Phyre^2

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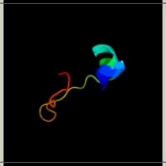
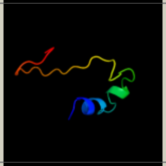
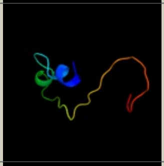
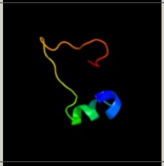
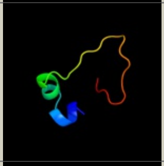
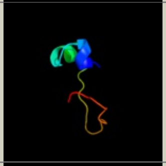
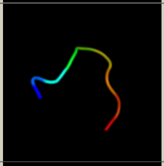
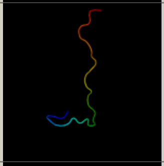
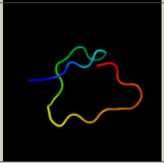
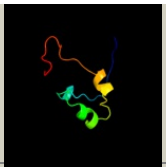
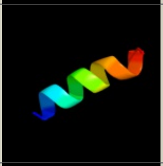
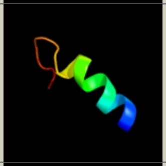
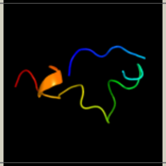
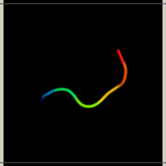
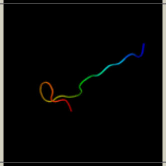
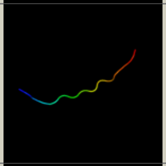
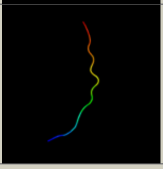
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jala2	Alignment		39.1	67	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
2	d1ni3a2	Alignment		38.6	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
3	c2hj1A_	Alignment		36.2	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
4	d2hj1a1	Alignment		36.2	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**HI0395-like
5	c1ni3A_	Alignment		25.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ychf gtp-binding protein; **PDBTitle:** structure of the schizosaccharomyces pombe ychf gtpase
6	c2ohfA_	Alignment		25.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein 9; **PDBTitle:** crystal structure of human ola1 in complex with amppcp
7	c1jalA_	Alignment		21.4	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ychf protein; **PDBTitle:** ychf protein (hi0393)
8	c2dwqB_	Alignment		18.7	56	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**gtp-binding protein; **PDBTitle:** thermus thermophilus ychf gtp-binding protein
9	d2i9ca1	Alignment		11.9	29	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**RPA1889-like
10	d1hrti_	Alignment		9.3	33	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
11	c1wxqA_	Alignment		9.1	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3

12	c3b49A_	Alignment		8.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2189 protein; **PDBTitle:** crystal structure of an uncharacterized conserved protein from2 listeria innocua
13	c3cs5B_	Alignment		8.0	60	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**phycobilisome degradation protein nbla; **PDBTitle:** nbla protein from synechococcus elongatus pcc 7942
14	c3rh3A_	Alignment		7.3	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized duf3829-like protein; **PDBTitle:** crystal structure of an uncharacterized duf3829-like protein (bt_1908)2 from bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
15	d1nh2b_	Alignment		7.1	39	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
16	c3d6nB_	Alignment		6.6	17	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
17	c2kd3A_	Alignment		6.6	43	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sclerostin; **PDBTitle:** nmr structure of the wnt modulator protein sclerostin
18	d2iaya1	Alignment		6.6	39	**Fold:**Lp2179-like **Superfamily:**Lp2179-like **Family:**Lp2179-like
19	d2qqra2	Alignment		6.2	40	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
20	d2qqsa2	Alignment		6.1	47	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
21	c2ekiA_	Alignment	not modelled	5.8	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**developmentally-regulated gtp-binding protein 1; **PDBTitle:** solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
22	c1aikC_	Alignment	not modelled	5.7	43	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**hiv-1 gp41 glycoprotein; **PDBTitle:** hiv gp41 core structure
23	c3iuoA_	Alignment	not modelled	5.6	47	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase recq; **PDBTitle:** the crystal structure of the c-terminal domain of the atp-dependent2 dna helicase recq from porphyromonas gingivalis to 1.6a