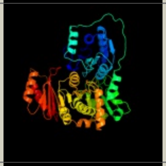
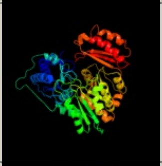
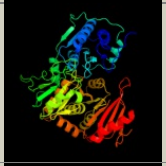
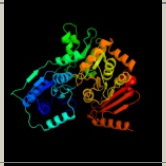
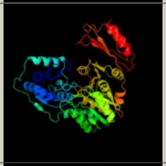
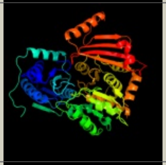
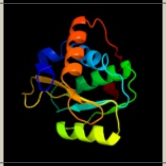
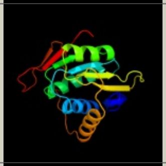
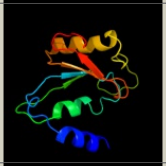
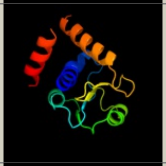
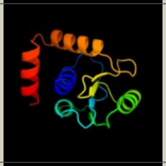
Email	l.a.kelley@imperial.ac.uk
Description	P24175
Date	Thu Jan 5 11:40:52 GMT 2012
Unique Job ID	c81f3aa0411e65f8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1wqaB_	Alignment		100.0	28	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phospho-sugar mutase; **PDBTitle:** crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
2	c3c04A_	Alignment		100.0	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphomannomutase/phosphoglucomutase; **PDBTitle:** structure of the p368g mutant of pmm/pgm from p. aeruginosa
3	c2f7lA_	Alignment		100.0	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**455aa long hypothetical phospho-sugar mutase; **PDBTitle:** crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
4	c3pdkB_	Alignment		100.0	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** crystal structure of phosphoglucosamine mutase from b. anthracis
5	c1tuoA_	Alignment		100.0	24	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative phosphomannomutase; **PDBTitle:** crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
6	c2fuvB_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucomutase; **PDBTitle:** phosphoglucomutase from salmonella typhimurium.
7	c1c4gB_	Alignment		100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (alpha-d-glucose 1-phosphate **PDBTitle:** phosphoglucomutase vanadate based transition state analog2 complex
8	c3i3wB_	Alignment		100.0	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** structure of a phosphoglucosamine mutase from francisella tularensis
9	c1kfiA_	Alignment		100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoglucomutase 1; **PDBTitle:** crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium
10	c2z0fA_	Alignment		100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphoglucomutase; **PDBTitle:** crystal structure of putative phosphoglucomutase from thermus2 thermophilus hb8
11	c2dkdA_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoacetylglucosamine mutase; **PDBTitle:** crystal structure of n-acetylglucosamine-phosphate mutase,2 a member of the alpha-d-phosphohexomutase superfamily, in3 the product complex

12	d1p5dx1	Alignment		100.0	35	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
13	d1kfia1	Alignment		100.0	19	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
14	d3pmga1	Alignment		100.0	18	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
15	d1p5dx3	Alignment		99.9	29	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
16	d1p5dx2	Alignment		99.9	37	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
17	d1kfia3	Alignment		99.9	20	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
18	d3pmga3	Alignment		99.9	16	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
19	d3pmga2	Alignment		99.8	31	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
20	d1kfia2	Alignment		99.8	24	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
21	d1p5dx4	Alignment	not modelled	99.8	17	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
22	d1wjwa_	Alignment	not modelled	99.2	16	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
23	d1kfia4	Alignment	not modelled	97.5	20	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
24	d3pmga4	Alignment	not modelled	97.5	23	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
25	d1nn4a_	Alignment	not modelled	91.7	33	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
26	c3he8A_	Alignment	not modelled	91.6	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
27	c3k7pA_	Alignment	not modelled	91.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
28	c3m1pA_	Alignment	not modelled	90.1	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
						Fold: Flavodoxin-like

29	d3bula2	Alignment	not modelled	90.1	19	**Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
30	c3s5pA_	Alignment	not modelled	90.1	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
31	d2vvpa1	Alignment	not modelled	88.7	23	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
32	c2ppwA_	Alignment	not modelled	84.9	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
33	c1k98A_	Alignment	not modelled	84.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
34	d1ccwa_	Alignment	not modelled	83.1	29	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
35	d1o1xa_	Alignment	not modelled	78.5	23	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
36	c3c5yD_	Alignment	not modelled	78.5	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
37	c1bmtB_	Alignment	not modelled	77.7	18	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.o angstrom x-ray structure of2 the b12-binding domains of methionine synthase
38	c2i2xD_	Alignment	not modelled	72.8	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**methyltransferase 1; **PDBTitle:** crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
39	c3qayC_	Alignment	not modelled	71.4	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**endolysin; **PDBTitle:** catalytic domain of cd27l endolysin targeting clostridia difficile
40	c3onoA_	Alignment	not modelled	69.7	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
41	c3ezxA_	Alignment	not modelled	69.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1; **PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein
42	c1y80A_	Alignment	not modelled	69.1	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
43	c3hlyA_	Alignment	not modelled	67.4	19	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
44	d1vmea1	Alignment	not modelled	64.6	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
45	c3fniA_	Alignment	not modelled	64.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
46	d1ycga1	Alignment	not modelled	60.9	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
47	d1fmfa_	Alignment	not modelled	59.4	32	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
48	d1vr6a1	Alignment	not modelled	56.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
49	d1e5da1	Alignment	not modelled	55.5	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
50	c3qd5B_	Alignment	not modelled	55.0	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
51	d1xrsb1	Alignment	not modelled	51.4	18	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
52	c3cinA_	Alignment	not modelled	48.5	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**myo-inositol-1-phosphate synthase-related protein; **PDBTitle:** crystal structure of a myo-inositol-1-phosphate synthase-related2 protein (tm_1419) from thermotoga maritima msb8 at 1.70 a resolution
53	d1gvfa_	Alignment	not modelled	46.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
54	c3ne8A_	Alignment	not modelled	44.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase;

54	c3ne8A_	Alignment	not modelled	44.0	15	**PDBTitle:** the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1
55	c2ohiB_	Alignment	not modelled	44.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
56	c3nvtA_	Alignment	not modelled	43.1	12	**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
57	d1d9ea_	Alignment	not modelled	40.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
58	d1t71a_	Alignment	not modelled	40.6	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
59	d1rvga_	Alignment	not modelled	38.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
60	c2q9uB_	Alignment	not modelled	37.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
61	c3k6qB_	Alignment	not modelled	35.4	15	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative ligand binding protein; **PDBTitle:** crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
62	c2pfsA_	Alignment	not modelled	35.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
63	d1vjza_	Alignment	not modelled	35.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
64	c2rejA_	Alignment	not modelled	34.7	10	**PDB header:**choline-binding protein **Chain:** A: **PDB Molecule:**putative glycine betaine abc transporter protein; **PDBTitle:** abc-transporter choline binding protein in unliganded semi-2 closed conformation
65	c1keeH_	Alignment	not modelled	33.6	20	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
66	d1b1ca_	Alignment	not modelled	33.4	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
67	d1ws6a1	Alignment	not modelled	31.4	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
68	c3f93D_	Alignment	not modelled	31.4	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of exo-1,3/1,4-beta-glucanase (exop) from2 pseudoalteromonas sp. bb1
69	d1dxha2	Alignment	not modelled	29.9	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
70	c2jpiA_	Alignment	not modelled	29.9	13	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
71	d2a5la1	Alignment	not modelled	28.7	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
72	c2vyoA_	Alignment	not modelled	28.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitooligosaccharide deacetylase; **PDBTitle:** chitin deacetylase family member from encephalitozoon2 cuniculi
73	c3op1A_	Alignment	not modelled	28.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
74	c3qqzA_	Alignment	not modelled	27.9	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein yjik; **PDBTitle:** crystal structure of the c-terminal domain of the yjik protein from2 escherichia coli cft073
75	c3nolA_	Alignment	not modelled	27.7	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** crystal structure of zymomonas mobilis glutaminyl cyclase (trigonal2 form)
76	c2iswB_	Alignment	not modelled	27.3	25	**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
77	c1xrsB_	Alignment	not modelled	26.9	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-lysine 5,6-aminomutase beta subunit; **PDBTitle:** crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
78	c1vmeB_	Alignment	not modelled	26.6	12	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
						PDB header:chaperone

79	c3s3tD_	Alignment	not modelled	25.6	8	**Chain:** D: **PDB Molecule:**nucleotide-binding protein, universal stress protein uspa **PDBTitle:** universal stress protein uspa from lactobacillus plantarum
80	c3sz8D_	Alignment	not modelled	25.5	14	**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
81	d1q77a_	Alignment	not modelled	23.9	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
82	d2z3va1	Alignment	not modelled	22.6	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
83	c3a9gA_	Alignment	not modelled	22.5	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pqq-dependent sugar dehydrogenase apo-form
84	d7reqa2	Alignment	not modelled	21.9	16	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
85	c1w17A_	Alignment	not modelled	21.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
86	c3gxxB_	Alignment	not modelled	21.4	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
87	d1t6t1_	Alignment	not modelled	21.2	21	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
88	c2c1iA_	Alignment	not modelled	21.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan glcnac deacetylase; **PDBTitle:** structure of streptococcus pnemoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant.
89	d1xk7a1	Alignment	not modelled	20.9	38	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
90	d1p9oa_	Alignment	not modelled	20.2	10	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
91	c2zkiH_	Alignment	not modelled	20.2	20	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
92	c2ismA_	Alignment	not modelled	19.4	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of the putative oxidoreductase (glucose2 dehydrogenase) (ttha0570) from thermus theromophilus hb8
93	d2c1ia1	Alignment	not modelled	19.2	15	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
94	c2dumD_	Alignment	not modelled	18.4	7	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ph0823; **PDBTitle:** crystal structure of hypothetical protein, ph0823
95	d1m40a_	Alignment	not modelled	18.4	21	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
96	c3c52B_	Alignment	not modelled	18.2	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
97	c1vs1B_	Alignment	not modelled	18.2	19	**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
98	c3hzpA_	Alignment	not modelled	18.2	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of ntf2-like protein of unknown function mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 natl2a at 1.40 a resolution
99	c1xa3B_	Alignment	not modelled	18.0	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**crotonobetainyl-coa:carnitine coa-transferase; **PDBTitle:** crystal structure of caib, a type iii coa transferase in2 carnitine metabolism