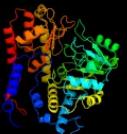
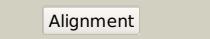
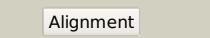
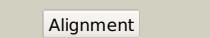
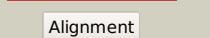
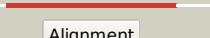
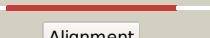
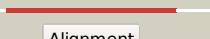
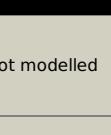


Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD1093_(glyA)_1220579_1221859
Date	Wed Jul 31 22:05:17 BST 2019
Unique Job ID	d6b3a18b8509cd98

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h7fB_			100.0	100	PDB header: transferase Chain: B; PDB Molecule: serine hydroxymethyltransferase 1; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
2	d1ejia_			100.0	47	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
3	d1bj4a_			100.0	48	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
4	c3n0lA_			100.0	49	PDB header: transferase Chain: A; PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
5	c6cd1A_			100.0	49	PDB header: transferase Chain: A; PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of medicago truncatula serine2 hydroxymethyltransferase 3 (mtshmt3), complexes with reaction3 intermediates
6	d1rv3a_			100.0	48	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
7	c2a7vA_			100.0	53	PDB header: transferase Chain: A; PDB Molecule: serine hydroxymethyltransferase; PDBTitle: human mitochondrial serine hydroxymethyltransferase 2
8	d2a7val			100.0	53	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
9	c4n0wA_			100.0	53	PDB header: transferase Chain: A; PDB Molecule: serine hydroxymethyltransferase; PDBTitle: x-ray crystal structure of a serine hydroxymethyltransferase from2 burkholderia cenocepacia with covalently attached pyridoxal phosphate
10	c4j5uB_			100.0	48	PDB header: transferase Chain: B; PDB Molecule: serine hydroxymethyltransferase; PDBTitle: x-ray crystal structure of a serine hydroxymethyltransferase with2 covalently bound plp from rickettsia rickettsii str. sheila smith
11	c4o6zC_			100.0	40	PDB header: transferase Chain: C; PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase with covalently2 bound plp schiff-base from plasmodium falciparum

12	c4wxFC	Alignment		100.0	52	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of l-serine hydroxymethyltransferase in complex with 2 glycine
13	c5vc2A	Alignment		100.0	46	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of a serine hydroxymethyltransferase from 2 helicobacter pylori
14	c3ecdC	Alignment		100.0	53	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase 2; PDBTitle: crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
15	d1dfa	Alignment		100.0	55	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
16	c4bhel	Alignment		100.0	31	PDB header: transferase Chain: I: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: methanococcus jannaschii serine hydroxymethyltransferase2 in complex with plp
17	d1kl1a	Alignment		100.0	58	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
18	c2dkjB	Alignment		100.0	61	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
19	c5z0yA	Alignment		100.0	40	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystallization and structure determination of cytoplasm serine2 hydroxymethyltransferase (shmt) from pichia pastoris
20	c5txtA	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinate synthase, mitochondrial; PDBTitle: structure of asymmetric apo/holo alas dimer from s. cerevisiae
21	c6hrhA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 5-aminolevulinate synthase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
22	d1c4ka2	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
23	c3bcxA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
24	c1c4kA	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: protein (ornithine decarboxylase); PDBTitle: ornithine decarboxylase mutant (gly121tyr)
25	c2vyca	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: biodegradative arginine decarboxylase; PDBTitle: crystal structure of acid induced arginine decarboxylase2 from e. coli
26	c5w70B	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: l-glutamine:2-deoxy-scyllo-inosose aminotransferase; PDBTitle: x-ray structure of rbmb from streptomyces ribosidificus
27	c5fkzE	Alignment	not modelled	100.0	16	PDB header: lyase Chain: E: PDB Molecule: lysine decarboxylase, constitutive; PDBTitle: structure of e.coli constitutive lysine decarboxylase
28	c2w8wA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser

29	c3hqtB	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsA
30	c3n75E	Alignment	not modelled	100.0	15	PDB header: lyase Chain: E: PDB Molecule: lysine decarboxylase, inducible; PDBTitle: x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldcI
31	c2c7tA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: glutamine-2-deoxy-scyllo-inosose aminotransferase; PDBTitle: crystal structure of the plp-bound form of btrr, a dual functional2 aminotransferase involved in butirosin biosynthesis.
32	c4k2ba	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: ntd biosynthesis operon protein ntda; PDBTitle: crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
33	c5k8bA	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: 8-amino-3,8-dideoxy-alpha-d-manno-octulosonate PDBTitle: x-ray structure of kdna, 8-amino-3,8-dideoxy-alpha-d-manno-2 octulosonate transaminase, from shewanella oneidensis in the presence3 of the external aldimine with plp and glutamate
34	c2ogeC	Alignment	not modelled	100.0	16	PDB header: transferase Chain: C: PDB Molecule: transaminase; PDBTitle: x-ray structure of s. venezuelae desv in its internal2 aldimine form
35	c4q6rB	Alignment	not modelled	100.0	14	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: sphingosine-1-phosphate lyase 1; PDBTitle: crystal structure of human sphingosine-1-phosphate lyase in complex2 with inhibitor 6-[(2r)-4-(4-benzyl-7-chlorophthalazin-1-yl)-2-3 methylpiperazin-1-yl]pyridine-3-carbonitrile
36	c3wy7D	Alignment	not modelled	100.0	25	PDB header: transferase Chain: D: PDB Molecule: 8-amino-7-oxonanoate synthase; PDBTitle: crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
37	d1b9ha	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: GABA-aminotransferase-like
38	c5k1rB	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: burkholderia pseudomallei sphingosine-1-phosphate lyase PDBTitle: structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021
39	c2r0tA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: pyridoxamine 5-phosphate-dependent dehydrase; PDBTitle: crystal structure of gdp-4-keto-6-deoxymannose-3-dehydratase with a2 trapped plp-glutamate geminal diamine
40	d1o69a	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: GABA-aminotransferase-like
41	c2po3B	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
42	d1bs0a	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: GABA-aminotransferase-like
43	d1c7ga	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: Beta-eliminating lyases
44	c3tqxA	Alignment	not modelled	100.0	16	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
45	d1vjoa	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: Cystathionine synthase-like
46	c4qgrA	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: degt/dnrj/eryc1/strs aminotransferase; PDBTitle: crystal structure of a degt dnrj eryc1 strs aminotransferase from2 brucella abortus
47	d1mdoa	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: GABA-aminotransferase-like
48	c3a2ba	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
49	d2bwna1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: GABA-aminotransferase-like
50	d1qgna	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: Cystathionine synthase-like
51	d1jf9a	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: Cystathionine synthase-like
52	c3nnkC	Alignment	not modelled	100.0	18	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
						Fold: PLP-dependent transferase-like

53	d2fnua1	Alignment	not modelled	100.0	12	Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
54	d2v1pa1	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
55	d1wyub1	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
56	d1tpla_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
57	c3hbxB_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: B: PDB Molecule: glutamate decarboxylase 1; PDBTitle: crystal structure of gad1 from arabidopsis thaliana
58	c3nysA_	Alignment	not modelled	100.0	16	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
59	c5kz5M_	Alignment	not modelled	100.0	15	PDB header: transferase/oxidoreductase Chain: M: PDB Molecule: cysteine desulfurase, mitochondrial; PDBTitle: architecture of the human mitochondrial iron-sulfur cluster assembly2 machinery: the complex formed by the iron donor, the sulfur donor,3 and the scaffold
60	c2cb1A_	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
61	c3mafB_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
62	c3frkB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: qdtb; PDBTitle: x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine
63	c4j8IA_	Alignment	not modelled	100.0	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yhfs; PDBTitle: crystal structure of the pyridoxal-5'-phosphate dependent protein yhfs2 from escherichia coli
64	d1fc4a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
65	c3wgcB_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: B: PDB Molecule: l-allo-threonine aldolase; PDBTitle: aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
66	c2z9wA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
67	c4oc9N_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: N: PDB Molecule: putative o-acetylhomoserine (thiol)-lyase; PDBTitle: 2.35 angstrom resolution crystal structure of putative o-2 acetylhomoserine (thiol)-lyase (mety) from campylobacter jejuni3 subsp. jejuni nctc 11168 with n'-pyridoxyl-lysine-5'-monophosphate at4 position 205
68	c3dr4B_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter crescentus with bound sugar ligand
69	c3zrrB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: serine-pyruvate aminotransferase (agxt); PDBTitle: crystal structure and substrate specificity of a thermophilic2 archaeal serine : pyruvate aminotransferase from sulfolobus3 solfataricus
70	c3is1A_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
71	d2ctza1	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
72	c3madA_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (symmetric form)
73	c5gp4C_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: C: PDB Molecule: glutamate decarboxylase; PDBTitle: lactobacillus brevis cgmcc 1306 glutamate decarboxylase
74	c4obuG_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: G: PDB Molecule: pyridoxal-dependent decarboxylase domain protein; PDBTitle: ruminococcus gnavaus tryptophan decarboxylase rumgna_01526 (apo)
75	c4ritB_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: pyridoxal-dependent decarboxylase; PDBTitle: the yellow crystal structure of pyridoxal-dependent decarboxylase from2 sphaerobacter thermophilus dsm 20745
76	c3e9kA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
77	c3uwca_	Alignment	not modelled	100.0	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
						PDB header: lyase

78	c1i41J	Alignment	not modelled	100.0	20	Chain: J: PDB Molecule: cystathione gamma-synthase; PDBTitle: cystathione gamma-synthase in complex with the inhibitor2 appa PDB header: lyase
79	c2jisA	Alignment	not modelled	100.0	12	Chain: A: PDB Molecule: cysteine sulfenic acid decarboxylase; PDBTitle: human cysteine sulfenic acid decarboxylase (csad) in2 complex with plp.
80	c3hvyc	Alignment	not modelled	100.0	21	PDB header: lyase Chain: C: PDB Molecule: cystathione beta-lyase family protein, ynbb b.subtilis PDBTitle: crystal structure of putative cystathione beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution
81	c3fd0B	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: putative cystathione beta-lyase involved in aluminum PDBTitle: crystal structure of putative cystathione beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
82	c3f9tB	Alignment	not modelled	100.0	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
83	c5dx5B	Alignment	not modelled	100.0	16	PDB header: lyase Chain: B: PDB Molecule: methionine gamma-lyase; PDBTitle: crystal structure of methionine gamma-lyase from clostridium2 sporogenes
84	d1m6sa	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
85	c6ewqA	Alignment	not modelled	100.0	12	PDB header: sugar binding protein Chain: A: PDB Molecule: putative capsular polysaccharide biosynthesis protein; PDBTitle: putative sugar aminotransferase spr1654 from streptococcus pneumoniae,2 plp-form
86	d2c0ra1	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
87	d2ch1a1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathione synthase-like
88	c3ndnC	Alignment	not modelled	100.0	19	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
89	c4lc3B	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: putative udp-4-amino-4-deoxy-l-arabinose-oxoglutarate PDBTitle: x-ray crystal structure of a putative udp-4-amino-4-deoxy-l-arabinose-2-oxoglutarate aminotransferase from burkholderia cenocepacia
90	c5j8gA	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase sufs; PDBTitle: crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis
91	c5u20C	Alignment	not modelled	99.9	12	PDB header: transferase Chain: C: PDB Molecule: putative aminotransferase; PDBTitle: x-ray structure of the wlarg aminotransferase from campylobacter2 jejuni, internal plp-aldimine
92	d1pmma	Alignment	not modelled	99.9	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
93	d1wyua1	Alignment	not modelled	99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
94	c4xauG	Alignment	not modelled	99.9	18	PDB header: transferase Chain: G: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of ats13 from actinomadura melliaura
95	c4xk1A	Alignment	not modelled	99.9	10	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: crystal structure of a phosphoserine/phosphohydroxythreonine2 aminotransferase (psat) from pseudomonas aeruginosa with cofactor3 pyridoxal phosphate and bound glutamate
96	c4InjA	Alignment	not modelled	99.9	20	PDB header: lyase Chain: A: PDB Molecule: low-specificity l-threonine aldolase; PDBTitle: structure of escherichia coli threonine aldolase in unliganded form
97	c2okkA	Alignment	not modelled	99.9	13	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)
98	c5ijgb	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: cys/met metabolism pyridoxal-phosphate-dependent enzyme; PDBTitle: crystal structure of o-acetylhomoserine sulfhydrolase from brucella2 melitensis at 2.0 a resolution
99	d1h0ca	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathione synthase-like
100	c6c9eB	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
						PDB header: lyase Chain: D: PDB Molecule: methionine gamma-lyase;

101	c3aemD	Alignment	not modelled	99.9	17	PDBTitle: reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate
102	c3mc6C	Alignment	not modelled	99.9	16	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
103	c6enzA	Alignment	not modelled	99.9	13	PDB header: lyase Chain: A: PDB Molecule: acidic amino acid decarboxylase gadl1; PDBTitle: crystal structure of mouse gadl1
104	d1js3a	Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
105	c4e1oC	Alignment	not modelled	99.9	12	PDB header: lyase Chain: C: PDB Molecule: histidine decarboxylase; PDBTitle: human histidine decarboxylase complex with histidine methyl ester2 (hme)
106	c2dr1A	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
107	d1qz9a	Alignment	not modelled	99.9	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathione synthase-like
108	c3caIA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
109	c3f0hA	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
110	d1y4ia1	Alignment	not modelled	99.9	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathione synthase-like
111	c6jrlA	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 3,4-dihydroxyphenylacetaldehyde synthase; PDBTitle: crystal structure of drosophila alpha methylldopa-resistant protein/3,2 4-dihydroxyphenylacetaldehyde synthase
112	d3bc8a1	Alignment	not modelled	99.9	8	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
113	c6eeewC	Alignment	not modelled	99.9	13	PDB header: lyase Chain: C: PDB Molecule: aromatic-l-amino-acid decarboxylase; PDBTitle: crystal structure of catharanthus roseus tryptophan decarboxylase in2 complex with l-tryptophan
114	c2gqnB	Alignment	not modelled	99.9	17	PDB header: lyase Chain: B: PDB Molecule: cystathione beta-lyase; PDBTitle: cystathione beta-lyase (cbl) from escherichia coli in complex with 2-hydrazinocarbonylmethyl-2-nitro-benzamide
115	c2x3IA	Alignment	not modelled	99.9	14	PDB header: lyase Chain: A: PDB Molecule: orn/lys/arg decarboxylase family protein; PDBTitle: crystal structure of the orn_lys_arg decarboxylase family2 protein saro482 from methicillin-resistant staphylococcus3 aureus
116	d1cl1a	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathione synthase-like
117	c5uidC	Alignment	not modelled	99.9	16	PDB header: transferase Chain: C: PDB Molecule: aminotransferase tlmj; PDBTitle: the crystal structure of an aminotransferase tlmj from2 streptoalloteichus hindustanus
118	c4lw2C	Alignment	not modelled	99.9	19	PDB header: lyase Chain: C: PDB Molecule: cysteine sulfinate desulfinase; PDBTitle: structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration
119	d1t3ia	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathione synthase-like
120	c3ju7B	Alignment	not modelled	99.9	12	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