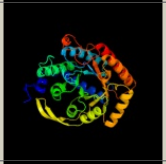
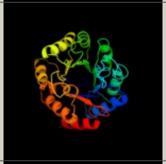
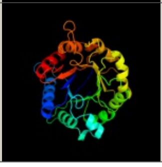
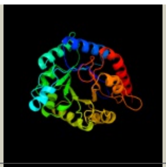
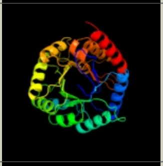
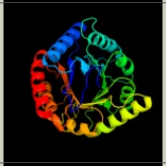
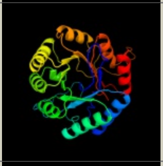
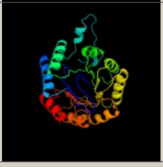
Email	l.a.kelley@imperial.ac.uk
Description	P0AB91
Date	Thu Jan 5 11:14:55 GMT 2012
Unique Job ID	6197988fe10126de

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1n8fa_	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
2	c3tqkA_	Alignment		100.0	54	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** structure of phospho-2-dehydro-3-deoxyheptonate aldolase from2 francisella tularensis schu s4
3	d1of8a_	Alignment		100.0	58	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
4	c1ofaB_	Alignment		100.0	59	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** crystal structure of the tyrosine-regulated2 3-deoxy-d-arabino-heptulosonate-7-phosphate synthase3 from saccharomyces cerevisiae in complex with4 phosphoenolpyruvate and cobalt(ii)
5	d1vr6a1	Alignment		100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
6	c1vs1B_	Alignment		100.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-deoxy-7-phosphoheptulonate synthase; **PDBTitle:** crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
7	c1zcoA_	Alignment		100.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphoheptonate aldolase; **PDBTitle:** crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
8	d2a21a1	Alignment		100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
9	c3nvtA_	Alignment		100.0	27	**PDB header:**transferase/isomerase **Chain:** A: **PDB Molecule:**3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; **PDBTitle:** 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
10	c3stgA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
11	c3fs2A_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate2 aldolase from bruciella melitensis at 1.85a resolution

12	d1d9ea_	Alignment		100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
13	d1o60a_	Alignment		100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
14	c3t4cD_	Alignment		100.0	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 1; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
15	c3sz8D_	Alignment		100.0	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
16	c3pg8B_	Alignment		100.0	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
17	d2zdra2	Alignment		99.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
18	d1vlia2	Alignment		99.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
19	c1xuzA_	Alignment		98.8	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
20	c1vliA_	Alignment		98.2	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
21	c3g8rA_	Alignment	not modelled	97.5	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
22	d2b7oa1	Alignment	not modelled	97.5	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase
23	d1ajza_	Alignment	not modelled	94.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
24	d1ad1a_	Alignment	not modelled	88.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
25	c3tr9A_	Alignment	not modelled	85.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
26	c3eb2A_	Alignment	not modelled	84.8	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
27	c2y5sA_	Alignment	not modelled	82.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
28	c3e5bB_	Alignment	not modelled	81.4	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**isocitrate lyase; **PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2

						melitensis
29	c2bmbA_	Alignment	not modelled	79.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**folic acid synthesis protein fol1; **PDBTitle:** x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae
30	c2dzaA_	Alignment	not modelled	74.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
31	d1tx2a_	Alignment	not modelled	71.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
32	c1tx2A_	Alignment	not modelled	71.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
33	d1eyea_	Alignment	not modelled	67.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
34	c2p2sA_	Alignment	not modelled	64.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
35	c2p90B_	Alignment	not modelled	52.1	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein cgl1923; **PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
36	c2ze5A_	Alignment	not modelled	50.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl transferase; **PDBTitle:** crystal structure of adenosine phosphate-isopentenyltransferase
37	d2p62a1	Alignment	not modelled	48.7	17	**Fold:**PH0156-like **Superfamily:**PH0156-like **Family:**PH0156-like
38	c3btuD_	Alignment	not modelled	46.6	15	**PDB header:**transcription **Chain:** D: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
39	d1ydwa1	Alignment	not modelled	46.1	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
40	d2v3za1	Alignment	not modelled	45.9	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
41	c3fhlC_	Alignment	not modelled	45.7	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
42	c3fa4D_	Alignment	not modelled	45.7	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase; **PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
43	c2e3zB_	Alignment	not modelled	44.6	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of intracellular family 1 beta-2 glucosidase bgl1a from the basidiomycete phanerochaete3 chrysosporium in substrate-free form
44	c3d3qB_	Alignment	not modelled	43.2	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
45	c3oqbF_	Alignment	not modelled	41.4	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
46	d1o5ka_	Alignment	not modelled	40.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
47	d1u1ia1	Alignment	not modelled	40.3	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	c1ofgF_	Alignment	not modelled	38.1	22	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
49	c1h6dL_	Alignment	not modelled	38.1	22	**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
50	c1zlpA_	Alignment	not modelled	37.5	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
51	c2ixaA_	Alignment	not modelled	36.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
52	c3si9B_	Alignment	not modelled	35.4	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
53	c3euwB	Alignment	not modelled	35.3	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase;

		Alignment	not modelled			**PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
54	c3a8tA_	Alignment	not modelled	35.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate isopentenyltransferase; **PDBTitle:** plant adenylate isopentenyltransferase in complex with atp
55	c3e35A_	Alignment	not modelled	34.7	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco1997; **PDBTitle:** actinobacteria-specific protein of unknown function, sco1997
56	c3ptkB_	Alignment	not modelled	34.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase os4bglu12; **PDBTitle:** the crystal structure of rice (oryza sativa l.) os4bglu12
57	d1f74a_	Alignment	not modelled	31.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
58	c2vqqA_	Alignment	not modelled	31.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histone deacetylase 4; **PDBTitle:** structure of hdac4 catalytic domain (a double cysteine-to-2 alanine mutant) bound to a trifluoromethylketone inhbitor
59	d1pffa_	Alignment	not modelled	30.8	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
60	d2v89a1	Alignment	not modelled	30.4	21	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**PHD domain
61	c2qw5B_	Alignment	not modelled	30.3	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
62	c3h5dD_	Alignment	not modelled	30.1	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
63	c3cprB_	Alignment	not modelled	29.4	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
64	d2auwa1	Alignment	not modelled	29.3	75	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
65	c3dtyA_	Alignment	not modelled	29.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from pseudomonas2 syringae
66	c3oixA_	Alignment	not modelled	29.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative dihydroorotate dehydrogenase; dihydroorotate **PDBTitle:** crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
67	d1auaa2	Alignment	not modelled	28.7	13	**Fold:**SpoIIaa-like **Superfamily:**CRAL/TRIO domain **Family:**CRAL/TRIO domain
68	c3na8A_	Alignment	not modelled	28.3	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
69	c3q2kB_	Alignment	not modelled	28.3	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaca
70	d1ryda1	Alignment	not modelled	28.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
71	d1sq5a_	Alignment	not modelled	28.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
72	c3kuxA_	Alignment	not modelled	27.3	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis
73	c2wamB_	Alignment	not modelled	27.2	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical alanine and leucine rich **PDBTitle:** crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714
74	c2hjpA_	Alignment	not modelled	27.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
75	c2bdqA_	Alignment	not modelled	26.6	20	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
76	c3exaD_	Alignment	not modelled	26.3	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of the full-length trna2 isopentenylpyrophosphate transferase (bh2366) from3 bacillus halodurans, northeast structural genomics4 consortium target bhr41.
77	c2auwB_	Alignment	not modelled	26.1	75	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
						PDB header:oxidoreductase

78	c3c1aB_	Alignment	not modelled	25.9	23	**Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
79	d1ulza3	Alignment	not modelled	25.9	12	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
80	c3moiA_	Alignment	not modelled	25.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
81	c3noeA_	Alignment	not modelled	24.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
82	c3f4lF_	Alignment	not modelled	24.5	29	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative oxidoreductase yhhx; **PDBTitle:** crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
83	d1t6ua_	Alignment	not modelled	24.1	30	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nickel-containing superoxide dismutase, NiSOD **Family:**Nickel-containing superoxide dismutase, NiSOD
84	d1olma3	Alignment	not modelled	24.0	11	**Fold:**SpoIIaa-like **Superfamily:**CRAL/TRIO domain **Family:**CRAL/TRIO domain
85	c3fd8A_	Alignment	not modelled	23.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
86	c3ahyD_	Alignment	not modelled	23.5	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of beta-glucosidase 2 from fungus trichoderma reesei2 in complex with tris
87	c3e18A_	Alignment	not modelled	22.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
88	d1w79a1	Alignment	not modelled	22.4	21	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
89	c3db2C_	Alignment	not modelled	22.2	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative nadph-dependent oxidoreductase; **PDBTitle:** crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
90	d1igwa_	Alignment	not modelled	22.1	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
91	c3crqA_	Alignment	not modelled	22.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** structure of trna dimethylallyltransferase: rna2 modification through a channel
92	d2ex2a1	Alignment	not modelled	22.1	23	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
93	d1n8pa_	Alignment	not modelled	21.5	45	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
94	c2nmpC_	Alignment	not modelled	21.3	45	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine gamma-lyase; **PDBTitle:** crystal structure of human cystathionine gamma lyase
95	c1f9cA_	Alignment	not modelled	21.3	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein (muconate cycloisomerase i); **PDBTitle:** crystal structure of mle d178n variant
96	c3m2tA_	Alignment	not modelled	20.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
97	c3e82A_	Alignment	not modelled	20.7	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
98	c3daqB_	Alignment	not modelled	20.7	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
99	d1qgna_	Alignment	not modelled	20.6	30	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
100	c1zh8B_	Alignment	not modelled	20.5	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
101	c3fozB_	Alignment	not modelled	20.5	26	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate transferase; **PDBTitle:** structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
102	c2jf7B_	Alignment	not modelled	20.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**strictosidine-o-beta-d-glucosidase; **PDBTitle:** structure of strictosidine glucosidase