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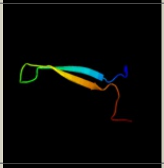
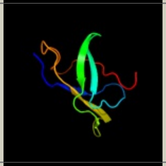
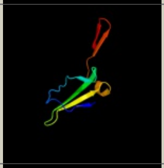
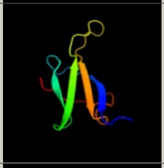
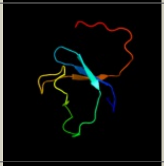
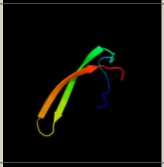
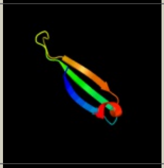
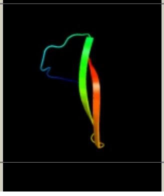
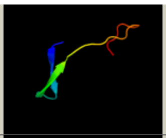
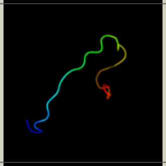
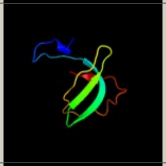
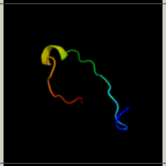
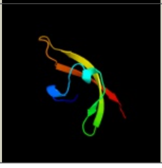
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v5va1	Alignment		64.8	16	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
2	c2j5uB_	Alignment		63.6	9	**PDB header:**cell shape regulation **Chain:** B: **PDB Molecule:**mrec protein; **PDBTitle:** mrec lysteria monocytogenes
3	c1v5vA_	Alignment		40.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of a component of glycine cleavage system: t-protein2 from pyrococcus horikoshii ot3 at 1.5 a resolution
4	c2qf4A_	Alignment		32.2	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cell shape determining protein mrec; **PDBTitle:** high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
5	d1pj5a1	Alignment		15.2	17	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
6	d1wosa1	Alignment		13.9	10	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
7	c1yx2B_	Alignment		12.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of the probable aminomethyltransferase2 from bacillus subtilis
8	c1cz5A_	Alignment		11.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vcp-like atpase; **PDBTitle:** nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
9	c2k6zA_	Alignment		10.5	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1943; **PDBTitle:** solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
10	d1h9ra2	Alignment		9.2	8	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
11	d1x9la_	Alignment		8.1	9	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**DR1885-like metal-binding protein **Family:**DR1885-like metal-binding protein

12	c3htrB_	Alignment		7.9	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized prc-barrel domain protein; **PDBTitle:** crystal structure of prc-barrel domain protein from2 rhodopseudomonas palustris
13	c1t5eB_	Alignment		7.8	22	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
14	d1nnxa_	Alignment		7.5	16	**Fold:**OB-fold **Superfamily:**Hypothetical protein YgiW **Family:**Hypothetical protein YgiW
15	d1vf7a_	Alignment		7.3	22	**Fold:**HlyD-like secretion proteins **Superfamily:**HlyD-like secretion proteins **Family:**HlyD-like secretion proteins
16	d2cp6a1	Alignment		6.9	20	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
17	d1gtra1	Alignment		6.8	8	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain

18	d2vv5a1	Alignment		6.5	33	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain