Phyre^2

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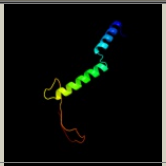
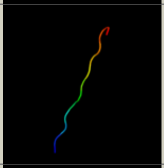
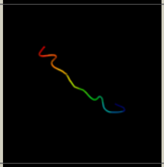
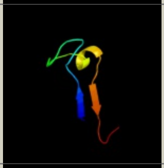
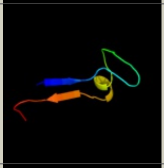
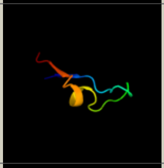
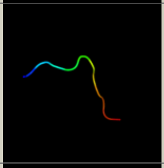
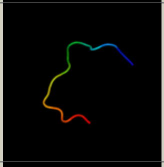
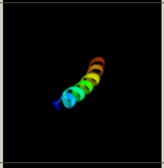
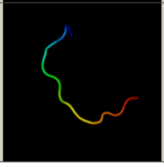
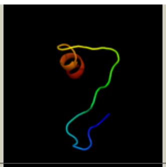
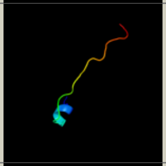
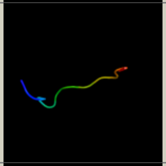
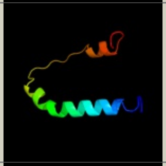
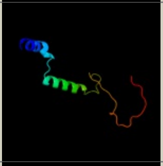
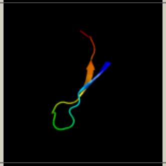
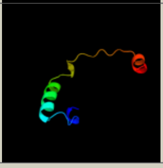
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ig8a1	Alignment		32.1	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
2	c3f1zF_	Alignment		23.2	69	**PDB header:**dna binding protein **Chain:** F: **PDB Molecule:**putative nucleic acid-binding lipoprotein; **PDBTitle:** crystal structure of putative nucleic acid-binding lipoprotein2 (yp_001337197.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.46 a resolution
3	d1tu2b2	Alignment		14.2	57	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
4	d1ikop_	Alignment		13.4	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Ephrin ectodomain
5	c1ikoP_	Alignment		13.4	14	**PDB header:**signaling protein **Chain:** P: **PDB Molecule:**ephrin-b2; **PDBTitle:** crystal structure of the murine ephrin-b2 ectodomain
6	c3d12E_	Alignment		13.2	16	**PDB header:**hydrolase/membrane protein **Chain:** E: **PDB Molecule:**ephrin-b3; **PDBTitle:** crystal structures of nipah virus g attachment glycoprotein in complex2 with its receptor ephrin-b3
7	d1x9ya2	Alignment		12.9	67	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Staphopain B, prodomain
8	c2v0xB_	Alignment		10.9	67	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**lamina-associated polypeptide 2 isoforms **PDBTitle:** the dimerization domain of lap2alpha
9	d1bg3a3	Alignment		9.6	47	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
10	d1m7ka_	Alignment		9.0	22	**Fold:**Spectrin repeat-like **Superfamily:**BAG domain **Family:**BAG domain
11	d1v4sa1	Alignment		8.8	40	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase

12	d1j6wa_	Alignment		8.4	37	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
13	d1uhza_	Alignment		8.4	22	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
14	d1czan3	Alignment		8.1	43	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
15	d2ilka_	Alignment		8.0	21	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
16	d1czan1	Alignment		7.8	25	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
17	d2nn6g2	Alignment		7.6	39	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
18	c3fmaD_	Alignment		6.8	23	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**protein smy2; **PDBTitle:** crystal structure of the gyf domain of smy2 in complex with a proline-2 rich peptide from bbp/scsf1
19	d3b2ua2	Alignment		6.6	80	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Growth factor receptor domain **Family:**Growth factor receptor domain
20	d2pbka1	Alignment		6.4	12	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
21	d1j6xa_	Alignment	not modelled	6.4	22	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
22	d1y74b1	Alignment	not modelled	6.1	42	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
23	c3adjA_	Alignment	not modelled	6.1	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
24	c2wa0A_	Alignment	not modelled	6.0	18	**PDB header:**immune system **Chain:** A: **PDB Molecule:**melanoma-associated antigen 4; **PDBTitle:** crystal structure of the human magea4
25	c2kpeB_	Alignment	not modelled	5.2	35	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glycophorin-a; **PDBTitle:** refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles