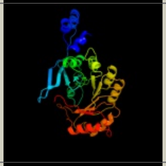
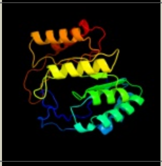
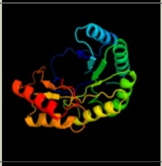
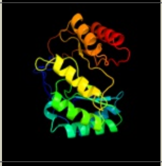
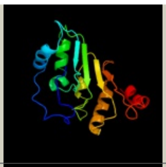
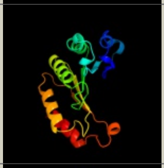
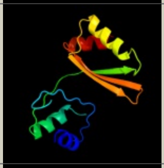
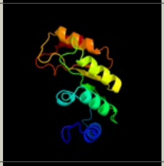
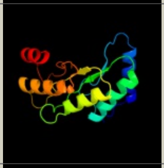
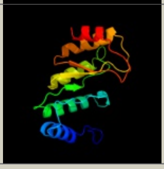
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P39280
Date	Thu Jan 5 11:58:50 GMT 2012
Unique Job ID	4a00e695611c5bac

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2a5hC_	Alignment		100.0	32	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-lysine 2,3-aminomutase; **PDBTitle:** 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
2	c3rfaA_	Alignment		99.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase n; **PDBTitle:** x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
3	d1tv8a_	Alignment		99.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**MoCo biosynthesis proteins
4	c2yx0A_	Alignment		99.7	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam enzyme; **PDBTitle:** crystal structure of p. horikoshii tyw1
5	c3c8fA_	Alignment		99.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate formate-lyase 1-activating enzyme; **PDBTitle:** 4fe-4s-pyruvate formate-lyase activating enzyme with2 partially disordered adomet
6	c3cixA_	Alignment		99.6	12	**PDB header:**adomet binding protein **Chain:** A: **PDB Molecule:**fefe-hydrogenase maturase; **PDBTitle:** x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
7	c3t7vA_	Alignment		99.5	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylornithine synthase pylb; **PDBTitle:** crystal structure of methylornithine synthase (pylb)
8	c1r30A_	Alignment		99.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**biotin synthase; **PDBTitle:** the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
9	d1r30a_	Alignment		99.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Biotin synthase
10	c2qgqF_	Alignment		99.5	12	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**protein tm_1862; **PDBTitle:** crystal structure of tm_1862 from thermotoga maritima.2 northeast structural genomics consortium target vr77
11	d1olta_	Alignment		99.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN

12	c2z2uA_	Alignment		99.1	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**upf0026 protein mj0257; **PDBTitle:** crystal structure of archaeal tyw1
13	c3canA_	Alignment		99.0	15	**PDB header:**lyase activator **Chain:** A: **PDB Molecule:**pyruvate-formate lyase-activating enzyme; **PDBTitle:** crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
14	c2f06B_	Alignment		92.4	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
15	d2nu7b1	Alignment		87.0	16	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
16	c2rfgB_	Alignment		82.2	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
17	c2r8wB_	Alignment		79.0	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
18	c3daqB_	Alignment		78.6	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
19	d1f74a_	Alignment		76.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
20	c2vc6A_	Alignment		75.7	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
21	c2nu9E_	Alignment	not modelled	74.2	15	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
22	c3lerA_	Alignment	not modelled	74.1	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
23	d1hl2a_	Alignment	not modelled	73.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
24	c3lciA_	Alignment	not modelled	73.4	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
25	c3na8A_	Alignment	not modelled	72.5	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
26	c3si9B_	Alignment	not modelled	71.1	7	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
27	c3e96B_	Alignment	not modelled	70.4	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
28	c3h5dD_	Alignment	not modelled	70.3	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
						PDB header:lyase

29	c2yxgD_	Alignment	not modelled	69.1	9	**Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
30	c3fkkA_	Alignment	not modelled	68.2	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
31	c3dz1A_	Alignment	not modelled	67.7	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
32	c3n2xB_	Alignment	not modelled	66.9	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uncharacterized protein yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
33	c3eb2A_	Alignment	not modelled	64.6	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
34	c3bi8A_	Alignment	not modelled	63.6	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
35	c2ehhE_	Alignment	not modelled	63.0	11	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
36	c2kboA_	Alignment	not modelled	61.7	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna dc->du-editing enzyme apobec-3g; **PDBTitle:** structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
37	d2hiya1	Alignment	not modelled	61.1	22	**Fold:**SP0830-like **Superfamily:**SP0830-like **Family:**SP0830-like
38	c3pueA_	Alignment	not modelled	59.5	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
39	c3g0sA_	Alignment	not modelled	58.8	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
40	c3cprB_	Alignment	not modelled	57.2	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
41	d2a6na1	Alignment	not modelled	56.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
42	c3ewbX_	Alignment	not modelled	56.2	15	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
43	d1m1ha2	Alignment	not modelled	55.6	23	**Fold:**Ferredoxin-like **Superfamily:**N-utilization substance G protein NusG, N-terminal domain **Family:**N-utilization substance G protein NusG, N-terminal domain
44	c2fmoA_	Alignment	not modelled	55.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate reductase; **PDBTitle:** ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
45	c3noeA_	Alignment	not modelled	54.1	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
46	d1eucb1	Alignment	not modelled	54.0	15	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
47	c2v9dB_	Alignment	not modelled	49.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
48	c3lkeA_	Alignment	not modelled	48.9	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from bacillus2 halodurans
49	d1qwga_	Alignment	not modelled	47.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
50	c3b4uB_	Alignment	not modelled	47.2	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
51	c1eucB_	Alignment	not modelled	46.2	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**succinyl-coa synthetase, beta chain; **PDBTitle:** crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
52	c2pg8C_	Alignment	not modelled	46.0	21	**PDB header:**ligand binding protein **Chain:** C: **PDB Molecule:**dpgc; **PDBTitle:** crystal structure of r254k mutanat of dpgc with bound substrate analog
53	c1zcoA_	Alignment	not modelled	44.2	12	**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
54	c3fluD	Alignment	not modelled	43.7	10	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase;

54	c3fluD_	Alignment	not modelled	43.7	10	**PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
55	d1o5ka_	Alignment	not modelled	43.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
56	c3c52B_	Alignment	not modelled	43.4	10	**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
57	c2nx9B_	Alignment	not modelled	42.1	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxaloacetate decarboxylase 2, subunit alpha; **PDBTitle:** crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
58	c3ndcB_	Alignment	not modelled	41.1	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-4 c(11)-methyltransferase; **PDBTitle:** crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
59	c3kwpA_	Alignment	not modelled	40.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**predicted methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase from lactobacillus2 brevis
60	c2nytB_	Alignment	not modelled	40.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable c->u-editing enzyme apobec-2; **PDBTitle:** the apobec2 crystal structure and functional implications2 for aid
61	c2zf8A_	Alignment	not modelled	40.1	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
62	c3d0cB_	Alignment	not modelled	40.0	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
63	d1va0a1	Alignment	not modelled	39.9	23	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
64	d1xxxa1	Alignment	not modelled	38.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
65	d1nvma2	Alignment	not modelled	35.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
66	c1vs1B_	Alignment	not modelled	35.8	10	**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
67	d1xkya1	Alignment	not modelled	35.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
68	c2r94B_	Alignment	not modelled	35.4	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxy-(6-phospho-)gluconate aldolase; **PDBTitle:** crystal structure of kd(p)ga from t.tenax
69	c3rrvC_	Alignment	not modelled	34.1	7	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
70	c3nvtA_	Alignment	not modelled	33.3	11	**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
71	c2nuxB_	Alignment	not modelled	32.6	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate **PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
72	c1xuzA_	Alignment	not modelled	32.6	16	**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
73	c2higA_	Alignment	not modelled	31.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phospho-1-fructokinase; **PDBTitle:** crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
74	d2deka1	Alignment	not modelled	31.5	21	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
75	c2k06A_	Alignment	not modelled	31.1	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of the aminoterminal domain of e. coli2 nusg
76	d1g5ta_	Alignment	not modelled	30.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
77	d1xx4a_	Alignment	not modelled	30.5	15	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
78	d1gvfa_	Alignment	not modelled	30.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase

						Family: Class II FBP aldolase
79	c3rsiA_	Alignment	not modelled	30.1	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196
80	d1cc5a_	Alignment	not modelled	29.6	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
81	c3gkbA_	Alignment	not modelled	28.8	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis
82	d1rjma_	Alignment	not modelled	28.6	15	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
83	c2i55C_	Alignment	not modelled	28.5	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphomannomutase; **PDBTitle:** complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
84	d2cg4a2	Alignment	not modelled	28.2	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
85	c2ppyE_	Alignment	not modelled	28.1	15	**PDB header:**lyase **Chain:** E: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426
86	c1m1gB_	Alignment	not modelled	27.4	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
87	c3bh1A_	Alignment	not modelled	27.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0371 protein dip2346; **PDBTitle:** crystal structure of protein dip2346 from corynebacterium diphtheriae
88	d2ex2a1	Alignment	not modelled	27.3	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
89	c2hmcA_	Alignment	not modelled	27.1	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
90	c2iswB_	Alignment	not modelled	26.8	10	**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
91	c3a3eB_	Alignment	not modelled	26.8	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**penicillin-binding protein 4; **PDBTitle:** crystal structure of penicillin binding protein 4 (dacb)2 from haemophilus influenzae, complexed with novel beta-3 lactam (cmv)
92	c3q94B_	Alignment	not modelled	26.5	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
93	c3g64A_	Alignment	not modelled	26.0	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2)
94	c2djwF_	Alignment	not modelled	25.9	19	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**probable transcriptional regulator, asnc family; **PDBTitle:** crystal structure of ttha0845 from thermus thermophilus hb8
95	c2e0kA_	Alignment	not modelled	25.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 c20-methyltransferase; **PDBTitle:** crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
96	c3e2vA_	Alignment	not modelled	25.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3'-5'-exonuclease; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
97	d1w3ia_	Alignment	not modelled	25.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
98	d2ffja1	Alignment	not modelled	25.5	10	**Fold:**AF1104-like **Superfamily:**AF1104-like **Family:**AF1104-like
99	d1q52a_	Alignment	not modelled	25.4	15	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
100	c3g8rA_	Alignment	not modelled	25.3	16	**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
101	c3fkjA_	Alignment	not modelled	24.9	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerases; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
102	c2ftpA_	Alignment	not modelled	24.8	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa

103	d1i1ga2	Alignment	not modelled	24.5	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
104	c3h02F_	Alignment	not modelled	24.4	15	**PDB header:**lyase **Chain:** F: **PDB Molecule:**naphthoate synthase; **PDBTitle:** 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.
105	d1wz8a1	Alignment	not modelled	24.3	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
106	c3r0oA_	Alignment	not modelled	24.1	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carnitinyl-coa dehydratase; **PDBTitle:** crystal structure of carnitinyl-coa hydratase from mycobacterium avium
107	d1qt1a_	Alignment	not modelled	23.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
108	c2w3pB_	Alignment	not modelled	23.2	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**benzoyl-coa-dihydrodiol lyase; **PDBTitle:** boxc crystal structure
109	c3tqkA_	Alignment	not modelled	23.2	13	**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
110	d1mj3a_	Alignment	not modelled	22.5	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
111	d1nz8a_	Alignment	not modelled	22.5	22	**Fold:**Ferredoxin-like **Superfamily:**N-utilization substance G protein NusG, N-terminal domain **Family:**N-utilization substance G protein NusG, N-terminal domain
112	c3hsiC_	Alignment	not modelled	22.5	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphatidylserine synthase; **PDBTitle:** crystal structure of phosphatidylserine synthase haemophilus2 influenzae rd kw20
113	c2iexA_	Alignment	not modelled	22.0	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroxynapthoic acid synthetase; **PDBTitle:** crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
114	c3ktsA_	Alignment	not modelled	22.0	14	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**glycerol uptake operon antiterminator regulatory protein; **PDBTitle:** crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
115	d3bexa2	Alignment	not modelled	21.9	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**CoaX-like
116	c3bleA_	Alignment	not modelled	21.1	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
117	c3o8nA_	Alignment	not modelled	21.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase, muscle type; **PDBTitle:** structure of phosphofructokinase from rabbit skeletal muscle
118	c2vzvB_	Alignment	not modelled	20.5	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
119	d1sg4a1	Alignment	not modelled	20.5	15	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
120	c3sllC_	Alignment	not modelled	20.4	6	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus