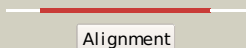
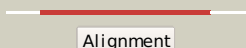
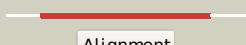
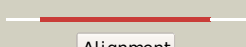
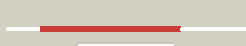
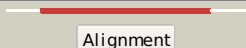
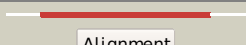
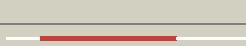
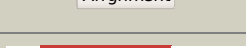
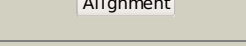
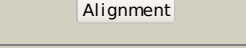
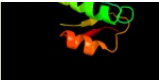


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3e6eC_	 Alignment		100.0	17	PDB header: isomerase Chain: C; PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
2	c1niuA_	 Alignment		100.0	18	PDB header: isomerase Chain: A; PDB Molecule: alanine racemase; PDBTitle: alanine racemase with bound inhibitor derived from l-2 cycloserine
3	c1vftA_	 Alignment		100.0	18	PDB header: isomerase Chain: A; PDB Molecule: alanine racemase; PDBTitle: crystal structure of l-cycloserine-bound form of alanine2 racemase from d-cycloserine-producing streptomyces3 lavendulae
4	c3hurA_	 Alignment		100.0	15	PDB header: isomerase Chain: A; PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from oenococcus oeni
5	c3mubB_	 Alignment		100.0	18	PDB header: isomerase Chain: B; PDB Molecule: alanine racemase; PDBTitle: the crystal structure of alanine racemase from streptococcus2 pneumoniae
6	c3kw3B_	 Alignment		100.0	14	PDB header: isomerase Chain: B; PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
7	c3oo2A_	 Alignment		100.0	14	PDB header: isomerase Chain: A; PDB Molecule: alanine racemase 1; PDBTitle: 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
8	c1xfcb_	 Alignment		100.0	16	PDB header: isomerase Chain: B; PDB Molecule: alanine racemase; PDBTitle: the 1.9 a crystal structure of alanine racemase from mycobacterium2 tuberculosis contains a conserved entryway into the active site
9	c2rigC_	 Alignment		100.0	16	PDB header: isomerase Chain: C; PDB Molecule: alanine racemase; PDBTitle: crystal structure of biosynthetic alaine racemase from escherichia2 coli
10	c2odoC_	 Alignment		100.0	15	PDB header: isomerase Chain: C; PDB Molecule: alanine racemase; PDBTitle: crystal structure of pseudomonas fluorescens alanine racemase
11	c3oo2B_	 Alignment		100.0	15	PDB header: isomerase Chain: B; PDB Molecule: alanine racemase 1; PDBTitle: 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col

12	c3co8B_	 Alignment		100.0	14	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from oenococcus oeni
13	c2dy3B_	 Alignment		100.0	17	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from corynebacterium glutamicum
14	c2vd9A_	 Alignment		100.0	19	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: the crystal structure of alanine racemase from bacillus2 anthracis (ba0252) with bound l-alap
15	c3anuA_	 Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of d-serine dehydratase from chicken kidney
16	c3llxA_	 Alignment		100.0	18	PDB header: isomerase Chain: A: PDB Molecule: predicted amino acid aldolase or racemase; PDBTitle: crystal structure of an ala racemase-like protein (il1761) from2 idiomarina loihiensis at 1.50 a resolution
17	c3gwqB_	 Alignment		100.0	14	PDB header: lyase Chain: B: PDB Molecule: d-serine deaminase; PDBTitle: crystal structure of a putative d-serine deaminase (bx_e_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution
18	d1vfsa2	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
19	d1bd0a2	 Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
20	d1rcqa2	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
21	c1w8gA_	 Alignment	not modelled	100.0	16	PDB header: plp-binding protein Chain: A: PDB Molecule: hypothetical upf0001 protein yggs; PDBTitle: crystal structure of e. coli k-12 yggs
22	c2p3eA_	 Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of aq1208 from aquifex aeolicus
23	c3n2bD_	 Alignment	not modelled	100.0	16	PDB header: lyase Chain: D: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
24	c2qghA_	 Alignment	not modelled	100.0	10	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
25	c2j66A_	 Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: btrk; PDBTitle: structural characterisation of btrk decarboxylase from2 butirosin biosynthesis
26	c3r79B_	 Alignment	not modelled	100.0	19	PDB header: structure genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from agrobacterium2 tumefaciens
27	c3cpgA_	 Alignment	not modelled	100.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an unknown protein from bifidobacterium2 adolescentis
28	d1ct5a_	 Alignment	not modelled	100.0	13	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: "Hypothetical" protein ybl036c
		 Alignment				PDB header: lyase

29	c1njjC_	Alignment	not modelled	100.0	13	Chain: C: PDB Molecule: ornithine decarboxylase; PDBTitle: crystal structure determination of t. brucei ornithine2 decarboxylase bound to d-ornithine and to g418
30	c1tufA_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase from m.2 jannaschi
31	c2nvaH_	Alignment	not modelled	100.0	10	PDB header: lyase Chain: H: PDB Molecule: arginine decarboxylase, a207r protein; PDBTitle: the x-ray crystal structure of the paramecium bursaria2 chlorella virus arginine decarboxylase bound to agmatine
32	c2pljA_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: lysine/ornithine decarboxylase; PDBTitle: crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
33	c2o0tB_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: the three dimensional structure of diaminopimelate decarboxylase from2 mycobacterium tuberculosis reveals a tetrameric enzyme organisation
34	c2yxxA_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure analysis of diaminopimelate decarboxylate (lysa)
35	c1knwA_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase
36	c2on3A_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: ornithine decarboxylase; PDBTitle: a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminooxy-3 1-aminopropane
37	c3btuA_	Alignment	not modelled	99.9	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: antizyme inhibitor 1; PDBTitle: crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
38	c1d7kB_	Alignment	not modelled	99.9	17	PDB header: lyase Chain: B: PDB Molecule: human ornithine decarboxylase; PDBTitle: crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
39	d1hkva2	Alignment	not modelled	99.9	17	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
40	d1f3ta2	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
41	d1twia2	Alignment	not modelled	99.9	13	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
42	d7odca2	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
43	c3n29A_	Alignment	not modelled	99.9	15	PDB header: lyase Chain: A: PDB Molecule: carboxynorspermidine decarboxylase; PDBTitle: crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
44	c3nzqB_	Alignment	not modelled	99.9	13	PDB header: lyase Chain: B: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
45	d1d7ka2	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
46	c3mt1B_	Alignment	not modelled	99.9	12	PDB header: lyase Chain: B: PDB Molecule: putative carboxynorspermidine decarboxylase protein; PDBTitle: crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
47	c3nzpA_	Alignment	not modelled	99.8	16	PDB header: lyase Chain: A: PDB Molecule: arginine decarboxylase; PDBTitle: crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
48	c3n2oA_	Alignment	not modelled	99.8	12	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
49	d1knwa2	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
50	d1bd0a1	Alignment	not modelled	99.7	13	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Alanine racemase
51	d1vfsa1	Alignment	not modelled	99.6	15	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Alanine racemase
52	d1rcqa1	Alignment	not modelled	99.6	22	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Alanine racemase
53	c2y85D_	Alignment	not modelled	97.1	17	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
54	c3ciaA_	Alignment	not modelled	96.6	14	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase;

54	c3qjaA	Alignment	not modelled	90.0	14	PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
55	dlvc4a	Alignment	not modelled	96.1	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
56	dlrpxa	Alignment	not modelled	96.1	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
57	c2c3zA	Alignment	not modelled	95.6	17	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
58	dl10ea	Alignment	not modelled	94.6	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
59	dl1tja	Alignment	not modelled	94.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
60	c3inpA	Alignment	not modelled	94.4	14	PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
61	dlh5ya	Alignment	not modelled	94.1	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
62	c3ct7E	Alignment	not modelled	92.9	13	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
63	c3ivuB	Alignment	not modelled	91.9	17	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
64	dlizca	Alignment	not modelled	91.9	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/HpaI aldolase
65	clizcA	Alignment	not modelled	91.9	17	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
66	dlj5ta	Alignment	not modelled	91.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
67	d2flia1	Alignment	not modelled	90.9	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
68	dlznn1	Alignment	not modelled	90.5	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: PdxS-like
69	dlvzwa1	Alignment	not modelled	90.4	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
70	clznnF	Alignment	not modelled	90.0	10	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
71	c2w6rA	Alignment	not modelled	88.1	11	PDB header: lyase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit PDBTitle: crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
72	dl1thfd	Alignment	not modelled	88.1	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
73	c3igsB	Alignment	not modelled	87.6	19	PDB header: isomerase Chain: B: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase 2; PDBTitle: structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
74	dli4na	Alignment	not modelled	86.1	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
75	c3qz6A	Alignment	not modelled	85.9	14	PDB header: lyase Chain: A: PDB Molecule: hpcH/hpaI aldolase; PDBTitle: the crystal structure of hpcH/hpaI aldolase from desulfitobacterium2 hafniense dcb-2
76	dlka9f	Alignment	not modelled	83.3	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
77	c2ftpA	Alignment	not modelled	81.1	15	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
78	dla53a	Alignment	not modelled	80.5	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
79	dlmxsa	Alignment	not modelled	77.7	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
80	c2wvh4	Alignment		77.0	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase;

80	c2wyhA	Alignment		77.0	13	PDBTitle: structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
81	c1ydcC	Alignment	not modelled	77.0	18	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
82	d1qo2a	Alignment	not modelled	76.7	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
83	d1dxea	Alignment	not modelled	76.7	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/HpaI aldolase
84	d1h1ya	Alignment	not modelled	76.2	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
85	d1tqxa	Alignment	not modelled	76.1	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
86	c2h9aA	Alignment	not modelled	73.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoid/iron- PDBTitle: corrinoid iron-sulfur protein
87	c2vefB	Alignment	not modelled	73.3	19	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
88	d7reqa2	Alignment	not modelled	72.2	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
89	d1eyea	Alignment	not modelled	72.2	15	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
90	c2bdqA	Alignment	not modelled	70.7	15	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 structural genomics target sar15.
91	c2h90A	Alignment	not modelled	70.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
92	c2v82A	Alignment	not modelled	67.7	14	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpGal complexed to kdpGal
93	c1x1oC	Alignment	not modelled	67.7	15	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
94	c3q58A	Alignment	not modelled	66.5	16	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
95	c3bolB	Alignment	not modelled	66.1	20	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
96	c3ghfA	Alignment	not modelled	65.7	20	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein2 minc from salmonella typhimurium
97	d1ps9a1	Alignment	not modelled	65.3	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
98	c3qc3B	Alignment	not modelled	64.9	14	PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
99	c1k1yA	Alignment	not modelled	64.5	21	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
100	d1yxya1	Alignment	not modelled	64.5	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
101	c3cu2A	Alignment	not modelled	64.4	17	PDB header: isomerase Chain: A: PDB Molecule: ribulose-5-phosphate 3-epimerase; PDBTitle: crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
102	c3rfaA	Alignment	not modelled	61.5	7	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
103	c2b7pA	Alignment	not modelled	61.2	14	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
104	c2qv5A	Alignment	not modelled	60.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2773; PDBTitle: crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58

105	d1olta_	Alignment	not modelled	60.5	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
106	d1lt7a_	Alignment	not modelled	60.0	17	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
107	d1umya_	Alignment	not modelled	59.9	17	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
108	d1piia2	Alignment	not modelled	58.8	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
109	c3hf3A_	Alignment	not modelled	57.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
110	c1qapA_	Alignment	not modelled	57.6	14	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
111	d1gvfa_	Alignment	not modelled	57.0	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
112	c3bdkB_	Alignment	not modelled	55.7	17	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
113	c3kruC_	Alignment	not modelled	54.1	11	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
114	c1ydnA_	Alignment	not modelled	53.4	15	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
115	d1xcfa_	Alignment	not modelled	52.5	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
116	d1njib1	Alignment	not modelled	52.4	12	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
117	d1wa3a1	Alignment	not modelled	50.2	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
118	d1vcfa1	Alignment	not modelled	50.0	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
119	c3gnna_	Alignment	not modelled	49.8	10	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
120	c2dzaA_	Alignment	not modelled	47.7	20	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate