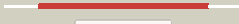



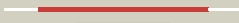



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0884c_(serC)_981427_982557
Date	Fri Jul 26 01:50:47 BST 2019
Unique Job ID	d84e05ed74f4d267

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fyfB_	 Alignment		100.0	99	PDB header: transferase Chain: B: PDB Molecule: phosphoserine aminotransferase; PDBTitle: structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
2	d2c0ra1	 Alignment		100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
3	c4xk1A_	 Alignment		100.0	20	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
4	d1w23a_	 Alignment		100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
5	c3m5uA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
6	c6czyA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase 1, chloroplastic; PDBTitle: crystal structure of arabidopsis thaliana phosphoserine2 aminotransferase isoform 1 (atpsat1) in complex with pyridoxamine-5'-3 phosphate (pmp)
7	d1bjna_	 Alignment		100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
8	c5yb0I_	 Alignment		100.0	21	PDB header: transferase Chain: I: PDB Molecule: phosphoserine aminotransferase; PDBTitle: crystal structure of wild type phosphoserine aminotransferase (psat)2 from e. histolytica
9	c5f8vH_	 Alignment		100.0	19	PDB header: transferase Chain: H: PDB Molecule: aminotransferase, class v family protein; PDBTitle: crystal structure of plp bound phosphoserine aminotransferase (psat)2 from trichomonas vaginalis
10	c3e77A_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: human phosphoserine aminotransferase in complex with plp
11	c3qm2A_	 Alignment		100.0	21	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

12	c3ffrA_	Alignment		100.0	22	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
13	c3nnkC_	Alignment		100.0	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
14	c5yiiA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: crystal structure of 45 amino acid deleted from n-terminal of2 phosphoserine aminotransferase (psat) of entamoeba histolytica
15	d1vjoa_	Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
16	c3islA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
17	d2ch1a1	Alignment		100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
18	d1h0ca_	Alignment		100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
19	c3f0hA_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
20	c2huuA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate aminotransferase2 in complex with alanine
21	c2z9wA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
22	c3zrrB_	Alignment	not modelled	100.0	20	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 sulfobolus3 solfataricus
23	c2dr1A_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
24	d1iuga_	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
25	c2yrrA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
26	d2bkwa1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
27	d1m32a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
28	c5utsC_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: C: PDB Molecule: c-s lyase egt2; PDBTitle: carbon sulfoxide lyase, egt2 in the ergothioneine biosynthesis pathway PDB header: lyase

29	c4lw2C_	Alignment	not modelled	100.0	17	Chain: C: PDB Molecule: cysteine sulfinate desulfurase; PDBTitle: structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration
30	d1qz9a_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
31	c6c9eB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
32	c4q76B_	Alignment	not modelled	100.0	14	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
33	c3caiA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
34	d1jf9a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
35	c3e9kA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
36	d1t3ia_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
37	c4w91C_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp
38	c5b87B_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of a cysteine desulfurase from thermococcus2 onnurineus na1 in complex with alanine at 2.3 angstrom resolution
39	c5j8qA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase sufs; PDBTitle: crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis
40	c5vprA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from elizabethkingia2 anophelis with covalently bound pyridoxal phosphate
41	c2hzpA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
42	c5j90A_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: pvdn; PDBTitle: crystal structure of pvdn from pseudomonas aeruginosa
43	c3vaxA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein dnda; PDBTitle: crystal structure of dnda from streptomyces lividans
44	c3ke3A_	Alignment	not modelled	100.0	16	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
45	d1elua_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
46	c5zsqA_	Alignment	not modelled	100.0	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: nifs from hydrogenimonas thermophila, soaked with l-cysteine for 4 min
47	c5kz5M_	Alignment	not modelled	100.0	16	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
48	c5k1rB_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: B: PDB Molecule: burkholderia pseudomallei sphingosine-1-phosphate lyase PDBTitle: structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021
49	c4q6rB_	Alignment	not modelled	100.0	13	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
50	c3f9tB_	Alignment	not modelled	100.0	17	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
51	c3mafB_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
52	c4ixoB_	Alignment	not modelled	100.0	12	PDB header: protein binding Chain: B: PDB Molecule: nifs-like protein; PDBTitle: x-ray structure of nifs-like protein from rickettsia africae esf-5
						Fold: PLP-dependent transferase-like

53	d1js3a_	Alignment	not modelled	100.0	15	Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
54	c4eb5B_	Alignment	not modelled	100.0	15	PDB header: transferase/metal binding protein Chain: B: PDB Molecule: probable cysteine desulfurase 2; PDBTitle: a. fulgidus iscs-iscu complex structure
55	c3mc6C_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
56	c4e1oC_	Alignment	not modelled	100.0	11	PDB header: lyase Chain: C: PDB Molecule: histidine decarboxylase; PDBTitle: human histidine decarboxylase complex with histidine methyl ester2 (hme)
57	c6enzA_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: acidic amino acid decarboxylase gad11; PDBTitle: crystal structure of mouse gad11
58	c4isyB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of iscs from mycobacterium tuberculosis
59	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
60	d1eg5a_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
61	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
62	c5usrG_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: G: PDB Molecule: cysteine desulfurase, mitochondrial; PDBTitle: crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
63	c4obuG_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: G: PDB Molecule: pyridoxal-dependent decarboxylase domain protein; PDBTitle: ruminococcus gnavus tryptophan decarboxylase rumgna_01526 (apo)
64	c5gp4C_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: C: PDB Molecule: glutamate decarboxylase; PDBTitle: lactobacillus brevis cgmc 1306 glutamate decarboxylase
65	c3madA_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of tspl (symmetric form)
66	d1pmma_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
67	c6eeqA_	Alignment	not modelled	100.0	11	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxyphenylacetaldehyde synthase; PDBTitle: crystal structure of rhodiola rosea 4-hydroxyphenylacetaldehyde2 synthase
68	c2hdyA_	Alignment	not modelled	100.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
69	d1p3wa_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
70	c5o5cD_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: D: PDB Molecule: putative decarboxylase involved in desferrioxamine PDBTitle: the crystal structure of dfoj, the desferrioxamine biosynthetic2 pathway lysine decarboxylase from the fire blight disease pathogen3 erwinia amylovora
71	c5usrC_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: C: PDB Molecule: cysteine desulfurase, mitochondrial; PDBTitle: crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
72	c6eeiA_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: A: PDB Molecule: tyrosine decarboxylase 1; PDBTitle: crystal structure of arabidopsis thaliana phenylacetaldehyde synthase2 in complex with l-phenylalanine
73	d1wsta1	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
74	c2jisA_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
75	c3lvmB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
76	c3eucB_	Alignment	not modelled	100.0	14	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
77	c4wbtA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: probable histidinol-phosphate aminotransferase; PDBTitle: crystal structure of histidinol-phosphate aminotransferase from2 sinorhizobium meliloti in complex with pyridoxal-5'-phosphate
78	c5wt2A_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase iscs; PDBTitle: nifs from helicobacter pylori

79	d1x0ma1	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
80	c3hdoB_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
81	c2okkA_	Alignment	not modelled	100.0	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)
82	d1wyua1	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
83	c3cbfA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
84	c3h14A_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
85	c3fkdC_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: C: PDB Molecule: l-threonine-o-3-phosphate decarboxylase; PDBTitle: the crystal structure of l-threonine-o-3-phosphate decarboxylase from2 porphyromonas gingivalis
86	c6jrlA_	Alignment	not modelled	100.0	12	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
87	c5uidC_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: C: PDB Molecule: aminotransferase tlmj; PDBTitle: the crystal structure of an aminotransferase tlmj from2 streptoalloeichus hindustanus
88	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
89	c5yvhA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
90	d2fnua1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
91	c3ffhA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
92	c6eemB_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: B: PDB Molecule: tyrosine/dopa decarboxylase; PDBTitle: crystal structure of papaver somniferum tyrosine decarboxylase in2 complex with l-tyrosine
93	d1bw0a_	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
94	c3jtxB_	Alignment	not modelled	100.0	9	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
95	c4j8lA_	Alignment	not modelled	100.0	12	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
96	c3eibB_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
97	c3getA_	Alignment	not modelled	100.0	11	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
98	c3ly1C_	Alignment	not modelled	100.0	11	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
99	d1b9ha_	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
100	c3l8aB_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
101	c3b1dD_	Alignment	not modelled	100.0	14	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
102	c3bcxA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
103	c3d7zB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: putative pyridoxal 5'-phosphate-dependent c-s lyase;

103	c3uzzb_	Alignment	not modelled	100.0	14	PDBTitle: crystal structure of a putative plp-dependent aminotransferase2 (lbul_1103) from lactobacillus delbrueckii subsp. at 1.61 a3 resolution
104	c3uwca_	Alignment	not modelled	100.0	13	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
105	c3ftbA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate aminotransferase2 from clostridium acetobutylicum
106	c4f10A_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: aminotransferase ald1; PDBTitle: crystal structure of ald1 from arabidopsis thaliana
107	c3op7A_	Alignment	not modelled	100.0	11	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
108	c3qguB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: l,l-diaminopimelate aminotransferase from chalmymdomonas reinhardtii
109	c3b46B_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
110	d1w71a_	Alignment	not modelled	100.0	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
111	c5jayB_	Alignment	not modelled	100.0	14	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
112	c3dr4B_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
113	c5dj3B_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: plp-dependent l-arginine hydroxylase mppp; PDBTitle: structure of the plp-dependent l-arginine hydroxylase mppp with d-2 arginine bound
114	d1c4ka2	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
115	d2r5ea1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
116	d1j32a_	Alignment	not modelled	100.0	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
117	d1mdoa_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
118	c2ogeC_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: transaminase; PDBTitle: x-ray structure of s. venezuelae desv in its internal2 aldimine form
119	d1v2da_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
120	c6eewC_	Alignment	not modelled	100.0	15	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