

Phyre²

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Description	RVBD0858c_(-)_953730_954923
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2o0rA_			100.0	99	PDB header: transferase Chain: A; PDB Molecule: rv0858c (n-succinylaminopimelate aminotransferase); PDBTitle: the three-dimensional structure of n-succinylaminopimelate2 aminotransferase from mycobacterium tuberculosis
2	c3e2yB_			100.0	38	PDB header: transferase, lyase Chain: B; PDB Molecule: kynurenine-oxoglutarate transaminase 3; PDBTitle: crystal structure of mouse kynureanine aminotransferase iii in complex2 with glutamine
3	d1u08a_			100.0	38	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: AAT-like
4	d2r5ea1			100.0	37	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: AAT-like
5	d1w7la_			100.0	35	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: AAT-like
6	c4my5C_			100.0	28	PDB header: transferase Chain: C; PDB Molecule: putative amino acid aminotransferase; PDBTitle: crystal structure of the aromatic amino acid aminotransferase from2 streptococcus mutants
7	c3g0tA_			100.0	18	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
8	c3b1dD_			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
9	d1gdea_			100.0	35	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfers Family: AAT-like
10	c3tcmb_			100.0	22	PDB header: transferase Chain: B; PDB Molecule: alanine aminotransferase 2; PDBTitle: crystal structure of alanine aminotransferase from hordeum vulgare
11	c6f35B_			100.0	26	PDB header: transferase Chain: B; PDB Molecule: aspartate aminotransferase b; PDBTitle: crystal structure of the aspartate aminotranferase from rhizobium2 meliloti

12	c5yhvA		100.0	27	PDB header: transferase Chain: A; PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
13	c6f77D		100.0	25	PDB header: transferase Chain: D; PDB Molecule: aspartate aminotransferase a; PDBTitle: crystal structure of the prephenate aminotransferase from rhizobium2 mellotii
14	d1j32a		100.0	29	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
15	c3h14A		100.0	26	PDB header: transferase Chain: A; PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
16	c3dzzB		100.0	20	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
17	c2o1bA		100.0	24	PDB header: transferase Chain: A; PDB Molecule: aminotransferase, class i; PDBTitle: structure of aminotransferase from staphylococcus aureus
18	c5wmiA		100.0	27	PDB header: transferase Chain: A; PDB Molecule: bifunctional aspartate aminotransferase and PDBTitle: arabidopsis thaliana prephenate aminotransferase mutant- t84v
19	c3b46B		100.0	30	PDB header: transferase Chain: B; PDB Molecule: aminotransferase bna3p; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
20	d1o4sa		100.0	27	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
21	c6hnuA	Alignment	not modelled	100.0	21 PDB header: transferase Chain: A; PDB Molecule: aromatic amino acid aminotransferase i; PDBTitle: crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
22	c3nraA	Alignment	not modelled	100.0	22 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
23	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
24	c2x5dD	Alignment	not modelled	100.0	27 PDB header: transferase Chain: D; PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a probable aminotransferase from pseudomonas2 aeruginosa
25	c4dgtA	Alignment	not modelled	100.0	19 PDB header: transferase Chain: A; PDB Molecule: putative pyridoxal phosphate-dependent transferase; PDBTitle: crystal structure of plp-bound putative aminotransferase from clostridium difficile 630 crystallized with magnesium formate
26	c3gguB	Alignment	not modelled	100.0	22 PDB header: transferase Chain: B; PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: ll-diaminopimelate aminotransferase from chlamydomonas reinhardtii
27	c3l8aB	Alignment	not modelled	100.0	20 PDB header: lyase Chain: B; PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans
28	d1wsta1	Alignment	not modelled	100.0	21 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

					Family: AAT-like
29	d2gb3a1	Alignment	not modelled	100.0	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
30	d1xi9a	Alignment	not modelled	100.0	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
31	d1vp4a	Alignment	not modelled	100.0	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
32	c1ynuA	Alignment	not modelled	100.0	PDB header: lyase Chain: A: PDB Molecule: 1-aminocyclopropane-1-carboxylate synthase; PDBTitle: crystal structure of apple acc synthase in complex with l-vinylglycine
33	c3eibB	Alignment	not modelled	100.0	PDB header: transferase Chain: B: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
34	d1bw0a	Alignment	not modelled	100.0	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
35	c3ezsB	Alignment	not modelled	100.0	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
36	c2zc0C	Alignment	not modelled	100.0	PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
37	d1c7na	Alignment	not modelled	100.0	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathione synthase-like
38	c4je5C	Alignment	not modelled	100.0	PDB header: transferase Chain: C: PDB Molecule: aromatic/aminoacid aminotransferase 1; PDBTitle: crystal structure of the aromatic aminotransferase aro8, a putative2 alpha-aminoacid aminotransferase in saccharomyces cerevisiae
39	d1b5pa	Alignment	not modelled	100.0	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
40	c3kaxB	Alignment	not modelled	100.0	PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
41	c3if2B	Alignment	not modelled	100.0	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
42	d1x0ma1	Alignment	not modelled	100.0	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
43	c4fl0A	Alignment	not modelled	100.0	PDB header: transferase Chain: A: PDB Molecule: aminotransferase ald1; PDBTitle: crystal structure of ald1 from arabidopsis thaliana
44	c6hndA	Alignment	not modelled	100.0	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
45	c3eleB	Alignment	not modelled	100.0	PDB header: transferase Chain: B: PDB Molecule: amino transferase; PDBTitle: crystal structure of amino transferase (rer070207001803) from2 eubacterium rectale at 2.10 a resolution
46	c3pplB	Alignment	not modelled	100.0	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
47	c3ihjA	Alignment	not modelled	100.0	PDB header: transferase Chain: A: PDB Molecule: alanine aminotransferase 2; PDBTitle: human alanine aminotransferase 2 in complex with plp
48	c3fdbA	Alignment	not modelled	100.0	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
49	d1m7ya	Alignment	not modelled	100.0	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
50	d1iaya	Alignment	not modelled	100.0	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
51	c2douA	Alignment	not modelled	100.0	PDB header: transferase Chain: A: PDB Molecule: probable n-succinylaminopimelate aminotransferase; PDBTitle: probable n-succinylaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
52	c4cvqB	Alignment	not modelled	100.0	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
53	c5z0qG	Alignment	not modelled	100.0	24 PDB header: transferase Chain: G: PDB Molecule: aminotransferase, class i and ii; PDBTitle: crystal structure of ovob
54	c2z61A	Alignment	not modelled	100.0	25 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
55	d1v2da	Alignment	not modelled	100.0	44 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
56	c1d2fB	Alignment	not modelled	100.0	20 PDB header: transferase Chain: B: PDB Molecule: maly protein; PDBTitle: x-ray structure of maly from escherichia coli: a pyridoxal-5'-phosphate-dependent enzyme acting as a modulator in mal gene3 expression
57	c3asaA	Alignment	not modelled	100.0	21 PDB header: transferase Chain: A: PDB Molecule: ll-diaminopimelate aminotransferase; PDBTitle: crystal structure of apo-ll-diaminopimelate aminotransferase from2 chlamydia trachomatis
58	c3t18D	Alignment	not modelled	100.0	19 PDB header: transferase Chain: D: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
59	c5c6uA	Alignment	not modelled	100.0	17 PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: rv3722c aminotransferase from mycobacterium tuberculosis
60	d1d2fa	Alignment	not modelled	100.0	20 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
61	c4ix8B	Alignment	not modelled	100.0	24 PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structure of tyrosine aminotransferase from leishmania2 infantum
62	c2x5fB	Alignment	not modelled	100.0	20 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
63	c3ez1A	Alignment	not modelled	100.0	17 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
64	c3dc1A	Alignment	not modelled	100.0	21 PDB header: transferase Chain: A: PDB Molecule: kynurenine/alpha-amino adipate aminotransferase PDBTitle: crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
65	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
66	c4m2jA	Alignment	not modelled	100.0	23 PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of plp-dependent cyclase orfr in complex with au
67	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
68	d2csta	Alignment	not modelled	100.0	17 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
69	c3pdxA	Alignment	not modelled	100.0	22 PDB header: transferase Chain: A: PDB Molecule: tyrosine aminotransferase; PDBTitle: crystal structural of mouse tyrosine aminotransferase
70	c3dydB	Alignment	not modelled	100.0	23 PDB header: transferase Chain: B: PDB Molecule: tyrosine aminotransferase; PDBTitle: human tyrosine aminotransferase
71	c4n0bA	Alignment	not modelled	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
72	c3cbfA	Alignment	not modelled	100.0	23 PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminodipate2 aminotransferase, from thermus thermophilus hb27
73	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
74	c4rkda	Alignment	not modelled	100.0	15 PDB header: transferase Chain: A: PDB Molecule: aromatic amino acid aminotransferase; PDBTitle: psychrophilic aromatic amino acids aminotransferase from psychrobacter2 sp. b6 cocrystallized with aspartic acid
75	c3rq1A	Alignment	not modelled	100.0	17 PDB header: transferase Chain: A: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase class i and ii from veillonella2 parvula
76	c3k7yA	Alignment	not modelled	100.0	13 PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase;

						PDBTitle: aspartate aminotransferase of plasmodium falciparum
77	c3op7A_	Alignment	not modelled	100.0	21	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
78	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
79	d1ajsa_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfersases Family: AAT-like
80	d7aata_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfersases Family: AAT-like
81	d2ay1a_	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfersases Family: AAT-like
82	d1yaaa_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfersases Family: AAT-like
83	c4effA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: aromatic-amino-acid aminotransferase; PDBTitle: crystal structure of aromatic-amino-acid aminotransferase from2 burkholderia pseudomallei
84	c4h51B_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of a putative aspartate aminotransferase from2 leishmania major friedlin
85	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
86	c2zy4F_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: F: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
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	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfersases Family: AAT-like
89	c4wbtA_	Alignment	not modelled	100.0	19	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
90	c2zy3A_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
91	d3tata_	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfersases Family: AAT-like
92	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
93	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
94	c3f6tA_	Alignment	not modelled	100.0	22	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
95	c3getA_	Alignment	not modelled	100.0	14	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
96	c3bwnF_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: F: PDB Molecule: l-tryptophan aminotransferase; PDBTitle: l-tryptophan aminotransferase
97	c3cq6E_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: E: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
98	c6ezLB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of aspartate aminotransferase from trypanosoma cruzi2 at 2.07 angstrom resolution
99	c4r2nA_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: putative phenylalanine aminotransferase; PDBTitle: crystal structure of rv3772 in complex with its substrate
100	d1lc5a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transfersases Family: AAT-like
						PDB header: transferase Chain: B: PDB Molecule: plp-dependent l-arginine hydroxylase

101	c5dj3B_	Alignment	not modelled	100.0	17	mppp; PDBTitle: structure of the plp-dependent l-arginine hydroxylase mppp with d-2 arginine bound
102	d2f8ja1	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
103	c3eucB_	Alignment	not modelled	100.0	19	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
104	d1fg7a_	Alignment	not modelled	100.0	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
105	d2hoxa1	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
106	c3hdoB_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
107	c3ffhA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
108	c3ftbA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of the histidinol-phosphate aminotransferase2 from clostridium acetobutylicum
109	c3fkdc_	Alignment	not modelled	100.0	18	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
110	c3p1tB_	Alignment	not modelled	100.0	24	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	17	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	c5jayB_	Alignment	not modelled	100.0	13	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	d1tpla_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
115	c3wy7D_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: D: PDB Molecule: 8-amino-7-oxononanoate synthase; PDBTitle: crystal structure of mycobacterium smegmatis 7-keto-8-aminopalpegaronic2 acid (kapa) synthase biof
116	c3hqtB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsA
117	c3a2ba_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorans with substrate l-serine
118	c3f0hA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
119	d1v72a1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
120	c2w8wA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with pip-ser