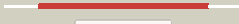



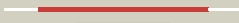



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1600_(hisC1)_1800903_1802045
Date	Fri Aug 2 13:30:19 BST 2019
Unique Job ID	ece86b97bafd9314

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4r8dB_	 Alignment		100.0	100	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
2	c3cq6E_	 Alignment		100.0	60	PDB header: transferase Chain: E: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
3	c3hdoB_	 Alignment		100.0	31	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
4	c3ly1C_	 Alignment		100.0	23	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
5	c4r2nA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: putative phenylalanine aminotransferase; PDBTitle: crystal structure of rv3772 in complex with its substrate
6	c3eucB_	 Alignment		100.0	31	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
7	c3getA_	 Alignment		100.0	19	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
8	d1lc5a_	 Alignment		100.0	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
9	c4wbtA_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: probable histidinol-phosphate aminotransferase; PDBTitle: crystal structure of histidinol-phosphate aminotransferase from2 sinorhizobium melliloti in complex with pyridoxal-5'-phosphate
10	d2f8ja1	 Alignment		100.0	30	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
11	d1fg7a_	 Alignment		100.0	28	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like

12	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
13	c3b1dD_	Alignment		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
14	d1o4sa_	Alignment		100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
15	c3h14A_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
16	c3p1tB_	Alignment		100.0	25	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
17	c3ffhA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
18	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
19	c3eleB_	Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: amino transferase; PDBTitle: crystal structure of amino transferase (rer070207001803) from2 eubacterium rectale at 2.10 a resolution
20	c5yhvA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
21	c3dzzB_	Alignment	not modelled	100.0	13	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
22	d1j32a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
23	c3tcmB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: alanine aminotransferase 2; PDBTitle: crystal structure of alanine aminotransferase from hordeum vulgare
24	d1w7la_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
25	c4my5C_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: C: PDB Molecule: putative amino acid aminotransferase; PDBTitle: crystal structure of the aromatic amino acid aminotransferase from2 streptococcus mutants
26	d1c7na_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
27	d1b5pa_	Alignment	not modelled	100.0	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
28	d2r5ea1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
						PDB header: transferase, lyase

29	c3e2yB_	Alignment	not modelled	100.0	17	Chain: B; PDB Molecule: kynurenine-oxoglutarate transaminase 3; PDBTitle: crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
30	c5wmiA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A; PDB Molecule: bifunctional aspartate aminotransferase and PDBTitle: arabidopsis thaliana prephenate aminotransferase mutant- t84v
31	c2o1bA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A; PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus aureus
32	c6f77D_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: D; PDB Molecule: aspartate aminotransferase a; PDBTitle: crystal structure of the prephenate aminotransferase from rhizobium2 melliloti
33	d1u08a_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
34	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
35	c3l8aB_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B; PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
36	d1iaya_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
37	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
38	c3jtxB_	Alignment	not modelled	100.0	22	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
39	c5z0qG_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: G; PDB Molecule: aminotransferase, class i and ii; PDBTitle: crystal structure of ovob
40	c2o0rA_	Alignment	not modelled	100.0	18	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
41	c3fdbA_	Alignment	not modelled	100.0	16	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
42	c3ftbA_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A; PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate aminotransferase2 from clostridium acetobutylicum
43	c3pplB_	Alignment	not modelled	100.0	16	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
44	d2gb3a1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
45	d1xi9a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
46	d1m7ya_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
47	c2z61A_	Alignment	not modelled	100.0	19	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
48	c2douA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A; PDB Molecule: probable n-succinyl diaminopimelate aminotransferase; PDBTitle: probable n-succinyl diaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
49	c4fi0A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A; PDB Molecule: aminotransferase ald1; PDBTitle: crystal structure of ald1 from arabidopsis thaliana
50	c3fkdC_	Alignment	not modelled	100.0	23	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
51	c3b46B_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B; PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
52	d1gdea_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like

53	c3kaxB	Alignment	not modelled	100.0	11	PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
54	c3eibB	Alignment	not modelled	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
55	c4ix8B	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structure of tyrosine aminotransferase from leishmania2 infantum
56	d1wsta1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
57	c3ezsB	Alignment	not modelled	100.0	17	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
58	c3qguB	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: l,l-diaminopimelate aminotransferase from chalmymdomonas reinhardtii
59	c2x5dD	Alignment	not modelled	100.0	16	PDB header: transferase Chain: D: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a probable aminotransferase from pseudomonas2 aeruginosa
60	c1d2fB	Alignment	not modelled	100.0	12	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
61	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
62	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
63	d1vp4a	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
64	d1x0ma1	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
65	d1d2fa	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
66	c3nraA	Alignment	not modelled	100.0	16	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
67	d1bw0a	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
68	c3t18D	Alignment	not modelled	100.0	15	PDB header: transferase Chain: D: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
69	c3rq1A	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase class i and ii from veillonella2 parvula
70	c4je5C	Alignment	not modelled	100.0	16	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
71	c4n0bA	Alignment	not modelled	100.0	11	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
72	c3ihjA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: alanine aminotransferase 2; PDBTitle: human alanine aminotransferase 2 in complex with plp
73	c5c6uA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: rv3722c aminotransferase from mycobacterium tuberculosis
74	c4rkdA	Alignment	not modelled	100.0	17	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
75	d2csta	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
76	c4effA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: aromatic-amino-acid aminotransferase; PDBTitle: crystal structure of aromatic-amino-acid aminotransferase from2 burkholderia pseudomallei
77	d1v2da	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like

78	c6hndA	Alignment	not modelled	100.0	17	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
79	c6hnuA	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: aromatic amino acid aminotransferase i; PDBTitle: crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
80	c3asaA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
81	c6c3aB	Alignment	not modelled	100.0	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: o2-, plp-dependent l-arginine hydroxylase rohp 4-hydroxy-2-2 ketoarginine complex
82	c3ez1A	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: aminotransferase mocr family; PDBTitle: crystal structure of apo-ll-diaminopimelate (mocr family)2 (yp_604413.1) from deinococcus geothermalis dsm 11300 at 2.60 a3 resolution
83	c4cvqB	Alignment	not modelled	100.0	17	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
84	c2x5fB	Alignment	not modelled	100.0	12	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
85	c3dydB	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: human tyrosine aminotransferase
86	c3k7yA	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: aspartate aminotransferase of plasmodium falciparum
87	d1ajsa	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
88	d1yaaa	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
89	d2q7wa1	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
90	c3cbfA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
91	c4wd2A	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aromatic-amino-acid transaminase tyrb; PDBTitle: crystal structure of an aromatic amino acid aminotransferase from2 burkholderia cenocepacia j2315
92	c3g7qA	Alignment	not modelled	100.0	18	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
93	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
94	c3pdxA	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structural of mouse tyrosine aminotransferase
95	d7aata	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
96	d2ay1a	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
97	c3mebB	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
98	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
99	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
100	c2zy4F	Alignment	not modelled	100.0	16	PDB header: lyase Chain: F: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
101	d3tata	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
						PDB header: transferase

102	c3d6kB	Alignment	not modelled	100.0	16	Chain: B; PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from <i>2 corynebacterium diphtheriae</i>
103	c3bwnF	Alignment	not modelled	100.0	17	PDB header: transferase Chain: F; PDB Molecule: l-tryptophan aminotransferase; PDBTitle: l-tryptophan aminotransferase
104	c2zy3A	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A; PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
105	c6ouxB	Alignment	not modelled	100.0	22	PDB header: lyase Chain: B; PDB Molecule: threonine phosphate decarboxylase-like enzyme; PDBTitle: structure of smul_1544, a decarboxylase from <i>sulfurospirillum2 multivorans</i>
106	c4m2jA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A; PDB Molecule: aminotransferase; PDBTitle: crystal structure of plp-dependent cyclase orfr in complex with au
107	c3op7A	Alignment	not modelled	100.0	17	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 <i>streptococcus suis</i> 89-1591 at 1.70 a resolution
108	c6ezbB	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B; PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of aspartate aminotransferase from <i>trypanosoma cruzi</i> 2 at 2.07 angstrom resolution
109	d2hoxa1	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
110	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
111	c3f6tA	Alignment	not modelled	100.0	14	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 <i>lactobacillus acidophilus</i> ncfm at 2.15 a3 resolution
112	c5jayB	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B; PDB Molecule: 8-amino-7-oxononoate synthase; PDBTitle: crystal structure of an 8-amino-7-oxononoate synthase from <i>2 burkholderia xenovorans</i>
113	d2aeua1	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SelA-like
114	c3hqtB	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B; PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
115	d2e7ja1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
116	c3wy7D	Alignment	not modelled	100.0	19	PDB header: transferase Chain: D; PDB Molecule: 8-amino-7-oxononoate synthase; PDBTitle: crystal structure of <i>mycobacterium smegmatis</i> 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
117	c3a2bA	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A; PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from <i>sphingobacterium2 multivorum</i> with substrate l-serine
118	c2w8wA	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A; PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
119	d1vjoa	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
120	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) from <i>2 coxiella burnetii</i>