Phyre^2

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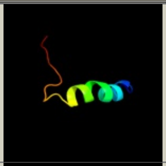
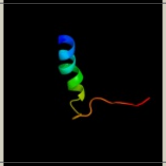
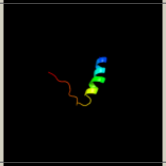
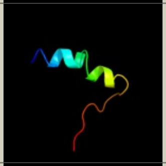
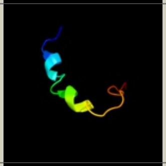
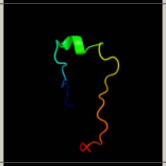
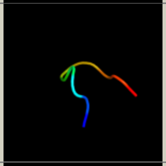
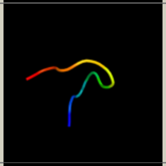
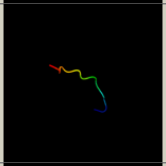
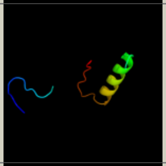
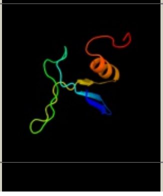
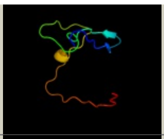
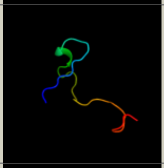
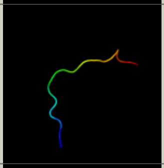
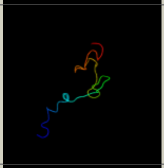
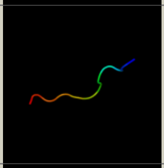
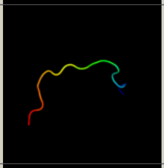
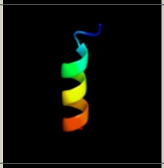
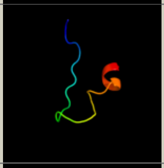
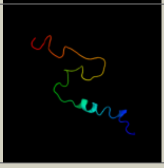
Description	Q9XB42
Date	Thu Jan 5 12:38:30 GMT 2012
Unique Job ID	ddd3c13c5b1f0cd8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2cqma1	Alignment		58.6	30	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
2	d1gd8a_	Alignment		53.1	30	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
3	d2zjrk1	Alignment		53.1	25	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
4	c3bboP_	Alignment		34.8	25	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**ribosomal protein l17; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
5	d2qamn1	Alignment		30.5	29	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
6	d1bnla_	Alignment		15.5	18	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Endostatin
7	c2qh7A_	Alignment		12.3	40	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**zinc finger cdgsh-type domain 1; **PDBTitle:** mitoneet is a uniquely folded 2fe-2s outer mitochondrial membrane2 protein stabilized by pioglitazone
8	c3fnvB_	Alignment		12.3	40	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**cdgsh iron sulfur domain-containing protein 2; **PDBTitle:** crystal structure of miner1: the redox-active 2fe-2s protein causative2 in wolfram syndrome 2
9	c2gyrB_	Alignment		11.2	38	**PDB header:**hormone/growth factor **Chain:** B: **PDB Molecule:**neurotrophic factor artemin, isoform 3; **PDBTitle:** crystal structure of human artemin
10	d1ir1s_	Alignment		11.1	25	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
11	d2j7qa1	Alignment		8.7	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**M48USP-like

12	c3fkaD_	Alignment		8.5	13	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized ntf-2 like protein; **PDBTitle:** crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
13	d1koea_	Alignment		8.4	19	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Endostatin
14	d1ztxe1	Alignment		8.2	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
15	c2wsfN_	Alignment		7.3	20	**PDB header:**photosynthesis **Chain:** N: **PDB Molecule:**photosystem i-n subunit; **PDBTitle:** improved model of plant photosystem i
16	c3egpA_	Alignment		7.3	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure analysis of dengue-1 envelope protein2 domain iii
17	d1ok8a1	Alignment		6.8	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
18	c2kztA_	Alignment		6.7	20	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** structure of the tandem ma-3 region of pdcd4
19	d1hd2a_	Alignment		6.6	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
20	c2o01N_	Alignment		5.9	20	**PDB header:**photosynthesis **Chain:** N: **PDB Molecule:**photosystem i-n subunit; **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
21	c2riqA_	Alignment	not modelled	5.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** crystal structure of the third zinc-binding domain of human parp-1
22	d2j01s1	Alignment	not modelled	5.7	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
23	c3ccjU_	Alignment	not modelled	5.7	23	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**50s ribosomal protein l24e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u
24	d1vqou1	Alignment	not modelled	5.6	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Ribosomal protein L24e
25	c2iosA_	Alignment	not modelled	5.5	40	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**programmed cell death 4, pdcd4; **PDBTitle:** crystal structure of the c-terminal ma3 domain of pdcd42 (mouse); form 3
26	c2rg8A_	Alignment	not modelled	5.5	20	**PDB header:**apoptosis, translation **Chain:** A: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** crystal structure of programmed for cell death 4 middle ma32 domain
27	d1m9sa3	Alignment	not modelled	5.4	18	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**GW domain
28	c2h0pA_	Alignment	not modelled	5.2	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** nmr structure of the dengue-4 virus envelope protein domain2 iii
29	c3oe3B_	Alignment	not modelled	5.1	16	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**putative periplasmic protein; **PDBTitle:** crystal structure of plic-st, periplasmic lysozyme

						inhibitor of c-type2 lysozyme from salmonella typhimurium
30	d1pjwa_	Alignment	not modelled	5.1	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
31	c2jqmA_	Alignment	not modelled	5.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**envelope protein e; **PDBTitle:** yellow fever envelope protein domain iii nmr structure2 (s288-k398)