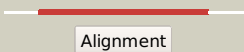

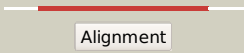

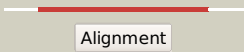

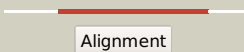

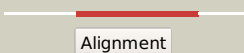

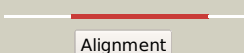

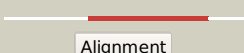





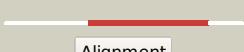

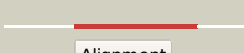










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2531c_(-)_2854948_2857791
Date	Wed Aug 7 12:50:16 BST 2019
Unique Job ID	066272529cb3fa7d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vycA_	 Alignment		100.0	24	PDB header: lyase Chain: A: PDB Molecule: biodegradative arginine decarboxylase; PDBTitle: crystal structure of acid induced arginine decarboxylase2 from e. coli
2	c5fkzE_	 Alignment		100.0	25	PDB header: lyase Chain: E: PDB Molecule: lysine decarboxylase, constitutive; PDBTitle: structure of e.coli constitutive lysine decarboxylase
3	c3n75E_	 Alignment		100.0	25	PDB header: lyase Chain: E: PDB Molecule: lysine decarboxylase, inducible; PDBTitle: x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldci
4	c1c4kA_	 Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: protein (ornithine decarboxylase); PDBTitle: ornithine decarboxylase mutant (gly121tyr)
5	d1c4ka2	 Alignment		100.0	25	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
6	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
7	d1rv3a_	 Alignment		100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
8	d1bj4a_	 Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
9	c6cd1A_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of medicago truncatula serine2 hydroxymethyltransferase 3 (mtshmt3), complexes with reaction3 intermediates
10	d1ejja_	 Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
11	d2z67a1	 Alignment		100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like

12	d2a7va1	Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
13	c2a7vA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: human mitochondrial serine hydroxymethyltransferase 2
14	c4o6zC_	Alignment		100.0	18	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase with covalently2 bound plp schiff-base from plasmodium falciparum
15	c3h7fB_	Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase 1; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
16	c5z0yA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystallization and structure determination of cytoplasm serine2 hydroxymethyltransferase (shmt) from pichia pastoris
17	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
18	d3bc8a1	Alignment		100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
19	c3ecdC_	Alignment		100.0	18	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase 2; PDBTitle: crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
20	c4wxfC_	Alignment		100.0	18	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of l-serine hydroxymethyltransferase in complex with2 glycine
21	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
22	c3n0lA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
23	c5vc2A_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of a serine hydroxymethyltransferase from2 helicobacter pylori
24	d1dfoa_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
25	c4j5uB_	Alignment	not modelled	99.9	19	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
26	c4bhel_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: I: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: methanococcus jannaschii serine hydroxymethyltransferase2 in complex with plp
27	d1kl1a_	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
28	c2dkjB_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine

						hydroxymethyltransferase
29	d2e7ja1	Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
30	c4n0wA_	Alignment	not modelled	99.9	20	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
31	c6hrhA_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 5-aminolevulinatase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinatase synthase,2 alas2
32	c5k1rB_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: B: PDB Molecule: burkholderia pseudomallei sphingosine-1-phosphate lyase PDBTitle: structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021
33	c3madA_	Alignment	not modelled	99.9	17	PDB header: lyase Chain: A: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (symmetric form)
34	c3mafB_	Alignment	not modelled	99.9	16	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
35	c3mc6C_	Alignment	not modelled	99.9	12	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
36	d1vjoa_	Alignment	not modelled	99.9	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
37	c5xtxA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinatase, mitochondrial; PDBTitle: structure of asymmetric apo/holo alas dimer from s. cerevisiae
38	d1wyua1	Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
39	d1wyub1	Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
40	c3f9tB_	Alignment	not modelled	99.9	14	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
41	c5o5cD_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: D: PDB Molecule: putative decarboxylase involved in desferrioxamine biosynthesis2 PDBTitle: the crystal structure of dfoj, the desferrioxamine biosynthetic2 pathway lysine decarboxylase from the fire blight disease pathogen3 erwinia amylovora
42	c6ewqA_	Alignment	not modelled	99.9	15	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
43	d1js3a_	Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
44	c4ritB_	Alignment	not modelled	99.9	14	PDB header: lyase Chain: B: PDB Molecule: pyridoxal-dependent decarboxylase; PDBTitle: the yellow crystal structure of pyridoxal-dependent decarboxylase from2 sphaerobacter thermophilus dsm 20745
45	c4obuG_	Alignment	not modelled	99.9	16	PDB header: lyase Chain: G: PDB Molecule: pyridoxal-dependent decarboxylase domain protein; PDBTitle: ruminococcus onavus tryptophan decarboxylase rumgna_01526 (apo)
46	d1m6sa_	Alignment	not modelled	99.9	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
47	c2jisA_	Alignment	not modelled	99.9	17	PDB header: lyase Chain: A: PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
48	c3nnkC_	Alignment	not modelled	99.9	16	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
49	c2z9wA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
50	c2w8wA_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
51	c3bcxA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
52	d1h0ca_	Alignment	not modelled	99.9	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

						Family: Cystathionine synthase-like
53	d1o69a_	Alignment	not modelled	99.8	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
54	c2hzpA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
55	c5utsC_	Alignment	not modelled	99.8	10	PDB header: lyase Chain: C: PDB Molecule: c-s lyase egt2; PDBTitle: carbon sulfoxide lyase, egt2 in the ergothioneine biosynthesis pathway
56	c4e1oC_	Alignment	not modelled	99.8	16	PDB header: lyase Chain: C: PDB Molecule: histidine decarboxylase; PDBTitle: human histidine decarboxylase complex with histidine methyl ester2 (hme)
57	c6jrlA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 3,4-dihydroxyphenylacetaldehyde synthase; PDBTitle: crystal structure of drosophila alpha methyl dopa-resistant protein/3,2 4-dihydroxyphenylacetaldehyde synthase
58	c3e9kA_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
59	c6eewC_	Alignment	not modelled	99.8	19	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
60	c3l8aB_	Alignment	not modelled	99.8	17	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
61	c3hbxB_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: B: PDB Molecule: glutamate decarboxylase 1; PDBTitle: crystal structure of gad1 from arabidopsis thaliana
62	c2po3B_	Alignment	not modelled	99.8	12	PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
63	c4qgrA_	Alignment	not modelled	99.8	13	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
64	c6eeqA_	Alignment	not modelled	99.8	16	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxyphenylacetaldehyde synthase; PDBTitle: crystal structure of rhodiola rosea 4-hydroxyphenylacetaldehyde2 synthase
65	c3islA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
66	d1tpla_	Alignment	not modelled	99.8	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
67	c5k8bA_	Alignment	not modelled	99.8	14	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
68	c6enzA_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: A: PDB Molecule: acidic amino acid decarboxylase gadl1; PDBTitle: crystal structure of mouse gadl1
69	d1mdoa_	Alignment	not modelled	99.8	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
70	c5gp4C_	Alignment	not modelled	99.8	17	PDB header: lyase Chain: C: PDB Molecule: glutamate decarboxylase; PDBTitle: lactobacillus brevis cgmcc 1306 glutamate decarboxylase
71	c3a2bA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
72	c3wgcB_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: B: PDB Molecule: l-allo-threonine aldolase; PDBTitle: aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
73	d2v1pa1	Alignment	not modelled	99.8	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
74	d1v72a1	Alignment	not modelled	99.8	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
75	c3hqtB_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
76	c2r0tA_	Alignment	not modelled	99.8	19	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
77	d1fc4a_	Alignment	not modelled	99.8	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
						PDB header: lyase

78	c4lnjA_	Alignment	not modelled	99.8	16	Chain: A: PDB Molecule: low-specificity l-threonine aldolase; PDBTitle: structure of escherichia coli threonine aldolase in unliganded form
79	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
80	d2ch1a1	Alignment	not modelled	99.8	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
81	c2ogeC_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: C: PDB Molecule: transaminase; PDBTitle: x-ray structure of s. venezuelae desv in its internal2 aldimine form
82	c3zrrB_	Alignment	not modelled	99.8	16	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
83	c2dr1A_	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
84	c3tqxA_	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
85	d2bwna1	Alignment	not modelled	99.8	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
86	c3wy7D_	Alignment	not modelled	99.8	18	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
87	c3uwcA_	Alignment	not modelled	99.8	16	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
88	d1bs0a_	Alignment	not modelled	99.8	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
89	c3nysA_	Alignment	not modelled	99.8	17	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
90	c2c7tA_	Alignment	not modelled	99.8	21	PDB header: transferase Chain: A: PDB Molecule: glutamine-2-deoxy-scylo-inosose aminotransferase; PDBTitle: crystal structure of the plp-bound form of bttr, a dual functional2 aminotransferase involved in butirosin biosynthesis.
91	c3w1hB_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) selenium transferase; PDBTitle: crystal structure of the selenocysteine synthase sela from aquifex2 aeolicus
92	c3ffrA_	Alignment	not modelled	99.8	12	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
93	c5w70B_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: B: PDB Molecule: l-glutamine:2-deoxy-scylo-inosose aminotransferase; PDBTitle: x-ray structure of rbmb from streptomyces ribosidificus
94	d1c7na_	Alignment	not modelled	99.8	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
95	c2huuA_	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate aminotransferase2 in complex with alanine
96	c6eeiA_	Alignment	not modelled	99.8	20	PDB header: lyase Chain: A: PDB Molecule: tyrosine decarboxylase 1; PDBTitle: crystal structure of arabidopsis thaliana phenylacetaldehyde synthase2 in complex with l-phenylalanine
97	d1svva_	Alignment	not modelled	99.8	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
98	d2aeva1	Alignment	not modelled	99.8	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SelA-like
99	c3kaxB_	Alignment	not modelled	99.8	17	PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
100	c3b1dD_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: D: PDB Molecule: betac-s lyase; PDBTitle: crystal structure of betac-s lyase from streptococcus anginosus in2 complex with l-serine: external aldimine form
101	c3frkB_	Alignment	not modelled	99.8	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
102	c3ke3A_	Alignment	not modelled	99.8	14	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
103	d1c4ka3	Alignment	not modelled	99.8	19	Fold: Ornithine decarboxylase C-terminal domain Superfamily: Ornithine decarboxylase C-terminal domain Family: Ornithine decarboxylase C-terminal domain
104	c5jayB_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: B: PDB Molecule: 8-amino-7-oxononoate synthase; PDBTitle: crystal structure of an 8-amino-7-oxononoate synthase from2 burkholderia xenovorans
105	c3pj0D_	Alignment	not modelled	99.8	16	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
106	c3f0hA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
107	c3dr4B_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
108	c4q76B_	Alignment	not modelled	99.8	13	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
109	c6eemB_	Alignment	not modelled	99.8	18	PDB header: lyase Chain: B: PDB Molecule: tyrosine/dopa decarboxylase; PDBTitle: crystal structure of papaver somniferum tyrosine decarboxylase in2 complex with l-tyrosine
110	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)
111	c3ju7B_	Alignment	not modelled	99.8	11	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
112	c2cb1A_	Alignment	not modelled	99.8	19	PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
113	d1qgna_	Alignment	not modelled	99.7	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
114	d1c7ga_	Alignment	not modelled	99.7	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
115	d1jf9a_	Alignment	not modelled	99.7	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
116	c3op7A_	Alignment	not modelled	99.7	16	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
117	c1d2fB_	Alignment	not modelled	99.7	14	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
118	d1b9ha_	Alignment	not modelled	99.7	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
119	c4ytjC_	Alignment	not modelled	99.7	12	PDB header: transferase Chain: C: PDB Molecule: cals13; PDBTitle: crystal structure of sugar aminotransferase cals13 from micromonospora2 echinospora
120	c5vyeA_	Alignment	not modelled	99.7	15	PDB header: lyase Chain: A: PDB Molecule: l-threonine aldolase; PDBTitle: crystal structure of l-threonine aldolase from pseudomonas putida