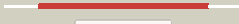



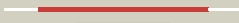



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3025c_iscS_3383896_3385077
Date	Thu Aug 8 16:20:19 BST 2019
Unique Job ID	11f51d3c6176a2da

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4isyB_	 Alignment		100.0	99	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of iscS from mycobacterium tuberculosis
2	c4eb5B_	 Alignment		100.0	38	PDB header: transferase/metal binding protein Chain: B: PDB Molecule: probable cysteine desulfurase 2; PDBTitle: a. fulgidus iscS-iscU complex structure
3	c5zsqA_	 Alignment		100.0	36	PDB header: biosynthetic protein Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: nifs from hydrogenimonas thermophila, soaked with l-cysteine for 4 min
4	c2hdyA_	 Alignment		100.0	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
5	d1eg5a_	 Alignment		100.0	32	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
6	c4ixob_	 Alignment		100.0	33	PDB header: protein binding Chain: B: PDB Molecule: nifs-like protein; PDBTitle: x-ray structure of nifs-like protein from rickettsia africae esf-5
7	c3vaxA_	 Alignment		100.0	35	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein dnda; PDBTitle: crystal structure of dnda from streptomyces lividans
8	d1jf9a_	 Alignment		100.0	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
9	d1t3ia_	 Alignment		100.0	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
10	c5wt2A_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase iscS; PDBTitle: nifs from helicobacter pylori
11	c5kz5M_	 Alignment		100.0	39	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

12	c3caiA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
13	d1p3wa_	Alignment		100.0	39	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
14	c4q76B_	Alignment		100.0	23	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
15	c5j8qa_	Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase sufs; PDBTitle: crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis
16	c4lw2C_	Alignment		100.0	25	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
17	c6c9eB_	Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
18	c5utsC_	Alignment		100.0	16	PDB header: lyase Chain: C: PDB Molecule: c-s lyase egt2; PDBTitle: carbon sulfoxide lyase, egt2 in the ergothioneine biosynthesis pathway
19	c3e9kA_	Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
20	c3lvmB_	Alignment		100.0	39	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
21	c5b87B_	Alignment	not modelled	100.0	24	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
22	c4w91C_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp
23	d1qz9a_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
24	c5usrC_	Alignment	not modelled	100.0	34	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
25	c2hzaA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
26	c5vprA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from elizabethkingia2 anophelis with covalently bound pyridoxal phosphate
27	c5i90A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: pvdn; PDBTitle: crystal structure of pvdn from pseudomonas aeruginosa
28	d1elua_	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like

29	d2c0ra1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
30	d1w23a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
31	c5usrG_	Alignment	not modelled	100.0	38	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
32	c6czyA_	Alignment	not modelled	100.0	12	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)
33	c4xk1A_	Alignment	not modelled	100.0	14	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
34	d1bjna_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
35	c5f8vH_	Alignment	not modelled	100.0	14	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
36	c3m5uA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
37	c3ffrA_	Alignment	not modelled	100.0	10	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
38	c2dr1A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: 3866aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
39	c2z9wA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
40	c3e77A_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: phosphoserine aminotransferase; PDBTitle: human phosphoserine aminotransferase in complex with plp
41	c3qm2A_	Alignment	not modelled	100.0	13	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
42	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
43	c3nnkC_	Alignment	not modelled	100.0	14	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
44	c3zrrB_	Alignment	not modelled	100.0	15	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
45	d1h0ca_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
46	c3ly1C_	Alignment	not modelled	100.0	15	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
47	d2ch1a1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
48	c2huuA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: alanine glyoxylate aminotransferase; PDBTitle: crystal structure of aedes aegypti alanine glyoxylate aminotransferase2 in complex with alanine
49	c3islA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: purine catabolism protein pucg; PDBTitle: crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
50	d2bkwa1	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
51	c4q6rB_	Alignment	not modelled	100.0	17	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

52	c2fyfB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: phosphoserine aminotransferase; PDBTitle: structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
53	c3hdoB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
54	d1vjoa_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
55	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
56	c4dgtA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: putative pyridoxal phosphate-dependent transferase; PDBTitle: crystal structure of plp-bound putative aminotransferase from2 clostridium difficile 630 crystallized with magnesium formate
57	c4wbtA_	Alignment	not modelled	100.0	16	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
58	c4qgrA_	Alignment	not modelled	100.0	16	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
59	c5yb0l_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: I: PDB Molecule: phosphoserine aminotransferase; PDBTitle: crystal structure of wild type phosphoserine aminotransferase (psat)2 from e. histolytica
60	c3pplB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
61	c3eucB_	Alignment	not modelled	100.0	18	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
62	c3h14A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
63	d1iuga_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
64	c3if2B_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of putative amino-acid aminotransferase2 (yp_265399.1) from psychrobacter arcticum 273-4 at 2.50 a resolution
65	d1m32a_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
66	c3b1dD_	Alignment	not modelled	100.0	13	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
67	c3kaxB_	Alignment	not modelled	100.0	10	PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
68	c3p1tB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: putative histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a putative aminotransferase (bpsl1724) from2 burkholderia pseudomallei k96243 at 2.60 a resolution
69	d1x0ma1	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
70	c2yrrA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class v; PDBTitle: hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
71	c6hrhA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 5-aminolevulinate synthase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
72	c3cbfA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
73	c3wy7D_	Alignment	not modelled	100.0	19	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
74	c3madA_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stsp1 (symmetric form)
75	c2w8wA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser

76	d1c7na_	Alignment	not modelled	100.0	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
77	c5yhvA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
78	c3mafB_	Alignment	not modelled	100.0	23	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stsp1 (asymmetric form)
79	c5uidC_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: C: PDB Molecule: aminotransferase tlmj; PDBTitle: the crystal structure of an aminotransferase tlmj from2 streptoalloteichus hindustanus
80	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
81	d1xi9a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
82	c5c6uA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: rv3722c aminotransferase from mycobacterium tuberculosis
83	c4f10A_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: aminotransferase ald1; PDBTitle: crystal structure of ald1 from arabidopsis thaliana
84	d1j32a_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
85	c3ftbA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate aminotransferase2 from clostridium acetobutylicum
86	d1d2fa_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
87	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
88	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
89	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
90	c3eleB_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: amino transferase; PDBTitle: crystal structure of amino transferase (rer070207001803) from2 eubacterium rectale at 2.10 a resolution
91	d1b5pa_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
92	c5txtA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinate synthase, mitochondrial; PDBTitle: structure of asymmetric apo/holo alas dimer from s. cerevisiae
93	c3dzzB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: putative pyridoxal 5'-phosphate-dependent c-s lyase; PDBTitle: crystal structure of a putative plp-dependent aminotransferase2 (lbul_1103) from lactobacillus delbrueckii subsp. at 1.61 a3 resolution
94	c4je5C_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: C: PDB Molecule: aromatic/aminoadipate aminotransferase 1; PDBTitle: crystal structure of the aromatic aminotransferase aro8, a putative2 alpha-aminoadipate aminotransferase in saccharomyces cerevisiae
95	d1vp4a_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
96	d2bwna1	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
97	c5wmiA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: bifunctional aspartate aminotransferase and PDBTitle: arabidopsis thaliana prephenate aminotransferase mutant- t84v
98	c3cq6E_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: E: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
99	c3g7qA_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A: PDB Molecule: valine-pyruvate aminotransferase; PDBTitle: crystal structure of valine-pyruvate aminotransferase avta2 (np_462565.1) from salmonella typhimurium lt2 at 1.80 a resolution
						PDB header: transferase Chain: B: PDB Molecule: maly protein;

100	c1d2fB_	Alignment	not modelled	100.0	13	PDBTitle: x-ray structure of maly from escherichia coli: a pyridoxal-5'-2 phosphate-dependent enzyme acting as a modulator in mal gene3 expression
101	c3ez1A_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: aminotransferase mocr family; PDBTitle: crystal structure of putative aminotransferase (mocr family)2 (yp_604413.1) from deinococcus geothermalis dsm 11300 at 2.60 a3 resolution
102	c3l8aB_	Alignment	not modelled	100.0	11	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
103	c5z0qG_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: G: PDB Molecule: aminotransferase, class i and ii; PDBTitle: crystal structure of ovob
104	c4ppmB_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of pige: a transaminase involved in the biosynthesis2 of 2-methyl-3-n-amy-l-pyrrole (map) from serratia sp. fs14
105	c4r8dB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of rv1600 encoded aminotransferase in complex with2 plp-mes from mycobacterium tuberculosis
106	c3ffhA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
107	d1o4sa_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
108	c3tqxA_	Alignment	not modelled	100.0	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
109	c3getA_	Alignment	not modelled	100.0	12	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
110	c3g0tA_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution
111	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)
112	d1wsta1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
113	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
114	c3a2bA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
115	c3dydB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: human tyrosine aminotransferase
116	d1bw0a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
117	c3mc6C_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdp11
118	c3fkdC_	Alignment	not modelled	100.0	12	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
119	c6jrlA_	Alignment	not modelled	100.0	16	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
120	c5k1rB_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: B: PDB Molecule: burkholderia pseudomallei sphingosine-1-phosphate lyase PDBTitle: structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021