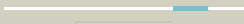
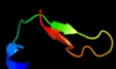
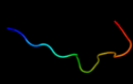
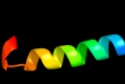
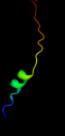


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A6X970
Date	Sun Jul 8 11:45:01 BST 2012
Unique Job ID	9818a44b6aad2fd1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2oeea1	 Alignment		60.0	26	Fold: YheA-like Superfamily: YheA/YmcA-like Family: YheA-like
2	d2iaza1	 Alignment		39.5	30	Fold: YheA-like Superfamily: YheA/YmcA-like Family: YheA-like
3	c3uamD_	 Alignment		34.7	33	PDB header: protein binding Chain: D: PDB Molecule: chitin binding domain; PDBTitle: crystal structure of a chitin binding domain from burkholderia2 pseudomallei
4	d2bema_	 Alignment		30.3	40	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
5	c3h43F_	 Alignment		28.1	25	PDB header: hydrolase Chain: F: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii
6	d2oeqa1	 Alignment		26.9	30	Fold: YheA-like Superfamily: YheA/YmcA-like Family: YheA-like
7	c2wg6L_	 Alignment		26.4	31	PDB header: transcription,hydrolase Chain: L: PDB Molecule: general control protein gcn4, PDBTitle: proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant
8	c4a02A_	 Alignment		26.3	40	PDB header: chitin binding protein Chain: A: PDB Molecule: chitin binding protein; PDBTitle: x-ray crystallographic structure of efcbm33a
9	c2xwxB_	 Alignment		22.8	47	PDB header: chitin-binding protein Chain: B: PDB Molecule: glcnac-binding protein a; PDBTitle: vibrio cholerae colonization factor gbpa crystal structure
10	c2pihA_	 Alignment		22.2	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ymca; PDBTitle: crystal structure of protein ymca from bacillus subtilis,2 northeast structural genomics target sr375
11	d2piha1	 Alignment		22.2	9	Fold: YheA-like Superfamily: YheA/YmcA-like Family: YmcA-like

12	dlxoub_	Alignment		16.2	67	Fold: EspA/CesA-like Superfamily: EspA/CesA-like Family: EspA chaperone CesA
13	d2bcgg2	Alignment		13.8	50	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
14	d2in1a1	Alignment		13.5	55	Fold: UBC-like Superfamily: UBC-like Family: UFC1-like
15	c2lhkB_	Alignment		13.0	67	PDB header: chaperone Chain: B: PDB Molecule: l0052; PDBTitle: structural analysis of a chaperone in type iii secretion system
16	c2reuA_	Alignment		10.3	21	PDB header: hydrolase Chain: A: PDB Molecule: type ii restriction enzyme sau3ai; PDBTitle: crystal structure of the c-terminal of sau3ai fragment
17	c3bc1F_	Alignment		9.5	28	PDB header: signaling protein/transport protein Chain: F: PDB Molecule: synaptotagmin-like protein 2; PDBTitle: crystal structure of the complex rab27a-slp2a
18	c3kpaB_	Alignment		9.3	45	PDB header: ligase Chain: B: PDB Molecule: probable ubiquitin fold modifier conjugating enzyme; PDBTitle: ubiquitin fold modifier conjugating enzyme from leishmania major2 (probable)
19	c3lo3E_	Alignment		9.2	50	PDB header: structure genomics, unknown function Chain: E: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 colwellia psychrerythraea 34h.
20	c2e7vA_	Alignment		9.1	36	PDB header: hydrolase Chain: A: PDB Molecule: transmembrane protease; PDBTitle: crystal structure of sea domain of transmembrane protease2 from mus musculus
21	d2ffta1	Alignment	not modelled	9.0	45	Fold: Intrinsically disordered proteins Superfamily: TSP9-like Family: TSP9-like
22	c1jlxB_	Alignment	not modelled	8.5	36	PDB header: lectin Chain: B: PDB Molecule: agglutinin; PDBTitle: agglutinin in complex with t-disaccharide
23	d2qtva4	Alignment	not modelled	7.6	17	Fold: Gelsolin-like Superfamily: C-terminal, gelsolin-like domain of Sec23/24 Family: C-terminal, gelsolin-like domain of Sec23/24
24	c2kc1A_	Alignment	not modelled	7.3	23	PDB header: structural protein Chain: A: PDB Molecule: mkiaa1027 protein; PDBTitle: nmr structure of the f0 domain (residues 0-85) of the talin2 ferm domain
25	d1m47a_	Alignment	not modelled	6.9	42	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines
26	c1kcfB_	Alignment	not modelled	6.6	29	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical 30.2 kd protein c25g10.02 in PDBTitle: crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
27	d1r6fa_	Alignment	not modelled	6.2	41	Fold: Virulence-associated V antigen Superfamily: Virulence-associated V antigen Family: Virulence-associated V antigen
28	c3go5A_	Alignment	not modelled	6.0	56	PDB header: gene regulation Chain: A: PDB Molecule: multidomain protein with s1 rna-binding domains; PDBTitle: crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae

