



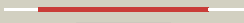



















# Phyre2

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Description	P50457
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3oksB_</a>	 Alignment		100.0	43	<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
2	<a href="#">d1sffa_</a>	 Alignment		100.0	55	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
3	<a href="#">c3fcrA_</a>	 Alignment		100.0	28	<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
4	<a href="#">c3n5mD_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate aminotransferase; <b>PDBTitle:</b> crystals structure of a bacillus anthracis aminotransferase
5	<a href="#">c3hmuA_</a>	 Alignment		100.0	25	<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 from2 silicibacter pomeroyi
6	<a href="#">d1s0aa_</a>	 Alignment		100.0	27	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
7	<a href="#">d1zoda1</a>	 Alignment		100.0	28	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
8	<a href="#">c3lv2A_</a>	 Alignment		100.0	25	<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
9	<a href="#">c3i5tB_</a>	 Alignment		100.0	26	<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
10	<a href="#">c3bv0A_</a>	 Alignment		100.0	25	<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
11	<a href="#">c3dxvA_</a>	 Alignment		100.0	32	<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

12	<a href="#">d1ohwa_</a>	Alignment		100.0	29	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
13	<a href="#">c2eo5A_</a>	Alignment		100.0	33	<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 sulfolobus2 tokodaii strain7
14	<a href="#">c2e7uA_</a>	Alignment		100.0	29	<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
15	<a href="#">d2gsaa_</a>	Alignment		100.0	26	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
16	<a href="#">c2cjdA_</a>	Alignment		100.0	27	<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 external2 aldimine form
17	<a href="#">c3bs8A_</a>	Alignment		100.0	24	<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
18	<a href="#">c3a8uX_</a>	Alignment		100.0	25	<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
19	<a href="#">d2byla1</a>	Alignment		100.0	32	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
20	<a href="#">c2zsmA_</a>	Alignment		100.0	26	<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
21	<a href="#">c1oatB_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> aminotransferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine aminotransferase; <b>PDBTitle:</b> ornithine aminotransferase
22	<a href="#">c3l44A_</a>	Alignment	not modelled	100.0	24	<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
23	<a href="#">c3nuiA_</a>	Alignment	not modelled	100.0	26	<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
24	<a href="#">c3ruiB_</a>	Alignment	not modelled	100.0	34	<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
25	<a href="#">d1vefa1</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
26	<a href="#">d1z7da1</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
27	<a href="#">c2pb2B_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetylornithine/succinyldiaminopimelate aminotransferase; <b>PDBTitle:</b> structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-

28	<a href="#">c3dodA_</a>	Alignment	not modelled	100.0	27	oxononanoate aminotransferase; <b>PDBTitle:</b> crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
29	<a href="#">c1z7dE_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> ornithine aminotransferase; <b>PDBTitle:</b> ornithine aminotransferase py00104 from plasmodium yoelii
30	<a href="#">c2cy8A_</a>	Alignment	not modelled	100.0	27	<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
31	<a href="#">c2ordA_</a>	Alignment	not modelled	100.0	35	<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
32	<a href="#">c3nx3A_</a>	Alignment	not modelled	100.0	32	<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
33	<a href="#">c3i4jC_</a>	Alignment	not modelled	100.0	28	<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 from2 deinococcus radiodurans
34	<a href="#">d2cfba1</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
35	<a href="#">c2eh6A_</a>	Alignment	not modelled	100.0	33	<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
36	<a href="#">c2w8wA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser
37	<a href="#">c3a2bA_</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> crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
38	<a href="#">d1fc4a_</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
39	<a href="#">d2bwna1</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
40	<a href="#">d1bs0a_</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
41	<a href="#">c3tqxA_</a>	Alignment	not modelled	100.0	16	<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
42	<a href="#">c3hqtB_</a>	Alignment	not modelled	100.0	16	<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
43	<a href="#">d1wsta1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
44	<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
45	<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
46	<a href="#">d1m6sa_</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
47	<a href="#">c2zc0C_</a>	Alignment	not modelled	100.0	15	<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
48	<a href="#">d1vp4a_</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
49	<a href="#">d1tpla_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
50	<a href="#">c3lwsF_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> aromatic amino acid beta-eliminating <b>PDBTitle:</b> crystal structure of putative aromatic amino acid beta-2 eliminating lyase/threonine aldolase. (yp_001813866.1) from3 exiguobacterium sp. 255-15 at 2.00 a resolution
51	<a href="#">d1c7ga_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
52	<a href="#">c3pplB_</a>	Alignment	not modelled	100.0	13	<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
53	<a href="#">d1c7na_</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like

54	<a href="#">c3jtxB_</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 aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
55	<a href="#">c2douA_</a>	Alignment	not modelled	100.0	13	<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
56	<a href="#">c3kaxB_</a>	Alignment	not modelled	100.0	11	<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
57	<a href="#">d1xi9a_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
58	<a href="#">c3ke3A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine-pyruvate aminotransferase; <b>PDBTitle:</b> crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution
59	<a href="#">c3l8aB_</a>	Alignment	not modelled	100.0	12	<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
60	<a href="#">d1svva_</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
61	<a href="#">c1ynuA_</a>	Alignment	not modelled	100.0	11	<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
62	<a href="#">d1o4sa_</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
63	<a href="#">d1b5pa_</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
64	<a href="#">d1iaya_</a>	Alignment	not modelled	100.0	8	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
65	<a href="#">d1v72a1</a>	Alignment	not modelled	100.0	9	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
66	<a href="#">d1lc5a_</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
67	<a href="#">c2x5dD_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> probable aminotransferase; <b>PDBTitle:</b> crystal structure of a probable aminotransferase from2 pseudomonas aeruginosa
68	<a href="#">c3b46B_</a>	Alignment	not modelled	100.0	15	<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
69	<a href="#">c3op7A_</a>	Alignment	not modelled	100.0	13	<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="#">d1w7la_</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
71	<a href="#">c3if2B_</a>	Alignment	not modelled	100.0	12	<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
72	<a href="#">d2r5ea1</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
73	<a href="#">d1v2da_</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
74	<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
75	<a href="#">d1j32a_</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
76	<a href="#">c3dc1A_</a>	Alignment	not modelled	100.0	14	<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
77	<a href="#">c3cbfA_</a>	Alignment	not modelled	100.0	17	<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
						<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative pyridoxal 5'-phosphate-

78	<a href="#">c3dzdB</a>	Alignment	not modelled	100.0	14	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
79	<a href="#">d1m7ya</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
80	<a href="#">c3e2yB</a>	Alignment	not modelled	100.0	15	<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
81	<a href="#">c3nraA</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> crystal structure of an aspartate aminotransferase (yp_354942.1) from2 rhodobacter sphaeroides 2.4.1 at 2.15 a resolution
82	<a href="#">c3h14A</a>	Alignment	not modelled	100.0	13	<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
83	<a href="#">d1u08a</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
84	<a href="#">c3qguB</a>	Alignment	not modelled	100.0	11	<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
85	<a href="#">d1ax4a</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
86	<a href="#">d2v1pa1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
87	<a href="#">c3fdbA</a>	Alignment	not modelled	100.0	11	<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
88	<a href="#">c3eibB</a>	Alignment	not modelled	100.0	12	<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
89	<a href="#">d2csta</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
90	<a href="#">c2o0rA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rv0858c (n-succinyl-diaminopimelate aminotransferase); <b>PDBTitle:</b> the three-dimensional structure of n-succinyl-diaminopimelate2 aminotransferase from mycobacterium tuberculosis
91	<a href="#">c3k7yA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> aspartate aminotransferase of plasmodium falciparum
92	<a href="#">d1gdea</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
93	<a href="#">c3g0tA</a>	Alignment	not modelled	99.9	15	<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
94	<a href="#">c2o1bA</a>	Alignment	not modelled	99.9	12	<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
95	<a href="#">c3pdxA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine aminotransferase; <b>PDBTitle:</b> crystal structural of mouse tyrosine aminotransferase
96	<a href="#">d7aata</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
97	<a href="#">c3d6kB</a>	Alignment	not modelled	99.9	13	<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
98	<a href="#">c3ftbA</a>	Alignment	not modelled	99.9	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
99	<a href="#">c3ezsB</a>	Alignment	not modelled	99.9	10	<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
100	<a href="#">c1d2fB</a>	Alignment	not modelled	99.9	12	<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
101	<a href="#">c3f9tB</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> l-tyrosine decarboxylase mfa; <b>PDBTitle:</b> crystal structure of l-tyrosine decarboxylase mfa (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution
						<b>Fold:</b> PLP-dependent transferase-like



102	<a href="#">d1ajsa_</a>	Alignment	not modelled	99.9	11	<b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
103	<a href="#">d2ay1a_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
104	<a href="#">d2gb3a1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
105	<a href="#">d2q7wa1</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
106	<a href="#">d1qz9a_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
107	<a href="#">d1yaaa_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
108	<a href="#">c3ihja_</a>	Alignment	not modelled	99.9	15	<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
109	<a href="#">c3tl8D_</a>	Alignment	not modelled	99.9	11	<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.
110	<a href="#">c3g7qA_</a>	Alignment	not modelled	99.9	13	<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
111	<a href="#">c3mebB_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> structure of cytoplasmic aspartate aminotransferase from giardia lamblia
112	<a href="#">d1d2fa_</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
113	<a href="#">c3getA_</a>	Alignment	not modelled	99.9	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
114	<a href="#">c3rq1A_</a>	Alignment	not modelled	99.9	11	<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
115	<a href="#">d1bw0a_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
116	<a href="#">c3dydB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine aminotransferase; <b>PDBTitle:</b> human tyrosine aminotransferase
117	<a href="#">c2x5fB_</a>	Alignment	not modelled	99.9	11	<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
118	<a href="#">c3hdoB_</a>	Alignment	not modelled	99.9	13	<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
119	<a href="#">c3asaA_</a>	Alignment	not modelled	99.9	15	<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
120	<a href="#">c3ly1C_</a>	Alignment	not modelled	99.9	12	<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