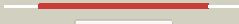
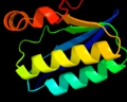


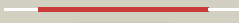






















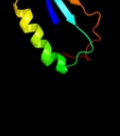
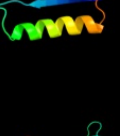
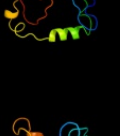



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P60070
Date	Tue Jul 17 17:05:11 BST 2012
Unique Job ID	b44f4842317fef9e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vc1a_	 Alignment		99.9	33	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
2	d1th8b_	 Alignment		99.9	30	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
3	c3t6oA_	 Alignment		99.9	14	PDB header: transport protein Chain: A; PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
4	d1lauza_	 Alignment		99.9	30	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
5	c3f43A_	 Alignment		99.8	16	PDB header: transcription Chain: A; PDB Molecule: putative anti-sigma factor antagonist tm1081; PDBTitle: crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
6	d1h4xa_	 Alignment		99.8	25	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
7	c3mg1A_	 Alignment		99.7	17	PDB header: transport protein Chain: A; PDB Molecule: sulfate permease family protein; PDBTitle: crystal structure of permease family protein from vibrio2 cholerae
8	c2vy9A_	 Alignment		99.7	12	PDB header: gene regulation Chain: A; PDB Molecule: anti-sigma-factor antagonist; PDBTitle: molecular architecture of the stressosome, a signal2 integration and transduction hub
9	c3oirA_	 Alignment		99.7	17	PDB header: transport protein Chain: A; PDB Molecule: sulfate transporter sulfate transporter family protein; PDBTitle: crystal structure of sulfate transporter family protein from wolinetella2 succinogenes
10	c2klnA_	 Alignment		99.7	11	PDB header: transport protein Chain: A; PDB Molecule: probable sulphate-transport transmembrane protein, cog0659; PDBTitle: solution structure of stas domain of rv1739c from m. tuberculosis
11	c3ny7A_	 Alignment		99.7	21	PDB header: membrane protein Chain: A; PDB Molecule: sulfate transporter; PDBTitle: stas domain of ychm bound to acp

12	c3lloA	Alignment		99.6	11	PDB header: motor protein Chain: A: PDB Molecule: prestini; PDBTitle: crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
13	c3lklB	Alignment		99.6	11	PDB header: transport protein Chain: B: PDB Molecule: antisigma-factor antagonist stas; PDBTitle: crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
14	d2q3la1	Alignment		95.3	12	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
15	c3ih9A	Alignment		95.2	17	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form
16	c3bezC	Alignment		89.5	15	PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
17	d2ooka1	Alignment		85.1	12	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
18	c2deoA	Alignment		83.9	23	PDB header: hydrolase Chain: A: PDB Molecule: 441aa long hypothetical nfed protein; PDBTitle: 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
19	c3bl4B	Alignment		69.9	12	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function (arth_0117) from2 arthrobacter sp. fb24 at 2.20 a resolution
20	c2pr7A	Alignment		64.4	15	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
21	c3rstH	Alignment	not modelled	40.4	14	PDB header: hydrolase Chain: H: PDB Molecule: signal peptide peptidase sppa; PDBTitle: crystal structure of bacillus subtilis signal peptide peptidase a
22	d2ap9a1	Alignment	not modelled	37.8	17	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
23	d2btya1	Alignment	not modelled	32.8	15	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
24	c2v5hB	Alignment	not modelled	32.6	15	PDB header: transcription Chain: B: PDB Molecule: acetylglutamate kinase; PDBTitle: controlling the storage of nitrogen as arginine: the2 complex of pii and acetylglutamate kinase from3 synechococcus elongatus pcc 7942
25	c2rd5A	Alignment	not modelled	32.1	17	PDB header: protein binding Chain: A: PDB Molecule: acetylglutamate kinase-like protein; PDBTitle: structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
26	c3ghfA	Alignment	not modelled	29.8	10	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein2 minc from salmonella typhi murium
27	c3qmjA	Alignment	not modelled	27.2	7	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase, echa8_6; PDBTitle: crystal structure of enoyl-coa hydratase echa8_6 from mycobacterium2 marinum
28	c3trrA	Alignment	not modelled	26.9	6	PDB header: isomerase Chain: A: PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus

29	c2dfwA	Alignment	not modelled	26.8	10	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
30	c3efaA	Alignment	not modelled	25.9	13	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of putative n-acetyltransferase from lactobacillus2 plantarum
31	d2zeqa1	Alignment	not modelled	25.9	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
32	c2f6iG	Alignment	not modelled	25.6	17	PDB header: hydrolase Chain: G: PDB Molecule: atp-dependent clp protease, putative; PDBTitle: crystal structure of the clpp protease catalytic domain from2 plasmodium falciparum
33	d2bufa1	Alignment	not modelled	23.7	13	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
34	d2f6ia1	Alignment	not modelled	23.6	17	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
35	d1r5ja	Alignment	not modelled	23.4	16	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
36	d1xcoa	Alignment	not modelled	21.2	9	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
37	c2q8fA	Alignment	not modelled	18.6	11	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
38	c3isaA	Alignment	not modelled	17.5	9	PDB header: hydrolase Chain: A: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis
39	d1ro5a	Alignment	not modelled	17.4	16	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Autoinducer synthetase
40	c3i42A	Alignment	not modelled	17.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey- PDBTitle: structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
41	d1yg6a1	Alignment	not modelled	16.7	9	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
42	d1ef8a	Alignment	not modelled	15.3	19	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
43	d2i71a1	Alignment	not modelled	13.9	10	Fold: SSO1389-like Superfamily: SSO1389-like Family: Cas DxTHG
44	d3c9ua2	Alignment	not modelled	13.8	21	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
45	d1nzya	Alignment	not modelled	13.5	19	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
46	c1o6uA	Alignment	not modelled	12.9	12	PDB header: transferase Chain: A: PDB Molecule: sec14-like protein 2; PDBTitle: the crystal structure of human supernatant protein factor
47	d2af4c1	Alignment	not modelled	12.7	14	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
48	c2fdsA	Alignment	not modelled	12.7	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: orotidine-monophosphate-decarboxylase; PDBTitle: crystal structure of plasmodium berghei orotidine 5'-2 monophosphate decarboxylase (ortholog of plasmodium3 falciparum pf10_0225)
49	d2fdsa1	Alignment	not modelled	12.7	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
50	d1qsra	Alignment	not modelled	12.3	13	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
51	c3fb3A	Alignment	not modelled	12.2	18	PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase; PDBTitle: crystal structure of trypanosoma brucei acetyltransferase,2 tb11.01.2886
52	c2g0bG	Alignment	not modelled	12.1	10	PDB header: transferase Chain: G: PDB Molecule: feem; PDBTitle: the structure of feem, an n-acyl amino acid synthase from uncultured2 soil microbes
53	c2hroA	Alignment	not modelled	12.0	19	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the full-length enzyme i of the pts system from2 staphylococcus carnosus
54	d2q8za1	Alignment	not modelled	11.8	9	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
						Fold: Acyl-CoA N-acyltransferases (Nat)

55	d1q2ya_	Alignment	not modelled	11.7	16	Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
56	c3kc2A_	Alignment	not modelled	11.7	17	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
57	c2cbyG_	Alignment	not modelled	11.2	14	PDB header: hydrolase Chain: G: PDB Molecule: atp-dependent clp protease proteolytic subunit 1; PDBTitle: crystal structure of the atp-dependent clp protease2 proteolytic subunit 1 (clpp1) from mycobacterium3 tuberculosis
58	c1tg6G_	Alignment	not modelled	11.1	14	PDB header: hydrolase Chain: G: PDB Molecule: putative atp-dependent clp protease proteolytic subunit; PDBTitle: crystallography and mutagenesis point to an essential role for the n-2 terminus of human mitochondrial clpp
59	c4e4rA_	Alignment	not modelled	11.1	14	PDB header: transferase Chain: A: PDB Molecule: phosphate acetyltransferase; PDBTitle: eutd phosphotransacetylase from staphylococcus aureus
60	d2nu7b1	Alignment	not modelled	10.7	13	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
61	c1oizA_	Alignment	not modelled	10.7	8	PDB header: transport Chain: A: PDB Molecule: alpha-tocopherol transfer protein; PDBTitle: the molecular basis of vitamin e retention: structure of2 human alpha-tocopherol transfer protein
62	d1ptma_	Alignment	not modelled	10.5	13	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
63	c1yqtA_	Alignment	not modelled	10.1	11	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: rnase-l inhibitor
64	d1vmia_	Alignment	not modelled	10.1	8	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
65	c1vmiA_	Alignment	not modelled	10.1	8	PDB header: transferase Chain: A: PDB Molecule: putative phosphate acetyltransferase; PDBTitle: crystal structure of putative phosphate acetyltransferase2 (np_416953.1) from escherichia coli k12 at 2.32 a resolution
66	c3t90A_	Alignment	not modelled	9.6	15	PDB header: transferase Chain: A: PDB Molecule: glucose-6-phosphate acetyltransferase 1; PDBTitle: crystal structure of glucosamine-6-phosphate n-acetyltransferase from2 arabidopsis thaliana
67	c3lkeA_	Alignment	not modelled	9.6	15	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from bacillus2 halodurans
68	c2bg5C_	Alignment	not modelled	9.5	16	PDB header: transferase Chain: C: PDB Molecule: phosphoenolpyruvate-protein kinase; PDBTitle: crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts)
69	c3jywF_	Alignment	not modelled	9.3	5	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
70	c3hy5A_	Alignment	not modelled	9.2	12	PDB header: transport protein Chain: A: PDB Molecule: retinaldehyde-binding protein 1; PDBTitle: crystal structure of cralbp
71	c2nnzA_	Alignment	not modelled	8.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
72	d1z4ra1	Alignment	not modelled	8.8	12	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
73	c2klcA_	Alignment	not modelled	8.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr solution structure of human ubiquitin-like domain of ubiquilin 1,2 northeast structural genomics consortium (nesg) target ht5a
74	c2qq3F_	Alignment	not modelled	8.8	11	PDB header: lyase Chain: F: PDB Molecule: enoyl-coa hydratase subunit i; PDBTitle: crystal structure of enoyl-coa hydrates subunit i (gk_2039)2 other form from geobacillus kaustophilus hta426
75	c3uosH_	Alignment	not modelled	8.7	11	PDB header: ribosome Chain: H: PDB Molecule: 50s ribosomal protein l10; PDBTitle: crystal structure of release factor rf3 trapped in the gtp state on a2 rotated conformation of the ribosome (without viomycin)
76	d1tg6a1	Alignment	not modelled	8.6	15	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
77	d2fiwa1	Alignment	not modelled	8.5	19	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
78	c2k42A_	Alignment	not modelled	8.3	14	PDB header: signaling protein Chain: A: PDB Molecule: wiskott-aldrich syndrome protein; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehcc effector
79	c3mgdB_	Alignment	not modelled	8.3	13	PDB header: transferase Chain: B: PDB Molecule: predicted acetyltransferase; PDBTitle: crystal structure of predicted acetyltransferase with acetyl-coa from2 clostridium acetobutylicum at the resolution 1.9a, northeast3 structural genomics consortium target car165

80	c3hp0B_	Alignment	not modelled	8.3	11	PDB header: lyase Chain: B: PDB Molecule: putative polyketide biosynthesis enoyl-coa PDBTitle: crystal structure of a putative polyketide biosynthesis2 enoyl-coa hydratase (pksh) from bacillus subtilis
81	c2ej5B_	Alignment	not modelled	8.1	13	PDB header: lyase Chain: B: PDB Molecule: enoyl-coa hydratase subunit ii; PDBTitle: crystal structure of gk2038 protein (enoyl-coa hydratase subunit ii)2 from geobacillus kaustophilus
82	d1cm0a_	Alignment	not modelled	8.0	11	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
83	c4fd5A_	Alignment	not modelled	7.9	7	PDB header: transferase Chain: A: PDB Molecule: arylalkylamine n-acetyltransferase 2; PDBTitle: crystal structure of arylalkylamine n-acetyltransferase 2 from aedes2 aegypti
84	d2qale1	Alignment	not modelled	7.9	11	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
85	c3rsiA_	Alignment	not modelled	7.8	7	PDB header: isomerase Chain: A: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196
86	c2q0yA_	Alignment	not modelled	7.7	14	PDB header: transferase Chain: A: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: crystal structure of gcn5-related n-acetyltransferase (yp_295895.1)2 from ralstonia eutropha jmp134 at 1.80 a resolution
87	c1f2uD_	Alignment	not modelled	7.7	5	PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
88	d1a9xa3	Alignment	not modelled	7.6	14	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
89	c1e5IA_	Alignment	not modelled	7.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
90	d1pkpa1	Alignment	not modelled	7.5	17	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
91	d1olma3	Alignment	not modelled	7.4	12	Fold: Spollaa-like Superfamily: CRAL/TRIO domain Family: CRAL/TRIO domain
92	d1b0ua_	Alignment	not modelled	7.3	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
93	c2hwgA_	Alignment	not modelled	7.2	21	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
94	c3kthD_	Alignment	not modelled	6.9	10	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: structure of clpp from bacillus subtilis in orthorhombic crystal form
95	c2p11A_	Alignment	not modelled	6.9	19	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative haloacid dehalogenase-like hydrolase2 (bx_e_b1342) from burkholderia xenovorans lb400 at 2.20 a resolution
96	c3fduF_	Alignment	not modelled	6.8	11	PDB header: isomerase Chain: F: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a putative enoyl-coa hydratase/isomerase from2 acinetobacter baumannii
97	d2ffca1	Alignment	not modelled	6.8	9	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
98	c3te4A_	Alignment	not modelled	6.7	16	PDB header: transferase Chain: A: PDB Molecule: dopamine n acetyltransferase, isoform a; PDBTitle: crystal structure of dopamine n acetyltransferase in complex with2 acetyl-coa from drosophila melanogaster
99	d2uube1	Alignment	not modelled	6.7	17	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components