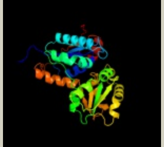
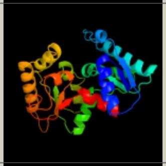
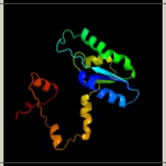
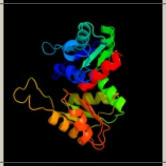
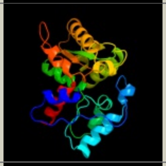
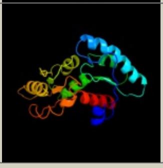
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P22634
Date	Thu Jan 5 11:39:02 GMT 2012
Unique Job ID	d71b015145d3f128

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jfnA_	Alignment		100.0	100	**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
2	c3hfrA_	Alignment		100.0	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from listeria monocytogenes
3	c2jfoB_	Alignment		100.0	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
4	c2jfqA_	Alignment		100.0	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
5	c2dwuA_	Alignment		100.0	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
6	c2gzmB_	Alignment		100.0	28	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis
7	c1zuwA_	Alignment		100.0	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase 1; **PDBTitle:** crystal structure of b.subtilis glutamate racemase (race) with d-glu
8	c2ohoA_	Alignment		100.0	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** structural basis for glutamate racemase inhibitor
9	c3outC_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
10	c2jfzB_	Alignment		100.0	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
11	c1b74A_	Alignment		100.0	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus

12	c2zskA_	Alignment		100.0	18	**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
13	d1b74a1	Alignment		100.0	34	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
14	c3ojcD_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative aspartate/glutamate racemase; **PDBTitle:** crystal structure of a putative asp/glu racemase from yersinia pestis
15	c3s81A_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium
16	c2dx7B_	Alignment		100.0	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**aspartate racemase; **PDBTitle:** crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
17	d1b74a2	Alignment		100.0	23	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
18	c2vlbC_	Alignment		100.0	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**arylmalonate decarboxylase; **PDBTitle:** structure of unliganded arylmalonate decarboxylase
19	c3qvjB_	Alignment		99.9	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative hydantoin racemase; **PDBTitle:** allantoin racemase from klebsiella pneumoniae
20	c2eq5D_	Alignment		99.9	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**228aa long hypothetical hydantoin racemase; **PDBTitle:** crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
21	c2dgdD_	Alignment	not modelled	99.8	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**223aa long hypothetical arylmalonate decarboxylase; **PDBTitle:** crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
22	d1jfla2	Alignment	not modelled	99.8	16	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
23	d2dx7a1	Alignment	not modelled	99.8	14	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
24	d1jfla1	Alignment	not modelled	99.1	15	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
25	c2xecD_	Alignment	not modelled	98.6	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
26	c3dahB_	Alignment	not modelled	94.4	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
27	c1dkrB_	Alignment	not modelled	94.0	15	**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.
28	c2dpyA_	Alignment	not modelled	93.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flagellum-specific atp synthase; **PDBTitle:** crystal structure of the flagellar type iii atpase flii

29	d1m3ua_	Alignment	not modelled	93.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
30	c3a5dM_	Alignment	not modelled	93.4	15	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**v-type atp synthase beta chain; **PDBTitle:** inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
31	d1oy0a_	Alignment	not modelled	91.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
32	d1skye3	Alignment	not modelled	91.1	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
33	c3lp6D_	Alignment	not modelled	90.7	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
34	c3ez4B_	Alignment	not modelled	87.5	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase; **PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
35	c2pjuD_	Alignment	not modelled	87.1	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
36	d1wbha1	Alignment	not modelled	86.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
37	c1kjjA_	Alignment	not modelled	85.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
38	d1o5oa_	Alignment	not modelled	84.7	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
39	c2q5cA_	Alignment	not modelled	84.7	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
40	c2xd4A_	Alignment	not modelled	84.6	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
41	d2pjua1	Alignment	not modelled	82.8	14	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
42	c2c61A_	Alignment	not modelled	82.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**a-type atp synthase non-catalytic subunit b; **PDBTitle:** crystal structure of the non-catalytic b subunit of a-type2 atpase from m. mazei go1
43	c3ouzA_	Alignment	not modelled	81.9	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
44	c1fx0B_	Alignment	not modelled	80.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase beta chain; **PDBTitle:** crystal structure of the chloroplast f1-atpase from spinach
45	c2axqA_	Alignment	not modelled	80.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
46	d1o66a_	Alignment	not modelled	80.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
47	d1skyb3	Alignment	not modelled	79.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
48	c2gr2A_	Alignment	not modelled	78.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin reductase; **PDBTitle:** crystal structure of ferredoxin reductase, bpha4 (oxidized form)
49	c3gkaB_	Alignment	not modelled	76.7	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-ethylmaleimide reductase; **PDBTitle:** crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
50	d1cjca2	Alignment	not modelled	76.6	16	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
51	c3h5lB_	Alignment	not modelled	76.2	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative branched-chain amino acid abc **PDBTitle:** crystal structure of a putative branched-chain amino acid2 abc transporter from silicibacter pomeroyi
52	c3bolB_	Alignment	not modelled	75.3	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
53	c2jizD_	Alignment	not modelled	75.3	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp synthase subunit beta; **PDBTitle:** the structure of f1-atpase inhibited by resveratrol.
						PDB header:oxidoreductase

54	c3noyA_	Alignment	not modelled	75.0	21	**Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** crystal structure of ispg (gcpe)
55	c3hf3A_	Alignment	not modelled	74.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
56	c3d2fC_	Alignment	not modelled	74.3	19	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein homolog sse1; **PDBTitle:** crystal structure of a complex of sse1p and hsp70
57	c2v7yA_	Alignment	not modelled	74.2	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein dnak; **PDBTitle:** crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
58	d1v9sa1	Alignment	not modelled	73.7	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
59	c2c4kD_	Alignment	not modelled	73.4	14	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
60	c1dkgD_	Alignment	not modelled	72.8	26	**PDB header:**complex (hsp24/hsp70) **Chain:** D: **PDB Molecule:**molecular chaperone dnak; **PDBTitle:** crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
61	c2oblA_	Alignment	not modelled	72.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**escn; **PDBTitle:** structural and biochemical analysis of a prototypical atpase from the2 type iii secretion system of pathogenic bacteria
62	c3gr7A_	Alignment	not modelled	72.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
63	c2ys6A_	Alignment	not modelled	72.1	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide synthetase; **PDBTitle:** crystal structure of gar synthetase from geobacillus kaustophilus
64	c3a5dB_	Alignment	not modelled	71.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**v-type atp synthase alpha chain; **PDBTitle:** inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
65	c2w6jD_	Alignment	not modelled	71.5	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp synthase subunit beta, mitochondrial; **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
66	c1skyE_	Alignment	not modelled	70.0	11	**PDB header:**atp synthase **Chain:** E: **PDB Molecule:**f1-atpase; **PDBTitle:** crystal structure of the nucleotide free alpha3beta3 sub-complex of2 f1-atpase from the thermophilic bacillus ps3
67	c1kmhA_	Alignment	not modelled	69.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atpase alpha subunit; **PDBTitle:** crystal structure of spinach chloroplast f1-atpase2 complexed with tentoxin
68	c2o14A_	Alignment	not modelled	67.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yxim; **PDBTitle:** x-ray crystal structure of protein yxim_bacsu from bacillus2 subtilis. northeast structural genomics consortium target3 sr595
69	d1fx0b3	Alignment	not modelled	67.4	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
70	c2h31A_	Alignment	not modelled	65.4	17	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
71	c1m6iA_	Alignment	not modelled	64.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**programmed cell death protein 8; **PDBTitle:** crystal structure of apoptosis inducing factor (aif)
72	c3zu0A_	Alignment	not modelled	64.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nad nucleotidase; **PDBTitle:** structure of haemophilus influenzae nad nucleotidase (nadn)
73	d1vhca_	Alignment	not modelled	64.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
74	d1gv4a1	Alignment	not modelled	63.9	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
75	c1ulzA_	Alignment	not modelled	63.9	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
76	c2v3aA_	Alignment	not modelled	63.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin reductase; **PDBTitle:** crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.
77	c3sg0A_	Alignment	not modelled	63.5	18	**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
78	c2h90A_	Alignment	not modelled	63.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
79	c3jz3B_	Alignment	not modelled	63.1	43	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein qsec; **PDBTitle:** structure of the cytoplasmic segment of histidine kinase

						qsec
80	c3dmpD_	Alignment	not modelled	62.5	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
81	c2iswB_	Alignment	not modelled	62.4	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
82	d1e5qa1	Alignment	not modelled	62.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
83	c3lwzC_	Alignment	not modelled	60.3	24	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis
84	c3u9sE_	Alignment	not modelled	59.9	13	**PDB header:**ligase **Chain:** E: **PDB Molecule:**methylcrotonyl-coa carboxylase, alpha-subunit; **PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
85	c2khoA_	Alignment	not modelled	59.0	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 70; **PDBTitle:** nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone2 (1-605) complexed with adp and substrate
86	d1gqoa_	Alignment	not modelled	59.0	15	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
87	c3lp8A_	Alignment	not modelled	57.7	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
88	c2ywrA_	Alignment	not modelled	57.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of gar transformylase from aquifex2 aeolicus
89	c2qe7C_	Alignment	not modelled	56.6	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
90	c1yqzA_	Alignment	not modelled	56.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a disulfide reductase; **PDBTitle:** structure of coenzyme a-disulfide reductase from2 staphylococcus aureus refined at 1.54 angstrom resolution
91	c2ip4A_	Alignment	not modelled	56.3	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
92	c3bg5C_	Alignment	not modelled	56.1	13	**PDB header:**ligase **Chain:** C: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of staphylococcus aureus pyruvate2 carboxylase
93	c3n6rK_	Alignment	not modelled	55.9	9	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
94	c2vpqA_	Alignment	not modelled	54.9	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
95	d1jkxa_	Alignment	not modelled	54.8	19	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
96	c1h6dL_	Alignment	not modelled	54.4	7	**PDB header:**protein translocation **Chain:** L: **PDB Molecule:**precursor form of glucose-fructose **PDBTitle:** oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
97	c1ofgF_	Alignment	not modelled	54.4	7	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
98	d1m6ia1	Alignment	not modelled	54.4	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
99	c3l0oB_	Alignment	not modelled	53.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcription termination factor rho; **PDBTitle:** structure of rna-free rho transcription termination factor from2 thermotoga maritima
100	c3lpnB_	Alignment	not modelled	53.5	5	**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).
101	d1ujqa_	Alignment	not modelled	53.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
102	c3cr8C_	Alignment	not modelled	53.2	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sulfate adenylyltranferase, adenylylsulfate **PDBTitle:** hexameric aps kinase from thiobacillus denitrificans
103	d2ffca1	Alignment	not modelled	53.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
						PDB header:ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small

104	c1keeH_	Alignment	not modelled	52.8	16	chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
105	c3lxdA_	Alignment	not modelled	52.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans
106	d1uqra_	Alignment	not modelled	52.2	16	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
107	c2xdqA_	Alignment	not modelled	51.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
108	d1dkgd2	Alignment	not modelled	51.1	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
109	c3cpqB_	Alignment	not modelled	50.9	16	**PDB header:**ribosomal protein **Chain:** B: **PDB Molecule:**50s ribosomal protein l30e; **PDBTitle:** crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
110	c2wjxA_	Alignment	not modelled	50.2	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glutamate receptor 2; **PDBTitle:** crystal structure of the human ionotropic glutamate2 receptor glur2 atd region at 4.1 a resolution
111	d1gvfa_	Alignment	not modelled	49.9	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
112	c1gv4A_	Alignment	not modelled	49.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**programed cell death protein 8; **PDBTitle:** murine apoptosis-inducing factor (aif)
113	c3tsuA_	Alignment	not modelled	49.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
114	d1fmta2	Alignment	not modelled	49.3	12	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
115	c3dcjA_	Alignment	not modelled	49.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide **PDBTitle:** crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
116	c2qrvA_	Alignment	not modelled	49.0	25	**PDB header:**transferase/transferase regulator **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 3a; **PDBTitle:** structure of dnmt3a-dnmt3l c-terminal domain complex
117	d1xtta1	Alignment	not modelled	48.9	8	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
118	c3kwlA_	Alignment	not modelled	48.3	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from helicobacter pylori
119	d1t0kb_	Alignment	not modelled	48.2	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
120	c2dzdB_	Alignment	not modelled	48.1	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase