

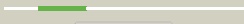


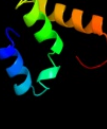
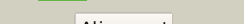

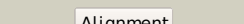

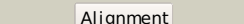

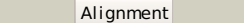

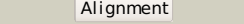

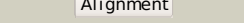

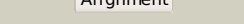

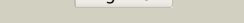












Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P77297
Date	Thu Jan 5 12:27:24 GMT 2012
Unique Job ID	2e0a8191685ab0ba

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gpaa_	 Alignment		62.6	20	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
2	d2f3ga_	 Alignment		58.5	18	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
3	d1u0ma2	 Alignment		56.5	9	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
4	d1glaf_	 Alignment		52.1	18	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
5	d2gpaa_	 Alignment		38.1	19	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
6	d1pkla1	 Alignment		23.5	13	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
7	c2dchX	 Alignment		23.5	50	PDB header: hydrolase Chain: X: PDB Molecule: putative homing endonuclease; PDBTitle: crystal structure of archaeal intron-encoded homing endonuclease i-2 tsp061i
8	c2l55A	 Alignment		20.8	20	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
9	d1pkma1	 Alignment		18.7	20	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
10	d1teda_	 Alignment		17.2	8	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
11	d1ycna_	 Alignment		15.3	17	Fold: Annexin Superfamily: Annexin Family: Annexin

12	c1zeqX	Alignment		15.2	20	PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
13	d1e0ta1	Alignment		15.0	18	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
14	d1apja	Alignment		13.6	26	Fold: TB module/8-cys domain Superfamily: TB module/8-cys domain Family: TB module/8-cys domain
15	d2g50a1	Alignment		13.1	20	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
16	d1liua1	Alignment		12.9	11	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
17	c1u0mA	Alignment		12.7	8	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative polyketide synthase; PDBTitle: crystal structure of 1,3,6,8-tetrahydroxynaphthalene synthase (thns)2 from streptomyces coelicolor a3(2): a bacterial type iii polyketide3 synthase (pks) provides insights into enzymatic control of reactive4 polyketide intermediates
18	c3aleB	Alignment		11.3	12	PDB header: transferase Chain: B: PDB Molecule: os07g0271500 protein; PDBTitle: a type iii polyketide synthase that produces diarylheptanoid
19	d1ksqa	Alignment		11.0	22	Fold: TB module/8-cys domain Superfamily: TB module/8-cys domain Family: TB module/8-cys domain
20	c2d1kC	Alignment		10.5	36	PDB header: structural protein Chain: C: PDB Molecule: metastasis suppressor protein 1; PDBTitle: ternary complex of the wh2 domain of mim with actin-dnase i
21	c3oitB	Alignment	not modelled	10.1	13	PDB header: transferase Chain: B: PDB Molecule: os07g0271500 protein; PDBTitle: crystal structure of curcuminoid synthase cus from oryza sativa
22	c3ov3A	Alignment	not modelled	9.4	17	PDB header: transferase Chain: A: PDB Molecule: curcumin synthase; PDBTitle: g211f mutant of curcumin synthase 1 from curcuma longa
23	d1a3xa1	Alignment	not modelled	9.1	9	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
24	c2p0uB	Alignment	not modelled	9.0	10	PDB header: transferase Chain: B: PDB Molecule: stilbenecarboxylate synthase 2; PDBTitle: crystal structure of marchantia polymorpha stilbenecarboxylate2 synthase 2 (stcs2)
25	c2e28A	Alignment	not modelled	8.7	20	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
26	d1u0ua2	Alignment	not modelled	8.6	11	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
27	c3mmIE	Alignment	not modelled	8.3	18	PDB header: hydrolase Chain: E: PDB Molecule: allophanate hydrolase subunit 2; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
28	c3u1nC	Alignment	not modelled	8.1	19	PDB header: hydrolase Chain: C: PDB Molecule: sam domain and hd domain-containing protein 1; PDBTitle: structure of the catalytic core of human samhd1
						PDB header: transferase

29	c3a5qA_	Alignment	not modelled	7.6	13	Chain: A: PDB Molecule: benzalacetone synthase; PDBTitle: benzalacetone synthase from rheum palmatum
30	d1fasa_	Alignment	not modelled	7.1	57	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
31	c3t07D_	Alignment	not modelled	7.0	15	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
32	c2h84A_	Alignment	not modelled	7.0	15	PDB header: biosynthetic protein, transferase Chain: A: PDB Molecule: steely1; PDBTitle: crystal structure of the c-terminal type iii polyketide synthase (pks2 iii) domain of 'steely1' (a type i/iii pks hybrid from dictyostelium)
33	d1m98a1	Alignment	not modelled	6.9	9	Fold: Orange carotenoid protein, N-terminal domain Superfamily: Orange carotenoid protein, N-terminal domain Family: Orange carotenoid protein, N-terminal domain
34	d1ve2a1	Alignment	not modelled	6.8	47	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
35	d1twda_	Alignment	not modelled	6.7	100	Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like
36	c1ee0A_	Alignment	not modelled	6.5	6	PDB header: transferase Chain: A: PDB Molecule: 2-pyrone synthase; PDBTitle: 2-pyrone synthase complexed with acetoacetyl-coa
37	d1cnza_	Alignment	not modelled	6.5	33	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
38	c3iwpK_	Alignment	not modelled	6.4	80	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein cutc
39	c2q14A_	Alignment	not modelled	6.4	19	PDB header: hydrolase Chain: A: PDB Molecule: phosphohydrolase; PDBTitle: crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
40	c1m98A_	Alignment	not modelled	6.3	9	PDB header: unknown function Chain: A: PDB Molecule: orange carotenoid protein; PDBTitle: crystal structure of orange carotenoid protein
41	d1h9ma1	Alignment	not modelled	5.9	22	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
42	c2e0kA_	Alignment	not modelled	5.9	41	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 c20-methyltransferase; PDBTitle: crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
43	d1quta_	Alignment	not modelled	5.9	14	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
44	c3nutC_	Alignment	not modelled	5.5	41	PDB header: transferase Chain: C: PDB Molecule: precorrin-3 methylase; PDBTitle: crystal structure of the methyltransferase cobj
45	c3eoeC_	Alignment	not modelled	5.5	12	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
46	d1drsa_	Alignment	not modelled	5.5	38	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Dendroaspin
47	c2bb3B_	Alignment	not modelled	5.3	22	PDB header: transferase Chain: B: PDB Molecule: cobalamin biosynthesis precorrin-6y methylase (cbie); PDBTitle: crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
48	c2j5dA_	Alignment	not modelled	5.2	21	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: nmr structure of bnip3 transmembrane domain in lipid2 bicelles