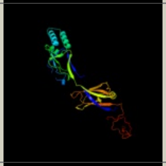
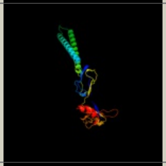
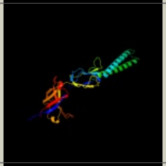
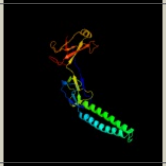
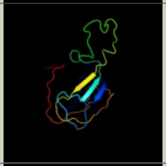
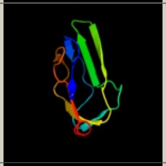
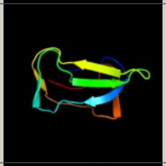
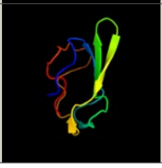
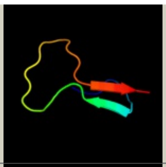
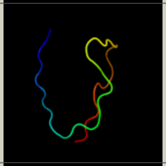
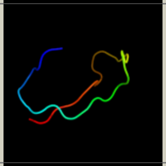
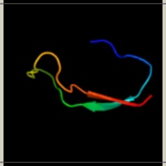
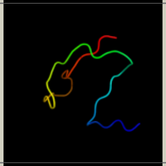
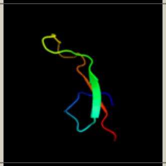
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P27303
Date	Thu Jan 5 11:43:50 GMT 2012
Unique Job ID	601f55121cf433a5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fppB_	Alignment		99.9	22	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**macrolide-specific efflux protein maca; **PDBTitle:** crystal structure of e.coli maca
2	c3h9iB_	Alignment		99.9	18	**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
3	c2f1mA_	Alignment		99.9	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
4	c3lnnB_	Alignment		99.9	22	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**membrane fusion protein (mfp) heavy metal cation efflux **PDBTitle:** crystal structure of zneb from cupriavidus metallidurans
5	c1t5eB_	Alignment		99.9	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
6	d1vf7a_	Alignment		99.8	18	**Fold:**HlyD-like secretion proteins **Superfamily:**HlyD-like secretion proteins **Family:**HlyD-like secretion proteins
7	c2k33A_	Alignment		99.1	35	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**acra; **PDBTitle:** solution structure of an n-glycosylated protein using in2 vitro glycosylation
8	c2b8gA_	Alignment		97.5	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)
9	d1o78a_	Alignment		97.3	27	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
10	c3n6rK_	Alignment		97.3	27	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
11	d1dcza_	Alignment		97.2	33	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains

12	c2ejgD_	Alignment		96.7	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
13	c2l5tA_	Alignment		96.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
14	c2dn8A_	Alignment		96.3	16	**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
15	c2ejmA_	Alignment		96.3	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methylcrotonoyl-coa carboxylase subunit alpha; **PDBTitle:** solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
16	c2kccA_	Alignment		96.2	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
17	d1iyua_	Alignment		96.2	31	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
18	d1bdoa_	Alignment		96.2	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
19	d1ghja_	Alignment		96.0	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
20	d1k8ma_	Alignment		95.9	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
21	d1qjoa_	Alignment	not modelled	95.5	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
22	d1gjxa_	Alignment	not modelled	95.2	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
23	d1laba_	Alignment	not modelled	95.1	29	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
24	d1y8ob1	Alignment	not modelled	94.7	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
25	c2qf7A_	Alignment	not modelled	94.4	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
26	d1pmra_	Alignment	not modelled	94.4	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
27	c2q8iB_	Alignment	not modelled	94.4	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
28	d2pnrc1	Alignment	not modelled	94.4	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
						PDB header:transferase

29	c2dncA_	Alignment	not modelled	93.8	8	**Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component; **PDBTitle:** solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
30	c2dneA_	Alignment	not modelled	93.3	10	**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
31	c2jkuA_	Alignment	not modelled	93.2	27	**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
32	d1glaf_	Alignment	not modelled	91.4	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
33	d2gpra_	Alignment	not modelled	91.1	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
34	d1uoua3	Alignment	not modelled	91.0	22	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
35	d2f3ga_	Alignment	not modelled	91.0	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
36	d2tpta3	Alignment	not modelled	90.6	28	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
37	d1gpra_	Alignment	not modelled	90.2	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
38	d1brwa3	Alignment	not modelled	89.9	30	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
39	c2gu1A_	Alignment	not modelled	89.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
40	c2hsiB_	Alignment	not modelled	88.4	17	**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
41	c1otpA_	Alignment	not modelled	87.3	24	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
42	c2j0fC_	Alignment	not modelled	85.5	24	**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
43	c3h5qA_	Alignment	not modelled	85.2	48	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
44	c1brwB_	Alignment	not modelled	84.4	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
45	c2aukA_	Alignment	not modelled	82.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
46	c2qj8B_	Alignment	not modelled	79.5	30	**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
47	c3nyyA_	Alignment	not modelled	79.2	23	**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
48	c3fmcC_	Alignment	not modelled	78.6	23	**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
49	d1qwya_	Alignment	not modelled	78.0	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Peptidoglycan hydrolase LytM
50	d2ix0a1	Alignment	not modelled	77.9	8	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
51	d1ci3m2	Alignment	not modelled	76.2	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
52	d1e2wa2	Alignment	not modelled	75.9	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
						PDB header:transferase

53	c2dsjA_	Alignment	not modelled	75.4	18	**Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
54	d1qpoa2	Alignment	not modelled	74.5	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
55	c3na6A_	Alignment	not modelled	70.9	25	**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
56	c3cdxB_	Alignment	not modelled	68.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
57	d1o4ua2	Alignment	not modelled	67.5	11	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
58	c2b44A_	Alignment	not modelled	67.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm; **PDBTitle:** truncated s. aureus lytm, p 32 2 1 crystal form
59	d1qapa2	Alignment	not modelled	65.6	16	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
60	c2xhaB_	Alignment	not modelled	64.1	28	**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)
61	c2aujD_	Alignment	not modelled	63.9	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
62	c3it5B_	Alignment	not modelled	63.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protease lasa; **PDBTitle:** crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
63	c3d4rE_	Alignment	not modelled	63.2	25	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**domain of unknown function from the pfam-b_34464 family; **PDBTitle:** crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
64	d1krha1	Alignment	not modelled	59.7	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
65	c1e2vB_	Alignment	not modelled	58.3	13	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
66	c1ctmA_	Alignment	not modelled	58.2	13	**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
67	c2jxmB_	Alignment	not modelled	57.4	25	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
68	c1tu2B_	Alignment	not modelled	55.8	25	**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
69	c2xhcA_	Alignment	not modelled	55.3	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
70	c1q90A_	Alignment	not modelled	54.7	13	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**apocytochrome f; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
71	d1whla_	Alignment	not modelled	54.1	17	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
72	d1tu2b2	Alignment	not modelled	53.9	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
73	c3gnnA_	Alignment	not modelled	53.2	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
74	d1h9ma2	Alignment	not modelled	52.6	17	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
75	d1ek9a_	Alignment	not modelled	52.6	19	**Fold:**Outer membrane efflux proteins (OEP) **Superfamily:**Outer membrane efflux proteins (OEP) **Family:**Outer membrane efflux proteins (OEP)
76	c1tqqC_	Alignment	not modelled	52.0	19	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**outer membrane protein tolc; **PDBTitle:** structure of tolc in complex with hexamminecobalt
						PDB header:photosynthesis

77	c2e75C_	Alignment	not modelled	51.5	25	**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
78	d1fr3a_	Alignment	not modelled	49.3	18	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
79	c1o4uA_	Alignment	not modelled	48.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
80	c1yc9A_	Alignment	not modelled	48.1	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein; **PDBTitle:** the crystal structure of the outer membrane protein vcec from the2 bacterial pathogen vibrio cholerae at 1.8 resolution
81	c1qapA_	Alignment	not modelled	47.5	16	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
82	c3csqC_	Alignment	not modelled	47.5	27	**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
83	c3pajA_	Alignment	not modelled	46.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
84	d1hcza2	Alignment	not modelled	46.0	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
85	c3tqvA_	Alignment	not modelled	45.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
86	c2b7pA_	Alignment	not modelled	45.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
87	d1h9ma1	Alignment	not modelled	45.5	15	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
88	c2jbmA_	Alignment	not modelled	44.5	0	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** qprtase structure from human
89	c3pikA_	Alignment	not modelled	44.2	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusc; **PDBTitle:** outer membrane protein cusc
90	d1wp1a_	Alignment	not modelled	42.2	16	**Fold:**Outer membrane efflux proteins (OEP) **Superfamily:**Outer membrane efflux proteins (OEP) **Family:**Outer membrane efflux proteins (OEP)
91	c3hd7A_	Alignment	not modelled	42.1	21	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
92	c1qpoA_	Alignment	not modelled	40.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
93	c3l0gD_	Alignment	not modelled	40.7	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
94	c3ipkA_	Alignment	not modelled	40.6	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**agi/ii; **PDBTitle:** crystal structure of a3vp1 of agi/ii of streptococcus mutans
95	c2jz2A_	Alignment	not modelled	38.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
96	d1pw4a_	Alignment	not modelled	37.7	19	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
97	d2rdea2	Alignment	not modelled	37.4	13	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain-associated domain
98	d1guta_	Alignment	not modelled	37.1	33	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
99	c1x1oC_	Alignment	not modelled	37.0	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
100	c2jvvA_	Alignment	not modelled	35.8	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg;

						PDBTitle: solution structure of e. coli nusg carboxyterminal domain
101	c2kvqG_	Alignment	not modelled	35.8	29	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
102	c2k21A_	Alignment	not modelled	35.7	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
103	d1nz9a_	Alignment	not modelled	34.6	25	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
104	d1tova_	Alignment	not modelled	34.6	15	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
105	d1nppa2	Alignment	not modelled	34.0	24	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
106	d1h9ra2	Alignment	not modelled	33.9	21	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
107	c3dtpA_	Alignment	not modelled	33.2	8	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
108	d1onla_	Alignment	not modelled	30.7	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
109	d1qfja1	Alignment	not modelled	30.3	31	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
110	c3iftA_	Alignment	not modelled	29.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
111	c2edgA_	Alignment	not modelled	29.0	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** solution structure of the gcv_h domain from mouse glycine
112	d1efca1	Alignment	not modelled	27.9	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
113	d1h9ra1	Alignment	not modelled	27.0	21	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
114	c3d33B_	Alignment	not modelled	26.8	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**domain of unknown function with an immunoglobulin-like **PDBTitle:** crystal structure of a duf3244 family protein with an immunoglobulin-2 like beta-sandwich fold (bvu_0276) from bacteroides vulgatus atcc3 8482 at 1.70 a resolution
115	d2cp3a1	Alignment	not modelled	26.2	18	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
116	d1vf5c2	Alignment	not modelled	24.7	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
117	c3mxuA_	Alignment	not modelled	23.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from bartonella2 henselae
118	d2je6i2	Alignment	not modelled	23.7	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
119	d1ixda_	Alignment	not modelled	23.3	10	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
120	c3ojaB_	Alignment	not modelled	23.2	8	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex