Phyre2

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Description	P11864
Date	Thu Jan 5 11:32:51 GMT 2012
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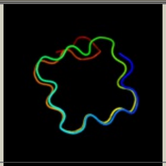
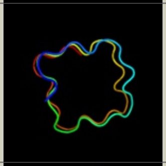
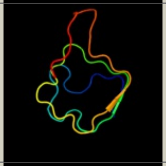
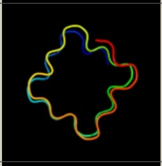
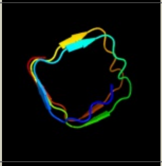
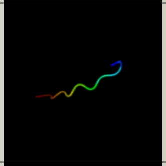
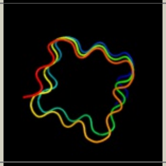
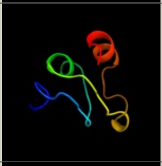
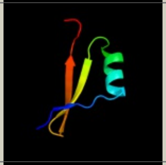
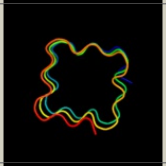
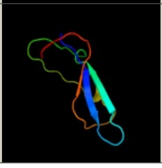
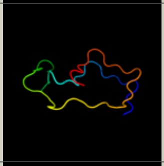
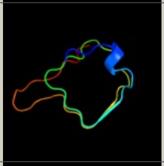
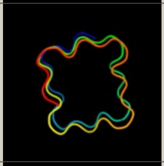
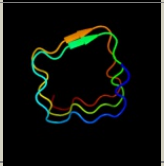
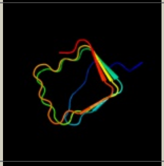
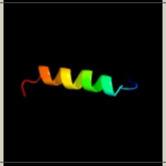
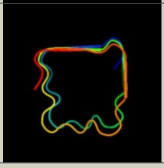
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3du1X_	Alignment		34.3	19	**PDB header:**structural protein **Chain:** X: **PDB Molecule:**all3740 protein; **PDBTitle:** the 2.0 angstrom resolution crystal structure of hetl, a pentapeptide2 repeat protein involved in heterocyst differentiation regulation from3 the cyanobacterium nostoc sp. strain pcc 7120
2	c3nb2B_	Alignment		33.9	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**secreted effector protein; **PDBTitle:** crystal structure of e. coli o157:h7 effector protein nlel
3	c2xtwB_	Alignment		18.7	12	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**qnrb1; **PDBTitle:** structure of qnrb1 (full length), a plasmid-mediated2 fluoroquinolone resistance protein
4	d2j8ia1	Alignment		17.6	23	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
5	c2xt4B_	Alignment		11.9	18	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mcbg-like protein; **PDBTitle:** structure of the pentapeptide repeat protein albg, a2 resistance factor for the topoisomerase poison albicidin.
6	d1z0aa1	Alignment		11.6	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
7	c2j8iB_	Alignment		10.9	17	**PDB header:**toxin **Chain:** B: **PDB Molecule:**np275; **PDBTitle:** structure of np275, a pentapeptide repeat protein from2 nostoc punctiforme
8	d2naca2	Alignment		10.7	33	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
9	c3r67A_	Alignment		10.6	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycosidase; **PDBTitle:** crystal structure of a putative glycosidase (bt_4094) from bacteroides2 thetaiotaomicron vpi-5482 at 2.30 a resolution
10	d2j8ka1	Alignment		10.4	17	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
11	d1wmxa_	Alignment		10.3	19	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)

12	d2b4wa1	Alignment		10.1	50	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**LmjF10.1260-like
13	c2o6wA_	Alignment		9.6	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**repeat five residue (rfr) protein or **PDBTitle:** crystal structure of a pentapeptide repeat protein (rfr23)2 from the cyanobacterium cyanothece 51142
14	c3pssB_	Alignment		9.0	14	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**qnr; **PDBTitle:** crystal structure of ahqnr, the qnr protein from aeromonas hydrophila2 (p21 crystal form)
15	c2yuiA_	Alignment		8.5	21	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**anamorsin; **PDBTitle:** solution structure of the n-terminal domain in human2 cytokine-induced apoptosis inhibitor anamorsin
16	c3n90A_	Alignment		8.2	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**thylakoid lumenal 15 kda protein 1, chloroplastic; **PDBTitle:** the 1.7 angstrom resolution crystal structure of at2g44920, a2 pentapeptide repeat protein from arabidopsis thaliana thylakoid3 lumen.
17	d2f3la1	Alignment		8.0	18	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
18	c2w7zB_	Alignment		7.8	15	**PDB header:**inhibitor **Chain:** B: **PDB Molecule:**pentapeptide repeat family protein; **PDBTitle:** structure of the pentapeptide repeat protein efsqnr, a dna2 gyrase inhibitor. free amines modified by cyclic3 pentylation with glutaraldehyde.
19	d2zjrj1	Alignment		7.7	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L16p
20	d2bm5a1	Alignment		7.7	12	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
21	d2coba1	Alignment	not modelled	7.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
22	c2g0yA_	Alignment	not modelled	7.2	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**pentapeptide repeat protein; **PDBTitle:** crystal structure of a lumenal pentapeptide repeat protein from2 cyanothece sp 51142 at 2.3 angstrom resolution. tetragonal crystal3 form
23	d2j01q1	Alignment	not modelled	6.9	35	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L16p
24	c3e3uA_	Alignment	not modelled	6.6	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of mycobacterium tuberculosis peptide2 deformylase in complex with inhibitor
25	c3bboO_	Alignment	not modelled	6.5	35	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**ribosomal protein l16; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
26	d2gyck1	Alignment	not modelled	6.4	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L16p
27	d1iuqa_	Alignment	not modelled	6.1	21	**Fold:**Glycerol-3-phosphate (1)-acyltransferase **Superfamily:**Glycerol-3-phosphate (1)-acyltransferase **Family:**Glycerol-3-phosphate (1)-acyltransferase
28	c3aqoD_	Alignment	not modelled	5.6	21	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** structure and function of a membrane component secdf that enhances2 protein export

29	c2k3jA_	Alignment	not modelled	5.6	78	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mitochondrial intermembrane space import and **PDBTitle:** the solution structure of human mia40
30	c2jx0A_	Alignment	not modelled	5.6	20	**PDB header:**cell adhesion, signaling protein **Chain:** A: **PDB Molecule:**arf gtpase-activating protein git1; **PDBTitle:** the paxillin-binding domain (pbd) of g protein coupled2 receptor (gpcr)-kinase (grk) interacting protein 1 (git1)
31	d1kshb_	Alignment	not modelled	5.6	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
32	c3nw8B_	Alignment	not modelled	5.4	19	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**envelope glycoprotein b; **PDBTitle:** glycoprotein b from herpes simplex virus type 1, y179s mutant, high-ph