Phyre2

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Description	P0A780
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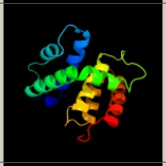
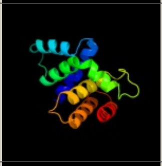
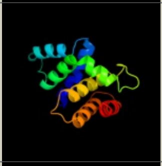
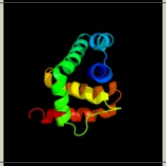
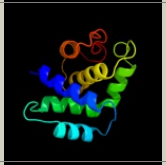
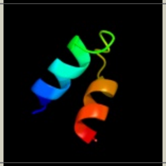
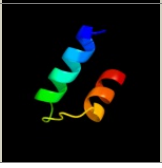
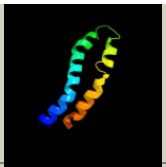
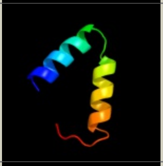
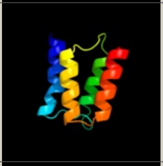
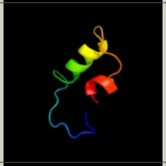
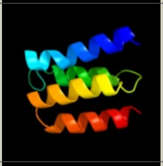
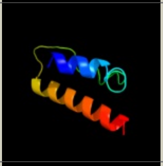
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ey1a_	Alignment		100.0	100	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**Antitermination factor NusB
2	d1tzva_	Alignment		100.0	35	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**Antitermination factor NusB
3	c2jr0A_	Alignment		100.0	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n utilization substance protein b homolog; **PDBTitle:** solution structure of nusb from aquifex aeolicus
4	d1eyva_	Alignment		100.0	34	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**Antitermination factor NusB
5	c1eyvA_	Alignment		100.0	34	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n-utilizing substance protein b homolog; **PDBTitle:** the crystal structure of nusb from mycobacterium2 tuberculosis
6	d1sqga1	Alignment		100.0	23	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**RmsB N-terminal domain-like
7	c1sqgA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sun protein; **PDBTitle:** the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
8	c2yxlA_	Alignment		99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**450aa long hypothetical fmu protein; **PDBTitle:** crystal structure of ph0851
9	d1q8ca_	Alignment		81.4	18	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**Hypothetical protein MG027
10	c2zc2A_	Alignment		42.8	15	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnad-like replication protein; **PDBTitle:** crystal structure of dnad-like replication protein from2 streptococcus mutans ua159, gi 24377835, residues 127-199
11	d2i5ua1	Alignment		35.7	24	**Fold:**DnaD domain-like **Superfamily:**DnaD domain-like **Family:**DnaD domain

12	c3ls1A_	Alignment		32.8	8	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
13	c3pubA_	Alignment		30.8	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**30kda protein; **PDBTitle:** crystal structure of the bombyx mori low molecular weight lipoprotein2 7 (bmlp7)
14	d1v54e_	Alignment		24.5	18	**Fold:**alpha-alpha superhelix **Superfamily:**Cytochrome c oxidase subunit E **Family:**Cytochrome c oxidase subunit E
15	c2kebA_	Alignment		21.6	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
16	c2y69R_	Alignment		20.9	19	**PDB header:**electron transport **Chain:** R: **PDB Molecule:**cytochrome c oxidase subunit 5a; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
17	d3c8ga1	Alignment		12.1	14	**Fold:**MtlR-like **Superfamily:**MtlR-like **Family:**MtlR-like
18	c2kz5A_	Alignment		11.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor nf-e2 45 kda subunit; **PDBTitle:** solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
19	c2hv8D_	Alignment		11.0	4	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**rab11 family-interacting protein 3; **PDBTitle:** crystal structure of gtp-bound rab11 in complex with fip3
20	d2ga1a1	Alignment		10.9	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Alr1493-like
21	c2z1dA_	Alignment	not modelled	9.3	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hypd; **PDBTitle:** crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
22	c3kaeC_	Alignment	not modelled	7.6	21	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**possible protein of nuclear scaffold; **PDBTitle:** cdc27 n-terminus
23	d1xmka1	Alignment	not modelled	6.9	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
24	c2vckC_	Alignment	not modelled	6.7	39	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**cyanobacterial phycoerythrobilin; **PDBTitle:** structure of phycoerythrobilin synthase pebs from the2 cyanophage p-ssm2 in complex with the bound substrate3 biliverdin ixa
25	c3c9pA_	Alignment	not modelled	6.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sp1917; **PDBTitle:** crystal structure of uncharacterized protein sp1917
26	c1dxzA_	Alignment	not modelled	5.7	15	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**acetylcholine receptor protein, alpha chain; **PDBTitle:** m2 transmembrane segment of alpha-subunit of nicotinic2 acetylcholine receptor from torpedo californica, nmr, 203 structures
27	d1rkta2	Alignment	not modelled	5.6	9	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
						Fold:DLC

28	d1cmia_	Alignment	not modelled	5.6	5	**Superfamily:**DLC **Family:**DLC
29	d1x4pa1	 Alignment	not modelled	5.3	25	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)