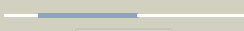
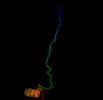
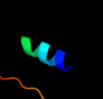
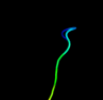
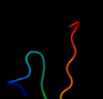
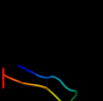
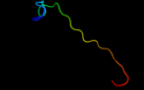
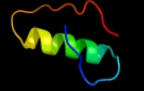
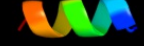
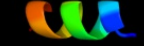
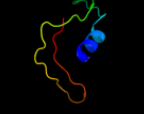


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P76172
Date	Thu Jan 5 12:20:05 GMT 2012
Unique Job ID	a4b1e40923dcaaf5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wy3B_	 Alignment		28.6	56	PDB header: immune system/viral protein Chain: B: PDB Molecule: uncharacterized protein ul16; PDBTitle: structure of the hcmv ul16-micb complex elucidates select2 binding of a viral immunoevasin to diverse nkg2d ligands
2	d2jnaa1	 Alignment		27.6	35	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
3	c2y69S_	 Alignment		17.3	23	PDB header: electron transport Chain: S: PDB Molecule: cytochrome c oxidase subunit 5b; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
4	c2dhmA_	 Alignment		16.4	26	PDB header: protein binding Chain: A: PDB Molecule: protein bola; PDBTitle: solution structure of the bola protein from escherichia coli
5	d1v54f_	 Alignment		15.7	23	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Cytochrome c oxidase Subunit F
6	c3k2tA_	 Alignment		12.5	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2511 protein; PDBTitle: crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
7	d2fz5a1	 Alignment		11.0	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
8	c3ka5A_	 Alignment		9.8	13	PDB header: chaperone Chain: A: PDB Molecule: ribosome-associated protein y (psrp-1); PDBTitle: crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
9	c1xs3A_	 Alignment		9.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein xc975; PDBTitle: solution structure analysis of the xc975 protein
10	d1ea9c2	 Alignment		8.2	18	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
11	d5nula_	 Alignment		8.1	24	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related

12	c1v60A	Alignment		7.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: riken cdna 1810037g04; PDBTitle: solution structure of bola1 protein from mus musculus
13	d1u9da	Alignment		7.6	8	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: VC0714-like
14	d1pgsa	Alignment		7.6	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
15	d1xrsb2	Alignment		7.3	18	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
16	c1q90L	Alignment		7.1	25	PDB header: photosynthesis Chain: L: PDB Molecule: cytochrome b6f complex subunit peti; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
17	d1q90L	Alignment		7.1	25	Fold: Single transmembrane helix Superfamily: PetL subunit of the cytochrome b6f complex Family: PetL subunit of the cytochrome b6f complex
18	d1go3e2	Alignment		6.7	18	Fold: Dodecin subunit-like Superfamily: N-terminal, heterodimerisation domain of RBP7 (RpoE) Family: N-terminal, heterodimerisation domain of RBP7 (RpoE)
19	c2k8sA	Alignment		6.5	36	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution nmr structure of dimeric thioredoxin-like protein2 ne0084 from nitrosomonas europaea: northeast structural3 genomics target net6
20	c2jo1A	Alignment		6.5	25	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
21	d2cu6a1	Alignment	not modelled	6.3	12	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
22	d1l7da2	Alignment	not modelled	6.1	7	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: L-alanine dehydrogenase-like
23	d1pjca2	Alignment	not modelled	6.0	9	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: L-alanine dehydrogenase-like
24	d1r17a1	Alignment	not modelled	6.0	22	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Fibrinogen-binding domain
25	c1ib8A	Alignment	not modelled	5.8	15	PDB header: nucleic acid binding protein Chain: A: PDB Molecule: conserved protein sp14.3; PDBTitle: solution structure and function of a conserved protein2 sp14.3 encoded by an essential streptococcus pneumoniae3 gene
26	d1ylea1	Alignment	not modelled	5.7	27	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: AstA-like
27	c3hyjD	Alignment	not modelled	5.5	21	PDB header: transcription regulator Chain: D: PDB Molecule: protein duf199/whia; PDBTitle: crystal structure of the n-terminal laglidag domain of duf199/whia
28	c2kdnA	Alignment	not modelled	5.5	30	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein pfe0790c; PDBTitle: solution structure of pfe0790c, a putative bola-like2 protein from the protozoan parasite plasmodium falciparum.