
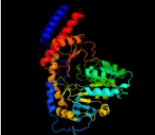
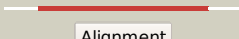

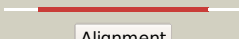














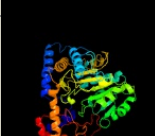













Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3722c_(-)_4166999_4168306
Date	Fri Aug 9 18:20:42 BST 2019
Unique Job ID	341abdb757cfca7c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5c6uA_	 Alignment		100.0	96	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: rv3722c aminotransferase from mycobacterium tuberculosis
2	c3pplB_	 Alignment		100.0	52	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
3	c3ez1A_	 Alignment		100.0	44	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
4	c3d6kB_	 Alignment		100.0	54	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
5	c4je5C_	 Alignment		100.0	17	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
6	c6hnuA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: aromatic amino acid aminotransferase i; PDBTitle: crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
7	c6hndA_	 Alignment		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
8	c3tcmB_	 Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: alanine aminotransferase 2; PDBTitle: crystal structure of alanine aminotransferase from hordeum vulgare
9	c3if2B_	 Alignment		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
10	c3g0tA_	 Alignment		100.0	13	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
11	d1vp4a_	 Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like

12	c4n0bA_	Alignment		100.0	15	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
13	d1wsta1	Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
14	c3dc1A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: kynurenine/alpha-aminoacidate aminotransferase PDBTitle: crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
15	c3ihjA_	Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: alanine aminotransferase 2; PDBTitle: human alanine aminotransferase 2 in complex with plp
16	c2x5fB_	Alignment		100.0	17	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
17	d1x0ma1	Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
18	c2zc0C_	Alignment		100.0	20	PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
19	c1ynuA_	Alignment		100.0	14	PDB header: lyase Chain: A: PDB Molecule: 1-aminocyclopropane-1-carboxylate synthase; PDBTitle: crystal structure of apple acc synthase in complex with l-vinylglycine
20	d1iaya_	Alignment		100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
21	d1m7ya_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
22	d2r5ea1	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
23	d1w7la_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
24	c3b1dD_	Alignment	not modelled	100.0	11	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
25	c3e2yB_	Alignment	not modelled	100.0	17	PDB header: transferase, lyase Chain: B: PDB Molecule: kynurenine-oxoglutarate transaminase 3; PDBTitle: crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
26	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
27	c3b46B_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
28	c3jtxB_	Alignment	not modelled	100.0	17	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
						PDB header: transferase

29	c5yhvA_	Alignment	not modelled	100.0	17	Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
30	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
31	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
32	d1u08a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
33	d2csta_	Alignment	not modelled	100.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
34	c6c3aB_	Alignment	not modelled	100.0	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: o2-, plp-dependent l-arginine hydroxylase rohp 4-hydroxy-2-2 ketoarginine complex
35	d2gb3a1	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
36	c3t18D_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: D: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
37	c3eibB_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
38	c3qguB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: l,l-diaminopimelate aminotransferase from chalmymdomonas reinhardtii
39	c4fl0A_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: aminotransferase ald1; PDBTitle: crystal structure of ald1 from arabidopsis thaliana
40	c3eleB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: amino transferase; PDBTitle: crystal structure of amino transferase (rer070207001803) from2 eubacterium rectale at 2.10 a resolution
41	c3cbfA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
42	c4wd2A_	Alignment	not modelled	100.0	14	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
43	c4cvqB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: glutamate-pyruvate aminotransferase alaa; PDBTitle: crystal structure of an aminotransferase from escherichia coli at 2.2 11 angstroem resolution
44	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
45	d1o4sa_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
46	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
47	d1yaaa_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
48	c4effA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: aromatic-amino-acid aminotransferase; PDBTitle: crystal structure of aromatic-amino-acid aminotransferase from2 burkholderia pseudomallei
49	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
50	c2zy4F_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: F: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
51	c6f77D_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: D: PDB Molecule: aspartate aminotransferase a; PDBTitle: crystal structure of the prephenate aminotransferase from rhizobium2 meliloti
52	c3ezsB_	Alignment	not modelled	100.0	18	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
53	c3k7yA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: aspartate aminotransferase of plasmodium falciparum
54	c2o0rA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: rv0858c (n-succinyldiaminopimelate aminotransferase);

54	c2001A	Alignment	not modelled	100.0	10	PDBTitle: the three-dimensional structure of n-succinyl-diaminopimelate 2-aminotransferase from mycobacterium tuberculosis
55	c5wmiA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: bifunctional aspartate aminotransferase and PDBTitle: arabidopsis thaliana prephenate aminotransferase mutant- t84v
56	d1xi9a	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
57	d1bw0a	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
58	d1gdea	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
59	c6f35B	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase b; PDBTitle: crystal structure of the aspartate aminotransferase from rhizobium2 meliloti
60	d1ajsa	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
61	c4h51B	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of a putative aspartate aminotransferase from2 leishmania major friedlin
62	d7aata	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
63	c3rq1A	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase class i and ii from veillonella2 parvula
64	d1j32a	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
65	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
66	d2q7wa1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
67	c2zy3A	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
68	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
69	d2ay1a	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
70	c4dgtA	Alignment	not modelled	100.0	12	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
71	c4ix8B	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structure of tyrosine aminotransferase from leishmania2 infantum
72	d1c7na	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
73	c3f6tA	Alignment	not modelled	100.0	13	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
74	d1b5pa	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
75	c2o1bA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus aureus
76	c2x5dD	Alignment	not modelled	100.0	18	PDB header: transferase Chain: D: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a probable aminotransferase from pseudomonas2 aeruginosa
77	c3asaA	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: l1-diaminopimelate aminotransferase; PDBTitle: crystal structure of apo-l1-diaminopimelate aminotransferase from2 chlamydia trachomatis
78	c3kaxB	Alignment	not modelled	100.0	12	PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
79	c2douA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: probable n-succinyl-diaminopimelate aminotransferase;

						PDBTitle: probable n-succinyldiaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
80	d3tata_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
81	c5z0qG_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: G: PDB Molecule: aminotransferase, class i and ii; PDBTitle: crystal structure of ovob
82	c6ezlB_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of aspartate aminotransferase from trypanosoma cruzi2 at 2.07 angstrom resolution
83	c3fdbA_	Alignment	not modelled	100.0	15	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
84	c3mebB_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
85	c3op7A_	Alignment	not modelled	100.0	13	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
86	c1d2fB_	Alignment	not modelled	100.0	14	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
87	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
88	c3pdxA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structural of mouse tyrosine aminotransferase
89	c2z61A_	Alignment	not modelled	100.0	15	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
90	c3dydB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: human tyrosine aminotransferase
91	d1v2da_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
92	c3bwnF_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: F: PDB Molecule: l-tryptophan aminotransferase; PDBTitle: l-tryptophan aminotransferase
93	d1d2fa_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
94	c5dj3B_	Alignment	not modelled	100.0	14	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
95	c3eucB_	Alignment	not modelled	100.0	13	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	d2hoxa1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
97	c3ly1C_	Alignment	not modelled	100.0	14	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
98	c3getA_	Alignment	not modelled	100.0	9	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
99	d1fg7a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
100	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
101	c4r8dB_	Alignment	not modelled	100.0	17	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
102	d2f8ja1	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
						PDB header: transferase

103	c3cq6E_	Alignment	not modelled	100.0	15	Chain: E: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
104	c4r2nA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: putative phenylalanine aminotransferase; PDBTitle: crystal structure of rv3772 in complex with its substrate
105	d1c5a_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
106	c3hdoB_	Alignment	not modelled	100.0	14	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	13	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	c3p1tB_	Alignment	not modelled	100.0	20	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
109	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.
110	c3ftbA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate aminotransferase2 from clostridium acetobutylicum
111	d2aeau1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SelA-like
112	c6ouxB_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: B: PDB Molecule: threonine phosphate decarboxylase-like enzyme; PDBTitle: structure of smul_1544, a decarboxylase from sulfurospirillum2 multivorans
113	d1tpla_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
114	c2z9wA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
115	d1vjoa_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
116	c3wy7D_	Alignment	not modelled	100.0	16	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
117	d1m6sa_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
118	c3hqtB_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
119	d1v72a1	Alignment	not modelled	100.0	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
120	c4j8lA_	Alignment	not modelled	100.0	15	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