Phyre²

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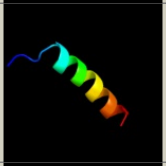
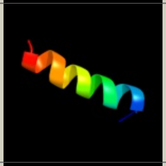
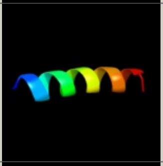
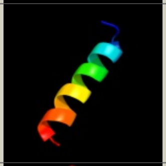
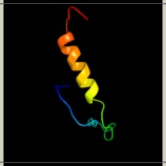
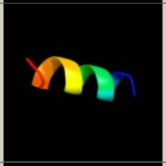
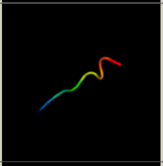
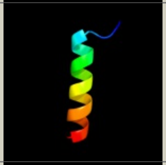
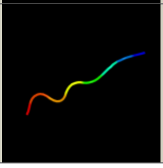
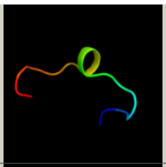
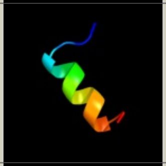
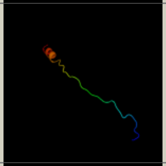
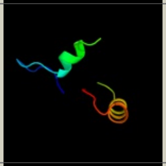
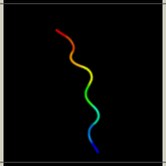
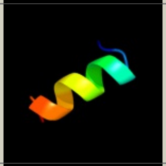
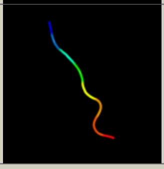
Description	P39351
Date	Thu Jan 5 11:59:39 GMT 2012
Unique Job ID	e358761d16067bdb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dxrA_	Alignment		33.2	26	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** crystal structure of the yeast inter-membrane space2 chaperone assembly tim9.10
2	c3dxrB_	Alignment		32.1	33	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** crystal structure of the yeast inter-membrane space2 chaperone assembly tim9.10
3	d2bska1	Alignment		28.1	32	**Fold:**Tim10-like **Superfamily:**Tim10-like **Family:**Tim10/DDP
4	c3cjhJ_	Alignment		28.1	32	**PDB header:**protein transport **Chain:** J: **PDB Molecule:**mitochondrial import inner membrane translocase subunit **PDBTitle:** tim8-tim13 complex
5	c2bskD_	Alignment		22.2	37	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** crystal structure of the tim9 tim10 hexameric complex
6	c2k19A_	Alignment		21.9	39	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**putative piscicolin 126 immunity protein; **PDBTitle:** nmr solution structure of pisi
7	c2iqcA_	Alignment		16.9	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fanconi anemia group f protein; **PDBTitle:** crystal structure of human fancf protein that functions in2 the assembly of a dna damage signaling complex
8	d2cvea1	Alignment		14.0	75	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
9	d2bskb1	Alignment		12.7	33	**Fold:**Tim10-like **Superfamily:**Tim10-like **Family:**Tim10/DDP
10	c2xglB_	Alignment		12.4	29	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m immunity protein; **PDBTitle:** the x-ray structure of the escherichia coli colicin m immunity2 protein demonstrates the presence of a disulphide bridge, which is3 functionally essential
11	d1vi7a1	Alignment		11.1	50	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like

12	d2incc1	Alignment		11.1	53	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TmoB-like **Family:**TmoB-like
13	c3hgkE_	Alignment		11.0	33	**PDB header:**transferase **Chain:** E: **PDB Molecule:**effector protein hopab2; **PDBTitle:** crystal structure of effect protein avrptob complexed with2 kinase pto
14	c3ol4B_	Alignment		11.0	40	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
15	d1x4pa1	Alignment		10.6	53	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)
16	c2k48A_	Alignment		10.6	36	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nucleoprotein; **PDBTitle:** nmr structure of the n-terminal coiled coil domain of the2 andes hantavirus nucleocapsid protein
17	d2tpta2	Alignment		9.6	21	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
18	c2cveA_	Alignment		8.6	75	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1053; **PDBTitle:** crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
19	c3sviA_	Alignment		8.5	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**type iii effector hopab2; **PDBTitle:** structure of the pto-binding domain of hoppmal generated by limited2 thermolysin digestion
20	c1vi7A_	Alignment		8.3	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yigz; **PDBTitle:** crystal structure of an hypothetical protein
21	c2kvcA_	Alignment	not modelled	7.8	60	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
22	d1ci3m2	Alignment	not modelled	7.7	39	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
23	c3p43A_	Alignment	not modelled	7.5	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure and activities of archaeal members of the ligd 3'2 phosphoesterase dna repair enzyme superfamily
24	c2lkyA_	Alignment	not modelled	7.4	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
25	d1zvsa1	Alignment	not modelled	7.1	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
26	c2xksA_	Alignment	not modelled	7.0	20	**PDB header:**immune system **Chain:** A: **PDB Molecule:**beta-2-microglobulin; **PDBTitle:** prion-like conversion during amyloid formation at atomic2 resolution
27	c3kxeD_	Alignment	not modelled	6.8	35	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**antitoxin protein pard-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
						PDB header:metal transport

28	c1xvlC_	Alignment	not modelled	6.8	30	**Chain:** C: **PDB Molecule:**mn transporter; **PDBTitle:** the three-dimensional structure of mntc from synechocystis2 6803
29	d1ffkw_	Alignment	not modelled	6.6	50	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
30	d1wgna_	Alignment	not modelled	6.4	67	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
31	d1qo3a1	Alignment	not modelled	6.1	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
32	c1s1i0_	Alignment	not modelled	6.1	38	**PDB header:**ribosome **Chain:** 0: **PDB Molecule:**60s ribosomal protein l32; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
33	c4a1cX_	Alignment	not modelled	6.1	55	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**60s ribosomal protein l32; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
34	d1ydpa1	Alignment	not modelled	6.0	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
35	c3ardB_	Alignment	not modelled	5.9	13	**PDB header:**immune system **Chain:** B: **PDB Molecule:**beta-2-microglobulin; **PDBTitle:** ternary crystal structure of the mouse nkt tcr-cd1d-3'deoxy-alpha-2 galactosylceramide
36	c3areB_	Alignment	not modelled	5.9	13	**PDB header:**immune system **Chain:** B: **PDB Molecule:**beta-2-microglobulin; **PDBTitle:** ternary crystal structure of the mouse nkt tcr-cd1d-4'deoxy-alpha-2 galactosylceramide
37	c2zkry_	Alignment	not modelled	5.6	75	**PDB header:**ribosomal protein/rna **Chain:** Y: **PDB Molecule:**5s ribosomal rna; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
38	d1a6tb2	Alignment	not modelled	5.3	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
39	d1sm3h2	Alignment	not modelled	5.2	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
40	d1de4a1	Alignment	not modelled	5.2	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
41	c3cceY_	Alignment	not modelled	5.2	50	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**50s ribosomal protein l32e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation u2535a
42	d1vqoy1	Alignment	not modelled	5.2	50	**Fold:**Barstar-like **Superfamily:**Ribosomal protein L32e **Family:**Ribosomal protein L32e
43	c1dfwA_	Alignment	not modelled	5.1	36	**PDB header:**immune system **Chain:** A: **PDB Molecule:**lung surfactant protein b; **PDBTitle:** conformational mapping of the n-terminal segment of2 surfactant protein b in lipid using 13c-enhanced fourier3 transform infrared spectroscopy (ftir)