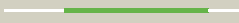
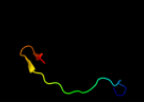
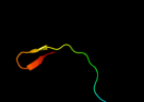
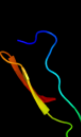
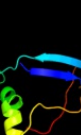


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0AF76
Date	Thu Jan 5 11:25:29 GMT 2012
Unique Job ID	7814dce8e3c264f9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jyoa_	 Alignment		86.1	15	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
2	d2plga1	 Alignment		54.5	16	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: TII0839-like
3	d2fm8a1	 Alignment		53.3	10	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
4	c2l6lA_	 Alignment		34.7	12	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 24; PDBTitle: solution structure of human j-protein co-chaperone, dph4
5	d1hdja_	 Alignment		30.8	26	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
6	c2ljoA_	 Alignment		25.3	24	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: polyprotein; PDBTitle: crystal structure of the west nile virus ns2b-ns3 protease2 complexed with bovine pancreatic trypsin inhibitor
7	c3e90C_	 Alignment		24.8	24	PDB header: hydrolase Chain: C: PDB Molecule: ns2b cofactor; PDBTitle: west nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kr-h
8	d2ga5a1	 Alignment		24.8	20	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
9	c2ieqC_	 Alignment		22.1	28	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
10	d1ry9a_	 Alignment		20.8	16	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
11	d1ew4a_	 Alignment		20.1	20	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like

12	c2v75A_	Alignment		19.8	26	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear polyadenylated rna-binding protein nab2; PDBTitle: n-terminal domain of nab2
13	d2fq1a1	Alignment		18.2	20	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
14	d1et9a1	Alignment		16.6	35	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
15	d1wjza_	Alignment		15.3	14	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
16	c3uc0B_	Alignment		12.2	21	PDB header: viral protein/immune system Chain: B: PDB Molecule: envelope protein; PDBTitle: crystal structure of domain i of the envelope glycoprotein ectodomain2 from dengue virus serotype 4 in complex with the fab fragment of the3 chimpanzee monoclonal antibody 5h2
17	d1iwga6	Alignment		11.7	16	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
18	d1ekga_	Alignment		11.1	22	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
19	c3kopB_	Alignment		10.7	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
20	c2hqnA_	Alignment		9.5	18	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
21	c3muwU_	Alignment	not modelled	8.8	5	PDB header: virus Chain: U: PDB Molecule: structural polyprotein; PDBTitle: pseudo-atomic structure of the e2-e1 protein shell in sindbis virus
22	c2ochA_	Alignment	not modelled	8.4	18	PDB header: chaperone Chain: A: PDB Molecule: hypothetical protein dnj-12; PDBTitle: j-domain of dnj-12 from caenorhabditis elegans
23	c3iwcD_	Alignment	not modelled	8.3	14	PDB header: lyase Chain: D: PDB Molecule: s-adenosylmethionine decarboxylase; PDBTitle: t. maritima adometdc complex with s-adenosylmethionine2 methyl ester
24	c2iiaA_	Alignment	not modelled	8.3	7	PDB header: lyase Chain: A: PDB Molecule: s-adenosylmethionine decarboxylase proenzyme; PDBTitle: crystal structure of the adenosylmethionine decarboxylase (aq_254)2 from aquifex aeolicus vf5
25	d1vlya2	Alignment	not modelled	8.2	6	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
26	c2bezC_	Alignment	not modelled	7.9	43	PDB header: viral protein Chain: C: PDB Molecule: e2 glycoprotein; PDBTitle: structure of a proteolitically resistant core from the2 severe acute respiratory syndrome coronavirus s2 fusion3 protein
27	c2o37A_	Alignment	not modelled	7.6	13	PDB header: chaperone Chain: A: PDB Molecule: protein sis1; PDBTitle: j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae.
28	c2ys8A_	Alignment	not modelled	7.5	11	PDB header: protein binding Chain: A: PDB Molecule: rab-related gtp-binding protein rabj; PDBTitle: solution structure of the dnaj-like domain from human ras-2 associated protein rap1

29	dlvr7a1	Alignment	not modelled	7.4	14	Fold: S-adenosylmethionine decarboxylase Superfamily: S-adenosylmethionine decarboxylase Family: Bacterial S-adenosylmethionine decarboxylase
30	c2dn9A	Alignment	not modelled	7.3	21	PDB header: apoptosis, chaperone Chain: A: PDB Molecule: dnaj homolog subfamily a member 3; PDBTitle: solution structure of j-domain from the dnaj homolog, human2 tid1 protein
31	c3r84O	Alignment	not modelled	7.3	30	PDB header: transcription Chain: O: PDB Molecule: mediator of rna polymerase ii transcription subunit 11; PDBTitle: structure of the mediator head subcomplex med11/22
32	c1vr7A	Alignment	not modelled	7.3	14	PDB header: lyase Chain: A: PDB Molecule: s-adenosylmethionine decarboxylase proenzyme; PDBTitle: crystal structure of s-adenosylmethionine decarboxylase proenzyme2 (tm0655) from thermotoga maritima at 1.2 a resolution
33	c3lkxB	Alignment	not modelled	7.0	38	PDB header: chaperone Chain: B: PDB Molecule: nascent polypeptide-associated complex subunit alpha; PDBTitle: human nac dimerization domain
34	c1wyvB	Alignment	not modelled	6.8	43	PDB header: viral protein Chain: B: PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
35	c2lgwA	Alignment	not modelled	6.7	19	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 2; PDBTitle: solution structure of the j domain of hsj1a
36	c2jzyA	Alignment	not modelled	6.6	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein pcor; PDBTitle: solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
37	d2gu3a2	Alignment	not modelled	6.5	50	Fold: Cystatin-like Superfamily: Cystatin/monellin Family: PepSY-like
38	d1wf9a1	Alignment	not modelled	6.2	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
39	d1yu0a1	Alignment	not modelled	6.0	38	Fold: Pseudo beta-prism Superfamily: Bacteriophage trimeric proteins domain Family: Mtd domain-like
40	c2ctqA	Alignment	not modelled	6.0	36	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 12; PDBTitle: solution structure of j-domain from human dnaj subfamily c2 member 12
41	c2ctrA	Alignment	not modelled	5.9	21	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 9; PDBTitle: solution structure of j-domain from human dnaj subfamily b2 member 9
42	d1aiea	Alignment	not modelled	5.8	21	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
43	d3saka	Alignment	not modelled	5.8	18	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
44	d1iqoa	Alignment	not modelled	5.8	24	Fold: Hypothetical protein MTH1880 Superfamily: Hypothetical protein MTH1880 Family: Hypothetical protein MTH1880
45	d1s6la1	Alignment	not modelled	5.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MerB N-terminal domain-like
46	c1zldA	Alignment	not modelled	5.6	33	PDB header: toxin Chain: A: PDB Molecule: ptr necrosis toxin; PDBTitle: crystal structure of a rgd-containing host-selective toxin:2 pyrenophora tritici-repentis ptr toxa
47	c2j10B	Alignment	not modelled	5.5	21	PDB header: transcription Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
48	c2j10D	Alignment	not modelled	5.5	21	PDB header: transcription Chain: D: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
49	c2j10A	Alignment	not modelled	5.5	21	PDB header: transcription Chain: A: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
50	d2i3oa1	Alignment	not modelled	5.3	10	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Gamma-glutamyltranspeptidase-like