

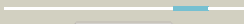
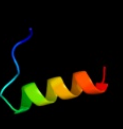



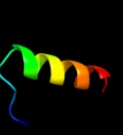
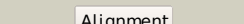




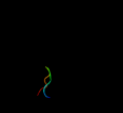










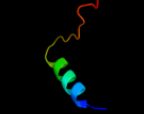

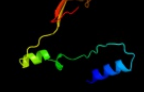

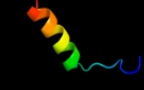
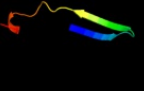



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P19932
Date	Thu Jan 5 11:37:41 GMT 2012
Unique Job ID	39c226ba5af61e5a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sb1B_	 Alignment		100.0	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hydrogenase expression protein; denitrificans2 atcc 25259
2	c1vp7D_	 Alignment		36.1	13	PDB header: hydrolase Chain: D: PDB Molecule: exodeoxyribonuclease vii small subunit; PDBTitle: crystal structure of exodeoxyribonuclease vii small subunit2 (np_881400.1) from bordetella pertussis at 2.40 a resolution
3	d1vp7a_	 Alignment		29.7	13	Fold: Spectrin repeat-like Superfamily: XseB-like Family: XseB-like
4	d1vp7b_	 Alignment		25.9	13	Fold: Spectrin repeat-like Superfamily: XseB-like Family: XseB-like
5	c2ka6B_	 Alignment		24.7	27	PDB header: transcription regulator Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: nmr structure of the cbp-taz2/stat1-tad complex
6	c2w56B_	 Alignment		24.1	13	PDB header: unknown function Chain: B: PDB Molecule: vc0508; PDBTitle: structure of the hypothetical protein vc0508 from vibrio cholerae2 vsp-ii pathogenicity island
7	d1vhib_	 Alignment		20.0	43	Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain
8	c3gkuB_	 Alignment		19.7	11	PDB header: rna binding protein Chain: B: PDB Molecule: probable rna-binding protein; PDBTitle: crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
9	d1p3wa_	 Alignment		18.5	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
10	d1b3ta_	 Alignment		16.4	50	Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain
11	c3h8dC_	 Alignment		14.6	15	PDB header: motor protein/signaling protein Chain: C: PDB Molecule: myosin-vi; PDBTitle: crystal structure of myosin vi in complex with dab2 peptide

12	c3lvmB_	Alignment		14.0	13	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
13	c3cvoA_	Alignment		13.3	15	PDB header: transferase Chain: A: PDB Molecule: methyltransferase-like protein of unknown function; PDBTitle: crystal structure of a methyltransferase-like protein (spo2022) from2 silicibacter pomeroyi dss-3 at 1.80 a resolution
14	c3d5jB_	Alignment		12.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: glutaredoxin-2, mitochondrial; PDBTitle: structure of yeast grx2-c30s mutant with glutathionyl mixed2 disulfide
15	d2f2ab1	Alignment		12.3	13	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like
16	c3if8B_	Alignment		12.3	15	PDB header: cell cycle Chain: B: PDB Molecule: protein zwilch homolog; PDBTitle: crystal structure of zwilch, a member of the rzz kinetochore complex
17	d1gyva_	Alignment		12.1	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: gamma-adaptin C-terminal appendage domain-like
18	c3n6qF_	Alignment		12.0	17	PDB header: oxidoreductase Chain: F: PDB Molecule: yghz aldo-keto reductase; PDBTitle: crystal structure of yghz from e. coli
19	d1gywb_	Alignment		11.9	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: gamma-adaptin C-terminal appendage domain-like
20	d2ns0a1	Alignment		11.5	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
21	d1th0a_	Alignment	not modelled	10.6	18	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Adenain-like
22	c2qf7A_	Alignment	not modelled	10.5	17	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
23	c3ipzA_	Alignment	not modelled	10.2	11	PDB header: electron transport, oxidoreductase Chain: A: PDB Molecule: monothiol glutaredoxin-s14, chloroplastic; PDBTitle: crystal structure of arabidopsis monothiol glutaredoxin atrxcp
24	c2wj8N_	Alignment	not modelled	9.9	13	PDB header: rna binding protein/rna Chain: N: PDB Molecule: nucleoprotein; PDBTitle: respiratory syncytial virus ribonucleoprotein
25	d2bz2a1	Alignment	not modelled	9.7	2	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
26	c1mszA_	Alignment	not modelled	9.0	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein smubp-2; PDBTitle: solution structure of the r3h domain from human smubp-2
27	d1msza_	Alignment	not modelled	9.0	19	Fold: IF3-like Superfamily: R3H domain Family: R3H domain
28	c2kwtA_	Alignment	not modelled	8.8	29	PDB header: viral protein Chain: A: PDB Molecule: protease ns2-3; PDBTitle: solution structure of ns2 [27-59]
						PDB header: transport protein

29	c2f3jA_	Alignment	not modelled	8.6	11	Chain: A: PDB Molecule: rna and export factor binding protein 2; PDBTitle: the solution structure of the ref2-i mrna export factor2 (residues 1-155).
30	d2ppqa1	Alignment	not modelled	8.2	10	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: APH phosphotransferases
31	c3exnA_	Alignment	not modelled	8.2	27	PDB header: transferase Chain: A: PDB Molecule: probable acetyltransferase; PDBTitle: crystal structure of acetyltransferase from thermus thermophilus hb8
32	c3c1sA_	Alignment	not modelled	8.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin-1; PDBTitle: crystal structure of grx1 in glutathionylated form
33	d1qk1a2	Alignment	not modelled	8.0	9	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
34	d2dwy1	Alignment	not modelled	7.8	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: gamma-adaptin C-terminal appendage domain-like
35	d1na8a_	Alignment	not modelled	6.9	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: gamma-adaptin C-terminal appendage domain-like
36	c2huuA_	Alignment	not modelled	6.8	22	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
37	d1j9ba_	Alignment	not modelled	6.8	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: ArsC-like
38	c2e9gA_	Alignment	not modelled	6.7	14	PDB header: protein binding Chain: A: PDB Molecule: ap-1 complex subunit gamma-2; PDBTitle: solution structure of the alpha adaptinc2 domain from human2 adapter-related protein complex 1 gamma 2 subunit
39	c2ee6A_	Alignment	not modelled	6.4	17	PDB header: structural protein Chain: A: PDB Molecule: filamin-b; PDBTitle: solution structure of the 21th filamin domain from human2 filamin-b
40	d1qmra_	Alignment	not modelled	6.3	14	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
41	d2bk0a1	Alignment	not modelled	6.2	12	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
42	d1t07a_	Alignment	not modelled	6.1	19	Fold: YggX-like Superfamily: YggX-like Family: YggX-like
43	c3e4fB_	Alignment	not modelled	5.9	17	PDB header: transferase Chain: B: PDB Molecule: aminoglycoside n3-acetyltransferase; PDBTitle: crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
44	d1bwwa_	Alignment	not modelled	5.8	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
45	c2hbpA_	Alignment	not modelled	5.8	17	PDB header: endocytosis, protein binding Chain: A: PDB Molecule: cytoskeleton assembly control protein sla1; PDBTitle: solution structure of sla1 homology domain 1
46	d2b79a1	Alignment	not modelled	5.7	11	Fold: TBP-like Superfamily: Bet v1-like Family: Smu440-like
47	d1y7ta2	Alignment	not modelled	5.7	11	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
48	d1c7na_	Alignment	not modelled	5.7	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
49	c2hqyB_	Alignment	not modelled	5.6	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of conserved protein of unknown function from2 bacteroides thetaiotaomicron vpi-5482
50	c3rv2B_	Alignment	not modelled	5.6	41	PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
51	d1hy7a_	Alignment	not modelled	5.5	24	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Matrix metalloproteases, catalytic domain
52	d2bp3a1	Alignment	not modelled	5.5	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
53	d3cmol1	Alignment	not modelled	5.4	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
54	c1y03A_	Alignment	not modelled	5.2	43	PDB header: antifreeze protein Chain: A: PDB Molecule: antifreeze peptide ss-3; PDBTitle: solution structure of a recombinant type i sculpin2 antifreeze protein
55	c1y04A_	Alignment	not modelled	5.2	43	PDB header: antifreeze protein Chain: A: PDB Molecule: antifreeze peptide ss-3; PDBTitle: solution structure of a recombinant type i sculpin2 antifreeze protein

56	d2ad9a1	Alignment	not modelled	5.1	21	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
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