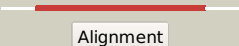



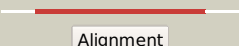





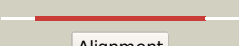













# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3565_(aspB)_4006379_4007545
Date	Fri Aug 9 18:20:24 BST 2019
Unique Job ID	539bed55eefcd921

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5yhvA_</a>	 Alignment		100.0	100	<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
2	<a href="#">c3h14A_</a>	 Alignment		100.0	45	<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
3	<a href="#">c3tcmB_</a>	 Alignment		100.0	24	<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
4	<a href="#">c3g0tA_</a>	 Alignment		100.0	17	<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
5	<a href="#">c6f35B_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase b; <b>PDBTitle:</b> crystal structure of the aspartate aminotranferase from rhizobium2 meliloti
6	<a href="#">d1j32a_</a>	 Alignment		100.0	30	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
7	<a href="#">c6f77D_</a>	 Alignment		100.0	27	<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
8	<a href="#">c3b1dD_</a>	 Alignment		100.0	19	<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
9	<a href="#">d1o4sa_</a>	 Alignment		100.0	31	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
10	<a href="#">c5wmiA_</a>	 Alignment		100.0	26	<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
11	<a href="#">c4my5C_</a>	 Alignment		100.0	25	<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

12	<a href="#">d1u08a_</a>	Alignment		100.0	24	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
13	<a href="#">d1xi9a_</a>	Alignment		100.0	24	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
14	<a href="#">c3dzzB_</a>	Alignment		100.0	19	<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 (Ibul_1103) from lactobacillus delbrueckii subsp. at 1.61 a3 resolution
15	<a href="#">d2gb3a1</a>	Alignment		100.0	24	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
16	<a href="#">c3e2yB_</a>	Alignment		100.0	23	<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
17	<a href="#">d1w7la_</a>	Alignment		100.0	23	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
18	<a href="#">d2r5ea1</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="#">c3b46B_</a>	Alignment		100.0	21	<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
20	<a href="#">c2zc0C_</a>	Alignment		100.0	23	<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
21	<a href="#">c3jtxB_</a>	Alignment	not modelled	100.0	22	<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
22	<a href="#">c2o0rA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rv0858c (n-succinyldiaminopimelate aminotransferase); <b>PDBTitle:</b> the three-dimensional structure of n-succinyldiaminopimelate2 aminotransferase from mycobacterium tuberculosis
23	<a href="#">d1b5pa_</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
24	<a href="#">c4dgtA_</a>	Alignment	not modelled	100.0	18	<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
25	<a href="#">c3l8aB_</a>	Alignment	not modelled	100.0	19	<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
26	<a href="#">c3qguB_</a>	Alignment	not modelled	100.0	22	<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
27	<a href="#">d1c7na_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
						<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase;

28	<a href="#">c3if2B_</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> crystal structure of putative amino-acid aminotransferase2 (yp_265399.1) from psychrobacter arcticum 273-4 at 2.50 a resolution
29	<a href="#">c2o1bA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase, class i; <b>PDBTitle:</b> structure of aminotransferase from staphylococcus aureus
30	<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
31	<a href="#">d1gdea_</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
32	<a href="#">c4fl0A_</a>	Alignment	not modelled	100.0	22	<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
33	<a href="#">c3eibB_</a>	Alignment	not modelled	100.0	22	<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
34	<a href="#">c3ezsB_</a>	Alignment	not modelled	100.0	20	<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
35	<a href="#">d1bw0a_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
36	<a href="#">c3ihjA_</a>	Alignment	not modelled	100.0	23	<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
37	<a href="#">c4cvqB_</a>	Alignment	not modelled	100.0	21	<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
38	<a href="#">c3pplB_</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> crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
39	<a href="#">c2z61A_</a>	Alignment	not modelled	100.0	30	<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
40	<a href="#">c2x5dD_</a>	Alignment	not modelled	100.0	26	<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
41	<a href="#">c3kaxB_</a>	Alignment	not modelled	100.0	16	<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
42	<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
43	<a href="#">c3fdbA_</a>	Alignment	not modelled	100.0	20	<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
44	<a href="#">d1m7ya_</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
45	<a href="#">c6hnuA_</a>	Alignment	not modelled	100.0	20	<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
46	<a href="#">c2douA_</a>	Alignment	not modelled	100.0	23	<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
47	<a href="#">c1d2fB_</a>	Alignment	not modelled	100.0	19	<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
48	<a href="#">c5z0qG_</a>	Alignment	not modelled	100.0	21	<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
49	<a href="#">c3eleB_</a>	Alignment	not modelled	100.0	23	<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
50	<a href="#">d1d2fa_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
51	<a href="#">d1wsta1</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
52	<a href="#">d1vp4a_</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
53	<a href="#">c3nraA_</a>	Alignment	not modelled	100.0	23	<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
54	<a href="#">c3t18D_</a>	Alignment	not modelled	100.0	16	<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.
55	<a href="#">c3asaA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ll-diaminopimelate aminotransferase; <b>PDBTitle:</b> crystal structure of apo-ll-diaminopimelate aminotransferase from2 chlamydia trachomatis
56	<a href="#">d1x0ma1</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
57	<a href="#">c5c6uA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> rv3722c aminotransferase from mycobacterium tuberculosis
58	<a href="#">c6hndA_</a>	Alignment	not modelled	100.0	20	<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
59	<a href="#">c4je5C_</a>	Alignment	not modelled	100.0	20	<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
60	<a href="#">c4ix8B_</a>	Alignment	not modelled	100.0	24	<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
61	<a href="#">c3pdxA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine aminotransferase; <b>PDBTitle:</b> crystal structural of mouse tyrosine aminotransferase
62	<a href="#">c3ez1A_</a>	Alignment	not modelled	100.0	18	<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
63	<a href="#">c4n0bA_</a>	Alignment	not modelled	100.0	17	<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
64	<a href="#">c3dydB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine aminotransferase; <b>PDBTitle:</b> human tyrosine aminotransferase
65	<a href="#">c6c3aB_</a>	Alignment	not modelled	100.0	12	<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
66	<a href="#">c2x5fB_</a>	Alignment	not modelled	100.0	17	<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
67	<a href="#">c3dc1A_</a>	Alignment	not modelled	100.0	19	<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
68	<a href="#">d1v2da_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
69	<a href="#">c4wd2A_</a>	Alignment	not modelled	100.0	18	<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
70	<a href="#">c3d6kB_</a>	Alignment	not modelled	100.0	19	<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
71	<a href="#">c4rkdA_</a>	Alignment	not modelled	100.0	17	<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
72	<a href="#">c3rq1A_</a>	Alignment	not modelled	100.0	18	<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
73	<a href="#">c3op7A_</a>	Alignment	not modelled	100.0	19	<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
74	<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
75	<a href="#">d2csta_</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

76	<a href="#">c3k7yA</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> aspartate aminotransferase of plasmodium falciparum
77	<a href="#">c3cbfA</a>	Alignment	not modelled	100.0	20	<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="#">d7aata</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
79	<a href="#">d2ay1a</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
80	<a href="#">c4effA</a>	Alignment	not modelled	100.0	20	<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
81	<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
82	<a href="#">d1yaaa</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
83	<a href="#">c4eu1A</a>	Alignment	not modelled	100.0	17	<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
84	<a href="#">c2zy4F</a>	Alignment	not modelled	100.0	22	<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
85	<a href="#">c4h51B</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 a putative aspartate aminotransferase from2 leishmania major friedlin
86	<a href="#">c3ly1C</a>	Alignment	not modelled	100.0	20	<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
87	<a href="#">d2q7wa1</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
88	<a href="#">c4m2jA</a>	Alignment	not modelled	100.0	24	<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
89	<a href="#">c4wbtA</a>	Alignment	not modelled	100.0	20	<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
90	<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
91	<a href="#">c3bwnF</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> l-tryptophan aminotransferase; <b>PDBTitle:</b> l-tryptophan aminotransferase
92	<a href="#">d3tata</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
93	<a href="#">c2zy3A</a>	Alignment	not modelled	100.0	20	<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
94	<a href="#">c3cq6E</a>	Alignment	not modelled	100.0	18	<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 )
95	<a href="#">c3eucB</a>	Alignment	not modelled	100.0	21	<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
96	<a href="#">d1lc5a</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
97	<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
98	<a href="#">c3mebB</a>	Alignment	not modelled	100.0	15	<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
99	<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
100	<a href="#">c3getA</a>	Alignment	not modelled	100.0	15	<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



101	<a href="#">c4r2nA_</a>	Alignment	not modelled	100.0	25	<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
102	<a href="#">c3f6tA_</a>	Alignment	not modelled	100.0	22	<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
103	<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
104	<a href="#">c5dj3B_</a>	Alignment	not modelled	100.0	18	<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
105	<a href="#">c3hdoB_</a>	Alignment	not modelled	100.0	20	<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
106	<a href="#">c6ezbB_</a>	Alignment	not modelled	100.0	20	<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
107	<a href="#">c3ffhA_</a>	Alignment	not modelled	100.0	22	<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.
108	<a href="#">c3ftbA_</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 the histidinol-phosphate aminotransferase2 from clostridium acetobutylicum
109	<a href="#">c3fkdC_</a>	Alignment	not modelled	100.0	18	<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
110	<a href="#">c3p1tB_</a>	Alignment	not modelled	100.0	24	<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	17	<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="#">d2aeua1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SelA-like
113	<a href="#">c5jayB_</a>	Alignment	not modelled	100.0	13	<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
114	<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 cgsa
115	<a href="#">c3wy7D_</a>	Alignment	not modelled	100.0	15	<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="#">d1tpla_</a>	Alignment	not modelled	100.0	10	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
117	<a href="#">c3a2bA_</a>	Alignment	not modelled	100.0	11	<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
118	<a href="#">c3tqxA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-3-ketobutyrate coenzyme a ligase; <b>PDBTitle:</b> structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii
119	<a href="#">d1m6sa_</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
120	<a href="#">c2w8wA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser