

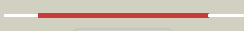
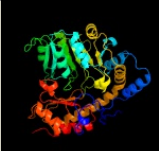




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2294 (-) _2565337_2566560
Date	Mon Aug 5 13:25:43 BST 2019
Unique Job ID	7a2271479373ca47

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dzzB_	 Alignment		100.0	26	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
2	c3b1dD_	 Alignment		100.0	30	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
3	c3fdbA_	 Alignment		100.0	32	PDB header: transferase Chain: A; PDB Molecule: putative plp-dependent beta-cystathionase; PDBTitle: crystal structure of a putative plp-dependent beta-cystathionase2 (aecd, dip1736) from corynebacterium diphtheriae at 1.99 a resolution
4	c3tcmB_	 Alignment		100.0	16	PDB header: transferase Chain: B; PDB Molecule: alanine aminotransferase 2; PDBTitle: crystal structure of alanine aminotransferase from hordeum vulgare
5	c4dgtA_	 Alignment		100.0	30	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
6	c3g0tA_	 Alignment		100.0	14	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
7	d1c7na_	 Alignment		100.0	29	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
8	c3l8aB_	 Alignment		100.0	29	PDB header: lyase Chain: B; PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
9	c3h14A_	 Alignment		100.0	22	PDB header: transferase Chain: A; PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
10	c3kaxB_	 Alignment		100.0	23	PDB header: lyase Chain: B; PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
11	c3eibB_	 Alignment		100.0	17	PDB header: transferase Chain: B; PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana

12	c4my5C_	Alignment		100.0	21	PDB header: transferase Chain: C: PDB Molecule: putative amino acid aminotransferase; PDBTitle: crystal structure of the aromatic amino acid aminotransferase from2 streptococcus mutants
13	c3qguB_	Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: l,l-diaminopimelate aminotransferase from chlamydomonas reinhardtii
14	c3e2yB_	Alignment		100.0	24	PDB header: transferase, lyase Chain: B: PDB Molecule: kynurenine-oxoglutarate transaminase 3; PDBTitle: crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
15	c2o1bA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus aureus
16	c5yhvA_	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
17	c4fl0A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: aminotransferase ald1; PDBTitle: crystal structure of ald1 from arabidopsis thaliana
18	c5z0qG_	Alignment		100.0	35	PDB header: transferase Chain: G: PDB Molecule: aminotransferase, class i and ii; PDBTitle: crystal structure of ovob
19	c3b46B_	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
20	c6f35B_	Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase b; PDBTitle: crystal structure of the aspartate aminotranferase from rhizobium2 meliloti
21	d1w7la_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
22	d1j32a_	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
23	c6f77D_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: D: PDB Molecule: aspartate aminotransferase a; PDBTitle: crystal structure of the prephenate aminotransferase from rhizobium2 meliloti
24	d2r5ea1	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
25	d1xi9a_	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
26	c1ynuA_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: 1-aminocyclopropane-1-carboxylate synthase; PDBTitle: crystal structure of apple acc synthase in complex with l-vinylglycine
27	c2o0rA_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: rv0858c (n-succinyl-diaminopimelate aminotransferase); PDBTitle: the three-dimensional structure of n-succinyl-diaminopimelate2 aminotransferase from mycobacterium tuberculosis
28	d1u08a_	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

						Family: AAT-like
29	c5wmiA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: bifunctional aspartate aminotransferase and PDBTitle: arabidopsis thaliana prephenate aminotransferase mutant- t84v
30	d1bw0a	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
31	d1o4sa	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
32	c3jtxB	Alignment	not modelled	100.0	18	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
33	d1iaya	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
34	c3if2B	Alignment	not modelled	100.0	16	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
35	d1vp4a	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
36	c3ezsB	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: aminotransferase aspb; PDBTitle: crystal structure of aminotransferase aspb (np_207418.1) from2 helicobacter pylori 26695 at 2.19 a resolution
37	c1d2fB	Alignment	not modelled	100.0	29	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
38	c3nraA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of an aspartate aminotransferase (yp_354942.1) from2 rhodobacter sphaeroides 2.4.1 at 2.15 a resolution
39	c3ihjA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: alanine aminotransferase 2; PDBTitle: human alanine aminotransferase 2 in complex with plp
40	d1m7ya	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
41	c2douA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: probable n-succinyl-diaminopimelate aminotransferase; PDBTitle: probable n-succinyl-diaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
42	d1gdea	Alignment	not modelled	100.0	23	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
43	d1d2fa	Alignment	not modelled	100.0	30	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
44	c2zc0C	Alignment	not modelled	100.0	16	PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
45	c2x5dD	Alignment	not modelled	100.0	20	PDB header: transferase Chain: D: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a probable aminotransferase from pseudomonas2 aeruginosa
46	d2gb3a1	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
47	c3pplB	Alignment	not modelled	100.0	18	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
48	c6hnuA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: aromatic amino acid aminotransferase i; PDBTitle: crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
49	c3eleB	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: amino transferase; PDBTitle: crystal structure of amino transferase (rer070207001803) from2 eubacterium rectale at 2.10 a resolution
50	c3asaA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of apo-ll-diaminopimelate aminotransferase from2 chlamydia trachomatis
51	c4cvqB	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: glutamate-pyruvate aminotransferase alaa; PDBTitle: crystal structure of an aminotransferase from escherichia coli at 2.2 11 angstrom resolution
52	d1wsta1	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
						PDB header: transferase Chain: C: PDB Molecule: aromatic/aminoadipate aminotransferase

53	c4je5C_	Alignment	not modelled	100.0	18	1; PDBTitle: crystal structure of the aromatic aminotransferase aro8, a putative2 alpha-aminoadipate aminotransferase in saccharomyces cerevisiae
54	d1b5pa_	Alignment	not modelled	100.0	25	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
55	d1x0ma1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
56	c6hndA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aromatic-amino-acid:2-oxoglutarate transaminase; PDBTitle: crystal structure of the aromatic aminotransferase aro9 from c.2 albicans
57	c5c6uA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: rv3722c aminotransferase from mycobacterium tuberculosis
58	c3t18D_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: D: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
59	c4ix8B_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structure of tyrosine aminotransferase from leishmania2 infantum
60	c2z61A_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: probable aspartate aminotransferase 2; PDBTitle: crystal structure of mj0684 from methanococcus jannaschii2 reveals its similarity in the active site to kynurenine3 aminotransferases
61	c2x5fB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: aspartate_tyrosine_phenylalanine pyridoxal-5' PDBTitle: crystal structure of the methicillin-resistant2 staphylococcus aureus sar2028, an3 aspartate_tyrosine_phenylalanine pyridoxal-5'-phosphate4 dependent aminotransferase
62	c6c3aB_	Alignment	not modelled	100.0	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: o2-, plp-dependent l-arginine hydroxylase rohp 4-hydroxy-2-2 ketoarginine complex
63	c3dc1A_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: kynurenine/alpha-aminoadipate aminotransferase PDBTitle: crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
64	c3dydB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: human tyrosine aminotransferase
65	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
66	c3pdxA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structural of mouse tyrosine aminotransferase
67	c3g7qA_	Alignment	not modelled	100.0	16	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
68	c2zy4F_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: F: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
69	c4rkdA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aromatic amino acid aminotransferase; PDBTitle: psychrophilic aromatic amino acids aminotransferase from psychrobacter2 sp. b6 cocrystalized with aspartic acid
70	c4n0bA_	Alignment	not modelled	100.0	12	PDB header: transcription activator Chain: A: PDB Molecule: hth-type transcriptional regulatory protein gabr; PDBTitle: crystal structure of bacillus subtilis gabr, an autorepressor and2 transcriptional activator of gabt
71	d2csta_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
72	c3rq1A_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase class i and ii from veillonella2 parvula
73	d1ajsa_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
74	c3d6kB_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
75	c3k7yA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: aspartate aminotransferase of plasmodium falciparum
76	d1v2da_	Alignment	not modelled	100.0	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like PDB header: transferase

77	c4wd2A_	Alignment	not modelled	100.0	16	Chain: A; PDB Molecule: aromatic-amino-acid transaminase tyrb; PDBTitle: crystal structure of an aromatic amino acid aminotransferase from2 burkholderia cenocepacia j2315
78	c3op7A_	Alignment	not modelled	100.0	18	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
79	c4effA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A; PDB Molecule: aromatic-amino-acid aminotransferase; PDBTitle: crystal structure of aromatic-amino-acid aminotransferase from2 burkholderia pseudomallei
80	c2zy3A_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A; PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
81	c3bwnF_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: F; PDB Molecule: l-tryptophan aminotransferase; PDBTitle: l-tryptophan aminotransferase
82	d7aata_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
83	c4m2jA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A; PDB Molecule: aminotransferase; PDBTitle: crystal structure of plp-dependent cyclase orfr in complex with au
84	c4eu1A_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A; PDB Molecule: mitochondrial aspartate aminotransferase; PDBTitle: structure of a mitochondrial aspartate aminotransferase from2 trypanosoma brucei
85	d2ay1a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
86	c4h51B_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B; PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of a putative aspartate aminotransferase from2 leishmania major friedlin
87	c3ly1C_	Alignment	not modelled	100.0	18	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
88	d2q7wa1	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
89	c3cbfA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A; PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
90	c3f6tA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A; PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
91	d1yaaa_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
92	c4wbtA_	Alignment	not modelled	100.0	17	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
93	d2hoxa1	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
94	d3tata_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
95	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
96	c4r8dB_	Alignment	not modelled	100.0	15	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
97	c5dj3B_	Alignment	not modelled	100.0	17	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
98	c6ezlB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B; PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of aspartate aminotransferase from trypanosoma cruzi2 at 2.07 angstrom resolution
99	c3mebB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B; PDB Molecule: aspartate aminotransferase; PDBTitle: structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
100	c3getA_	Alignment	not modelled	100.0	15	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
						PDB header: transferase

101	c3cq6E_	Alignment	not modelled	100.0	16	Chain: E; PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
102	d2f8ja1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
103	d1lc5a_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
104	d1fg7a_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
105	c3ffhA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A; PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
106	c3hdoB_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B; PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
107	c3fkdc_	Alignment	not modelled	100.0	14	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
108	c4r2na_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A; PDB Molecule: putative phenylalanine aminotransferase; PDBTitle: crystal structure of rv3772 in complex with its substrate
109	c3ftbA_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A; PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate aminotransferase2 from clostridium acetobutylicum
110	c3p1tB_	Alignment	not modelled	100.0	18	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
111	c6ouxB_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: B; PDB Molecule: threonine phosphate decarboxylase-like enzyme; PDBTitle: structure of smul_1544, a decarboxylase from sulfurospirillum2 multivorans
112	d2aeua1	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SelA-like
113	d1tpla_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
114	c3f0hA_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A; PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
115	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
116	c5jayB_	Alignment	not modelled	100.0	15	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
117	c3hqtB_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: B; PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
118	c3wy7D_	Alignment	not modelled	100.0	16	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
119	d1v72a1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
120	d1svva_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like