Phyre2

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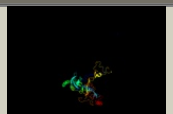
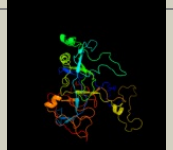
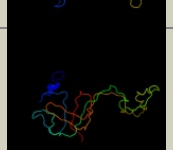
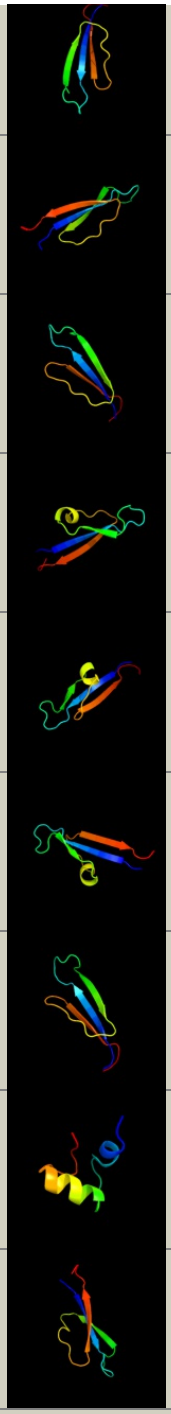
Description	P39023
Date	Thu Apr 26 09:26:30 BST 2012
Unique Job ID	fe687422d43f91ad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3iz5C_	Alignment		100.0	68	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**60s ribosomal protein l3 (l3p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
2	c4a1aB_	Alignment		100.0	63	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein l3; **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 3.
3	c3jywC_	Alignment		100.0	67	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**60s ribosomal protein l3; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
4	c2zkrb_	Alignment		100.0	98	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es4; **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
5	c1s1iC_	Alignment		100.0	67	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**60s ribosomal protein l3; **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.
6	d1vqob1	Alignment		100.0	37	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
7	d2gycb1	Alignment		100.0	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
8	d2zjrb1	Alignment		100.0	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
9	d2j01e1	Alignment		100.0	29	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Ribosomal protein L3
10	c2ftcC_	Alignment		100.0	21	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**mitochondrial 39s ribosomal protein l3; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
11	c3bboF_	Alignment		100.0	29	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**ribosomal protein l3; **PDBTitle:** homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome

12	c3rykB_	Alignment		59.7	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dtdp-4-dehydrorhamnose 3,5-epimerase; **PDBTitle:** 1.63 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 3,5-epimerase (rfbc) from bacillus anthracis str. ames with tdp and3 ppi bound
13	d1ep0a_	Alignment		46.8	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
14	c1upiA_	Alignment		42.7	14	**PDB header:**epimerase **Chain:** A: **PDB Molecule:**dtdp-4-dehydrorhamnose 3,5-epimerase; **PDBTitle:** mycobacterium tuberculosis rmlc epimerase (rv3465)
15	d1wlta1	Alignment		41.9	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
16	d1dzra_	Alignment		41.4	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
17	d1oi6a_	Alignment		35.5	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
18	d2ixca1	Alignment		34.9	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
19	c2qtxL_	Alignment		34.4	29	**PDB header:**rna binding protein **Chain:** L: **PDB Molecule:**uncharacterized protein mj1435; **PDBTitle:** crystal structure of an hfq-like protein from methanococcus2 jannaschii
20	c2c0zA_	Alignment		33.1	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**novw; **PDBTitle:** the 1.6 a resolution crystal structure of novw: a 4-keto-6-2 deoxy sugar epimerase from the novobiocin biosynthetic3 gene cluster of streptomyces spheroides
21	c3ejkA_	Alignment	not modelled	31.0	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dtdp sugar isomerase; **PDBTitle:** crystal structure of dtdp sugar isomerase (yp_390184.1) from2 desulfovibrio desulfuricans g20 at 1.95 a resolution
22	d2c0za1	Alignment	not modelled	30.1	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
23	d2ixha1	Alignment	not modelled	27.8	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
24	d1xhca3	Alignment	not modelled	13.5	45	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
25	d1ekga_	Alignment	not modelled	11.9	24	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
26	c1vbiA_	Alignment	not modelled	8.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type 2 malate/lactate dehydrogenase; **PDBTitle:** crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
27	d1vqoq1	Alignment	not modelled	8.1	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
28	c1htmB_	Alignment	not modelled	7.5	43	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin ha2 chain; **PDBTitle:** structure of influenza haemagglutinin at the ph of membrane2 fusion
						Fold:6-bladed beta-propeller

29	d1inva_	Alignment	not modelled	6.8	36	**Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
30	c3ij2B_	Alignment	not modelled	6.7	16	**PDB header:**hormone/protein binding **Chain:** B: **PDB Molecule:**beta-nerve growth factor; **PDBTitle:** ligand-receptor structure
31	c1s1iQ_	Alignment	not modelled	6.7	20	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l21-a; **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.
32	d1bndb_	Alignment	not modelled	6.7	14	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Neurotrophin
33	c2zkrq_	Alignment	not modelled	6.7	10	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 part ii; **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
34	d1wwwv_	Alignment	not modelled	6.5	21	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Neurotrophin
35	d2gqfa1	Alignment	not modelled	6.4	26	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
36	c1zuyB_	Alignment	not modelled	6.4	7	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin-5 isoform; **PDBTitle:** high-resolution structure of yeast myo5 sh3 domain
37	c1a3qA_	Alignment	not modelled	6.2	21	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (nuclear factor kappa-b p52); **PDBTitle:** human nf-kappa-b p52 bound to dna
38	c2rqrA_	Alignment	not modelled	6.0	0	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**engulfment and cell motility protein 1, linker, dedicator **PDBTitle:** the solution structure of human dock2 sh3 domain - elmo1 peptide2 chimera complex
39	c2eg9B_	Alignment	not modelled	5.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adp-ribosyl cyclase 1; **PDBTitle:** crystal structure of the truncated extracellular domain of2 mouse cd38
40	d1b7go1	Alignment	not modelled	5.8	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
41	c3hfkB_	Alignment	not modelled	5.7	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-methylmuconolactone methylisomerase; **PDBTitle:** crystal structure of 4-methylmuconolactone methylisomerase2 (h52a) in complex with 4-methylmuconolactone
42	d1t11a3	Alignment	not modelled	5.6	16	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
43	d1jjga_	Alignment	not modelled	5.5	8	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
44	c3fq6A_	Alignment	not modelled	5.4	45	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
45	c3iz5O_	Alignment	not modelled	5.4	26	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**60s ribosomal protein l27a (l15p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
46	d1s1da_	Alignment	not modelled	5.4	17	**Fold:**5-bladed beta-propeller **Superfamily:**Apyrase **Family:**Apyrase
47	c3fyfA_	Alignment	not modelled	5.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein bvu-3222; **PDBTitle:** crystal structure of uncharacterized protein bvu_3222 from2 bacteroides vulgatus