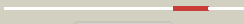
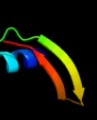
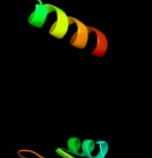
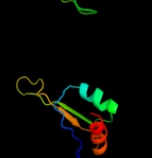
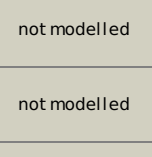


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P11557
Date	Thu Jan 5 11:32:47 GMT 2012
Unique Job ID	9bf04e37dec3f1f5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1utaa_	 Alignment		98.0	18	Fold: Ferredoxin-like Superfamily: Sporulation related repeat Family: Sporulation related repeat
2	c1x60A_	 Alignment		97.9	20	PDB header: hydrolase Chain: A: PDB Molecule: sporulation-specific n-acetylmuramoyl-l-alanine PDBTitle: solution structure of the peptidoglycan binding domain of 2 b. subtilis cell wall lytic enzyme cwlc
3	c3g5oA_	 Alignment		32.8	23	PDB header: toxin/antitoxin Chain: A: PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
4	c3kgkA_	 Alignment		25.3	13	PDB header: chaperone Chain: A: PDB Molecule: arsenical resistance operon trans-acting repressor arsd; PDBTitle: crystal structure of arsd
5	c3ktbD_	 Alignment		24.3	13	PDB header: transcription regulator Chain: D: PDB Molecule: arsenical resistance operon trans-acting repressor; PDBTitle: crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
6	d1xrsb2	 Alignment		20.0	17	Fold: Dodecin subunit-like Superfamily: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain Family: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
7	d2k49a1	 Alignment		19.1	20	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
8	d1qqka_	 Alignment		15.8	14	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
9	c2odkD_	 Alignment		13.6	29	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
10	c1ywlA_	 Alignment		12.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0213 protein ef2693; PDBTitle: solution nmr structure of the protein ef2693 from e.2 faecalis: northeast structural genomics consortium target3 efr36
11	d2odka1	 Alignment		12.5	29	Fold: YefM-like Superfamily: YefM-like Family: YefM-like

12	c2jvrA	Alignment		12.5	20	PDB header: rna binding protein Chain: A: PDB Molecule: nucleolar protein 3; PDBTitle: segmental isotope labeling of npl3p
13	d2a6qa1	Alignment		12.4	21	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
14	d2cqia1	Alignment		11.7	12	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
15	d1tuaa2	Alignment		11.6	33	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
16	c2osrA	Alignment		11.2	19	PDB header: rna binding protein Chain: A: PDB Molecule: nucleolar protein 3; PDBTitle: nmr structure of rrm-2 of yeast npl3 protein
17	d2k7ia1	Alignment		10.5	17	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
18	c2k7iB	Alignment		10.5	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: upf0339 protein atu0232; PDBTitle: solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223.
19	d1x5sa1	Alignment		10.1	21	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
20	c2dnzA	Alignment		9.7	17	PDB header: rna binding protein Chain: A: PDB Molecule: probable rna-binding protein 23; PDBTitle: solution structure of the second rna binding domain of rna2 binding motif protein 23
21	d1ihka	Alignment	not modelled	8.6	17	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
22	c3jtzA	Alignment	not modelled	8.3	19	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: structure of the arm-type binding domain of hpi integrase
23	c3ju0A	Alignment	not modelled	8.3	20	PDB header: dna binding protein Chain: A: PDB Molecule: phage integrase; PDBTitle: structure of the arm-type binding domain of hai7 integrase
24	c2dnmA	Alignment	not modelled	8.0	15	PDB header: rna binding protein Chain: A: PDB Molecule: srp46 splicing factor; PDBTitle: solution structure of rna binding domain in srp46 splicing2 factor
25	c2wbrA	Alignment	not modelled	7.9	24	PDB header: dna-binding protein Chain: A: PDB Molecule: gw182; PDBTitle: the rrm domain in gw182 proteins contributes to mirna-2 mediated gene silencing
26	c2dh9A	Alignment	not modelled	7.6	13	PDB header: rna binding protein Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein m; PDBTitle: solution structure of the c-terminal rna binding domain in2 heterogeneous nuclear ribonucleoprotein m
27	c1vjgB	Alignment	not modelled	7.3	27	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
28	c2oq8A	Alignment	not modelled	6.8	33	PDB header: dna binding protein Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of orf 157 from acidianus filamentous virus 1

29	d3e2ba1	Alignment	not modelled	6.5	18	Fold: DLC Superfamily: DLC Family: DLC
30	c3femB_	Alignment	not modelled	6.5	15	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
31	c2k49A_	Alignment	not modelled	6.4	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0339 protein so_3888; PDBTitle: solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
32	dlvka_	Alignment	not modelled	6.4	31	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: Putative nitroreductase TM1586
33	c3qbtH_	Alignment	not modelled	6.3	16	PDB header: protein transport/hydrolase Chain: H: PDB Molecule: inositol polyphosphate 5-phosphatase ocr1-1; PDBTitle: crystal structure of ocr1 540-678 in complex with rab8a:gpphph
34	dlkr4a_	Alignment	not modelled	6.0	25	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
35	c2rneA_	Alignment	not modelled	5.8	10	PDB header: rna binding protein Chain: A: PDB Molecule: tia1 protein; PDBTitle: solution structure of the second rna recognition motif2 (rrm) of tia-1
36	d2cq3a1	Alignment	not modelled	5.7	14	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
37	dlnuna_	Alignment	not modelled	5.6	24	Fold: beta-Trefoil Superfamily: Cytokine Family: Fibroblast growth factors (FGF)
38	c3i6pF_	Alignment	not modelled	5.6	20	PDB header: structural protein Chain: F: PDB Molecule: ethanolamine utilization protein eutm; PDBTitle: ethanolamine utilization microcompartment shell subunit, eutm
39	c3o4aC_	Alignment	not modelled	5.6	5	PDB header: de novo protein Chain: C: PDB Molecule: de novo designed beta-trefoil architecture with symmetric PDBTitle: crystal structure of symfoil-2: de novo designed beta-trefoil2 architecture with symmetric primary structure
40	c3ngkA_	Alignment	not modelled	5.5	25	PDB header: unknown function Chain: A: PDB Molecule: propanediol utilization protein pdua; PDBTitle: pdua from salmonella enterica typhimurium
41	dlr89a3	Alignment	not modelled	5.3	12	Fold: Ferredoxin-like Superfamily: PAP/Archaeal CCA-adding enzyme, C-terminal domain Family: Archaeal tRNA CCA-adding enzyme
42	d2ewha1	Alignment	not modelled	5.2	20	Fold: Ferredoxin-like Superfamily: CcmK-like Family: CcmK-like
43	dlrk8a_	Alignment	not modelled	5.2	14	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD