Phyre^2

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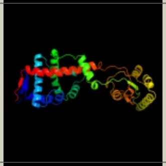
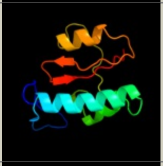
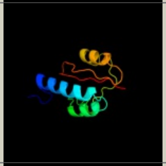
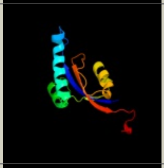
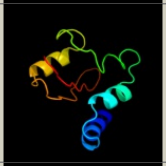
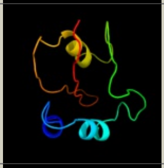
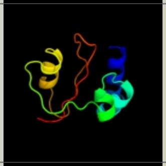
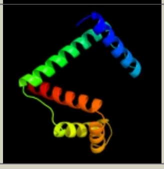
Description	P0ABZ6
Date	Thu Jan 5 11:16:47 GMT 2012
Unique Job ID	c22629b8a1e2112e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1m5yB_	Alignment		100.0	97	**PDB header:**isomerase, cell cycle **Chain:** B: **PDB Molecule:**survival protein sura; **PDBTitle:** crystallographic structure of sura, a molecular chaperone2 that facilitates outer membrane porin folding
2	c2pv3B_	Alignment		100.0	84	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**chaperone sura; **PDBTitle:** crystallographic structure of sura fragment lacking the second2 peptidyl-prolyl isomerase domain complexed with peptide nftlkfwdifrk
3	c3nrkA_	Alignment		100.0	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**lic12922; **PDBTitle:** the crystal structure of the leptospiral hypothetical protein lic12922
4	c3rgcB_	Alignment		100.0	22	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**possible periplasmic protein; **PDBTitle:** the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally related sura-like chaperones in the human pathogen3 campylobacter jejuni
5	c3rfwA_	Alignment		100.0	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cell-binding factor 2; **PDBTitle:** the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally-related sura-like chaperones in the human pathogen3 campylobacter jejuni
6	d1m5ya1	Alignment		99.9	86	**Fold:**Triger factor/SurA peptide-binding domain-like **Superfamily:**Triger factor/SurA peptide-binding domain-like **Family:**Porin chaperone SurA, peptide-binding domain
7	c1f8aB_	Alignment		99.8	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase nima- **PDBTitle:** structural basis for the phosphoserine-proline recognition2 by group iv ww domains
8	d1m5ya3	Alignment		99.8	100	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
9	c1yw5A_	Alignment		99.8	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl prolyl cis/trans isomerase; **PDBTitle:** peptidyl-prolyl isomerase ess1 from candida albicans
10	c2jzvA_	Alignment		99.7	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** solution structure of s. aureus prsa-ppiase
11	d2pv2a1	Alignment		99.7	100	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase

12	d1pina2	Alignment		99.7	21	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
13	d1j6ya_	Alignment		99.6	26	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
14	c3gpkA_	Alignment		99.6	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ppic-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution.
15	d1jnsa_	Alignment		99.6	31	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
16	c2rqsA_	Alignment		99.6	37	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**parvulin-like peptidyl-prolyl isomerase; **PDBTitle:** 3d structure of pin from the psychrophilic archeon cenarcheaum2 symbiosum (cspin)
17	d1eq3a_	Alignment		99.5	35	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
18	c2kgjA_	Alignment		99.5	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase d; **PDBTitle:** solution structure of parvulin domain of ppid from e.coli
19	c1zk6A_	Alignment		99.5	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** nmr solution structure of b. subtilis prsa ppiase
20	c2nsaA_	Alignment		97.3	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** structures of and interactions between domains of trigger factor from2 themotoga maritim
21	c3gtyX_	Alignment	not modelled	97.0	13	**PDB header:**chaperone/ribosomal protein **Chain:** X: **PDB Molecule:**trigger factor; **PDBTitle:** promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
22	d1w26a1	Alignment	not modelled	96.8	15	**Fold:**Triger factor/SurA peptide-binding domain-like **Superfamily:**Triger factor/SurA peptide-binding domain-like **Family:**TF C-terminus
23	c1w26B_	Alignment	not modelled	96.2	12	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
24	d1t11a1	Alignment	not modelled	93.7	16	**Fold:**Triger factor/SurA peptide-binding domain-like **Superfamily:**Triger factor/SurA peptide-binding domain-like **Family:**TF C-terminus
25	c1t11A_	Alignment	not modelled	91.6	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor
26	d1sknp_	Alignment	not modelled	20.8	18	**Fold:**A DNA-binding domain in eukaryotic transcription factors **Superfamily:**A DNA-binding domain in eukaryotic transcription factors **Family:**A DNA-binding domain in eukaryotic transcription factors
27	c2kz5A_	Alignment	not modelled	17.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor nf-e2 45 kda subunit; **PDBTitle:** solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
28	d1rwsa_	Alignment	not modelled	17.7	44	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS

29	d1a75a_	Alignment	not modelled	15.6	7	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
30	d1etob_	Alignment	not modelled	11.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
31	d1p5dx4	Alignment	not modelled	10.7	14	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
32	c2kycA_	Alignment	not modelled	10.1	6	**PDB header:**calcium binding protein **Chain:** A: **PDB Molecule:**parvalbumin, thymic cpv3; **PDBTitle:** solution structure of ca-free chicken parvalbumin 3 (cpv3)
33	d1zata2	Alignment	not modelled	8.8	15	**Fold:**L,D-transpeptidase pre-catalytic domain-like **Superfamily:**L,D-transpeptidase pre-catalytic domain-like **Family:**L,D-transpeptidase pre-catalytic domain-like
34	c1q6uA_	Alignment	not modelled	7.5	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase fkpa; **PDBTitle:** crystal structure of fkpa from escherichia coli
35	c3fs7D_	Alignment	not modelled	7.3	6	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**parvalbumin, thymic; **PDBTitle:** crystal structure of gallus gallus beta-parvalbumin (avian2 thymic hormone)
36	d1dq3a2	Alignment	not modelled	7.0	9	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**PI-Pfui intein middle domain
37	d1stza1	Alignment	not modelled	6.9	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
38	d1bu3a_	Alignment	not modelled	6.7	4	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
39	c3r9jD_	Alignment	not modelled	6.6	17	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** D: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 4.3a resolution structure of a mind-mine(i24n) protein complex
40	c3c04A_	Alignment	not modelled	6.6	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphomannomutase/phosphoglucomutase; **PDBTitle:** structure of the p368g mutant of pmm/pgm from p. aeruginosa
41	d1wdcb_	Alignment	not modelled	6.5	9	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
42	c3nr7A_	Alignment	not modelled	6.3	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein h-ns; **PDBTitle:** crystal structure of s. typhimurium h-ns 1-83
43	d2jnaa1	Alignment	not modelled	6.1	20	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
44	d1u2ma_	Alignment	not modelled	6.0	18	**Fold:**OmpH-like **Superfamily:**OmpH-like **Family:**OmpH-like
45	d1rwya_	Alignment	not modelled	5.9	9	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
46	d2pvba_	Alignment	not modelled	5.8	7	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
47	d2jn6a1	Alignment	not modelled	5.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
48	c3id5E_	Alignment	not modelled	5.4	7	**PDB header:**transferase/ribosomal protein/rna **Chain:** E: **PDB Molecule:**pre mrna splicing protein; **PDBTitle:** crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarin, l7ae and a split half c/d rna