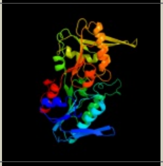
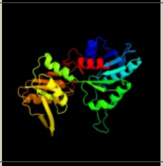
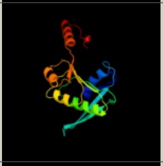
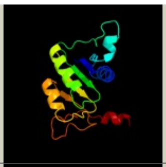
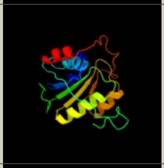
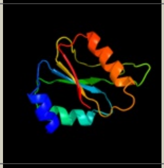
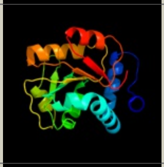
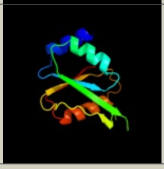
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A717
Date	Thu Jan 5 11:04:30 GMT 2012
Unique Job ID	fb5d7b4d4dc42227

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3efhB_	Alignment		100.0	49	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
2	c1dkrB_	Alignment		100.0	51	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
3	c3dahB_	Alignment		100.0	63	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
4	c2c4kD_	Alignment		100.0	41	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
5	c3lpnB_	Alignment		100.0	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
6	c1u9yD_	Alignment		100.0	34	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
7	d1dkua1	Alignment		100.0	55	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
8	d1u9ya1	Alignment		100.0	31	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
9	d2c4ka1	Alignment		100.0	42	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
10	d2c4ka2	Alignment		100.0	39	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
11	d1dkua2	Alignment		100.0	48	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like

12	d1u9ya2	Alignment		100.0	36	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
13	d1wd5a_	Alignment		99.7	27	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
14	d1zn7a1	Alignment		99.6	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
15	c3o7mD_	Alignment		99.6	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
16	c3dezA_	Alignment		99.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
17	d1g9sa_	Alignment		99.5	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
18	c2dy0A_	Alignment		99.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
19	c2yzkC_	Alignment		99.5	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
20	c1yfzA_	Alignment		99.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
21	d1yfza1	Alignment	not modelled	99.5	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
22	d1vdma1	Alignment	not modelled	99.5	27	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
23	d1z7ga1	Alignment	not modelled	99.5	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
24	d1hgxa_	Alignment	not modelled	99.5	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
25	d2aeea1	Alignment	not modelled	99.5	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
26	d1ecfa1	Alignment	not modelled	99.5	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
27	c3kb8A_	Alignment	not modelled	99.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
28	c2ywtA_	Alignment	not modelled	99.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus

						hb8
29	d1j7ja_	Alignment	not modelled	99.4	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
30	d1l1qa_	Alignment	not modelled	99.4	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
31	d1ufra_	Alignment	not modelled	99.4	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
32	d1gph11	Alignment	not modelled	99.4	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
33	d1cjba_	Alignment	not modelled	99.4	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
34	d1g2qa_	Alignment	not modelled	99.4	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
35	d1tc1a_	Alignment	not modelled	99.4	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
36	d1p17b_	Alignment	not modelled	99.4	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
37	d1y0ba1	Alignment	not modelled	99.4	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
38	c2wnsB_	Alignment	not modelled	99.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
39	d1vcha1	Alignment	not modelled	99.3	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
40	d1mzva_	Alignment	not modelled	99.3	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
41	d1w30a_	Alignment	not modelled	99.3	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
42	d1a3ca_	Alignment	not modelled	99.3	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
43	d2igba1	Alignment	not modelled	99.3	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
44	d1qb7a_	Alignment	not modelled	99.3	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
45	c1ecjB_	Alignment	not modelled	99.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
46	c2p1zA_	Alignment	not modelled	99.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase; **PDBTitle:** crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
47	c1gph1_	Alignment	not modelled	99.3	22	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
48	d1pzma_	Alignment	not modelled	99.2	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
49	d1o57a2	Alignment	not modelled	99.2	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
50	c1pzmB_	Alignment	not modelled	99.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
51	c3m3hA_	Alignment	not modelled	99.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
52	d1fsga_	Alignment	not modelled	99.2	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
53	d1lh0a_	Alignment	not modelled	99.2	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
54	c1o57A_	Alignment	not modelled	99.1	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pur operon repressor; **PDBTitle:** crystal structure of the purine operon repressor of2

						bacillus subtilis
55	c2jbhA_	Alignment	not modelled	99.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase domain-containing protein 1; **PDBTitle:** human phosphoribosyl transferase domain containing 1
56	c3mjdA_	Alignment	not modelled	99.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
57	c2jkzB_	Alignment	not modelled	99.0	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 -monophosphate) (orthorhombic crystal form)
58	c2przB_	Alignment	not modelled	99.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase 1; **PDBTitle:** s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
59	c3qw4B_	Alignment	not modelled	98.9	20	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**ump synthase; **PDBTitle:** structure of leishmania donovani ump synthase
60	d1o5oa_	Alignment	not modelled	98.9	26	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
61	d1i5ea_	Alignment	not modelled	98.9	25	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
62	c2ehjA_	Alignment	not modelled	98.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of uracil phosphoribosyl transferase
63	c2e55D_	Alignment	not modelled	98.9	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of aq2163 protein from aquifex aeolicus
64	c3n2lA_	Alignment	not modelled	98.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
65	d1nula_	Alignment	not modelled	98.8	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
66	c3dmpD_	Alignment	not modelled	98.7	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
67	d1xtta1	Alignment	not modelled	98.6	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
68	d1bd3a_	Alignment	not modelled	98.6	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
69	d1v9sa1	Alignment	not modelled	98.5	27	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
70	d1dqna_	Alignment	not modelled	98.5	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
71	c1zuwA_	Alignment	not modelled	88.3	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase 1; **PDBTitle:** crystal structure of b.subtilis glutamate racemase (race) with d-glu
72	c2zskA_	Alignment	not modelled	86.7	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**226aa long hypothetical aspartate racemase; **PDBTitle:** crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
73	c1sy7B_	Alignment	not modelled	85.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase 1; **PDBTitle:** crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
74	c2eggA_	Alignment	not modelled	83.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
75	c2hk8B_	Alignment	not modelled	82.5	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
76	c2xecD_	Alignment	not modelled	82.0	19	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
77	c3tfxB_	Alignment	not modelled	80.6	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**orotidine 5'-phosphate decarboxylase; **PDBTitle:** crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus
78	c2dx7B_	Alignment	not modelled	79.9	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**aspartate racemase; **PDBTitle:** crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
79	c2jfnA_	Alignment	not modelled	78.2	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala

80	c3fbtB_	Alignment	not modelled	77.3	14	**PDB header:**oxidoreductase, lyase **Chain:** B: **PDB Molecule:**chorismate mutase and shikimate 5-dehydrogenase **PDBTitle:** crystal structure of a chorismate mutase/shikimate 5-2 dehydrogenase fusion protein from clostridium3 acetobutylicum
81	c3hfrA_	Alignment	not modelled	77.2	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from listeria monocytogenes
82	d1gtea3	Alignment	not modelled	77.0	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
83	c1vi2B_	Alignment	not modelled	76.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase 2; **PDBTitle:** crystal structure of shikimate-5-dehydrogenase with nad
84	c2cnwF_	Alignment	not modelled	75.6	18	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
85	c3r2uC_	Alignment	not modelled	72.7	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
86	c2px0D_	Alignment	not modelled	72.4	11	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
87	c3donA_	Alignment	not modelled	71.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
88	c3tozA_	Alignment	not modelled	71.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
89	d1vi2a1	Alignment	not modelled	70.3	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
90	d1vmka_	Alignment	not modelled	68.5	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
91	c3sg0A_	Alignment	not modelled	68.4	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
92	d1efpb_	Alignment	not modelled	67.0	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
93	d1losc_	Alignment	not modelled	66.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
94	c3dmdA_	Alignment	not modelled	66.4	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
95	c3o8qB_	Alignment	not modelled	65.9	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase i alpha; **PDBTitle:** 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
96	c3hp7A_	Alignment	not modelled	65.0	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
97	c2gzmB_	Alignment	not modelled	64.9	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis
98	d1vp8a_	Alignment	not modelled	63.3	25	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
99	c2dgdD_	Alignment	not modelled	63.2	8	**PDB header:**lyase **Chain:** D: **PDB Molecule:**223aa long hypothetical arylmalonate decarboxylase; **PDBTitle:** crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
100	c3uagA_	Alignment	not modelled	63.2	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (udp-n-acetylmuramoyl-l-alanine:d- **PDBTitle:** udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
101	d1p77a1	Alignment	not modelled	63.1	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
102	c3dm5A_	Alignment	not modelled	62.1	13	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
103	c3euaD_	Alignment	not modelled	61.7	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
104	c2a3nA_	Alignment	not modelled	60.6	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative glucosamine-fructose-6-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella

						typhimurium lt2 at 1.353 a resolution
105	c3dfzB_	Alignment	not modelled	60.3	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**precorrin-2 dehydrogenase; **PDBTitle:** sirc, precorrin-2 dehydrogenase
106	d1j8yf2	Alignment	not modelled	60.1	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
107	d1eixa_	Alignment	not modelled	59.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
108	c2xf4A_	Alignment	not modelled	59.6	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydroxyacylglutathione hydrolase; **PDBTitle:** crystal structure of salmonella enterica serovar2 typhimurium ycbl
109	c3navB_	Alignment	not modelled	59.6	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
110	d1cjca1	Alignment	not modelled	59.2	32	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
111	c3lubE_	Alignment	not modelled	58.4	21	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**putative creatinine amidohydrolase; **PDBTitle:** crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
112	c3la8A_	Alignment	not modelled	58.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative purine nucleoside phosphorylase; **PDBTitle:** the crystal structure of smu.1229 from streptococcus mutans ua159
113	d1km4a_	Alignment	not modelled	57.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
114	c3pwzA_	Alignment	not modelled	57.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase 3; **PDBTitle:** crystal structure of an ael1 enzyme from pseudomonas putida
115	c3ek2D_	Alignment	not modelled	57.0	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of eonyl-(acyl carrier protein) reductase2 from burkholderia pseudomallei 1719b
116	c2j7pA_	Alignment	not modelled	56.9	11	**PDB header:**signal recognition **Chain:** A: **PDB Molecule:**signal recognition particle protein; **PDBTitle:** gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
117	c3shoA_	Alignment	not modelled	56.2	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
118	c3b9qA_	Alignment	not modelled	55.5	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
119	d1qsga_	Alignment	not modelled	55.4	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
120	c3qw3B_	Alignment	not modelled	55.4	16	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**orotidine-5-phosphate decarboxylase/orotate **PDBTitle:** structure of leishmania donovani omp decarboxylase