



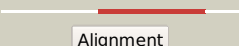


























# Phyre2

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 Description RVBD0032\_(bioF2)\_34295\_36610  
 Date Tue Jul 23 14:50:06 BST 2019  
 Unique Job ID 0efba217088c8244

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5txtA_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-aminolevulinate synthase, mitochondrial; <b>PDBTitle:</b> structure of asymmetric apo/holo alas dimer from s. cerevisiae
2	<a href="#">c6hrhA_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-aminolevulinate synthase, erythroid-specific, <b>PDBTitle:</b> structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
3	<a href="#">c2w8wA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser
4	<a href="#">c3a2bA_</a>	 Alignment		100.0	37	<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
5	<a href="#">c3hqtB_</a>	 Alignment		100.0	26	<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
6	<a href="#">d2bwna1</a>	 Alignment		100.0	31	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
7	<a href="#">c3tqxA_</a>	 Alignment		100.0	31	<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
8	<a href="#">d1bs0a_</a>	 Alignment		100.0	31	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
9	<a href="#">d1fc4a_</a>	 Alignment		100.0	31	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
10	<a href="#">c3wy7D_</a>	 Alignment		100.0	36	<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
11	<a href="#">c5jayB_</a>	 Alignment		100.0	35	<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

12	<a href="#">c4iw7A_</a>	Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-amino-7-oxononanoate synthase; <b>PDBTitle:</b> crystal structure of 8-amino-7-oxononanoate synthase (biof) from2 francisella tularensis.
13	<a href="#">c2eo5A_</a>	Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 419aa long hypothetical aminotransferase; <b>PDBTitle:</b> crystal structure of 4-aminobutyrate aminotransferase from sulfobolbus2 tokodaii strain7
14	<a href="#">c4ysvA_</a>	Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 4-aminobutyrate aminotransferase; <b>PDBTitle:</b> structure of aminoacid racemase in apo-form
15	<a href="#">d1s0aa_</a>	Alignment		100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
16	<a href="#">c5ghfB_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase class-iii; <b>PDBTitle:</b> transaminase with l-ala
17	<a href="#">c3nuuA_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate transaminase; <b>PDBTitle:</b> crystal structure of omega-transferase from vibrio fluvialis js17
18	<a href="#">c2eh6A_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
19	<a href="#">c3dxvA_</a>	Alignment		100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amino-epsilon-caprolactam racemase; <b>PDBTitle:</b> the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
20	<a href="#">c2e7uA_</a>	Alignment		100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-1-semialdehyde 2,1-aminomutase; <b>PDBTitle:</b> crystal structure of glutamate-1-semialdehyde 2,1-aminomutase from2 thermus thermophilus hb8
21	<a href="#">c2pb2B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetylornithine/succinyl-diaminopimelate aminotransferase; <b>PDBTitle:</b> structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
22	<a href="#">c4e77A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-1-semialdehyde 2,1-aminomutase; <b>PDBTitle:</b> 2.0a crystal structure of a glutamate-1-semialdehyde aminotransferase2 from yersinia pestis co92
23	<a href="#">c5viuB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase from2 elizabethkingia anophelis
24	<a href="#">c5g4iA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphorylase; <b>PDBTitle:</b> plp-dependent phosphorylase a1rdf1 from arthrobacter aurescens tc1
25	<a href="#">d1zoda1</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
26	<a href="#">c4addD_</a>	Alignment	not modelled	100.0	18	<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
27	<a href="#">c1z7dE_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> ornithine aminotransferase; <b>PDBTitle:</b> ornithine aminotransferase py00104 from plasmodium yoelii
						<b>PDB header:</b> transferase

28	<a href="#">c5g2pA_</a>	Alignment	not modelled	100.0	15	<b>Chain:</b> A: <b>PDB Molecule:</b> transaminase; <b>PDBTitle:</b> the crystal structure of a s-selective transaminase from2 arthrobacter sp.
29	<a href="#">c3h7fB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine hydroxymethyltransferase 1; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
30	<a href="#">c1oatB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> aminotransferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine aminotransferase; <b>PDBTitle:</b> ornithine aminotransferase
31	<a href="#">d2byla1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
32	<a href="#">c3ruyB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine aminotransferase; <b>PDBTitle:</b> crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis
33	<a href="#">d2cfba1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
34	<a href="#">c2zsmA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-1-semialdehyde 2,1-aminomutase; <b>PDBTitle:</b> crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form
35	<a href="#">c6fyqA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amine transaminase; <b>PDBTitle:</b> the crystal structure of a new transaminase from the marine bacterium2 virgibacillus
36	<a href="#">c6io1B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase, class iii; <b>PDBTitle:</b> crystal structure of a novel thermostable (s)-enantioselective omega-2 transaminase from thermomicrobium roseum
37	<a href="#">c5d95A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase class-iii; <b>PDBTitle:</b> structure of thermostable omega-transaminase
38	<a href="#">c4zm4B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> complex structure of pctv k276r mutant with pmp and 3-dehydroshkimate
39	<a href="#">c3nx3A_</a>	Alignment	not modelled	100.0	13	<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
40	<a href="#">c6erkB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of diaminopelargonic acid aminotransferase from2 psychrobacter cryohalolentis
41	<a href="#">c3oksB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-aminobutyrate transaminase; <b>PDBTitle:</b> crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis
42	<a href="#">d1kl1a_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
43	<a href="#">c4n0wA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> x-ray crystal structure of a serine hydroxymethyltransferase from2 burkholderia cenocepacia with covalently attached pyridoxal phosphate
44	<a href="#">c3bs8A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-1-semialdehyde 2,1-aminomutase; <b>PDBTitle:</b> crystal structure of glutamate 1-semialdehyde aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
45	<a href="#">d2gsaa_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
46	<a href="#">c3i4jC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aminotransferase, class iii; <b>PDBTitle:</b> crystal structure of aminotransferase, class iii from deinococcus2 radiodurans
47	<a href="#">c4atpD_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-aminobutyrate transaminase; <b>PDBTitle:</b> structure of gaba-transaminase a1r958 from arthrobacter aureescens in2 complex with plp
48	<a href="#">c5kqwD_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-aminobutyrate transaminase; <b>PDBTitle:</b> directed evolution of transaminases by ancestral reconstruction. using2 old proteins for new chemistries
49	<a href="#">c4aoaA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phenylalanine aminotransferase; <b>PDBTitle:</b> biochemical properties and crystal structure of a novel2 beta-phenylalanine aminotransferase from variovorax3 paradoxus
50	<a href="#">c4bhel_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> methanococcus jannaschii serine hydroxymethyltransferase2 in complex with plp
51	<a href="#">c3n0IA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
52	<a href="#">c3a8uX_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> omega-amino acid--pyruvate aminotransferase; <b>PDBTitle:</b> crystal structure of omega-amino acid:pyruvate aminotransferase

53	<a href="#">dlz7da1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
54	<a href="#">c4e3rC</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate transaminase; <b>PDBTitle:</b> plp-bound aminotransferase mutant crystal structure from vibrio2 fluvialis
55	<a href="#">c5i92E</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> glutamate-1-semialdehyde 2,1-aminomutase; <b>PDBTitle:</b> crystal structure of glutamate-1-semialdehyde 2,1-aminomutase (gsa)2 from pseudomonas aeruginosa
56	<a href="#">c3lv2A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate aminotransferase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
57	<a href="#">d1ohwa</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
58	<a href="#">c4ffcD</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 4-aminobutyrate aminotransferase (gabt); <b>PDBTitle:</b> crystal structure of a 4-aminobutyrate aminotransferase (gabt) from2 mycobacterium abscessus
59	<a href="#">c6g4dB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase family protein; <b>PDBTitle:</b> crystal structure of the omega transaminase from pseudomonas jessenii2 in complex with plp
60	<a href="#">c3bv0A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate aminotransferase; <b>PDBTitle:</b> crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 mycobacterium tuberculosis
61	<a href="#">c4j5uB</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> x-ray crystal structure of a serine hydroxymethyltransferase with2 covalently bound plp from rickettsia rickettsii str. sheila smith
62	<a href="#">c4a6tA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> omega transaminase; <b>PDBTitle:</b> crystal structure of the omega transaminase from chromobacterium2 violaceum in complex with plp
63	<a href="#">c5lhaC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> omega transaminase; <b>PDBTitle:</b> amine transaminase crystal structure from an uncultivated pseudomonas2 species in the pmp-bound form
64	<a href="#">c2ordA</a>	Alignment	not modelled	100.0	15	<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
65	<a href="#">c3i5tB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
66	<a href="#">d1vefa1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
67	<a href="#">d1dfoa</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
68	<a href="#">c4uoxB</a>	Alignment	not modelled	100.0	15	<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
69	<a href="#">c2ykyB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-transaminase; <b>PDBTitle:</b> structural determinants of the beta-selectivity of a bacterial2 aminotransferase
70	<a href="#">c4zm3C</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of plp-dependent 3-aminobenzoate synthase pctv wild-2 type
71	<a href="#">c4ysnD</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative 4-aminobutyrate aminotransferase; <b>PDBTitle:</b> structure of aminoacid racemase in complex with plp
72	<a href="#">c3lwsF</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> aromatic amino acid beta-eliminating lyase/threonine <b>PDBTitle:</b> crystal structure of putative aromatic amino acid beta-eliminating2 lyase/threonine aldolase. (yp_001813866.1) from exiguobacterium sp.3 255-15 at 2.00 a resolution
73	<a href="#">c4nogB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative ornithine aminotransferase, mitochondrial; <b>PDBTitle:</b> crystal structure of a putative ornithine aminotransferase from2 toxoplasma gondii me49 in complex with pyrodoxal-5'-phosphate
74	<a href="#">c2dkjB</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of t.th.hb8 serine hydroxymethyltransferase
75	<a href="#">c4wxfC</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of l-serine hydroxymethyltransferase in complex with2 glycine
						<b>PDB header:</b> transferase

76	<a href="#">c6gwiA_</a>	Alignment	not modelled	100.0	14	<b>Chain:</b> A: <b>PDB Molecule:</b> putrescine aminotransferase; <b>PDBTitle:</b> the crystal structure of halomonas elongata amino-transferase
77	<a href="#">c5ti8A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of an aspartate aminotransferase from pseudomonas
78	<a href="#">c3fcrA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> crystal structure of putative aminotransferase (yp_614685.1) from2 silicibacter sp. tm1040 at 1.80 a resolution
79	<a href="#">c3l44A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate-1-semialdehyde 2,1-aminomutase 1; <b>PDBTitle:</b> crystal structure of bacillus anthracis heml-1, glutamate semialdehyde2 aminotransferase
80	<a href="#">c6gioB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> amino acid amide racemase; <b>PDBTitle:</b> structure of amino acid amide racemase from ochrobactrum anthropi
81	<a href="#">c3pj0D_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> lmo0305 protein; <b>PDBTitle:</b> crystal structure of a putative l-allo-threonine aldolase (lmo0305)2 from listeria monocytogenes egd-e at 1.80 a resolution
82	<a href="#">d1sffa_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
83	<a href="#">c4ppmB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of pige: a transaminase involved in the biosynthesis2 of 2-methyl-3-n-amy-yl-pyrrole (map) from serratia sp. fs14
84	<a href="#">c2cy8A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-phenylglycine aminotransferase; <b>PDBTitle:</b> crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201
85	<a href="#">c5ykrB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable aminotransferase; <b>PDBTitle:</b> crystal structure of a glutamate-1-semialdehyde-aminomutase from2 pseudomonas aeruginosa pao1
86	<a href="#">c6iz9B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-transaminase; <b>PDBTitle:</b> crystal structure of the apo form of a beta-transaminase from2 mesorhizobium sp. strain luk
87	<a href="#">c3hmuA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase, class iii; <b>PDBTitle:</b> crystal structure of a class iii aminotransferase from silicibacter2 pomeroyi
88	<a href="#">c3dodA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononoate aminotransferase; <b>PDBTitle:</b> crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
89	<a href="#">c4o6zC_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase with covalently2 bound plp schiff-base from plasmodium falciparum
90	<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
91	<a href="#">c3hvyC_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cystathionine beta-lyase family protein, ynbb b.subtilis <b>PDBTitle:</b> crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution
92	<a href="#">c6cd1A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of medicago truncatula serine2 hydroxymethyltransferase 3 (mtshmt3), complexes with reaction3 intermediates
93	<a href="#">d1wsta1</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
94	<a href="#">c6cboB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> c-6' aminotransferase; <b>PDBTitle:</b> x-ray structure of genb1 from micromonospora echinospora in complex2 with neamine and plp (as the external aldimine)
95	<a href="#">d1svva_</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
96	<a href="#">c4obuG_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> pyridoxal-dependent decarboxylase domain protein; <b>PDBTitle:</b> ruminococcus gnavus tryptophan decarboxylase rumgna_01526 (apo)
97	<a href="#">d1m6sa_</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
98	<a href="#">c3ecdC_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> serine hydroxymethyltransferase 2; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
99	<a href="#">d1ejia_</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
100	<a href="#">d1qgna_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases

						<b>Family:</b> Cystathionine synthase-like
101	<a href="#">c4oc9N</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> N: <b>PDB Molecule:</b> putative o-acetylhomoserine (thiol)-lyase; <b>PDBTitle:</b> 2.35 angstrom resolution crystal structure of putative o-2 acetylhomoserine (thiol)-lyase (mety) from campylobacter jejuni3 subsp. jejuni nctc 11168 with n'-pyridoxyl-lysine-5'-monophosphate at4 position 205
102	<a href="#">c3f9tB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> l-tyrosine decarboxylase mfna; <b>PDBTitle:</b> crystal structure of l-tyrosine decarboxylase mfna (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution
103	<a href="#">c2ogeC</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> transaminase; <b>PDBTitle:</b> x-ray structure of s. venezuelae desv in its internal2 aldimine form
104	<a href="#">d1rv3a</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
105	<a href="#">c2x5dD</a>	Alignment	not modelled	100.0	16	<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
106	<a href="#">c3wgcB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> l-allo-threonine aldolase; <b>PDBTitle:</b> aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
107	<a href="#">c3n5mD</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononoate aminotransferase; <b>PDBTitle:</b> crystals structure of a bacillus anthracis aminotransferase
108	<a href="#">c6cbnA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> neamine transaminase neon; <b>PDBTitle:</b> x-ray structure of neob from streptomyces fradiae in complex with plp2 and neomycin (as the external aldimine) at ph 7.5
109	<a href="#">c5k8bA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-amino-3,8-dideoxy-alpha-d-manno-octulosonate <b>PDBTitle:</b> x-ray structure of kdna, 8-amino-3,8-dideoxy-alpha-d-manno-2 octulosonate transaminase, from shewanella oneidensis in the presence3 of the external aldimine with plp and glutamate
110	<a href="#">c4my5C</a>	Alignment	not modelled	100.0	15	<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
111	<a href="#">c3nysA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase wbpe; <b>PDBTitle:</b> x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution
112	<a href="#">c3e9kA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
113	<a href="#">c2cjdA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine-epsilon aminotransferase; <b>PDBTitle:</b> lysine aminotransferase from m. tuberculosis in external aldimine form
114	<a href="#">d1bj4a</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
115	<a href="#">c3frkB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> qdtb; <b>PDBTitle:</b> x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine
116	<a href="#">d1c4ka2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Ornithine decarboxylase major domain
117	<a href="#">c4j8lA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yhfs; <b>PDBTitle:</b> crystal structure of the pyridoxal-5'-phosphate dependent protein yhfs2 from escherichia coli
118	<a href="#">c4lnjA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> low-specificity l-threonine aldolase; <b>PDBTitle:</b> structure of escherichia coli threonine aldolase in unliganded form
119	<a href="#">d1o4sa</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="#">c3bcxA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; <b>PDBTitle:</b> e1 dehydrase