Phyre2

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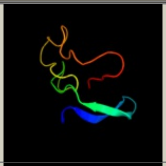
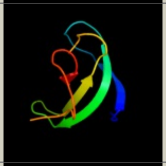
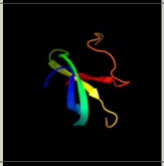
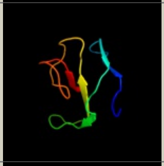
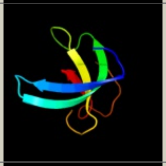
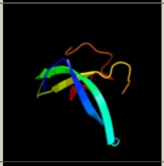
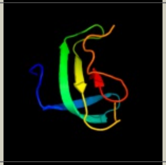
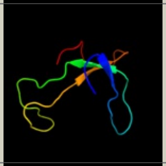
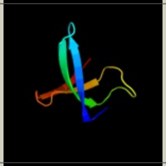
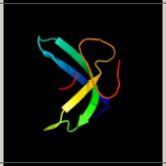
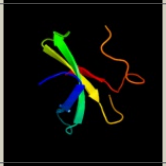
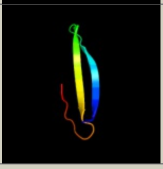
Description	P0AEG8
Date	Thu Jan 5 11:23:17 GMT 2012
Unique Job ID	8cb9b0e02ad48417

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1whma_	Alignment		88.3	29	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
2	d1tova_	Alignment		87.8	36	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
3	d1whga_	Alignment		87.1	38	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
4	d1whla_	Alignment		84.5	30	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
5	d1whka_	Alignment		80.3	21	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
6	c2e4hA_	Alignment		60.1	46	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**restin; **PDBTitle:** solution structure of cytoskeletal protein in complex with2 tubulin tail
7	d2cp6a1	Alignment		58.5	44	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
8	d2cp5a1	Alignment		55.1	35	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
9	d2cp3a1	Alignment		51.7	44	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
10	d1ixda_	Alignment		46.6	27	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
11	d2cowa1	Alignment		43.0	44	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain

12	c2equA_	Alignment		36.4	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1
13	c3qiiA_	Alignment		35.2	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 2 of human phd finger protein 20
14	c2a7yA_	Alignment		34.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv2302/mt2359; **PDBTitle:** solution structure of the conserved hypothetical protein2 rv2302 from the bacterium mycobacterium tuberculosis
15	d2a7ya1	Alignment		34.2	20	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Rv2302-like
16	d2e3ha1	Alignment		32.1	44	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
17	d2cp0a1	Alignment		31.8	35	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
18	c3p8dB_	Alignment		30.0	26	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**medulloblastoma antigen mu-mb-50.72; **PDBTitle:** crystal structure of the second tudor domain of human phf20 (homodimer2 form)
19	d2coza1	Alignment		25.4	40	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
20	c1q67B_	Alignment		24.5	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**decapping protein involved in mrna degradation- **PDBTitle:** crystal structure of dcp1p
21	c2qqsB_	Alignment	not modelled	23.7	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**jmjc domain-containing histone demethylation **PDBTitle:** jmjd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide
22	c1w4sA_	Alignment	not modelled	21.3	33	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**polybromo 1 protein; **PDBTitle:** crystal structure of the proximal bah domain of polybromo
23	c2z0wA_	Alignment	not modelled	20.4	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**cap-gly domain-containing linker protein 4; **PDBTitle:** crystal structure of the 2nd cap-gly domain in human restin-2 like protein 2 reveals a swapped-dimer
24	c2xdpA_	Alignment	not modelled	19.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 4c; **PDBTitle:** crystal structure of the tudor domain of human jmjd2c
25	c2l89A_	Alignment	not modelled	17.4	31	**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
26	d1whha_	Alignment	not modelled	17.1	37	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
27	c3tekA_	Alignment	not modelled	16.7	42	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**thermodbp-single stranded dna binding protein; **PDBTitle:** thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
28	c2w4eA	Alignment	not modelled	16.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein;

28	c2w4eA_	Alignment	not modelled	16.0	24	**PDBTitle:** structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
29	d1q67a_	Alignment	not modelled	16.0	12	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Dcp1
30	d2hqha1	Alignment	not modelled	14.9	30	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
31	c2k6dA_	Alignment	not modelled	11.8	22	**PDB header:**sh3 domain/ubiquitin **Chain:** A: **PDB Molecule:**sh3 domain-containing kinase-binding protein 1; **PDBTitle:** cin85 sh3-c domain in complex with ubiquitin
32	c2c1lA_	Alignment	not modelled	11.5	75	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease; **PDBTitle:** structure of the bfii restriction endonuclease
33	d1okga3	Alignment	not modelled	11.0	57	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**3-mercaptopyruvate sulfurtransferase, C-terminal domain
34	c1zq1B_	Alignment	not modelled	10.1	30	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
35	c2qkmG_	Alignment	not modelled	10.0	27	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**spbc3b9.21 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
36	d1whja_	Alignment	not modelled	10.0	24	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
37	d2e3ia1	Alignment	not modelled	9.5	37	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
38	d2coya1	Alignment	not modelled	9.2	28	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
39	d2cp2a1	Alignment	not modelled	8.7	28	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
40	d1o48a_	Alignment	not modelled	8.5	40	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
41	d2grea1	Alignment	not modelled	7.7	20	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
42	c3dlmA_	Alignment	not modelled	7.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setdb1; **PDBTitle:** crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
43	d1zq1a1	Alignment	not modelled	7.1	29	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
44	d3d03a1	Alignment	not modelled	7.0	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
45	d1b34b_	Alignment	not modelled	7.0	19	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
46	c1b34B_	Alignment	not modelled	7.0	19	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein (small nuclear ribonucleoprotein sm d2); **PDBTitle:** crystal structure of the d1d2 sub-complex from the human snrnp core2 domain
47	c1geaA_	Alignment	not modelled	6.8	63	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**pituitary adenylate cyclase activating **PDBTitle:** receptor-bound conformation of pacap21
48	d2cx1a1	Alignment	not modelled	6.4	29	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
49	d2d6fa1	Alignment	not modelled	6.2	26	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
50	d2pu9b1	Alignment	not modelled	6.1	55	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
51	c3d0fA_	Alignment	not modelled	6.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding 1 transmembrane protein mrca; **PDBTitle:** structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
52	c2ro0A_	Alignment	not modelled	5.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone acetyltransferase esa1; **PDBTitle:** solution structure of the knotted tudor domain of the yeast2 histone acetyltransferase, esa1
53	c2dlpA_	Alignment	not modelled	5.2	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**kiaa1783 protein; **PDBTitle:** solution structure of the sh3 domain of human kiaa17832 protein
						Fold:beta-Grasp (ubiquitin-like)

54	d2npta1	Alignment	not modelled	5.2	63	**Superfamily:**CAD & PB1 domains **Family:**PB1 domain