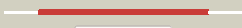
























Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3772_(hisC2)_4217312_4218373
 Date Fri Aug 9 18:20:47 BST 2019
 Unique Job ID 76b8905cab22f45

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4r2nA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: putative phenylalanine aminotransferase; PDBTitle: crystal structure of rv3772 in complex with its substrate
2	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
3	c3getA_	 Alignment		100.0	27	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
4	c4r8dB_	 Alignment		100.0	31	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
5	d1fg7a_	 Alignment		100.0	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
6	c3cq6E_	 Alignment		100.0	26	PDB header: transferase Chain: E: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
7	c4wbtA_	 Alignment		100.0	33	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
8	c3ffhA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
9	c3hdoB_	 Alignment		100.0	28	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
10	c3eucB_	 Alignment		100.0	26	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
11	d1lc5a_	 Alignment		100.0	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like

12	d2f8ja1	Alignment		100.0	28	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
13	c3p1tB	Alignment		100.0	28	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
14	c3h14A	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
15	c3g0tA	Alignment		100.0	17	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
16	d1o4sa	Alignment		100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
17	d1w7la	Alignment		100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
18	c3b1dD	Alignment		100.0	19	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
19	c3e2yB	Alignment		100.0	22	PDB header: transferase, lyase Chain: B: PDB Molecule: kynurenine-oxoglutarate transaminase 3; PDBTitle: crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
20	c3tcmB	Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: alanine aminotransferase 2; PDBTitle: crystal structure of alanine aminotransferase from hordeum vulgare
21	c3jtxB	Alignment	not modelled	100.0	21	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
22	c3ezsB	Alignment	not modelled	100.0	19	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
23	c3ftbA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate aminotransferase2 from clostridium acetobutylicum
24	c4my5C	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: putative amino acid aminotransferase; PDBTitle: crystal structure of the aromatic amino acid aminotransferase from2 streptococcus mutants
25	c1ynuA	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: 1-aminocyclopropane-1-carboxylate synthase; PDBTitle: crystal structure of apple acc synthase in complex with l-vinylglycine
26	c5yhvA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
27	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
28	c2o1bA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus

					aureus
29	d2r5ea1	Alignment	not modelled	100.0	21 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
30	d1iaya_	Alignment	not modelled	100.0	21 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
31	d1m7ya_	Alignment	not modelled	100.0	18 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
32	c3b46B_	Alignment	not modelled	100.0	17 PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
33	c3pplB_	Alignment	not modelled	100.0	19 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
34	c3dzzB_	Alignment	not modelled	100.0	17 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
35	c3eibB_	Alignment	not modelled	100.0	20 PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
36	c3l8aB_	Alignment	not modelled	100.0	17 PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
37	d1u08a_	Alignment	not modelled	100.0	22 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
38	c3fkdC_	Alignment	not modelled	100.0	19 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
39	d1j32a_	Alignment	not modelled	100.0	21 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
40	d1xi9a_	Alignment	not modelled	100.0	20 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
41	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
42	c4fl0A_	Alignment	not modelled	100.0	20 PDB header: transferase Chain: A: PDB Molecule: aminotransferase ald1; PDBTitle: crystal structure of ald1 from arabidopsis thaliana
43	d1b5pa_	Alignment	not modelled	100.0	25 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
44	c2o0rA_	Alignment	not modelled	100.0	26 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
45	c2zc0C_	Alignment	not modelled	100.0	19 PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
46	c2douA_	Alignment	not modelled	100.0	22 PDB header: transferase Chain: A: PDB Molecule: probable n-succinyl diaminopimelate aminotransferase; PDBTitle: probable n-succinyl diaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
47	c6f35B_	Alignment	not modelled	100.0	24 PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase b; PDBTitle: crystal structure of the aspartate aminotranferase from rhizobium2 meliloti
48	c3t18D_	Alignment	not modelled	100.0	18 PDB header: transferase Chain: D: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
49	d1c7na_	Alignment	not modelled	100.0	15 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
50	d2gb3a1	Alignment	not modelled	100.0	21 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
51	c3qguB_	Alignment	not modelled	100.0	22 PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: l,l-diaminopimelate aminotransferase from chlamydomonas reinhardtii
52	d1wsta1	Alignment	not modelled	100.0	18 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
53	d1vp4a_	Alignment	not modelled	100.0	20 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

						Family: AAT-like
54	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
55	c3kaxB	Alignment	not modelled	100.0	14	PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
56	d1bw0a	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
57	c6f77D	Alignment	not modelled	100.0	23	PDB header: transferase Chain: D: PDB Molecule: aspartate aminotransferase a; PDBTitle: crystal structure of the prephenate aminotransferase from rhizobium2 melliloti
58	c4je5C	Alignment	not modelled	100.0	18	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
59	c2x5dD	Alignment	not modelled	100.0	23	PDB header: transferase Chain: D: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a probable aminotransferase from pseudomonas2 aeruginosa
60	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
61	d1gdea	Alignment	not modelled	100.0	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
62	d1x0ma1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
63	c3fdbA	Alignment	not modelled	100.0	18	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
64	d1v2da	Alignment	not modelled	100.0	27	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
65	c3ihjA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: alanine aminotransferase 2; PDBTitle: human alanine aminotransferase 2 in complex with plp
66	c5c6uA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: rv3722c aminotransferase from mycobacterium tuberculosis
67	c4cvqB	Alignment	not modelled	100.0	20	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
68	c3if2B	Alignment	not modelled	100.0	19	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
69	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
70	c5z0qG	Alignment	not modelled	100.0	18	PDB header: transferase Chain: G: PDB Molecule: aminotransferase, class i and ii; PDBTitle: crystal structure of ovob
71	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
72	c3asaA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of apo-ll-diaminopimelate aminotransferase from2 chlamydia trachomatis
73	c3nraA	Alignment	not modelled	100.0	19	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
74	c2x5fB	Alignment	not modelled	100.0	15	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
75	c1d2fB	Alignment	not modelled	100.0	19	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
76	c3ez1A	Alignment	not modelled	100.0	18	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
77	c4rkdA	Alignment	not modelled	100.0	19	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
78	c2z61A	Alignment	not modelled	100.0	21	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
79	c6hndA	Alignment	not modelled	100.0	18	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
80	c6ouxB	Alignment	not modelled	100.0	20	PDB header: lyase Chain: B: PDB Molecule: threonine phosphate decarboxylase-like enzyme; PDBTitle: structure of smul_1544, a decarboxylase from sulfurospirillum2 multivorans
81	d1d2fa	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
82	c4effA	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: aromatic-amino-acid aminotransferase; PDBTitle: crystal structure of aromatic-amino-acid aminotransferase from2 burkholderia pseudomallei
83	d2csta	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
84	c3dc1A	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: kynurenine/alpha-aminoadipate aminotransferase PDBTitle: crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
85	d2ay1a	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
86	c4n0bA	Alignment	not modelled	100.0	17	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
87	c6c3aB	Alignment	not modelled	100.0	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: o2-, plp-dependent l-arginine hydroxylase rohp 4-hydroxy-2-2 ketoarginine complex
88	c3dydB	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: human tyrosine aminotransferase
89	d2q7wa1	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
90	c3d6kB	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
91	c3k7yA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: aspartate aminotransferase of plasmodium falciparum
92	c4wd2A	Alignment	not modelled	100.0	19	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
93	c3cbfA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
94	c3pdxA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structural of mouse tyrosine aminotransferase
95	d1ajsa	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
96	d7aata	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
97	c4eu1A	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: mitochondrial aspartate aminotransferase; PDBTitle: structure of a mitochondrial aspartate aminotransferase from2 trypanosoma brucei
98	c3g7qA	Alignment	not modelled	100.0	21	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
99	c4h51B	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of a putative aspartate aminotransferase from2 leishmania major friedlin
100	d1yaaa	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
						PDB header: lyase

101	c2zy3A_	Alignment	not modelled	100.0	19	Chain: A; PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
102	c2zy4F_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: F; PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
103	c6ezbB_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B; PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of aspartate aminotransferase from trypanosoma cruzi2 at 2.07 angstrom resolution
104	d3tata_	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
105	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
106	c3op7A_	Alignment	not modelled	100.0	16	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
107	c3bwnF_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: F; PDB Molecule: l-tryptophan aminotransferase; PDBTitle: l-tryptophan aminotransferase
108	c5dj3B_	Alignment	not modelled	100.0	18	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
109	c3f6tA_	Alignment	not modelled	100.0	17	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
110	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
111	d2hoxa1	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
112	d2aeua1	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SelA-like
113	c5jayB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B; PDB Molecule: 8-amino-7-oxononanoate synthase; PDBTitle: crystal structure of an 8-amino-7-oxononanoate synthase from2 burkholderia xenovorans
114	d1m6sa_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
115	d1svva_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
116	c3hqtB_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B; PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
117	d2e7ja1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
118	d1v72a1	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
119	c2eh6A_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A; PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
120	c3wgcB_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: B; PDB Molecule: l-allo-threonine aldolase; PDBTitle: aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant