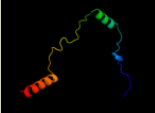
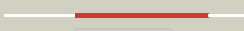
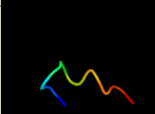
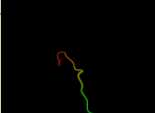
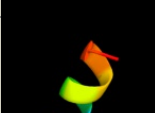


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	O94742
Date	Mon Jul 2 19:10:25 BST 2012
Unique Job ID	340681f75216abd1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3t5vC_	 Alignment		99.9	100	PDB header: transcription Chain: C: PDB Molecule: 26s proteasome complex subunit sem1; PDBTitle: sac3:thp1:sem1 complex
2	c1iyjC_	 Alignment		99.6	66	PDB header: gene regulation/antitumor protein Chain: C: PDB Molecule: deleted in split hand/split foot protein 1; PDBTitle: structure of a brca2-dss1 complex
3	c2xl4A_	 Alignment		53.3	33	PDB header: immune system Chain: A: PDB Molecule: lmo0438 protein; PDBTitle: Inta, a virulence factor from listeria monocytogenes
4	d1sv1a_	 Alignment		38.3	50	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
5	c1dpgA_	 Alignment		37.3	70	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib subunit; PDBTitle: solution structure of the constitutively active mutant of2 the integrin alpha iib cytoplasmic domain.
6	d1f3ub_	 Alignment		35.4	50	Fold: triple barrel Superfamily: Rap30/74 interaction domains Family: Rap30/74 interaction domains
7	c2kk9A_	 Alignment		35.2	21	PDB header: antimicrobial protein Chain: A: PDB Molecule: m protein, serotype 5; PDBTitle: anti-group a streptococcal vaccine epitope: structure, stability and2 its ability to interact with hla class ii molecules
8	d1r8ja1	 Alignment		30.3	40	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
9	d1p4ua_	 Alignment		22.6	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: gamma-adaptin C-terminal appendage domain-like
10	d1gyva_	 Alignment		18.4	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: gamma-adaptin C-terminal appendage domain-like
11	c1r8jB_	 Alignment		18.3	40	PDB header: circadian clock protein Chain: B: PDB Molecule: kaia; PDBTitle: crystal structure of circadian clock protein kaia from2 synechococcus elongatus

12	dlv2za_	Alignment		17.8	50	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
13	dlr5qa_	Alignment		17.7	38	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
14	c2e9ga_	Alignment		17.0	25	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
15	dlgywb_	Alignment		16.7	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: gamma-adaptin C-terminal appendage domain-like
16	d2dwya1	Alignment		15.7	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: gamma-adaptin C-terminal appendage domain-like
17	c3nmdA_	Alignment		11.1	30	PDB header: transferase Chain: A: PDB Molecule: cgmp dependent protein kinase; PDBTitle: crystal structure of the leucine zipper domain of cgmp dependent2 protein kinase i beta
18	d3etja2	Alignment		10.7	28	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
19	d2nsfa1	Alignment		9.5	33	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: Maleylpyruvate isomerase-like
20	d1na8a_	Alignment		9.3	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: gamma-adaptin C-terminal appendage domain-like
21	c3dnoC_	Alignment	not modelled	8.9	36	PDB header: viral protein Chain: C: PDB Molecule: hiv-1 envelope glycoprotein gp120; PDBTitle: molecular structure for the hiv-1 gp120 trimer in the cd4-2 bound state
22	d1wiza_	Alignment	not modelled	8.9	35	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
23	c3rrrM_	Alignment	not modelled	8.3	67	PDB header: viral protein Chain: M: PDB Molecule: fusion glycoprotein f0; PDBTitle: structure of the rsv f protein in the post-fusion conformation
24	d2rdva_	Alignment	not modelled	7.7	63	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
25	d1s24a_	Alignment	not modelled	7.3	75	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
26	c1s24A_	Alignment	not modelled	7.3	75	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin 2; PDBTitle: rubredoxin domain ii from pseudomonas oleovorans
27	d1iu5a_	Alignment	not modelled	6.8	63	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
28	d1dx8a_	Alignment	not modelled	6.5	38	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
29	d1qcva_	Alignment	not modelled	6.4	63	Fold: Rubredoxin-like Superfamily: Rubredoxin-like

						Family: Rubredoxin
30	d1h7va_	Alignment	not modelled	6.3	38	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
31	d1f3ud_	Alignment	not modelled	6.0	50	Fold: triple barrel Superfamily: Rap30/74 interaction domains Family: Rap30/74 interaction domains
32	d2csfa1	Alignment	not modelled	6.0	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
33	c2v3bB_	Alignment	not modelled	6.0	50	PDB header: oxidoreductase Chain: B: PDB Molecule: rubredoxin 2; PDBTitle: crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
34	d2dsxa1	Alignment	not modelled	5.9	75	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
35	c2yv5A_	Alignment	not modelled	5.7	21	PDB header: hydrolase Chain: A: PDB Molecule: yjeq protein; PDBTitle: crystal structure of yjeq from aquifex aeolicus
36	d1iroa_	Alignment	not modelled	5.6	63	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
37	d1rb9a_	Alignment	not modelled	5.5	50	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
38	d6rxna_	Alignment	not modelled	5.4	50	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
39	c2kn9A_	Alignment	not modelled	5.3	50	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin; PDBTitle: solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
40	d4rxna_	Alignment	not modelled	5.3	63	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
41	d2clyc1	Alignment	not modelled	5.2	25	Fold: Mitochondrial ATP synthase coupling factor 6 Superfamily: Mitochondrial ATP synthase coupling factor 6 Family: Mitochondrial ATP synthase coupling factor 6