Phyre2

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Description	P76613
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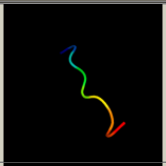
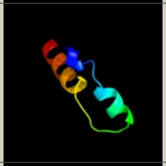
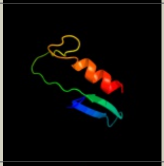
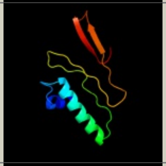
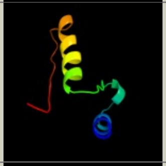
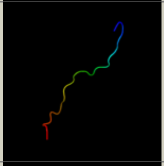
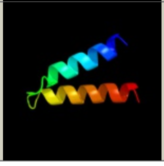
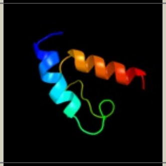
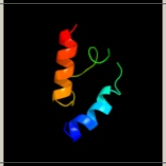
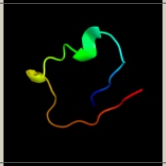
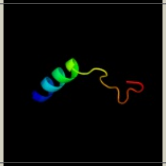
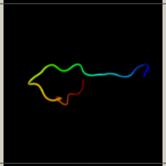
Unique Job ID	41926a2be4fb1912

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3c0na1	Alignment		16.8	67	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Aerolysin/Pertussis toxin (APT) domain
2	d1auua_	Alignment		15.7	25	**Fold:**GroES-like **Superfamily:**SacY-like RNA-binding domain **Family:**BglG-like antiterminator proteins
3	d1ho8a_	Alignment		15.4	42	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Regulatory subunit H of the V-type ATPase
4	d1gefa_	Alignment		14.3	19	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
5	c3mdnD_	Alignment		13.2	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamine aminotransferase class-ii domain protein; **PDBTitle:** structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
6	d1n6za_	Alignment		12.4	40	**Fold:**Hypothetical protein Yml108w **Superfamily:**Hypothetical protein Yml108w **Family:**Hypothetical protein Yml108w
7	d1e8ca2	Alignment		12.1	15	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
8	c3lr6A_	Alignment		10.4	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**major ampullate spidroin 1; **PDBTitle:** self-assembly of spider silk proteins is controlled by a ph-sensitive2 relay
9	d2o3ia1	Alignment		10.0	29	**Fold:**CV3147-like **Superfamily:**CV3147-like **Family:**CV3147-like
10	c1dmlG_	Alignment		8.9	33	**PDB header:**dna binding protein/transferase **Chain:** G: **PDB Molecule:**dna polymerase processivity factor; **PDBTitle:** crystal structure of herpes simplex ul42 bound to the c-2 terminus of hsv pol
11	d1q2za_	Alignment		8.6	11	**Fold:**alpha-alpha superhelix **Superfamily:**C-terminal domain of Ku80 **Family:**C-terminal domain of Ku80

12	d1lqya_	Alignment		8.6	17	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
13	c2is9A_	Alignment		8.2	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** structure of yeast dcn-1
14	c3bq3A_	Alignment		8.0	22	**PDB header:**cell cycle, ligase **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** crystal structure of s. cerevisiae dcn1
15	d2a6qb1	Alignment		7.9	12	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
16	c2wqqA_	Alignment		7.5	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-2,3-/2,8-sialyltransferase; **PDBTitle:** crystallographic analysis of monomeric cstii
17	d2cwla1	Alignment		7.4	32	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Manganese catalase (T-catalase)
18	d1ro7a_	Alignment		7.2	36	**Fold:**Alpha-2,3/8-sialyltransferase CstII **Superfamily:**Alpha-2,3/8-sialyltransferase CstII **Family:**Alpha-2,3/8-sialyltransferase CstII
19	d1mg4a_	Alignment		7.2	32	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
20	d1vl1a_	Alignment		7.2	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
21	c1kkhA_	Alignment	not modelled	7.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mevalonate kinase; **PDBTitle:** crystal structure of the methanococcus jannaschii2 mevalonate kinase
22	c2k3qA_	Alignment	not modelled	7.1	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**tusp1; **PDBTitle:** solution structure of the n-terminal domain (tusp1-n) of the2 egg case silk from nephila antipodiana
23	d1ob8a_	Alignment	not modelled	6.4	14	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
24	c2rp4C_	Alignment	not modelled	6.0	41	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription factor p53; **PDBTitle:** solution structure of the oligomerization domain in dmp53
25	d1ntga_	Alignment	not modelled	5.9	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
26	d1jx4a1	Alignment	not modelled	5.3	36	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
27	c3c0mB_	Alignment	not modelled	5.3	67	**PDB header:**toxin **Chain:** B: **PDB Molecule:**aerolysin; **PDBTitle:** crystal structure of the proaerolysin mutant y221g
28	d1nfpa_	Alignment	not modelled	5.1	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)

29	c2p2vA_	Alignment	not modelled	5.1	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-2,3-sialyltransferase; **PDBTitle:** crystal structure analysis of monofunctional alpha-2,3-2 sialyltransferase cst-i from campylobacter jejuni
30	d1mjda_	Alignment	not modelled	5.1	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
31	d3bdua1	Alignment	not modelled	5.0	32	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**YgdI/YgdR-like