

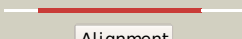


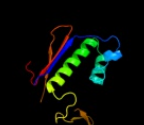










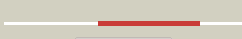




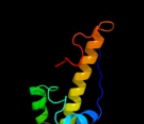






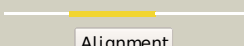

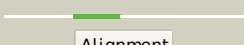
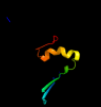
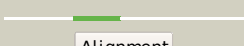

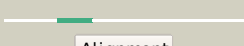
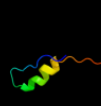




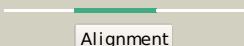
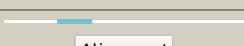
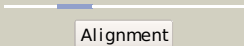

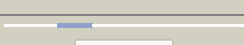





Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0ADM8
Date	Thu Jan 5 11:21:23 GMT 2012
Unique Job ID	c45863441bf35c40

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2cg5A_	 Alignment		100.0	18	PDB header: transferase/hydrolase Chain: A: PDB Molecule: l-aminoadipate-semialdehyde dehydrogenase- PDBTitle: structure of aminoadipate-semialdehyde dehydrogenase-2 phosphopantetheinyl transferase in complex with cytosolic c3 acyl carrier protein and coenzyme a
2	c1qr0A_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: 4'-phosphopantetheinyl transferase sfp; PDBTitle: crystal structure of the 4'-phosphopantetheinyl transferase sfp-2 coenzyme a complex
3	d1qr0a2	 Alignment		99.8	15	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: 4'-Phosphopantetheinyl transferase SFP
4	d1qr0a1	 Alignment		99.8	22	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: 4'-Phosphopantetheinyl transferase SFP
5	c2wasA_	 Alignment		99.4	16	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase; PDBTitle: structure of the fungal type i fas ppt domain
6	c3h88A_	 Alignment		99.4	10	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of 4'-phosphopantetheinyl transferase acps from2 vibrio cholerae o1 biovar eltor
7	c2jbzA_	 Alignment		99.3	17	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: crystal structure of the streptomyces coelicolor holo-2 [acyl-carrier-protein] synthase (acps) in complex with3 coenzyme a at 1.6 a
8	c3hykB_	 Alignment		99.2	13	PDB header: transferase Chain: B: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: 2.31 angstrom resolution crystal structure of a holo-(acyl-carrier-2 protein) synthase from bacillus anthracis str. ames in complex with3 coa (3',5'-adp)
9	d1f71a_	 Alignment		99.2	15	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: Holo-(acyl carrier protein) synthase ACPS
10	d1ftha_	 Alignment		99.2	13	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: Holo-(acyl carrier protein) synthase ACPS
11	c3ne9B_	 Alignment		99.1	13	PDB header: transferase Chain: B: PDB Molecule: phosphopantethiene protein transferase, ppt1p; PDBTitle: mycobacterium tuberculosis acyl carrier protein synthase adopts two2 different structural conformations: ph driven conformational changes3 of acps enzyme

12	c2qg8A_	 Alignment		98.9	10	PDB header: transferase Chain: A: PDB Molecule: acyl carrier protein synthase py06285; PDBTitle: plasmodium yoelii acyl carrier protein synthase py06285 with adp bound
13	c3f09B_	 Alignment		98.8	17	PDB header: transferase Chain: B: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: 1.82 angstrom resolution crystal structure of holo-(acyl-carrier-2 protein) synthase (acps) from staphylococcus aureus
14	c3hqjA_	 Alignment		98.1	22	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: structure-function analysis of mycobacterium tuberculosis2 acyl carrier protein synthase (acps).
15	c2ch4A_	 Alignment		79.8	22	PDB header: transferase/chemotaxis Chain: A: PDB Molecule: chemotaxis protein chea; PDBTitle: complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
16	c2q8fA_	 Alignment		56.9	14	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
17	c1y8oA_	 Alignment		54.7	12	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
18	c3k8aA_	 Alignment		47.5	24	PDB header: dna binding protein Chain: A: PDB Molecule: putative primosomal replication protein; PDBTitle: neisseria gonorrhoeae prib
19	c2bu8A_	 Alignment		45.2	10	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase kinase isoenzyme 2; PDBTitle: crystal structures of human pyruvate dehydrogenase kinase 22 containing physiological and synthetic ligands
20	c3d2rB_	 Alignment		44.3	12	PDB header: transferase Chain: B: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; PDBTitle: crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
21	c3a0rA_	 Alignment	not modelled	40.0	17	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein tra (tm1360)
22	d1bxya_	 Alignment	not modelled	33.2	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
23	c3en2A_	 Alignment	not modelled	28.2	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable primosomal replication protein n; PDBTitle: three-dimensional structure of the protein prib from2 ralstonia solanacearum at the resolution 2.3a. northeast3 structural genomics consortium target rsr213c.
24	c3fhwB_	 Alignment	not modelled	22.8	24	PDB header: dna binding protein Chain: B: PDB Molecule: primosomal replication protein n; PDBTitle: crystal structure of the protein prib from bordetella parapertussis.2 northeast structural genomics consortium target bpr162.
25	d1v1qa_	 Alignment	not modelled	20.0	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
26	c2z0rA_	 Alignment	not modelled	17.7	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein thha0547; PDBTitle: crystal structure of hypothetical protein thha0547
27	c1qjvA_	 Alignment	not modelled	17.4	12	PDB header: transferase Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase (bck)2 complexed with atp-gamma-s
28	c2oc4A_	 Alignment	not modelled	16.2	10	PDB header: protein binding Chain: A: PDB Molecule: pre-mrna-splicing factor 8;

28	c20g4A	Alignment	not modelled	10.2	19	PDBTitle: structure of an expanded jab1-mpn-like domain of splicing factor prp8p2 from yeast
29	d1i58a	Alignment	not modelled	15.5	20	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
30	c1pfoA	Alignment	not modelled	12.8	20	PDB header: toxin Chain: A: PDB Molecule: perfringolysin o; PDBTitle: perfringolysin o
31	d1pfoa	Alignment	not modelled	12.8	20	Fold: Perfringolysin Superfamily: Perfringolysin Family: Perfringolysin
32	d2cb2a1	Alignment	not modelled	9.8	18	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: SOR-like
33	c3fqmA	Alignment	not modelled	8.9	12	PDB header: metal binding protein Chain: A: PDB Molecule: non-structural protein 5a; PDBTitle: crystal structure of a novel dimeric form of hcv ns5a domain i protein
34	d1gxra	Alignment	not modelled	8.8	24	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like Family: WD40-repeat
35	d1ggla	Alignment	not modelled	8.8	18	Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
36	d2fr2a1	Alignment	not modelled	8.8	18	Fold: Lipocalins Superfamily: Lipocalins Family: Rv2717c-like
37	d1i8ya	Alignment	not modelled	8.2	21	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Granulin repeat Family: Granulin repeat
38	c1i8yA	Alignment	not modelled	8.2	21	PDB header: cytokine Chain: A: PDB Molecule: granulin-1; PDBTitle: semi-automatic structure determination of the cg1 3-302 peptide based on aria
39	d2a90a1	Alignment	not modelled	7.6	33	Fold: WWE domain Superfamily: WWE domain Family: WWE domain
40	d1kqwa	Alignment	not modelled	7.4	20	Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
41	d2a13a1	Alignment	not modelled	7.4	25	Fold: Lipocalins Superfamily: Lipocalins Family: Rv2717c-like
42	c2lazA	Alignment	not modelled	7.3	22	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
43	c21b0A	Alignment	not modelled	7.3	22	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
44	d1gprra	Alignment	not modelled	7.0	23	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
45	c1zy7A	Alignment	not modelled	6.9	16	PDB header: hydrolase Chain: A: PDB Molecule: rna-specific adenosine deaminase b1, isoform PDBTitle: crystal structure of the catalytic domain of an adenosine2 deaminase that acts on rna (hadar2) bound to inositol3 hexakisphosphate (ihp)
46	d1opaa	Alignment	not modelled	6.8	10	Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
47	d1ftpa	Alignment	not modelled	6.7	20	Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
48	c2yvqA	Alignment	not modelled	6.5	10	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase; PDBTitle: crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
49	d1fdqa	Alignment	not modelled	6.1	20	Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
50	c3pptA	Alignment	not modelled	6.0	20	PDB header: lipid binding protein Chain: A: PDB Molecule: sodium-calcium exchanger; PDBTitle: rep1-nxsq fatty acid transporter
51	d1p6pa	Alignment	not modelled	5.9	20	Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
52	d2ftba1	Alignment	not modelled	5.9	20	Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
53	d1mdca	Alignment	not modelled	5.9	30	Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
54	d2cbra	Alignment	not modelled	5.9	30	Fold: Lipocalins Superfamily: Lipocalins

					Family: Fatty acid binding protein-like
55	d1lpja_	Alignment	not modelled	5.9	10 Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
56	d1zq1a1	Alignment	not modelled	5.9	22 Fold: Sm-like fold Superfamily: GatD N-terminal domain-like Family: GatD N-terminal domain-like
57	d2fs6a1	Alignment	not modelled	5.8	30 Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
58	c3ia8A_	Alignment	not modelled	5.7	34 PDB header: metal binding protein Chain: A: PDB Molecule: thap domain-containing protein 4; PDBTitle: the structure of the c-terminal heme nitrobindin domain of thap2 domain-containing protein 4 from homo sapiens
59	d1pmpa_	Alignment	not modelled	5.7	20 Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
60	d2k4xa1	Alignment	not modelled	5.5	38 Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
61	d1g7na_	Alignment	not modelled	5.4	20 Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
62	d2f3ga_	Alignment	not modelled	5.4	23 Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
63	d1tw4a_	Alignment	not modelled	5.4	20 Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
64	c2lbaA_	Alignment	not modelled	5.3	20 PDB header: lipid binding protein Chain: A: PDB Molecule: babp protein; PDBTitle: solution structure of chicken ileal babp in complex with2 glycochenodeoxycholic acid
65	d1yiva1	Alignment	not modelled	5.3	20 Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
66	d2gpra_	Alignment	not modelled	5.2	27 Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
67	d1glaf_	Alignment	not modelled	5.2	23 Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
68	c1e0mA_	Alignment	not modelled	5.2	17 PDB header: de novo protein Chain: A: PDB Molecule: wwprototype; PDBTitle: prototype ww domain