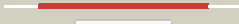



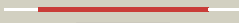



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3340_(metC)_3726298_3727647
Date	Thu Aug 8 16:20:55 BST 2019
Unique Job ID	b172a830758ce45f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ctza1	 Alignment		100.0	54	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
2	c3ndnC_	 Alignment		100.0	37	PDB header: lyase Chain: C: PDB Molecule: o-succinylhomoserine sulfhydrylase; PDBTitle: crystal structure of o-succinylhomoserine sulfhydrylase from 2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
3	c2cb1A_	 Alignment		100.0	38	PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
4	d1y4ia1	 Alignment		100.0	44	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
5	d1qgna_	 Alignment		100.0	35	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
6	d1e5ea_	 Alignment		100.0	37	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
7	c5dx5B_	 Alignment		100.0	41	PDB header: lyase Chain: B: PDB Molecule: methionine gamma-lyase; PDBTitle: crystal structure of methionine gamma-lyase from clostridium2 sporogenes
8	c4oc9N_	 Alignment		100.0	40	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
9	c1i41J_	 Alignment		100.0	35	PDB header: lyase Chain: J: PDB Molecule: cystathionine gamma-synthase; PDBTitle: cystathionine gamma-synthase in complex with the inhibitor2 appa
10	c2nmpC_	 Alignment		100.0	37	PDB header: lyase Chain: C: PDB Molecule: cystathionine gamma-lyase; PDBTitle: crystal structure of human cystathionine gamma lyase
11	d1n8pa_	 Alignment		100.0	37	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like

12	c5igB_	Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: cys/met metabolism pyridoxal-phosphate-dependent enzyme; PDBTitle: crystal structure of o-acetylhomoserine sulfhydrylase from brucella2 melitensis at 2.0 a resolution
13	c6cjbA_	Alignment		100.0	38	PDB header: lyase Chain: A: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from legionella2 pneumophila philadelphia 1 covalently bound to pyridoxal phosphate
14	c2gqnB_	Alignment		100.0	29	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-lyase; PDBTitle: cystathionine beta-lyase (cbl) from escherichia coli in complex with 2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
15	d1cl1a_	Alignment		100.0	29	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
16	c3aemD_	Alignment		100.0	37	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
17	c5x5hA_	Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: cystathionine beta-lyases/cystathionine gamma-synthases; PDBTitle: crystal structure of metb from corynebacterium glutamicum
18	d1csl1a_	Alignment		100.0	34	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
19	c1ibjC_	Alignment		100.0	37	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
20	d1libj_	Alignment		100.0	37	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
21	c3e6gA_	Alignment	not modelled	100.0	44	PDB header: lyase Chain: A: PDB Molecule: cystathionine gamma-lyase-like protein; PDBTitle: crystal structure of xometc, a cystathionine c-lyase-like2 protein from xanthomonas oryzae pv.oryzae
22	c4kamC_	Alignment	not modelled	100.0	93	PDB header: transferase Chain: C: PDB Molecule: o-acetylhomoserine sulfhydrylase metc; PDBTitle: x-ray crystal structure of o-acetylhomoserine sulfhydrylase metc from2 mycobacterium marinum atcc baa-535 / m
23	c3qi6B_	Alignment	not modelled	100.0	37	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
24	c4q31A_	Alignment	not modelled	100.0	35	PDB header: lyase Chain: A: PDB Molecule: cystathionine gamma lyase cale6; PDBTitle: the crystal structure of cystathionine gamma lyase (cale6) from2 micromonospora echinospora
25	c4l0oA_	Alignment	not modelled	100.0	43	PDB header: lyase Chain: A: PDB Molecule: cystathionine gamma-synthase; PDBTitle: structure determination of cystathionine gamma-synthase from2 helicobacter pylori
26	d1gc0a_	Alignment	not modelled	100.0	41	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
27	c5tt2D_	Alignment	not modelled	100.0	37	PDB header: lyase Chain: D: PDB Molecule: cystathionine gamma-lyase; PDBTitle: inactive conformation of engineered human cystathionine gamma lyase2 (e59n, r119l, e339v) to depleting methionine
28	c3ri6A_	Alignment	not modelled	100.0	42	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 wolinella3 succinogenes
29	c4j8A_	Alignment	not modelled	100.0	18	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
30	d1pffa_	Alignment	not modelled	100.0	37	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
31	c3ht4B_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: aluminum resistance protein; PDBTitle: crystal structure of the q81a77_baccr protein from bacillus cereus.2 northeast structural genomics consortium target bcr213
32	c5w70B_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: l-glutamine:2-deoxy-scylo-inosose aminotransferase; PDBTitle: x-ray structure of rbmb from streptomyces ribosidificus
33	c3hvyC_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-lyase family protein, ynbB b.subtilis PDBTitle: crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution
34	c3fd0B_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: putative cystathionine beta-lyase involved in aluminum PDBTitle: crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
35	c2po3B_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
36	c5k8bA_	Alignment	not modelled	100.0	15	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
37	c3bcxA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
38	c2c7tA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: glutamine-2-deoxy-scylo-inosose aminotransferase; PDBTitle: crystal structure of the plp-bound form of btrr, a dual functional2 aminotransferase involved in butirosin biosynthesis.
39	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
40	d1b9ha_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
41	c2r0tA_	Alignment	not modelled	100.0	14	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
42	c3caiA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
43	c5z0yA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystallization and structure determination of cytoplasm serine2 hydroxymethyltransferase (shmt) from pichia pastoris
44	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
45	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
46	c5utsC_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: C: PDB Molecule: c-s lyase egt2; PDBTitle: carbon sulfoxide lyase, egt2 in the ergothioneine biosynthesis pathway
47	d1o69a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
48	d1mdoa_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
49	d1qz9a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
50	c5uidC_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: aminotransferase tlmj; PDBTitle: the crystal structure of an aminotransferase tlmj from2 streptoalloteichus hindustanus
51	c3gwpA_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A: PDB Molecule: carbon-sulfur lyase involved in aluminum resistance; PDBTitle: crystal structure of carbon-sulfur lyase involved in aluminum2 resistance (yp_878183.1) from clostridium novyi nt at 2.90 a3 resolution

52	c3uwcA	Alignment	not modelled	100.0	15	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
53	c3ju7B	Alignment	not modelled	100.0	14	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
54	c3e9kA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
55	c3dr4B	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
56	c3frkB	Alignment	not modelled	100.0	15	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
57	c4ytjC	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: cals13; PDBTitle: crystal structure of sugar aminotransferase cals13 from micromonospora2 echinospora
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	c2hzpA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
60	c4xauG	Alignment	not modelled	100.0	16	PDB header: transferase Chain: G: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of ats13 from actinomadura melliaura
61	c3wy7D	Alignment	not modelled	100.0	20	PDB header: transferase Chain: D: PDB Molecule: 8-amino-7-oxononanoate synthase; PDBTitle: crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
62	c2w8wA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
63	c4j5uB	Alignment	not modelled	100.0	16	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
64	c6ewqA	Alignment	not modelled	100.0	16	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
65	d1jf9a	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
66	c3hqtB	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
67	c5u20C	Alignment	not modelled	100.0	12	PDB header: transferase Chain: C: PDB Molecule: putative aminotransferase; PDBTitle: x-ray structure of the wlarg aminotransferase from campylobacter2 jejuni, internal plp-aldimine
68	c3wgcB	Alignment	not modelled	100.0	20	PDB header: lyase Chain: B: PDB Molecule: l-allo-threonine aldolase; PDBTitle: aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
69	c3nnkC	Alignment	not modelled	100.0	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
70	c3vaxA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein dnda; PDBTitle: crystal structure of dnda from streptomyces lividans
71	c3hbxB	Alignment	not modelled	100.0	16	PDB header: lyase Chain: B: PDB Molecule: glutamate decarboxylase 1; PDBTitle: crystal structure of gad1 from arabidopsis thaliana
72	c4bhel	Alignment	not modelled	100.0	17	PDB header: transferase Chain: I: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: methanococcus jannaschii serine hydroxymethyltransferase2 in complex with plp
73	d2fnua1	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
74	c4q76B	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase 2, chloroplastic; PDBTitle: crystal structure of nfs2 c384s mutant, the plastidial cysteine2 desulfurase from arabidopsis thaliana
75	c4q6rB	Alignment	not modelled	100.0	16	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
76	c3mafB	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase;

						PDBTitle: crystal structure of stspl (asymmetric form)
77	c6c9eB	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
78	c3n0IA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
79	c6hrhA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 5-aminolevulinate synthase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
80	c4wxfC	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of l-serine hydroxymethyltransferase in complex with2 glycine
81	c2hdyA	Alignment	not modelled	100.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
82	d1m6sa	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
83	c4lnjA	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A: PDB Molecule: low-specificity l-threonine aldolase; PDBTitle: structure of escherichia coli threonine aldolase in unliganded form
84	c3ecdC	Alignment	not modelled	100.0	19	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase 2; PDBTitle: crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
85	d1wyua1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
86	c4lc3B	Alignment	not modelled	100.0	12	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
87	d1c4ka2	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
88	d1bs0a	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
89	c4w91C	Alignment	not modelled	100.0	16	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp
90	c5zsqA	Alignment	not modelled	100.0	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: nifs from hydrogenomonas thermophila, soaked with l-cysteine for 4 min
91	d1vjoa	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
92	d2bwna1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
93	d1k1la	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
94	c5vc2A	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of a serine hydroxymethyltransferase from2 helicobacter pylori
95	c5j8qA	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase sufs; PDBTitle: crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis
96	c3lwsF	Alignment	not modelled	100.0	18	PDB header: lyase Chain: F: PDB Molecule: aromatic amino acid beta-eliminating lyase/threonine PDBTitle: crystal structure of putative aromatic amino acid beta-eliminating2 lyase/threonine aldolase. (yp_001813866.1) from exiguobacterium sp.3 255-15 at 2.00 a resolution
97	c3a2bA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
98	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
99	c4e1oC	Alignment	not modelled	100.0	16	PDB header: lyase Chain: C: PDB Molecule: histidine decarboxylase; PDBTitle: human histidine decarboxylase complex with histidine methyl ester2 (hme)
100	c3madA	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (symmetric form)
						PDB header: lyase Chain: B: PDB Molecule: burkholderia pseudomallei sphingosine-1-

101	c5k1rB_	Alignment	not modelled	100.0	19	phosphate lyase PDBTitle: structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021
102	c5j90A_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: pvdn; PDBTitle: crystal structure of pvdn from pseudomonas aeruginosa
103	c4n0wA_	Alignment	not modelled	100.0	18	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
104	d1js3a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
105	d1t3ja_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
106	c2dkjB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
107	c4lw2C_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: C: PDB Molecule: cysteine sulfinic acid desulfurase; PDBTitle: structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration
108	c5xtaA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinic acid synthase, mitochondrial; PDBTitle: structure of asymmetric apo/holo alas dimer from s. cerevisiae
109	d1dfoa_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
110	c3pj0D_	Alignment	not modelled	100.0	18	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
111	c5gp4C_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: C: PDB Molecule: glutamate decarboxylase; PDBTitle: lactobacillus brevis cgmc 1306 glutamate decarboxylase
112	c5jayB_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: 8-amino-7-oxononanoate synthase; PDBTitle: crystal structure of an 8-amino-7-oxononanoate synthase from2 burkholderia xenovorans
113	c3mc6C_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
114	d2v1pa1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
115	c4eb5B_	Alignment	not modelled	100.0	17	PDB header: transferase/metal binding protein Chain: B: PDB Molecule: probable cysteine desulfurase 2; PDBTitle: a. fulgidus iscs-iscu complex structure
116	c2jisA_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
117	d1tpla_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
118	c4xk1A_	Alignment	not modelled	100.0	13	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
119	c4obuG_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: G: PDB Molecule: pyridoxal-dependent decarboxylase domain protein; PDBTitle: ruminococcus gnavus tryptophan decarboxylase rumgna_01526 (apo)
120	c3f0hA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution