Phyre^2

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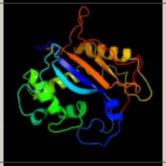
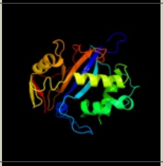
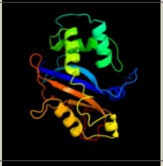
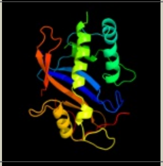
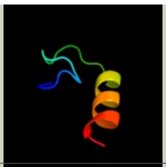
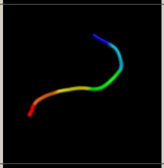
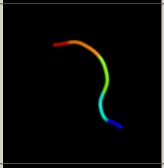
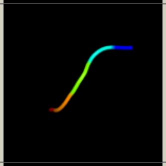
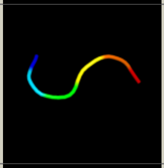
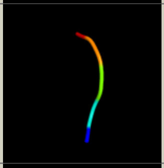
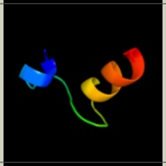
Description	P21338
Date	Thu Jan 5 11:38:03 GMT 2012
Unique Job ID	ccadd883d79760cc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pqxA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease i; **PDBTitle:** e. coli rnase 1 (in vivo folded)
2	d1sgla_	Alignment		100.0	20	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
3	d1iyba_	Alignment		100.0	23	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
4	d1dixa_	Alignment		100.0	19	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
5	c1vd3A_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rnase ngr3; **PDBTitle:** ribonuclease nt in complex with 2'-ump
6	d1jy5a_	Alignment		100.0	21	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
7	d1iooa_	Alignment		100.0	24	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
8	d1ucda_	Alignment		100.0	24	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
9	d1iqqa_	Alignment		100.0	20	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
10	c3d3zA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**actibind; **PDBTitle:** crystal structure of actibind a t2 rnase
11	d1bola_	Alignment		100.0	19	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like

12	d2ciwa1	Alignment		26.8	26	**Fold:**EF Hand-like **Superfamily:**Cloroperoxidase **Family:**Cloroperoxidase
13	d1dfxa1	Alignment		26.8	50	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Superoxide reductase-like **Family:**Superoxide reductase-like
14	c2amuA_	Alignment		25.3	80	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative superoxide reductase; **PDBTitle:** crystal structure of a putative superoxide reductase (tm0658) from2 thermotoga maritima at 2.00 a resolution
15	d1dqia_	Alignment		24.9	80	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Superoxide reductase-like **Family:**Superoxide reductase-like
16	c1y07A_	Alignment		23.7	50	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**desulfoferrodoxin (rbo); **PDBTitle:** crystal structure of the superoxide reductase from2 treponema pallidum
17	d1vzia1	Alignment		23.7	60	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Superoxide reductase-like **Family:**Superoxide reductase-like
18	c1vzhB_	Alignment		20.2	60	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**desulfoferrodoxin; **PDBTitle:** structure of superoxide reductase bound to ferrocyanide and2 active site expansion upon x-ray induced photoreduction
19	c3oqgA_	Alignment		14.4	38	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**hpy188i; **PDBTitle:** restriction endonuclease hpy188i in complex with substrate dna
20	c2cj0A_	Alignment		14.1	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chloroperoxidase; **PDBTitle:** chloroperoxidase complexed with nitrate
21	c2zkrs_	Alignment	not modelled	12.8	14	**PDB header:**ribosomal protein/rna **Chain:** S: **PDB Molecule:**rna expansion segment es39 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
22	c1s1iT_	Alignment	not modelled	10.3	11	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**60s ribosomal protein l25; **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.
23	c2cfaB_	Alignment	not modelled	9.3	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate synthase; **PDBTitle:** structure of viral flavin-dependant thymidylate synthase2 thyx
24	c3bboV_	Alignment	not modelled	9.2	11	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**ribosomal protein l23; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
25	d2dl2a1	Alignment	not modelled	8.8	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
26	c4a10A_	Alignment	not modelled	8.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**octenoyl-coa reductase/carboxylase; **PDBTitle:** apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomyces sp.
27	d1m4ka1	Alignment	not modelled	8.3	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
28	c2j42A_	Alignment	not modelled	8.2	23	**PDB header:**toxin **Chain:** A: **PDB Molecule:**c2 toxin component-ii;

28	c2j42A_	Alignment	not modelled	8.2	23	**PDBTitle:** low quality crystal structure of the transport component c2-2 ii of the c2-toxin from clostridium botulinum
29	c4a17R_	Alignment	not modelled	7.8	15	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**rpl23a; **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 2.
30	c3q13A_	Alignment	not modelled	7.7	22	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**spondin-1; **PDBTitle:** the structure of the ca2+-binding, glycosylated f-spondin domain of f-2 spondin, a c2-domain variant from extracellular matrix
31	d1nkra1	Alignment	not modelled	7.2	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
32	d1h7na_	Alignment	not modelled	6.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
33	c3f9xA_	Alignment	not modelled	6.7	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd8; **PDBTitle:** structural insights into lysine multiple methylation by set2 domain methyltransferases, set8-y334f / h4-lys20me2 /3 adohcy
34	d1vqos1	Alignment	not modelled	6.2	11	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**L23p
35	c1xa0B_	Alignment	not modelled	5.8	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative nadph dependent oxidoreductases; **PDBTitle:** crystal structure of mcsg target apc35536 from bacillus2 stearothermophilus
36	d1f66c_	Alignment	not modelled	5.6	16	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
37	c1f66C_	Alignment	not modelled	5.6	16	**PDB header:**structural protein/dna **Chain:** C: **PDB Molecule:**histone h2a.z; **PDBTitle:** 2.6 a crystal structure of a nucleosome core particle2 containing the variant histone h2a.z
38	d2qamt1	Alignment	not modelled	5.5	9	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**L23p
39	d1tp6a_	Alignment	not modelled	5.5	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PA1314-like
40	d1xtpa_	Alignment	not modelled	5.2	9	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
41	d1m4ua_	Alignment	not modelled	5.2	56	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Noggin
42	c2ww9K_	Alignment	not modelled	5.1	13	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein l25; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome