Phyre²

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Description	Q46919
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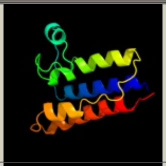
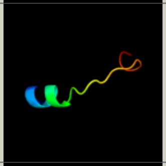
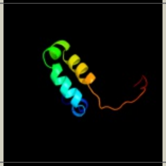
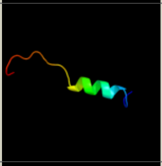
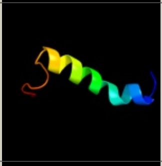
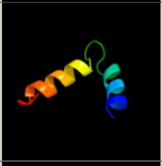
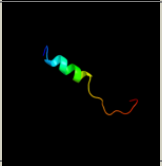
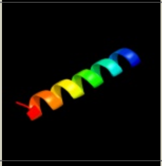
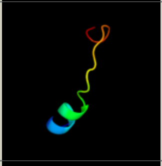
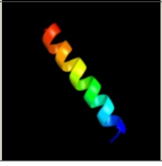
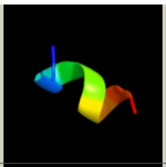
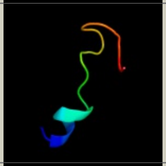
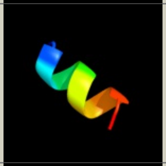
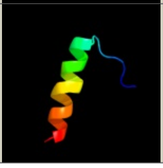
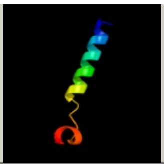
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hgka1	 Alignment		100.0	100	**Fold:**Bromodomain-like **Superfamily:**YqcC-like **Family:**YqcC-like
2	c2gc6A_	 Alignment		31.5	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase; **PDBTitle:** s73a mutant of l. casei fpgs
3	c3d1dC_	 Alignment		17.4	17	**PDB header:**nuclear protein **Chain:** C: **PDB Molecule:**rna-induced transcriptional silencing complex **PDBTitle:** hexagonal crystal structure of tas3 c-terminal alpha motif
4	d1ewfa2	 Alignment		17.1	28	**Fold:**Aha1/BPI domain-like **Superfamily:**Bactericidal permeability-increasing protein, BPI **Family:**Bactericidal permeability-increasing protein, BPI
5	d1eswa_	 Alignment		16.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
6	d1w1oa1	 Alignment		15.0	18	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Cytokinin dehydrogenase 1
7	c2yu0A_	 Alignment		11.1	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**interferon-activable protein 205; **PDBTitle:** solution structures of the paad_dapin domain of mus2 musculus interferon-activatable protein 205
8	c1bp1A_	 Alignment		9.7	28	**PDB header:**bactericidal **Chain:** A: **PDB Molecule:**bactericidal/permeability-increasing protein; **PDBTitle:** crystal structure of bpi, the human bactericidal2 permeability-increasing protein
9	d1x1na1	 Alignment		9.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
10	d2gc6a2	 Alignment		9.3	30	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase
11	d1tz7a1	 Alignment		8.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

12	d1jb0i_	Alignment		7.8	44	**Fold:**Single transmembrane helix **Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI **Family:**Subunit VIII of photosystem I reaction centre, PsaI
13	c1pnbB_	Alignment		7.5	11	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**napin bnib; **PDBTitle:** structure of napin bnib, nmr, 10 structures
14	c3if4C_	Alignment		6.9	30	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**integron cassette protein hfx_cass5; **PDBTitle:** structure from the mobile metagenome of north west arm2 sewage outfall: integron cassette protein hfx_cass5
15	d1v38a_	Alignment		6.1	13	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
16	d2r7ga2	Alignment		5.6	20	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Retinoblastoma tumor suppressor domains
17	c3k1qA_	Alignment		5.6	13	**PDB header:**virus **Chain:** A: **PDB Molecule:**vp1, the protein that forms the mrna-capping **PDBTitle:** backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics

18	d2fgea3	Alignment		5.3	14	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like