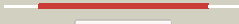







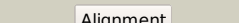

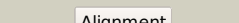

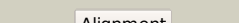











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1832_(gcvB)_2075884_2078709
Date	Fri Aug 2 13:30:44 BST 2019
Unique Job ID	42077ac13c70cedf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4lhdB_	 Alignment		100.0	55	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine dehydrogenase [decarboxylating]; PDBTitle: crystal structure of synechocystis sp. pcc 6803 glycine decarboxylase2 (p-protein), holo form with pyridoxal-5'-phosphate and glycine,3 closed flexible loop
2	d1wyub1	 Alignment		100.0	42	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
3	d1wyua1	 Alignment		100.0	37	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
4	c3madA_	 Alignment		100.0	15	PDB header: lyase Chain: A: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (symmetric form)
5	c4q6rB_	 Alignment		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
6	c5k1rB_	 Alignment		100.0	16	PDB header: lyase Chain: B: PDB Molecule: burkholderia pseudomallei sphingosine-1-phosphate lyase PDBTitle: structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021
7	d3bc8a1	 Alignment		100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
8	d1ax4a_	 Alignment		100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
9	c3hl2D_	 Alignment		100.0	17	PDB header: transferase Chain: D: PDB Molecule: o-phosphoseryl-trna(sec) selenium transferase; PDBTitle: the crystal structure of the human sepsecs-trnasec complex
10	d1pmma_	 Alignment		100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
11	c3mafB_	 Alignment		100.0	15	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)

12	c3hbxB_	Alignment		100.0	13	PDB header: lyase Chain: B; PDB Molecule: glutamate decarboxylase 1; PDBTitle: crystal structure of gad1 from arabidopsis thaliana
13	c3f9tB_	Alignment		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
14	c3mc6C_	Alignment		100.0	15	PDB header: lyase Chain: C; PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
15	c4ritB_	Alignment		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
16	c5gp4C_	Alignment		100.0	14	PDB header: lyase Chain: C; PDB Molecule: glutamate decarboxylase; PDBTitle: lactobacillus brevis cgmc 1306 glutamate decarboxylase
17	d1c7ga_	Alignment		100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
18	c4obuG_	Alignment		100.0	13	PDB header: lyase Chain: G; PDB Molecule: pyridoxal-dependent decarboxylase domain protein; PDBTitle: ruminococcus gnavus tryptophan decarboxylase rumgna_01526 (apo)
19	c4e1oC_	Alignment		100.0	14	PDB header: lyase Chain: C; PDB Molecule: histidine decarboxylase; PDBTitle: human histidine decarboxylase complex with histidine methyl ester2 (hme)
20	c4bhel_	Alignment		100.0	19	PDB header: transferase Chain: I; PDB Molecule: serine hydroxymethyltransferase; PDBTitle: methanococcus jannaschii serine hydroxymethyl-transferase2 in complex with plp
21	c2jisA_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A; PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
22	d1js3a_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
23	d1ejia_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
24	d1bj4a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
25	c6enzA_	Alignment	not modelled	100.0	11	PDB header: lyase Chain: A; PDB Molecule: acidic amino acid decarboxylase gad11; PDBTitle: crystal structure of mouse gadl1
26	d2z67a1	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
27	c2hzpA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A; PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
28	c5o5cD_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: D; PDB Molecule: putative decarboxylase involved in desferrioxamine biosynthesis PDBTitle: the crystal structure of dfoj, the desferrioxamine biosynthetic2 pathway lysine decarboxylase from the fire blight disease pathogen3 erwinia amylovora

29	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
30	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
31	c6eewC	Alignment	not modelled	100.0	11	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
32	c6jrlA	Alignment	not modelled	100.0	13	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
33	c2okkA	Alignment	not modelled	100.0	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)
34	c4w8iB	Alignment	not modelled	99.9	16	PDB header: lyase Chain: B: PDB Molecule: probable sphingosine-1-phosphate lyase; PDBTitle: crystal structure of lpspl/pp2128, legionella pneumophila2 sphingosine-1 phosphate lyase
35	c6eeqA	Alignment	not modelled	99.9	12	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxyphenylacetaldehyde synthase; PDBTitle: crystal structure of rhodiola rosea 4-hydroxyphenylacetaldehyde2 synthase
36	c4n0wA	Alignment	not modelled	99.9	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
37	d1rv3a	Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
38	c6hrhA	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 5-aminolevulinate synthase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
39	c6c9eB	Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
40	d2v1pa1	Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
41	c3ecdC	Alignment	not modelled	99.9	19	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase 2; PDBTitle: crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
42	c6eemB	Alignment	not modelled	99.9	14	PDB header: lyase Chain: B: PDB Molecule: tyrosine/dopa decarboxylase; PDBTitle: crystal structure of papaver somniferum tyrosine decarboxylase in2 complex with l-tyrosine
43	c4w91C	Alignment	not modelled	99.9	18	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp
44	c2qmaB	Alignment	not modelled	99.9	14	PDB header: transferase Chain: B: PDB Molecule: diaminobutyrate-pyruvate transaminase and l-2,4- PDBTitle: crystal structure of glutamate decarboxylase domain of2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus
45	c4o6zC	Alignment	not modelled	99.9	13	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase with covalently2 bound plp schiff-base from plasmodium falciparum
46	d1jf9a	Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
47	c4wxfC	Alignment	not modelled	99.9	17	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of l-serine hydroxymethyltransferase in complex with2 glycine
48	c3k40B	Alignment	not modelled	99.9	12	PDB header: lyase Chain: B: PDB Molecule: aromatic-l-amino-acid decarboxylase; PDBTitle: crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
49	d1dfoa	Alignment	not modelled	99.9	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
50	c5z0yA	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystallization and structure determination of cytoplasm serine2 hydroxymethyltransferase (shmt) from pichia pastoris
51	c5j8qA	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase sufs; PDBTitle: crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis
52	d1c4ka2	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
53	c6cd1A	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of medicago truncatula serine2

					hydroxymethyltransferase 3 (mtshmt3), complexes with reaction3 intermediates
54	c5vc2A_	Alignment	not modelled	99.9	15 PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of a serine hydroxymethyltransferase from2 helicobacter pylori
55	c2dkjB_	Alignment	not modelled	99.9	19 PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
56	c4q76B_	Alignment	not modelled	99.9	15 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
57	d1kl1a_	Alignment	not modelled	99.9	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
58	d1qz9a_	Alignment	not modelled	99.9	18 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
59	c5txtA_	Alignment	not modelled	99.9	19 PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinate synthase, mitochondrial; PDBTitle: structure of asymmetric apo/holo alas dimer from s. cerevisiae
60	c4lw2C_	Alignment	not modelled	99.9	17 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
61	d1tpla_	Alignment	not modelled	99.9	13 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
62	c3caiA_	Alignment	not modelled	99.9	16 PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
63	d1vjoa_	Alignment	not modelled	99.9	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
64	d1t3ia_	Alignment	not modelled	99.9	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
65	c3is1A_	Alignment	not modelled	99.9	13 PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
66	c3n01A_	Alignment	not modelled	99.9	17 PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
67	c5vprA_	Alignment	not modelled	99.9	14 PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from elizabethkingia2 anophelis with covalently bound pyridoxal phosphate
68	d1bs0a_	Alignment	not modelled	99.9	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
69	c6erkB_	Alignment	not modelled	99.9	14 PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of diamino-pelargonic acid aminotransferase from2 psychrobacter cryohalolentis
70	c5b87B_	Alignment	not modelled	99.9	19 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
71	c5i90A_	Alignment	not modelled	99.9	15 PDB header: transferase Chain: A: PDB Molecule: pvdn; PDBTitle: crystal structure of pvdn from pseudomonas aeruginosa
72	c3hmuA_	Alignment	not modelled	99.9	16 PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of a class iii aminotransferase from silicibacter2 pomeroyi
73	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
74	d2bwna1	Alignment	not modelled	99.9	16 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
75	d1o69a_	Alignment	not modelled	99.9	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
76	c5utsC_	Alignment	not modelled	99.9	14 PDB header: lyase Chain: C: PDB Molecule: c-s lyase egt2; PDBTitle: carbon sulfoxide lyase, egt2 in the ergothioneine biosynthesis pathway
77	d2ch1a1	Alignment	not modelled	99.9	13 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
78	c6fyqA_	Alignment	not modelled	99.9	18 PDB header: transferase Chain: A: PDB Molecule: amine transaminase; PDBTitle: the crystal structure of a new transaminase from the

					marine bacterium2 virgibacillus
79	c2w8wA_	Alignment	not modelled	99.9	13 PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
80	d2a7va1	Alignment	not modelled	99.9	19 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
81	c2a7vA_	Alignment	not modelled	99.9	19 PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: human mitochondrial serine hydroxymethyltransferase 2
82	c3zrrB_	Alignment	not modelled	99.9	11 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	d1h0ca_	Alignment	not modelled	99.9	13 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
84	c3dodA_	Alignment	not modelled	99.9	14 PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
85	d1s0aa_	Alignment	not modelled	99.9	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
86	c2dr1A_	Alignment	not modelled	99.9	16 PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
87	c5kz5M_	Alignment	not modelled	99.9	14 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
88	c5hsjB_	Alignment	not modelled	99.9	18 PDB header: lyase Chain: B: PDB Molecule: putative decarboxylase; PDBTitle: structure of tyrosine decarboxylase complex with plp at 1.9 angstroms2 resolution
89	c2po3B_	Alignment	not modelled	99.9	15 PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
90	c3bcxA_	Alignment	not modelled	99.9	14 PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
91	c4addD_	Alignment	not modelled	99.9	14 PDB header: transferase Chain: D: PDB Molecule: succinylornithine transaminase; PDBTitle: structural and functional study of succinyl-ornithine transaminase2 from e. coli
92	c3h7fB_	Alignment	not modelled	99.9	22 PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase 1; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
93	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
94	c2yrrA_	Alignment	not modelled	99.8	16 PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
95	c3f0hA_	Alignment	not modelled	99.8	10 PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
96	c3i4jC_	Alignment	not modelled	99.8	14 PDB header: transferase Chain: C: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of aminotransferase, class iii from deinococcus2 radiodurans
97	c4ixoB_	Alignment	not modelled	99.8	14 PDB header: protein binding Chain: B: PDB Molecule: nifs-like protein; PDBTitle: x-ray structure of nifs-like protein from rickettsia africae esf-5
98	d2e7ja1	Alignment	not modelled	99.8	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSec5-like
99	d1fc4a_	Alignment	not modelled	99.8	13 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
100	c2c7tA_	Alignment	not modelled	99.8	14 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.
101	d1mdoa_	Alignment	not modelled	99.8	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
102	c3nnkC_	Alignment	not modelled	99.8	13 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
103	c2huuA_	Alignment	not modelled	99.8	17 PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate aminotransferase2 in complex with alanine
104	c3a2bA_	Alignment	not modelled	99.8	17 PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
105	c2z9wA_	Alignment	not modelled	99.8	14 PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
106	c6cboB_	Alignment	not modelled	99.8	17 PDB header: transferase Chain: B: PDB Molecule: c-6' aminotransferase; PDBTitle: x-ray structure of genb1 from micromonospora echinospora in complex2 with neamine and plp (as the external aldimine)
107	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
108	c5jayB_	Alignment	not modelled	99.8	16 PDB header: transferase Chain: B: PDB Molecule: 8-amino-7-oxonanoate synthase; PDBTitle: crystal structure of an 8-amino-7-oxonanoate synthase from2 burkholderia xenovorans
109	c3dr4B_	Alignment	not modelled	99.8	13 PDB header: transferase Chain: B: PDB Molecule: putative perosamine synthetase; PDBTitle: gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
110	c2r0tA_	Alignment	not modelled	99.8	15 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
111	c3lv2A_	Alignment	not modelled	99.8	14 PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxonanoate aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
112	c4qgrA_	Alignment	not modelled	99.8	18 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
113	c3lvmB_	Alignment	not modelled	99.8	13 PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
114	c3hqtB_	Alignment	not modelled	99.8	14 PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
115	d1elua_	Alignment	not modelled	99.8	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
116	c3ffrA_	Alignment	not modelled	99.8	9 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
117	c3uwcA_	Alignment	not modelled	99.8	12 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
118	c4eb5B_	Alignment	not modelled	99.8	14 PDB header: transferase/metal binding protein Chain: B: PDB Molecule: probable cysteine desulfurase 2; PDBTitle: a. fulgidus iscs-iscu complex structure
119	c3wy7D_	Alignment	not modelled	99.8	15 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
120	c3tqxA_	Alignment	not modelled	99.8	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