







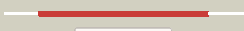















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0075 (-)_83993_85165
Date	Tue Jul 23 14:50:10 BST 2019
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dzzB_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative pyridoxal 5'-phosphate-dependent c-s lyase; <b>PDBTitle:</b> crystal structure of a putative plp-dependent aminotransferase2 (lbul_1103) from lactobacillus delbrueckii subsp. at 1.61 a3 resolution
2	<a href="#">c3b1dD_</a>	 Alignment		100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> betac-s lyase; <b>PDBTitle:</b> crystal structure of betac-s lyase from streptococcus anginosus in2 complex with l-serine: external aldimine form
3	<a href="#">c3fdbA_</a>	 Alignment		100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative plp-dependent beta-cystathionase; <b>PDBTitle:</b> crystal structure of a putative plp-dependent beta-cystathionase2 (aecd, dip1736) from corynebacterium diphtheriae at 1.99 a resolution
4	<a href="#">d1c7na_</a>	 Alignment		100.0	24	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
5	<a href="#">c4dgtA_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative pyridoxal phosphate-dependent transferase; <b>PDBTitle:</b> crystal structure of plp-bound putative aminotransferase from2 clostridium difficile 630 crystallized with magnesium formate
6	<a href="#">c3tcmB_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine aminotransferase 2; <b>PDBTitle:</b> crystal structure of alanine aminotransferase from hordeum vulgare
7	<a href="#">c3l8aB_</a>	 Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminotransferase, probable beta-cystathionase; <b>PDBTitle:</b> crystal structure of metc from streptococcus mutans
8	<a href="#">c5z0qG_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> aminotransferase, class i and ii; <b>PDBTitle:</b> crystal structure of ovob
9	<a href="#">c3kaxB_</a>	 Alignment		100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase, classes i and ii; <b>PDBTitle:</b> crystal structure of a putative c-s lyase from bacillus anthracis
10	<a href="#">c5yhvA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of an aminotransferase from mycobacterium2 tuberculosis
11	<a href="#">c3g0tA_</a>	 Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution

12	<a href="#">c3h14A_</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase, classes i and ii; <b>PDBTitle:</b> crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
13	<a href="#">c3b46B_</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase bna3; <b>PDBTitle:</b> crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
14	<a href="#">c3e2yB_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine-oxoglutarate transaminase 3; <b>PDBTitle:</b> crystal structure of mouse kynurenine aminotransferase iii in complex2 with glutamine
15	<a href="#">d1u08a_</a>	Alignment		100.0	21	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
16	<a href="#">d2r5ea1</a>	Alignment		100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
17	<a href="#">d1xi9a_</a>	Alignment		100.0	22	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
18	<a href="#">d1j32a_</a>	Alignment		100.0	23	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
19	<a href="#">d1w7la_</a>	Alignment		100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
20	<a href="#">c1d2fB_</a>	Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> maly protein; <b>PDBTitle:</b> x-ray structure of maly from escherichia coli: a pyridoxal-5'-2 phosphate-dependent enzyme acting as a modulator in mal gene3 expression
21	<a href="#">c3qguB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ll-diaminopimelate aminotransferase; <b>PDBTitle:</b> l,l-diaminopimelate aminotransferase from chlamydomonas reinhardtii
22	<a href="#">c4my5C_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> putative amino acid aminotransferase; <b>PDBTitle:</b> crystal structure of the aromatic amino acid aminotransferase from2 streptococcus mutants
23	<a href="#">c2o0rA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rv0858c (n-succinylldiaminopimelate aminotransferase); <b>PDBTitle:</b> the three-dimensional structure of n-succinylldiaminopimelate2 aminotransferase from mycobacterium tuberculosis
24	<a href="#">d1d2fa_</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
25	<a href="#">c3eibB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ll-diaminopimelate aminotransferase; <b>PDBTitle:</b> crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
26	<a href="#">d1o4sa_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
27	<a href="#">c3if2B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of putative amino-acid aminotransferase2 (yp_265399.1) from psychrobacter arcticum 273-4 at 2.50 a resolution
28	<a href="#">c3o1hA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase, class i;

28	<a href="#">c2010A</a>	Alignment	not modelled	100.0	18	<b>PDBTitle:</b> structure of aminotransferase from staphylococcus aureus <b>PDB header:</b> transferase
29	<a href="#">c6f35B</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> B; <b>PDB Molecule:</b> aspartate aminotransferase b; <b>PDBTitle:</b> crystal structure of the aspartate aminotranferase from rhizobium2 meliloti
30	<a href="#">c2zc0C</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> alanine glyoxylate transaminase; <b>PDBTitle:</b> crystal structure of an archaeal alanine:glyoxylate aminotransferase
31	<a href="#">c3jtxB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
32	<a href="#">c3ihjA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> alanine aminotransferase 2; <b>PDBTitle:</b> human alanine aminotransferase 2 in complex with plp
33	<a href="#">c1ynuA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> 1-aminocyclopropane-1-carboxylate synthase; <b>PDBTitle:</b> crystal structure of apple acc synthase in complex with l-vinylglycine
34	<a href="#">c6f77D</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> aspartate aminotransferase a; <b>PDBTitle:</b> crystal structure of the prephenate aminotransferase from rhizobium2 meliloti
35	<a href="#">c5wmiA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> bifunctional aspartate aminotransferase and <b>PDBTitle:</b> arabidopsis thaliana prephenate aminotransferase mutant- t84v
36	<a href="#">d1bw0a</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
37	<a href="#">c3nraA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of an aspartate aminotransferase (yp_354942.1) from2 rhodobacter sphaeroides 2.4.1 at 2.15 a resolution
38	<a href="#">c4f10A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aminotransferase ald1; <b>PDBTitle:</b> crystal structure of ald1 from arabidopsis thaliana
39	<a href="#">d1b5pa</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
40	<a href="#">d1gdea</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
41	<a href="#">c2x5dD</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> probable aminotransferase; <b>PDBTitle:</b> crystal structure of a probable aminotransferase from pseudomonas2 aeruginosa
42	<a href="#">d2gb3a1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
43	<a href="#">c4cvqB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> glutamate-pyruvate aminotransferase alaa; <b>PDBTitle:</b> crystal structure of an aminotransferase from escherichia coli at 2.2 11 angstroem resolution
44	<a href="#">c3eleB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> amino transferase; <b>PDBTitle:</b> crystal structure of amino transferase (rer070207001803) from2 eubacterium rectale at 2.10 a resolution
45	<a href="#">d1iaya</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
46	<a href="#">c3pp1B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
47	<a href="#">d1wsta1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
48	<a href="#">d1vp4a</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
49	<a href="#">c3ezsB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> aminotransferase aspb; <b>PDBTitle:</b> crystal structure of aminotransferase aspb (np_207418.1) from2 helicobacter pylori 26695 at 2.19 a resolution
50	<a href="#">d1m7ya</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
51	<a href="#">c6hnuA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aromatic amino acid aminotransferase i; <b>PDBTitle:</b> crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
52	<a href="#">c4je5C</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> aromatic/aminoadipate aminotransferase 1; <b>PDBTitle:</b> crystal structure of the aromatic aminotransferase aro8, a putative2 alpha-aminoadipate aminotransferase in saccharomyces cerevisiae <b>PDB header:</b> transferase

53	<a href="#">c3asaA</a>	Alignment	not modelled	100.0	21	<b>Chain:</b> A: <b>PDB Molecule:</b> ll-diaminopimelate aminotransferase; <b>PDBTitle:</b> crystal structure of apo-ll-diaminopimelate aminotransferase from2 chlamydia trachomatis
54	<a href="#">c2douA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable n-succinyldiaminopimelate aminotransferase; <b>PDBTitle:</b> probable n-succinyldiaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
55	<a href="#">d1x0ma1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
56	<a href="#">c6hndA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic-amino-acid:2-oxoglutarate transaminase; <b>PDBTitle:</b> crystal structure of the aromatic aminotransferase aro9 from c.2 albicans
57	<a href="#">c2x5fB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate_tyrosine_phenylalanine pyridoxal-5' <b>PDBTitle:</b> crystal structure of the methicillin-resistant2 staphylococcus aureus sar2028, an3 aspartate_tyrosine_phenylalanine pyridoxal-5'-phosphate4 dependent aminotransferase
58	<a href="#">c4ix8B</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine aminotransferase; <b>PDBTitle:</b> crystal structure of tyrosine aminotransferase from leishmania2 infantum
59	<a href="#">c5c6uA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> rv3722c aminotransferase from mycobacterium tuberculosis
60	<a href="#">c3pdxA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine aminotransferase; <b>PDBTitle:</b> crystal structural of mouse tyrosine aminotransferase
61	<a href="#">c3t18D</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> aminotransferase class i and ii; <b>PDBTitle:</b> crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
62	<a href="#">c3dydB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine aminotransferase; <b>PDBTitle:</b> human tyrosine aminotransferase
63	<a href="#">c3g7qA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> valine-pyruvate aminotransferase; <b>PDBTitle:</b> crystal structure of valine-pyruvate aminotransferase avta2 (np_462565.1) from salmonella typhimurium lt2 at 1.80 a resolution
64	<a href="#">c3dc1A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> kynurenine/alpha-aminoadipate aminotransferase <b>PDBTitle:</b> crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
65	<a href="#">c3ez1A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase mocr family; <b>PDBTitle:</b> crystal structure of putative aminotransferase (mocr family)2 (yp_604413.1) from deinococcus geothermalis dsm 11300 at 2.60 a3 resolution
66	<a href="#">c2z61A</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aspartate aminotransferase 2; <b>PDBTitle:</b> crystal structure of mj0684 from methanococcus jannaschii2 reveals its similarity in the active site to kynurenine3 aminotransferases
67	<a href="#">c4n0bA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulatory protein gabr; <b>PDBTitle:</b> crystal structure of bacillus subtilis gabr, an autorepressor and2 transcriptional activator of gabt
68	<a href="#">c6c3aB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> o2-, plp-dependent l-arginine hydroxylase rohp 4-hydroxy-2-2 ketoarginine complex
69	<a href="#">c3op7A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase class i and ii; <b>PDBTitle:</b> crystal structure of a plp-dependent aminotransferase (zp_03625122.1)2 from streptococcus suis 89-1591 at 1.70 a resolution
70	<a href="#">d2csta</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
71	<a href="#">d1v2da</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
72	<a href="#">c4rkdA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic amino acid aminotransferase; <b>PDBTitle:</b> psychrophilic aromatic amino acids aminotransferase from psychrobacter2 sp. b6 cocrystalized with aspartic acid
73	<a href="#">c2zy4F</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> l-aspartate beta-decarboxylase; <b>PDBTitle:</b> dodecameric l-aspartate beta-decarboxylase
74	<a href="#">c4wd2A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic-amino-acid transaminase tyrb; <b>PDBTitle:</b> crystal structure of an aromatic amino acid aminotransferase from2 burkholderia cenocepacia j2315
75	<a href="#">c3k7yA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> aspartate aminotransferase of plasmodium falciparum
76	<a href="#">c3rq1A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase class i and ii; <b>PDBTitle:</b> crystal structure of aminotransferase class i and ii from

						veillonella2 parvula
77	<a href="#">c3cbfA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-aminodipate aminotransferase; <b>PDBTitle:</b> crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
78	<a href="#">d1ajsa_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
79	<a href="#">c4effA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic-amino-acid aminotransferase; <b>PDBTitle:</b> crystal structure of aromatic-amino-acid aminotransferase from2 burkholderia pseudomallei
80	<a href="#">c2zy3A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate beta-decarboxylase; <b>PDBTitle:</b> dodecameric l-aspartate beta-decarboxylase
81	<a href="#">d2q7wa1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
82	<a href="#">c4eu1A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial aspartate aminotransferase; <b>PDBTitle:</b> structure of a mitochondrial aspartate aminotransferase from2 trypanosoma brucei
83	<a href="#">d2ay1a_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
84	<a href="#">c3f6tA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
85	<a href="#">d7aata_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
86	<a href="#">c4h51B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of a putative aspartate aminotransferase from2 leishmania major friedlin
87	<a href="#">c3ly1C_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> putative histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution
88	<a href="#">d1yaaa_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
89	<a href="#">c3d6kB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
90	<a href="#">c4m2jA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of plp-dependent cyclase orfr in complex with au
91	<a href="#">c4wbtA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of histidinol-phosphate aminotransferase from2 sinorhizobium meliloti in complex with pyridoxal-5'-phosphate
92	<a href="#">c4r8dB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of rv1600 encoded aminotransferase in complex with2 plp-mes from mycobacterium tuberculosis
93	<a href="#">c3bwnF_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> l-tryptophan aminotransferase; <b>PDBTitle:</b> l-tryptophan aminotransferase
94	<a href="#">d3tata_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
95	<a href="#">c3cq6E_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound )
96	<a href="#">c3mebB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> structure of cytoplasmic aspartate aminotransferase from giardia2 lamblia
97	<a href="#">d1lc5a_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
98	<a href="#">c3getA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution
99	<a href="#">c4r2nA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phenylalanine aminotransferase; <b>PDBTitle:</b> crystal structure of rv3772 in complex with its substrate
100	<a href="#">c6ezB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of aspartate aminotransferase from trypanosoma cruzi2 at 2.07 angstrom resolution
101	<a href="#">d2hoxa1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like



102	<a href="#">c5dj3B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> plp-dependent l-arginine hydroxylase mppp; <b>PDBTitle:</b> structure of the plp-dependent l-arginine hydroxylase mppp with d-2 arginine bound
103	<a href="#">c3eucB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> histidinol-phosphate aminotransferase 2; <b>PDBTitle:</b> crystal structure of histidinol-phosphate aminotransferase2 (yp_297314.1) from ralstonia eutropha jmp134 at 2.05 a resolution
104	<a href="#">c3hdoB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
105	<a href="#">d1fg7a_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
106	<a href="#">c3ftbA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
107	<a href="#">d2f8ja1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
108	<a href="#">c3fkdC_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> l-threonine-o-3-phosphate decarboxylase; <b>PDBTitle:</b> the crystal structure of l-threonine-o-3-phosphate decarboxylase from2 porphyromonas gingivalis
109	<a href="#">c3ffhA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
110	<a href="#">c3p1tB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> putative histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of a putative aminotransferase (bpsl1724) from2 burkholderia pseudomallei k96243 at 2.60 a resolution
111	<a href="#">c6ouxB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> threonine phosphate decarboxylase-like enzyme; <b>PDBTitle:</b> structure of smul_1544, a decarboxylase from sulfurospirillum2 multivorans
112	<a href="#">c2w8wA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser
113	<a href="#">c3a2bA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
114	<a href="#">c5jayB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> 8-amino-7-oxononanoate synthase; <b>PDBTitle:</b> crystal structure of an 8-amino-7-oxononanoate synthase from2 burkholderia xenovorans
115	<a href="#">c3wy7D_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> 8-amino-7-oxononanoate synthase; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
116	<a href="#">c3hqtB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> cai-1 autoinducer synthase; <b>PDBTitle:</b> plp-dependent acyl-coa transferase cqsa
117	<a href="#">c2ordA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution
118	<a href="#">c3nx3A_</a>	Alignment	not modelled	100.0	9	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
119	<a href="#">c4addD_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> succinylornithine transaminase; <b>PDBTitle:</b> structural and functional study of succinyl-ornithine transaminase2 from e. coli
120	<a href="#">c4uoxB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> putrescine aminotransferase; <b>PDBTitle:</b> crystal structure of ygig in complex with pyridoxal-5'-phosphate2 and putrescine