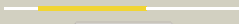
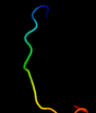
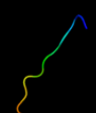
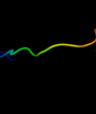
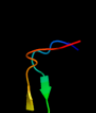
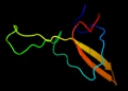
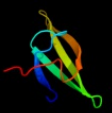
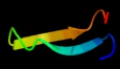


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0AB20
Date	Thu Jan 5 11:14:25 GMT 2012
Unique Job ID	3380201c221967c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vbva1	 Alignment		100.0	100	Fold: SH3-like barrel Superfamily: YccV-like Family: YccV-like
2	d1ugpb_	 Alignment		77.4	25	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
3	c2dxcG_	 Alignment		77.3	29	PDB header: hydrolase Chain: G: PDB Molecule: thiocyanate hydrolase subunit alpha; PDBTitle: recombinant thiocyanate hydrolase, fully-matured form
4	d1h3za_	 Alignment		76.5	19	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
5	c3qz9D_	 Alignment		66.3	22	PDB header: lyase Chain: D: PDB Molecule: co-type nitrile hydratase beta subunit; PDBTitle: crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
6	d2gy9p1	 Alignment		66.2	33	Fold: Ribosomal protein S16 Superfamily: Ribosomal protein S16 Family: Ribosomal protein S16
7	d2uubp1	 Alignment		63.9	27	Fold: Ribosomal protein S16 Superfamily: Ribosomal protein S16 Family: Ribosomal protein S16
8	d1v29b_	 Alignment		63.9	20	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
9	d3bn0a1	 Alignment		50.2	31	Fold: Ribosomal protein S16 Superfamily: Ribosomal protein S16 Family: Ribosomal protein S16
10	c3bbnP_	 Alignment		46.9	20	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein s16; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
11	c1g5vA_	 Alignment		39.4	21	PDB header: translation Chain: A: PDB Molecule: survival motor neuron protein 1; PDBTitle: solution structure of the tudor domain of the human smn2 protein

12	d1mhna_	Alignment		32.5	21	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
13	c2l89A_	Alignment		32.1	15	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
14	c4a4fA_	Alignment		29.5	21	PDB header: rna binding protein Chain: A: PDB Molecule: survival of motor neuron-related-splicing factor 30; PDBTitle: solution structure of spf30 tudor domain in complex with2 symmetrically dimethylated arginine
15	c3qiiA_	Alignment		24.4	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
16	d2rh2a1	Alignment		22.6	30	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: R67 dihydrofolate reductase
17	c2equA_	Alignment		22.1	20	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
18	d2diga1	Alignment		21.4	39	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
19	d2qdyb1	Alignment		17.5	25	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
20	dly71a1	Alignment		17.4	35	Fold: SH3-like barrel Superfamily: Kinase-associated protein B-like Family: Kinase-associated protein B-like
21	d1x61a2	Alignment	not modelled	15.4	27	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
22	d1g0da1	Alignment	not modelled	14.9	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
23	c3aicC_	Alignment	not modelled	13.1	16	PDB header: transferase Chain: C: PDB Molecule: glucosyltransferase-si; PDBTitle: crystal structure of glucansucrase from streptococcus mutans
24	d2imha1	Alignment	not modelled	12.1	17	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: SPO2555-like
25	d1n27a_	Alignment	not modelled	11.4	19	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
26	d1i3za_	Alignment	not modelled	10.8	50	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
27	c3sd7A_	Alignment	not modelled	10.2	17	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase; PDBTitle: 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
28	d2c9aa1	Alignment	not modelled	9.8	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
						Fold: WW domain-like

29	d1ed7a_	Alignment	not modelled	9.2	24	Superfamily: Carbohydrate binding domain Family: Carbohydrate binding domain
30	d2eyqa1	Alignment	not modelled	9.1	20	Fold: SH3-like barrel Superfamily: CarD-like Family: CarD-like
31	c2ftcK_	Alignment	not modelled	9.0	22	PDB header: ribosome Chain: K: PDB Molecule: 39s ribosomal protein l19, mitochondrial; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
32	c2crvA_	Alignment	not modelled	8.9	24	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: solution structure of c-terminal domain of mitochondrial2 translational initiationfactor 2
33	d1xg8a_	Alignment	not modelled	8.0	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: YuzD-like
34	d2imja1	Alignment	not modelled	7.9	23	Fold: Cystatin-like Superfamily: NTF2-like Family: PFL3262-like
35	d2nlua1	Alignment	not modelled	7.7	20	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
36	c3pnwX_	Alignment	not modelled	7.6	13	PDB header: protein binding/immune system Chain: X: PDB Molecule: tudor domain-containing protein 3; PDBTitle: crystal structure of the tudor domain of human tdrd3 in complex with2 an anti-tdrd3 fab
37	c2zg6A_	Alignment	not modelled	7.6	40	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein st2620; PDBTitle: crystal structure of hypothetical protein; probable 2-2 haloalkanoic acid dehalogenase from sulfolobus tokodaii
38	d1kzfa_	Alignment	not modelled	7.0	6	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Autoinducer synthetase
39	c2pqnB_	Alignment	not modelled	6.5	30	PDB header: apoptosis Chain: B: PDB Molecule: mitochondrial division protein 1; PDBTitle: crystal structure of yeast fis1 complexed with a fragment of yeast2 mdv1
40	c3fnnA_	Alignment	not modelled	6.2	25	PDB header: transferase Chain: A: PDB Molecule: thymidylate synthase thyx; PDBTitle: biochemical and structural analysis of an atypical thyx:2 corynebacterium glutamicum nchu 87078 depends on thya for3 thymidine biosynthesis
41	c1xnil_	Alignment	not modelled	6.1	20	PDB header: cell cycle Chain: I: PDB Molecule: tumor suppressor p53-binding protein 1; PDBTitle: tandem tudor domain of 53bp1
42	d1wvia_	Alignment	not modelled	5.9	44	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
43	d2qgra1	Alignment	not modelled	5.8	21	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
44	c1e0aB_	Alignment	not modelled	5.8	19	PDB header: signalling protein Chain: B: PDB Molecule: serine/threonine-protein kinase pak-alpha; PDBTitle: cdc42 complexed with the gtpase binding domain of p212 activated kinase
45	c3kzxA_	Alignment	not modelled	5.8	20	PDB header: hydrolase Chain: A: PDB Molecule: had-superfamily hydrolase, subfamily ia, variant 1; PDBTitle: crystal structure of a had-superfamily hydrolase from ehrlichia2 chaffeensis at 1.9a resolution
46	c3bboR_	Alignment	not modelled	5.7	32	PDB header: ribosome Chain: R: PDB Molecule: ribosomal protein l19; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
47	d2fcia1	Alignment	not modelled	5.7	23	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
48	c2kxgA_	Alignment	not modelled	5.4	32	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: aspartic protease inhibitor; PDBTitle: the solution structure of the squash aspartic acid proteinase2 inhibitor (sqapi)
49	d1a81e2	Alignment	not modelled	5.4	43	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
50	c3llrA_	Alignment	not modelled	5.4	24	PDB header: transferase Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: crystal structure of the pwp domain of human dna (cytosine-5)-2 methyltransferase 3 alpha
51	d2shpa2	Alignment	not modelled	5.2	29	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
52	d1ydfa1	Alignment	not modelled	5.2	44	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
53	d2j01t1	Alignment	not modelled	5.1	32	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal protein L19