































Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3n75E_	 Alignment		100.0	69	PDB header: lyase Chain: E: PDB Molecule: lysine decarboxylase, inducible; PDBTitle: x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldc1
2	c2vycA_	 Alignment		100.0	36	PDB header: lyase Chain: A: PDB Molecule: biodegradative arginine decarboxylase; PDBTitle: crystal structure of acid induced arginine decarboxylase2 from e. coli
3	c1c4kA_	 Alignment		100.0	30	PDB header: lyase Chain: A: PDB Molecule: protein (ornithine decarboxylase); PDBTitle: ornithine decarboxylase mutant (gly121tyr)
4	d1c4ka2	 Alignment		100.0	34	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
5	c2x3lA_	 Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: orn/lys/arg decarboxylase family protein; PDBTitle: crystal structure of the orn_lys_arg decarboxylase family2 protein sar0482 from methicillin-resistant staphylococcus3 aureus
6	d1rv3a_	 Alignment		100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
7	d1bj4a_	 Alignment		100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
8	d1ejja_	 Alignment		100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
9	d2z67a1	 Alignment		100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
10	c2a7vA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: human mitochondrial serine hydroxymethyltransferase 2
11	d2a7va1	 Alignment		100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like

12	d1c4ka3	Alignment		100.0	28	Fold: Ornithine decarboxylase C-terminal domain Superfamily: Ornithine decarboxylase C-terminal domain Family: Ornithine decarboxylase C-terminal domain
13	c3h7fB_	Alignment		100.0	14	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase 1; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
14	c3hl2D_	Alignment		100.0	13	PDB header: transferase Chain: D: PDB Molecule: o-phosphoseryl-trna(sec) selenium transferase; PDBTitle: the crystal structure of the human sepsecs-trnasec complex
15	d3bc8a1	Alignment		100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
16	c3ecdC_	Alignment		100.0	18	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase 2; PDBTitle: crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
17	c3n0lA_	Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
18	d1dfoa_	Alignment		99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
19	d1kl1a_	Alignment		99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
20	d2e7ja1	Alignment		99.9	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
21	c2dkjB_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
22	c3mc6C_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
23	c3mafB_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
24	d1o69a_	Alignment	not modelled	99.9	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
25	d1wyub1	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
26	c3f9tB_	Alignment	not modelled	99.9	16	PDB header: lyase Chain: B: PDB Molecule: l-tyrosine decarboxylase mfnA; PDBTitle: crystal structure of l-tyrosine decarboxylase mfnA (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution
27	d1vjoa_	Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
28	d1wyua1	Alignment	not modelled	99.9	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
						PDB header: transferase

29	c3bcxA	Alignment	not modelled	99.9	13	Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- PDBTitle: e1 dehydrase
30	c3e9kA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
31	c2w8wA	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
32	c2jisA	Alignment	not modelled	99.9	15	PDB header: lyase Chain: A: PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
33	c2hzpA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
34	c3nnkC	Alignment	not modelled	99.9	15	PDB header: transferase Chain: C: PDB Molecule: ureidoglycine-glyoxylate aminotransferase; PDBTitle: biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
35	c3hbxB	Alignment	not modelled	99.9	16	PDB header: lyase Chain: B: PDB Molecule: glutamate decarboxylase 1; PDBTitle: crystal structure of gad1 from arabidopsis thaliana
36	c2po3B	Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
37	d1mdoa	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
38	d1h0ca	Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
39	d1m6sa	Alignment	not modelled	99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
40	c3nysA	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: aminotransferase wbpe; PDBTitle: x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution
41	d1js3a	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
42	c2ogeC	Alignment	not modelled	99.8	14	PDB header: transferase Chain: C: PDB Molecule: transaminase; PDBTitle: x-ray structure of s. venezuelae desv in its internal2 aldimine form
43	c2z9wA	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
44	c2r0tA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: pyridoxamine 5-phosphate-dependent dehydrase; PDBTitle: crystal sructure of gdp-4-keto-6-deoxymannose-3-dehydratase2 with a trapped plp-glutamate geminal diamine
45	d1fc4a	Alignment	not modelled	99.8	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
46	c3uwCA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: nucleotide-sugar aminotransferase; PDBTitle: structure of an aminotransferase (degt-dnrj-eryc1-strs family) from2 coxiella burnetii in complex with pmp
47	c3a2bA	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
48	c3islA	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
49	d1bs0a	Alignment	not modelled	99.8	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
50	c3hqtB	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
51	d1svva	Alignment	not modelled	99.8	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
52	c2dr1A	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
53	c3k40B	Alignment	not modelled	99.8	13	PDB header: lyase Chain: B: PDB Molecule: aromatic-l-amino-acid decarboxylase; PDBTitle: crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
54	c3frkB	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: qdtb;

54	c3tkB_	Alignment	not modelled	99.8	14	PDBTitle: x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine PDB header: transferase Chain: A: PDB Molecule: glutamine-2-deoxy-scylo-ino- PDBTitle: crystal structure of the plp-bound form of btrr,2 a dual functional aminotransferase involved in butirosin3 biosynthesis.
55	c2c7tA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: 2-amino-3-ketobutyrate coenzyme a ligase; PDBTitle: structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii
56	c3tqxA_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase serc; PDBTitle: crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
57	c3ffrA_	Alignment	not modelled	99.8	10	PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
58	c3dr4B_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
59	c3l8aB_	Alignment	not modelled	99.8	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
60	d2ch1a1	Alignment	not modelled	99.8	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
61	d1pmma_	Alignment	not modelled	99.8	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
62	d2bwna1	Alignment	not modelled	99.8	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
63	c3pj0D_	Alignment	not modelled	99.8	17	PDB header: lyase Chain: D: PDB Molecule: lmo0305 protein; PDBTitle: crystal structure of a putative l-allo-threonine aldolase (lmo0305)2 from listeria monocytogenes egd-e at 1.80 a resolution
64	c3lwsF_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: F: PDB Molecule: aromatic amino acid beta-eliminating PDBTitle: crystal structure of putative aromatic amino acid beta-2 eliminating lyase/threonine aldolase. (yp_001813866.1) from3 exiguobacterium sp. 255-15 at 2.00 a resolution
65	c3ju7B_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: B: PDB Molecule: putative plp-dependent aminotransferase; PDBTitle: crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
66	d1v72a1	Alignment	not modelled	99.8	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
67	d2v1pa1	Alignment	not modelled	99.8	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
68	d2fnua1	Alignment	not modelled	99.8	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
69	d1b9ha_	Alignment	not modelled	99.8	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
70	c2okkA_	Alignment	not modelled	99.8	14	PDB header: lyase Chain: A: PDB Molecule: glutamate decarboxylase 2; PDBTitle: the x-ray crystal structure of the 65kda isoform of glutamic acid2 decarboxylase (gad65)
71	d1tp1a_	Alignment	not modelled	99.8	9	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
72	c2cb1A_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulphydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulphydrylase2 from thermus thermophilus hb8,oah2.
73	c2huuA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
74	d1m32a_	Alignment	not modelled	99.8	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
75	d1jf9a_	Alignment	not modelled	99.8	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
76	d1qgna_	Alignment	not modelled	99.8	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
77	c3ly1C_	Alignment	not modelled	99.8	12	PDB header: transferase Chain: C: PDB Molecule: putative histidinol-phosphate aminotransferase; PDBTitle: crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution
78	c3kaxB_	Alignment	not modelled	99.8	11	PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
						Fold: PLP-dependent transferase-like

79	d2aeua1	Alignment	not modelled	99.7	15	Superfamily: PLP-dependent transferases Family: SelA-like
80	d1cl1a	Alignment	not modelled	99.7	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
81	d1qz9a	Alignment	not modelled	99.7	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
82	c3f0ha	Alignment	not modelled	99.7	12	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
83	d1c7ga	Alignment	not modelled	99.7	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
84	d1cs1a	Alignment	not modelled	99.7	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
85	c3ke3A	Alignment	not modelled	99.7	15	PDB header: transferase Chain: A: PDB Molecule: putative serine-pyruvate aminotransferase; PDBTitle: crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution
86	c3qm2A	Alignment	not modelled	99.7	10	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
87	c3getA	Alignment	not modelled	99.7	7	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution
88	c2qmaB	Alignment	not modelled	99.7	12	PDB header: transferase Chain: B: PDB Molecule: diaminobutyrate-pyruvate transaminase and l-2,4- PDBTitle: crystal structure of glutamate decarboxylase domain of2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus
89	c1i41j	Alignment	not modelled	99.7	13	PDB header: lyase Chain: J: PDB Molecule: cystathionine gamma-synthase; PDBTitle: cystathionine gamma-synthase in complex with the inhibitor2 appa
90	d1c7na	Alignment	not modelled	99.7	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
91	d1elua	Alignment	not modelled	99.7	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
92	c2fyfB	Alignment	not modelled	99.7	16	PDB header: transferase Chain: B: PDB Molecule: phosphoserine aminotransferase; PDBTitle: structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
93	c1d2fB	Alignment	not modelled	99.7	12	PDB header: transferase Chain: B: PDB Molecule: maly protein; PDBTitle: x-ray structure of maly from escherichia coli: a pyridoxal-5'-2 phosphate-dependent enzyme acting as a modulator in mal gene3 expression
94	d1x0ma1	Alignment	not modelled	99.7	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
95	c3ri6A	Alignment	not modelled	99.7	12	PDB header: transferase Chain: A: PDB Molecule: o-acetylhomoserine sulfhydrylase; PDBTitle: a novel mechanism of sulfur transfer catalyzed by o-acetylhomoserine2 sulfhydrylase in methionine biosynthetic pathway of wolfinella3 succinogenes
96	d1lc5a	Alignment	not modelled	99.7	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
97	d1bw0a	Alignment	not modelled	99.7	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
98	c3caiA	Alignment	not modelled	99.7	13	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
99	d1gc0a	Alignment	not modelled	99.7	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
100	c3aemD	Alignment	not modelled	99.7	10	PDB header: lyase Chain: D: PDB Molecule: methionine gamma-lyase; PDBTitle: reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate
101	c3op7A	Alignment	not modelled	99.7	12	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of a plp-dependent aminotransferase (zp_03625122.1)2 from streptococcus suis 89-1591 at 1.70 a resolution
102	d2c0ra1	Alignment	not modelled	99.7	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
103	d1d2fa	Alignment	not modelled	99.7	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

						Family: Cystathionine synthase-like
104	c3eucB_	Alignment	not modelled	99.7	10	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase 2; PDBTitle: crystal structure of histidinol-phosphate aminotransferase2 (yp_297314.1) from ralstonia eutropha jmp134 at 2.05 a resolution
105	c2yrrA_	Alignment	not modelled	99.7	16	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
106	c2gqnB_	Alignment	not modelled	99.7	12	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-lyase; PDBTitle: cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
107	c3hdoB_	Alignment	not modelled	99.7	14	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
108	d1t3ia_	Alignment	not modelled	99.7	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
109	d1v2da_	Alignment	not modelled	99.7	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
110	c3qi6B_	Alignment	not modelled	99.7	12	PDB header: lyase Chain: B: PDB Molecule: cystathionine gamma-synthase metb (cgs); PDBTitle: crystal structure of cystathionine gamma-synthase metb (cgs) from2 mycobacterium ulcerans agy99
111	d1libja_	Alignment	not modelled	99.7	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
112	c3b46B_	Alignment	not modelled	99.7	12	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
113	dliaya_	Alignment	not modelled	99.7	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
114	c1ibjC_	Alignment	not modelled	99.7	13	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
115	c3fkdc_	Alignment	not modelled	99.7	12	PDB header: lyase Chain: C: PDB Molecule: l-threonine-o-3-phosphate decarboxylase; PDBTitle: the crystal structure of l-threonine-o-3-phosphate2 decarboxylase from porphyromonas gingivalis
116	c1ynuA_	Alignment	not modelled	99.7	13	PDB header: lyase Chain: A: PDB Molecule: 1-aminocyclopropane-1-carboxylate synthase; PDBTitle: crystal structure of apple acc synthase in complex with l-vinylglycine
117	c2nmpC_	Alignment	not modelled	99.7	10	PDB header: lyase Chain: C: PDB Molecule: cystathionine gamma-lyase; PDBTitle: crystal structure of human cystathionine gamma lyase
118	c2hdyA_	Alignment	not modelled	99.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
119	c3ndnC_	Alignment	not modelled	99.7	15	PDB header: lyase Chain: C: PDB Molecule: o-succinylhomoserine sulfhydrylase; PDBTitle: crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
120	c3dzzB_	Alignment	not modelled	99.7	10	PDB header: transferase Chain: B: PDB Molecule: putative pyridoxal 5'-phosphate-dependent c-s lyase; PDBTitle: crystal structure of a putative plp-dependent aminotransferase2 (lbul_1103) from lactobacillus delbrueckii subsp. at 1.61 a3 resolution