













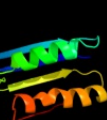







Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0ABV6
Date	Thu Jan 5 11:16:29 GMT 2012
Unique Job ID	2aa7d57323bd2e09

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pfuA_	 Alignment		99.6	22	PDB header: transport protein Chain: A: PDB Molecule: biopolymer transport exbd protein; PDBTitle: nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
2	c2jwlB_	 Alignment		99.4	51	PDB header: membrane protein Chain: B: PDB Molecule: protein tolR; PDBTitle: solution structure of periplasmic domain of tolR from h.2 influenzae with saxs data
3	d2e8aa1	 Alignment		49.1	9	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
4	d2axtk1	 Alignment		45.0	25	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein K, PsbK Family: PsbK-like
5	d1bupa1	 Alignment		40.6	8	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
6	c3a0bK_	 Alignment		40.4	25	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of br-substituted photosystem ii complex
7	d1jcea1	 Alignment		38.0	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
8	c2jvfA_	 Alignment		34.0	13	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein
9	c1qysA_	 Alignment		33.1	12	PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
10	c3a0bk_	 Alignment		30.6	25	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of br-substituted photosystem ii complex
11	c3a0hk_	 Alignment		24.1	25	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of i-substituted photosystem ii complex

12	c3bmaC_	Alignment		22.5	17	PDB header: ligase Chain: C: PDB Molecule: d-alanyl-lipoteichoic acid synthetase; PDBTitle: crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6
13	d1f75a_	Alignment		21.3	24	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
14	d1dkgd1	Alignment		21.1	9	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
15	d1qyia_	Alignment		20.9	42	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
16	d2d0oa1	Alignment		19.9	14	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Swiveling domain of dehydratase reactivase alpha subunit Family: Swiveling domain of dehydratase reactivase alpha subunit
17	c2vfwB_	Alignment		18.0	24	PDB header: transferase Chain: B: PDB Molecule: short-chain z-isoprenyl diphosphate synthetase; PDBTitle: rv1086 native
18	c1jp3A_	Alignment		17.9	14	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: structure of e.coli undecaprenyl pyrophosphate synthase
19	d1g8fa3	Alignment		17.8	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ATP sulfurylase C-terminal domain
20	c3qm3C_	Alignment		17.8	19	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
21	c3pm6B_	Alignment	not modelled	17.5	13	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
22	c3muxB_	Alignment	not modelled	17.1	18	PDB header: lyase Chain: B: PDB Molecule: putative 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
23	c3m6yA_	Alignment	not modelled	15.9	16	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
24	d1ueha_	Alignment	not modelled	15.7	14	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
25	c2d2rA_	Alignment	not modelled	15.3	5	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
26	c3m0zD_	Alignment	not modelled	14.0	20	PDB header: lyase Chain: D: PDB Molecule: putative aldolase; PDBTitle: crystal structure of putative aldolase from klebsiella2 pneumoniae.
27	d1gvfa_	Alignment	not modelled	13.6	28	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
28	d1olta_	Alignment	not modelled	13.2	13	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN

29	c3bz1y_	Alignment	not modelled	12.5	0	PDB header: electron transport Chain: Y: PDB Molecule: photosystem ii protein y; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
30	c3a0hy_	Alignment	not modelled	12.5	0	PDB header: electron transport Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: crystal structure of i-substituted photosystem ii complex
31	c3a0hY_	Alignment	not modelled	12.5	0	PDB header: electron transport Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: crystal structure of i-substituted photosystem ii complex
32	c3arcy_	Alignment	not modelled	12.1	0	PDB header: electron transport, photosynthesis Chain: Y: PDB Molecule: protein ycf12; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
33	c3arcY_	Alignment	not modelled	12.1	0	PDB header: electron transport, photosynthesis Chain: Y: PDB Molecule: protein ycf12; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
34	c3a0by_	Alignment	not modelled	11.8	0	PDB header: electron transport Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: crystal structure of br-substituted photosystem ii complex
35	c3gmgB_	Alignment	not modelled	11.1	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein rv1825/mt1873; PDBTitle: crystal structure of an uncharacterized conserved protein2 from mycobacterium tuberculosis
36	d1xr4a1	Alignment	not modelled	10.8	13	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
37	d2ohwa1	Alignment	not modelled	9.6	15	Fold: Bacillus chorismate mutase-like Superfamily: Yuel-like Family: Yuel-like
38	c3gk0H_	Alignment	not modelled	9.5	14	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
39	c3a0bY_	Alignment	not modelled	9.4	0	PDB header: electron transport Chain: Y: PDB Molecule: photosystem ii reaction center protein ycf12; PDBTitle: crystal structure of br-substituted photosystem ii complex
40	c3ivuB_	Alignment	not modelled	9.0	10	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
41	d1a9xa4	Alignment	not modelled	8.8	15	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
42	d1rvga_	Alignment	not modelled	8.2	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
43	c3iprC_	Alignment	not modelled	8.1	13	PDB header: transferase Chain: C: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
44	d1b0aa2	Alignment	not modelled	8.1	11	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
45	d2gycm1	Alignment	not modelled	8.0	12	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
46	d1nvma2	Alignment	not modelled	7.8	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
47	d1zhva2	Alignment	not modelled	7.6	32	Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
48	c3q94B_	Alignment	not modelled	7.6	19	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
49	d1edza2	Alignment	not modelled	7.6	15	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
50	c2vg2C_	Alignment	not modelled	6.9	19	PDB header: transferase Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp
51	d1ovya_	Alignment	not modelled	6.5	11	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
52	c2bdqA_	Alignment	not modelled	6.5	15	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
53	d1a4ia2	Alignment	not modelled	6.3	20	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
54	d1ujpa_	Alignment	not modelled	5.7	30	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
55	d1m5wa_	Alignment	not modelled	5.1	13	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase

