Phyre2

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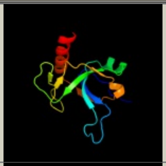
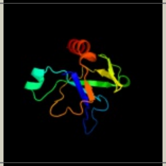
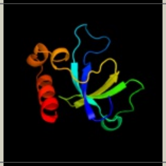
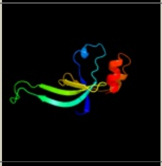
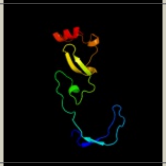
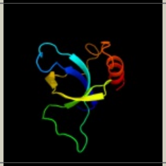
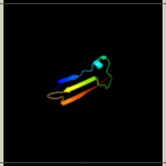
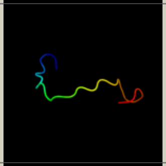
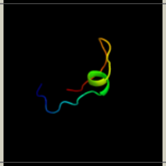
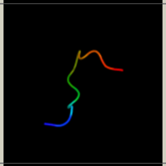
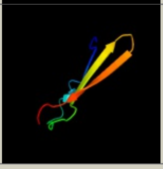
Description	P0AE70
Date	Thu Jan 5 11:22:39 GMT 2012
Unique Job ID	32861f8a3602467f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ub4a_	Alignment		100.0	100	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
2	d1m1fa_	Alignment		100.0	29	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
3	d1ne8a_	Alignment		100.0	25	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
4	c3jrzA_	Alignment		95.7	17	**PDB header:**toxin **Chain:** A: **PDB Molecule:**ccdb; **PDBTitle:** ccdbvfi-formii-ph5.6
5	d3vuba_	Alignment		94.9	15	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**CcdB
6	c3llrA_	Alignment		70.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 3a; **PDBTitle:** crystal structure of the pwwp domain of human dna (cytosine-5-)-2 methyltransferase 3 alpha
7	d2daqa1	Alignment		60.8	11	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
8	c2l89A_	Alignment		50.5	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pwwp domain-containing protein 1; **PDBTitle:** solution structure of pdp1 pwwp domain reveals its unique binding2 sites for methylated h4k20 and dna
9	d1h3za_	Alignment		48.8	10	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
10	d2nlua1	Alignment		43.6	14	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
11	c3mxuA_	Alignment		31.2	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from bartonella2 henselae

12	d1cxqa_	Alignment		27.9	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
13	d1n27a_	Alignment		23.8	15	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
14	c2edgA_	Alignment		23.5	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** solution structure of the gcv_h domain from mouse glycine
15	d1khca_	Alignment		21.0	15	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
16	d2je6i1	Alignment		20.9	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
17	c2h8kA_	Alignment		20.5	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sult1c3 splice variant d; **PDBTitle:** human sulfotranferase sult1c3 in complex with pap
18	c3a8jF_	Alignment		20.2	29	**PDB header:**transferase/transport protein **Chain:** F: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of et-ehred complex
19	d2ja9a1	Alignment		19.1	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
20	d1onla_	Alignment		18.4	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
21	c2x35A_	Alignment	not modelled	16.7	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**peregrin; **PDBTitle:** molecular basis of histone h3k36me3 recognition by the pwwp2 domain of brpf1.
22	c3pfsA_	Alignment	not modelled	16.2	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bromodomain and phd finger-containing protein 3; **PDBTitle:** pwwp domain of human bromodomain and phd finger-containing protein 3
23	c2ja9A_	Alignment	not modelled	15.7	33	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the n-terminal deletion of yeast exosome2 component rrp40
24	d2nn6g1	Alignment	not modelled	14.4	55	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
25	c3iftA_	Alignment	not modelled	14.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
26	d2nn6i1	Alignment	not modelled	13.8	31	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
27	d1aqua_	Alignment	not modelled	13.4	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
28	d2ba0a1	Alignment	not modelled	13.4	44	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

29	c2gfuA_	Alignment	not modelled	13.0	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna mismatch repair protein msh6; **PDBTitle:** nmr solution structure of the pwwp domain of mismatch2 repair protein hmsh6
30	d1vqoq1	Alignment	not modelled	12.8	24	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
31	d1b12a_	Alignment	not modelled	12.5	14	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**Type 1 signal peptidase
32	d1hpca_	Alignment	not modelled	12.3	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
33	d2nn6h1	Alignment	not modelled	11.9	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
34	d3bfxa1	Alignment	not modelled	11.1	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
35	c2jnsA_	Alignment	not modelled	10.8	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bromodomain-containing protein 4; **PDBTitle:** solution structure of the bromodomain-containing protein 42 et domain
36	d1xv1a_	Alignment	not modelled	9.8	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
37	c2zvpX_	Alignment	not modelled	9.6	16	**PDB header:**transferase **Chain:** X: **PDB Molecule:**tyrosine-ester sulfotransferase; **PDBTitle:** crystal structure of mouse cytosolic sulfotransferase msult1d1 complex2 with pap and p-nitrophenol
38	d1q44a_	Alignment	not modelled	9.3	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
39	d1zaka2	Alignment	not modelled	9.2	23	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
40	c2ba0A_	Alignment	not modelled	9.1	42	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**archeal exosome rna binding protein rrp4; **PDBTitle:** archaeal exosome core
41	d2z0sa1	Alignment	not modelled	7.9	56	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
42	c2gwhA_	Alignment	not modelled	7.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase 1c2; **PDBTitle:** human sulfotranferase sult1c2 in complex with pap and2 pentachlorophenol
43	c2jysA_	Alignment	not modelled	7.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease/reverse transcriptase; **PDBTitle:** solution structure of simian foamy virus (mac) protease
44	d1okja2	Alignment	not modelled	7.3	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
45	c2ky9A_	Alignment	not modelled	7.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ydhk; **PDBTitle:** solution nmr structure of ydhk c-terminal domain from b.subtilis,2 northeast structural genomics consortium target target sr518
46	d1j99a_	Alignment	not modelled	6.6	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
47	d1ubea2	Alignment	not modelled	6.4	24	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
48	c2nn6G_	Alignment	not modelled	6.4	50	**PDB header:**hydrolase/transferase **Chain:** G: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
49	d1ls6a_	Alignment	not modelled	6.3	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
50	c3u3oA_	Alignment	not modelled	6.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase 1a1; **PDBTitle:** crystal structure of human sult1a1 bound to pap and two 3-cyano-7-2 hydroxycoumarin
51	d1mo6a2	Alignment	not modelled	6.3	24	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
52	d1c0ma2	Alignment	not modelled	6.2	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
53	c2dgyA_	Alignment	not modelled	5.9	36	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
54	c2zkrq_	Alignment	not modelled	5.9	15	**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
55	d2a3ra1	Alignment	not modelled	5.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
56	c1zd1B_	Alignment	not modelled	5.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfotransferase 4a1; **PDBTitle:** human sulfortransferase sult4a1
57	c3lyiA_	Alignment	not modelled	5.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bromodomain-containing protein 1; **PDBTitle:** pwwp domain of human bromodomain-containing protein 1