
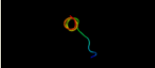

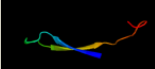
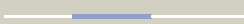
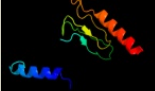

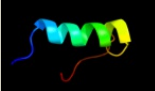









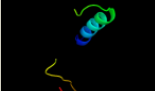





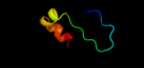






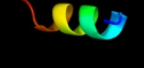


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P77206
Date	Thu Jan 5 12:26:20 GMT 2012
Unique Job ID	cd3b235fcd6b20a5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f9jp_	 Alignment		35.2	50	PDB header: rna binding protein Chain: P: PDB Molecule: splicing factor 3b subunit 1; PDBTitle: 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
2	c3kztB_	 Alignment		25.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_812423.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
3	d1xl7a2	 Alignment		24.8	17	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
4	d1w6ga2	 Alignment		16.0	17	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
5	c3hp7A_	 Alignment		12.9	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hemolysin, putative; PDBTitle: putative hemolysin from streptococcus thermophilus.
6	d2qi2a1	 Alignment		12.1	25	Fold: Sm-like fold Superfamily: Dom34/Pelota N-terminal domain-like Family: Dom34/Pelota N-terminal domain-like
7	c3lg8B_	 Alignment		10.9	25	PDB header: hydrolase Chain: B: PDB Molecule: a-type atp synthase subunit e; PDBTitle: crystal structure of the c-terminal part of subunit e (e101-206) from2 methanocaldococcus jannaschii of a1ao atp synthase
8	c3lydA_	 Alignment		10.4	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative uncharacterized protein from jonesia2 denitrificans
9	c1xl8B_	 Alignment		9.6	26	PDB header: transferase Chain: B: PDB Molecule: peroxisomal carnitine o-octanoyltransferase; PDBTitle: crystal structure of mouse carnitine octanoyltransferase in2 complex with octanoylcarnitine
10	d2vgna1	 Alignment		9.6	33	Fold: Sm-like fold Superfamily: Dom34/Pelota N-terminal domain-like Family: Dom34/Pelota N-terminal domain-like
11	d1whza_	 Alignment		9.0	19	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: YcfA-like

12	c2qi2A_	Alignment		8.7	21	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein pelota related protein; PDBTitle: crystal structure of the thermoplasma acidophilum pelota2 protein
13	d1em8b_	Alignment		8.6	19	Fold: DNA polymerase III psi subunit Superfamily: DNA polymerase III psi subunit Family: DNA polymerase III psi subunit
14	c1e2vB_	Alignment		8.3	67	PDB header: electron transport proteins Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii
15	d1vf5c1	Alignment		8.1	67	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
16	d1ci3m1	Alignment		8.0	67	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
17	d1e2wa1	Alignment		7.9	67	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
18	c3obyB_	Alignment		7.8	29	PDB header: hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
19	c1q6xA_	Alignment		7.7	19	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: crystal structure of rat choline acetyltransferase
20	c3agjD_	Alignment		7.7	21	PDB header: translation/hydrolase Chain: D: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
21	c3agjB_	Alignment	not modelled	7.7	21	PDB header: translation/hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
22	d1hcza1	Alignment	not modelled	7.5	67	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
23	c3m9vA_	Alignment	not modelled	7.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent oxidoreductase; PDBTitle: x-ray structure of a kijd3 in complex with dtdp
24	d1tlua2	Alignment	not modelled	7.0	17	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
25	d1vbk2	Alignment	not modelled	6.8	16	Fold: THUMP domain Superfamily: THUMP domain-like Family: THUMP domain
26	c3obwA_	Alignment	not modelled	6.7	21	PDB header: hydrolase Chain: A: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity
27	d1y1pa1	Alignment	not modelled	6.4	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
28	d1gsoa2	Alignment	not modelled	6.3	17	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
29	c2h4tB_	Alignment	not modelled	6.2	20	PDB header: transferase Chain: B: PDB Molecule: carnitine o-palmitoyltransferase ii, PDBTitle: crystal structure of rat carnitine palmitoyltransferase ii

30	c2e75C_	Alignment	not modelled	6.1	67	PDB header: photosynthesis Chain: C: PDB Molecule: apocytochrome f; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
31	c3b54A_	Alignment	not modelled	6.0	14	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: saccharomyces cerevisiae nucleoside diphosphate kinase
32	c1q90A_	Alignment	not modelled	5.8	67	PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
33	c3fa4D_	Alignment	not modelled	5.7	22	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
34	d1tu2b1	Alignment	not modelled	5.6	67	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
35	c2jxmB_	Alignment	not modelled	5.5	50	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
36	d1ndba2	Alignment	not modelled	5.5	16	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
37	c1ctmA_	Alignment	not modelled	5.4	67	PDB header: electron transport(cytochrome) Chain: A: PDB Molecule: cytochrome f; PDBTitle: crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
38	d1lukua_	Alignment	not modelled	5.4	35	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
39	c3jywW_	Alignment	not modelled	5.3	44	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l31(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
40	c2vu5A_	Alignment	not modelled	5.3	22	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: crystal structure of pndk from bacillus anthracis
41	d1xqia1	Alignment	not modelled	5.2	3	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
42	d1zs6a1	Alignment	not modelled	5.2	17	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
43	d1kx5b_	Alignment	not modelled	5.1	19	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
44	c2fipA_	Alignment	not modelled	5.1	30	PDB header: transcription Chain: A: PDB Molecule: late genes activator; PDBTitle: phage phi29 transcription regulator p4
45	d1vhfa_	Alignment	not modelled	5.0	24	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)