























Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	O33599
Date	Tue Jul 17 17:05:02 BST 2012
Unique Job ID	9adb4d7a0a807763

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gu1A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
2	c3sluB_	 Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315
3	c2hsiB_	 Alignment		100.0	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative peptidase m23; PDBTitle: crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
4	d1qwya_	 Alignment		100.0	96	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM
5	c2b44A_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form
6	c3nyyA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: putative glycyl-glycine endopeptidase lytm; PDBTitle: crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
7	c3tufB_	 Alignment		100.0	25	PDB header: signaling protein Chain: B: PDB Molecule: stage ii sporulation protein q; PDBTitle: structure of the spoiiiq-spoiiiiah pore forming complex.
8	c3uz0D_	 Alignment		100.0	24	PDB header: transport protein Chain: D: PDB Molecule: stage ii sporulation protein q; PDBTitle: crystal structure of spoiiiiah and spoiiiq complex
9	c3it5B_	 Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
10	c3csqC_	 Alignment		99.9	24	PDB header: hydrolase Chain: C: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
11	d2f3ga_	 Alignment		96.7	21	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like

12	d1glaf_	Alignment		96.5	21	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
13	d2gpaa_	Alignment		96.3	21	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
14	d1gpaa_	Alignment		96.2	19	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
15	d1ci3m2	Alignment		95.6	23	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
16	d1e2wa2	Alignment		95.5	26	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
17	c2lmcB_	Alignment		94.5	22	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex
18	c2aukA_	Alignment		94.1	18	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
19	c1e2vB_	Alignment		94.0	26	PDB header: electron transport proteins Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii
20	c1q90A_	Alignment		93.8	26	PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastoquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
21	c2jxmB_	Alignment	not modelled	92.8	25	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
22	c1tu2B_	Alignment	not modelled	90.3	26	PDB header: electron transport Chain: B: PDB Molecule: apocytochrome f; PDBTitle: the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
23	c1ctmA_	Alignment	not modelled	87.9	17	PDB header: electron transport(cytochrome) Chain: A: PDB Molecule: cytochrome f; PDBTitle: crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
24	c2l9yA_	Alignment	not modelled	87.6	4	PDB header: sugar binding protein Chain: A: PDB Molecule: cvnh-lysm lectin; PDBTitle: solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mzg_03307)
25	d1bdoa_	Alignment	not modelled	87.1	18	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
26	d1tu2b2	Alignment	not modelled	86.4	26	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
27	d1brwa3	Alignment	not modelled	86.3	25	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
28	c1t5eB_	Alignment	not modelled	85.3	26	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa

29	c3lnnB_	Alignment	not modelled	84.8	35	PDB header: metal transport Chain: B: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
30	c2ejgD_	Alignment	not modelled	84.8	26	PDB header: ligase Chain: D: PDB Molecule: 149aa long hypothetical methylmalonyl-coa decarboxylase PDBTitle: crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
31	c2k33A_	Alignment	not modelled	83.4	30	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: acra; PDBTitle: solution structure of an n-glycosylated protein using in2 vitro glycosylation
32	c2f1mA_	Alignment	not modelled	83.4	13	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
33	d1o78a_	Alignment	not modelled	82.9	30	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
34	c2e75C_	Alignment	not modelled	82.7	26	PDB header: photosynthesis Chain: C: PDB Molecule: apocytochrome f; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
35	c4dk1B_	Alignment	not modelled	82.4	35	PDB header: membrane protein Chain: B: PDB Molecule: putative maca, multidrug resistance protein mexa; PDBTitle: crystal structure of maca-mexa chimeric protein, containing the2 pseudomonas aeruginosa mexa alpha-hairpin domain.
36	c2djpA_	Alignment	not modelled	81.2	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein sb145; PDBTitle: the solution structure of the lysm domain of human2 hypothetical protein sb145
37	d1vf7a_	Alignment	not modelled	81.1	23	Fold: HlyD-like secretion proteins Superfamily: HlyD-like secretion proteins Family: HlyD-like secretion proteins
38	c2kccA_	Alignment	not modelled	79.8	17	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
39	c3fppB_	Alignment	not modelled	79.0	30	PDB header: membrane protein Chain: B: PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
40	c2ejmA_	Alignment	not modelled	78.4	43	PDB header: ligase Chain: A: PDB Molecule: methylcrotonoyl-coa carboxylase subunit alpha; PDBTitle: solution structure of ruh-072, an apo-biotin domain form2 human acetyl coenzyme a carboxylase
41	c2dn8A_	Alignment	not modelled	77.9	30	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
42	c2b8gA_	Alignment	not modelled	77.9	26	PDB header: biosynthetic protein Chain: A: PDB Molecule: biotin/lipoyl attachment protein; PDBTitle: solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
43	d1dcza_	Alignment	not modelled	76.2	17	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
44	c2l5tA_	Alignment	not modelled	74.5	22	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
45	c2q8iB_	Alignment	not modelled	74.2	26	PDB header: transferase Chain: B: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
46	c4dk0A_	Alignment	not modelled	73.5	35	PDB header: membrane protein Chain: A: PDB Molecule: putative maca; PDBTitle: crystal structure of maca from actinobacillus actinomycetemcomitans
47	d1jqoa_	Alignment	not modelled	72.8	34	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
48	c2dsjA_	Alignment	not modelled	72.1	24	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
49	d1uoua3	Alignment	not modelled	71.5	19	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
50	c3n6rK_	Alignment	not modelled	70.8	19	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
51	d1y8ob1	Alignment	not modelled	69.7	26	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
52	d1e0ga_	Alignment	not modelled	68.3	7	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
						Fold: Barrel-sandwich hybrid

53	d1laba_	Alignment	not modelled	67.9	14	Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
54	d2pnrc1	Alignment	not modelled	67.0	26	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
55	c2dneA_	Alignment	not modelled	65.1	35	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
56	c2xhaB_	Alignment	not modelled	64.8	21	PDB header: transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)
57	d2tpta3	Alignment	not modelled	64.7	21	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
58	c3fmcC_	Alignment	not modelled	64.3	17	PDB header: hydrolase Chain: C: PDB Molecule: putative succinylglutamate desuccinylase / aspartoacylase; PDBTitle: crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
59	c2jkuA_	Alignment	not modelled	64.1	26	PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, PDBTitle: crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase
60	c2qj8B_	Alignment	not modelled	63.9	29	PDB header: hydrolase Chain: B: PDB Molecule: mlr6093 protein; PDBTitle: crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
61	c2dncA_	Alignment	not modelled	63.8	22	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
62	d1gjxa_	Alignment	not modelled	63.3	24	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
63	c3h9iB_	Alignment	not modelled	62.4	22	PDB header: transport protein Chain: B: PDB Molecule: cation efflux system protein cusb; PDBTitle: crystal structure of the membrane fusion protein cusb from escherichia2 coli
64	d1y7ma2	Alignment	not modelled	61.3	7	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
65	d1hcza2	Alignment	not modelled	61.2	17	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
66	d1k8ma_	Alignment	not modelled	59.6	10	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
67	c2aujD_	Alignment	not modelled	59.6	14	PDB header: transferase Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert
68	c3va7A_	Alignment	not modelled	59.4	26	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
69	c3na6A_	Alignment	not modelled	58.1	30	PDB header: hydrolase Chain: A: PDB Molecule: succinylglutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
70	d1ghja_	Alignment	not modelled	54.8	14	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
71	d1pmra_	Alignment	not modelled	54.7	8	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
72	c3cdxB_	Alignment	not modelled	54.4	24	PDB header: hydrolase Chain: B: PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
73	c3t51C_	Alignment	not modelled	49.0	22	PDB header: transport protein Chain: C: PDB Molecule: cation efflux system protein cusb; PDBTitle: crystal structures of the pre-extrusion and extrusion states of the2 cusba adaptor-transporter complex
74	c3ozxA_	Alignment	not modelled	47.4	15	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
75	d1v8qa_	Alignment	not modelled	46.9	24	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: Ribosomal L27 protein
76	d1iyua_	Alignment	not modelled	46.3	20	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
77	d2zjrt1	Alignment	not modelled	46.1	28	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like

						Family: Ribosomal L27 protein
78	c2kw8A_	Alignment	not modelled	45.6	19	PDB header: protein binding Chain: A: PDB Molecule: lpxtg-site transpeptidase family protein; PDBTitle: solution structure of bacillus anthracis sortase a (srta)2 transpeptidase
79	d1vf5c2	Alignment	not modelled	44.1	28	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
80	c3fin0_	Alignment	not modelled	43.7	24	PDB header: ribosome Chain: 0: PDB Molecule: 50s ribosomal protein l27; PDBTitle: t. thermophilus 70s ribosome in complex with mrna, trnas and ef-2 tu.gdp.kirromycin ternary complex, fitted to a 6.4 a cryo-em map.3 this file contains the 50s subunit.
81	c3h5qA_	Alignment	not modelled	42.7	33	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
82	c1brwB_	Alignment	not modelled	42.4	32	PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
83	c2j0fC_	Alignment	not modelled	41.2	21	PDB header: transferase Chain: C: PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
84	c2xhcA_	Alignment	not modelled	40.6	21	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
85	c1otpA_	Alignment	not modelled	40.0	22	PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
86	c2x5cB_	Alignment	not modelled	39.8	17	PDB header: viral protein Chain: B: PDB Molecule: hypothetical protein orf131; PDBTitle: crystal structure of hypothetical protein orf131 from2 pyrobaculum spherical virus
87	c2ftcO_	Alignment	not modelled	36.5	24	PDB header: ribosome Chain: O: PDB Molecule: mitochondrial 39s ribosomal protein l27; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
88	c4ebzA_	Alignment	not modelled	34.3	12	PDB header: transferase Chain: A: PDB Molecule: chitin elicitor receptor kinase 1; PDBTitle: crystal structure of the ectodomain of a receptor like kinase
89	c2w1kB_	Alignment	not modelled	33.6	18	PDB header: transferase Chain: B: PDB Molecule: putative sortase; PDBTitle: crystal structure of sortase c-3 (src-3) from2 streptococcus pneumoniae
90	d1o4ua2	Alignment	not modelled	32.3	16	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
91	c3ilaG_	Alignment	not modelled	31.0	24	PDB header: signaling protein Chain: G: PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of rabbit ryanodine receptor 1 n-terminal domain (9-2 205)
92	c3camB_	Alignment	not modelled	29.5	23	PDB header: gene regulation Chain: B: PDB Molecule: cold-shock domain family protein; PDBTitle: crystal structure of the cold shock domain protein from neisseria2 meningitidis
93	c3n7xA_	Alignment	not modelled	28.7	20	PDB header: virus Chain: A: PDB Molecule: capsid protein; PDBTitle: crystal structure of penaeus stylirostris densovirus capsid
94	c3bboX_	Alignment	not modelled	28.6	28	PDB header: ribosome Chain: X: PDB Molecule: ribosomal protein l27; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
95	d2gycu1	Alignment	not modelled	27.5	21	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: Ribosomal L27 protein
96	c3o0pA_	Alignment	not modelled	26.6	22	PDB header: transferase , hydrolase Chain: A: PDB Molecule: sortase family protein; PDBTitle: pilus-related sortase c of group b streptococcus
97	d1qapa2	Alignment	not modelled	24.6	21	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
98	c2vbcA_	Alignment	not modelled	24.3	20	PDB header: hydrolase Chain: A: PDB Molecule: dengue 4 ns3 full-length protein; PDBTitle: crystal structure of the ns3 protease-helicase from dengue2 virus
99	c2qf7A_	Alignment	not modelled	23.0	19	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
100	c2boyC_	Alignment	not modelled	22.5	24	PDB header: oxidoreductase Chain: C: PDB Molecule: 3-chlorocatechol 1,2-dioxygenase; PDBTitle: crystal structure of 3-chlorocatechol 1,2-dioxygenase from2 rhodococcus opacus 1cp
101	d1k8ga2	Alignment	not modelled	21.1	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
102	c3howC_	Alignment	not modelled	20.7	16	PDB header: transcription,transferase/dna/rna hybrid Chain: C: PDB Molecule: dna-directed rna polymerase ii subunit rpb3;

