Phyre2

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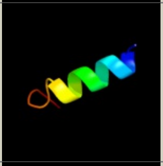
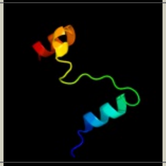
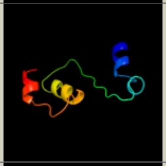
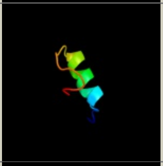
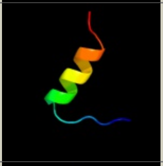
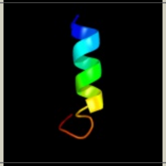
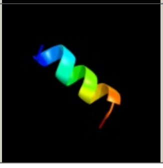
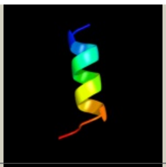
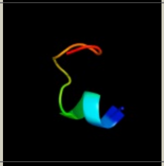
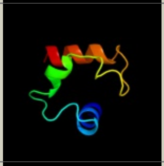
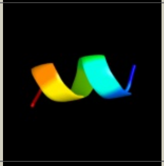
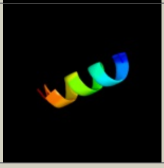
Description	P0C0L9
Date	Thu Jan 5 11:29:55 GMT 2012
Unique Job ID	d7cabf0792797834

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1uj8a1	Alignment		100.0	100	**Fold:**Another 3-helical bundle **Superfamily:**IscX-like **Family:**IscX-like
2	c2kzvA_	Alignment		82.1	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of cv_0373(175-257) protein from2 chromobacterium violaceum, northeast structural genomics consortium3 target cvr118a
3	c2kpmA_	Alignment		39.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein from gene2 locus ne0665 of nitrosomonas europaea. northeast structural3 genomics target ner103a
4	c3gr1A_	Alignment		20.4	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
5	d1gwca2	Alignment		15.6	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
6	c3ktbD_	Alignment		12.7	17	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**arsenical resistance operon trans-acting repressor; **PDBTitle:** crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
7	c3mg9A_	Alignment		9.3	19	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**teg12; **PDBTitle:** teg 12 binary structure complexed with the teicoplanin aglycone
8	d1mzba_	Alignment		8.0	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FUR-like
9	d1n2aa2	Alignment		7.8	35	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
10	d1gnwa2	Alignment		7.8	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
11	d1e6ba2	Alignment		7.7	40	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain

12	d1fw1a2	Alignment		7.0	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
13	c2o03A_	Alignment		6.6	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
14	d12asa_	Alignment		6.3	47	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
15	c2xigA_	Alignment		6.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
16	d1dgsa1	Alignment		6.2	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
17	d1rqta_	Alignment		6.0	33	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
18	c1rqtB_	Alignment		6.0	33	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
19	c1rqtA_	Alignment		6.0	33	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
20	d1oyja2	Alignment		5.5	40	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
21	d1qhma_	Alignment	not modelled	5.3	22	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
22	c2jg0A_	Alignment	not modelled	5.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**periplasmic trehalase; **PDBTitle:** family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin
23	d2jg0a1	Alignment	not modelled	5.3	12	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Trehalase-like