

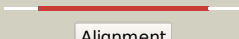

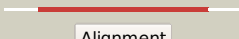











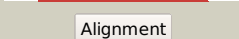







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1569_(bioF1)_1776708_1777868
Date	Fri Aug 2 13:30:16 BST 2019
Unique Job ID	4fe3f3481a28fdad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5txtA_</a>	 Alignment		100.0	27	<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="#">c3wy7D_</a>	 Alignment		100.0	76	<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
3	<a href="#">c6hrhA_</a>	 Alignment		100.0	29	<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
4	<a href="#">c2w8wA_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser
5	<a href="#">c3hqtB_</a>	 Alignment		100.0	21	<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="#">c3a2bA_</a>	 Alignment		100.0	28	<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
7	<a href="#">d2bwna1</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="#">d1bs0a_</a>	 Alignment		100.0	34	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
9	<a href="#">c3tqxA_</a>	 Alignment		100.0	28	<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
10	<a href="#">c5jayB_</a>	 Alignment		100.0	36	<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
11	<a href="#">d1fc4a_</a>	 Alignment		100.0	28	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like

12	<a href="#">c4iw7A_</a>	Alignment		100.0	25	<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="#">c4addD_</a>	Alignment		100.0	17	<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
14	<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
15	<a href="#">c4uoxB_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putrescine aminotransferase; <b>PDBTitle:</b> crystal structure of yggj in complex with pyridoxal-5'-phosphate2 and putrescine
16	<a href="#">c3ruyB_</a>	Alignment		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
17	<a href="#">c2eh6A_</a>	Alignment		100.0	16	<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
18	<a href="#">c2eo5A_</a>	Alignment		100.0	18	<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
19	<a href="#">c3nx3A_</a>	Alignment		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 (argd) from2 campylobacter jejuni
20	<a href="#">d1zoda1</a>	Alignment		100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
21	<a href="#">d2byla1</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
22	<a href="#">c4ysvA_</a>	Alignment	not modelled	100.0	17	<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 <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
23	<a href="#">c3dxvA_</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
24	<a href="#">c5g4iA_</a>	Alignment	not modelled	100.0	20	<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
25	<a href="#">c2ordA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> aminotransferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine aminotransferase; <b>PDBTitle:</b> ornithine aminotransferase
26	<a href="#">c1oatB_</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
27	<a href="#">d1vefa1</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of an aminotransferase from
28	<a href="#">c5yhvA_</a>	Alignment	not modelled	100.0	18	

					mycobacterium2 tuberculosis <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
29	<a href="#">c6fyqA_</a>	Alignment	not modelled	100.0	18
30	<a href="#">d1x0ma1</a>	Alignment	not modelled	100.0	13
31	<a href="#">c3h14A_</a>	Alignment	not modelled	100.0	19
32	<a href="#">d1wsta1</a>	Alignment	not modelled	100.0	14
33	<a href="#">c4nogB_</a>	Alignment	not modelled	100.0	18
34	<a href="#">c5viuB_</a>	Alignment	not modelled	100.0	15
35	<a href="#">d1sffa_</a>	Alignment	not modelled	100.0	16
36	<a href="#">c2pb2B_</a>	Alignment	not modelled	100.0	16
37	<a href="#">c4ffcD_</a>	Alignment	not modelled	100.0	18
38	<a href="#">c6erkB_</a>	Alignment	not modelled	100.0	17
39	<a href="#">c4e3rC_</a>	Alignment	not modelled	100.0	18
40	<a href="#">c5g2pA_</a>	Alignment	not modelled	100.0	20
41	<a href="#">c1z7dE_</a>	Alignment	not modelled	100.0	13
42	<a href="#">c3nuiA_</a>	Alignment	not modelled	100.0	17
43	<a href="#">c4ysnD_</a>	Alignment	not modelled	100.0	18
44	<a href="#">d1z7da1</a>	Alignment	not modelled	100.0	14
45	<a href="#">c3lv2A_</a>	Alignment	not modelled	100.0	19
46	<a href="#">c2zsmA_</a>	Alignment	not modelled	100.0	21
47	<a href="#">c2e7uA_</a>	Alignment	not modelled	100.0	18
48	<a href="#">d2r5ea1</a>	Alignment	not modelled	100.0	12
49	<a href="#">c5ghfB_</a>	Alignment	not modelled	100.0	16
50	<a href="#">c2ykyB_</a>	Alignment	not modelled	100.0	17
51	<a href="#">d1m6sa_</a>	Alignment	not modelled	100.0	18
52	<a href="#">c4zm4B_</a>	Alignment	not modelled	100.0	18

53	<a href="#">c3getA_</a>	Alignment	not modelled	100.0	12	<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
54	<a href="#">c4e77A_</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; <b>PDBTitle:</b> 2.0a crystal structure of a glutamate-1-semialdehyde aminotransferase2 from yersinia pestis co92
55	<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
56	<a href="#">c3bs8A_</a>	Alignment	not modelled	100.0	15	<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
57	<a href="#">c4aoaA_</a>	Alignment	not modelled	100.0	17	<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
58	<a href="#">c5i92E_</a>	Alignment	not modelled	100.0	17	<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
59	<a href="#">c3hdoB_</a>	Alignment	not modelled	100.0	16	<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
60	<a href="#">c3ly1C_</a>	Alignment	not modelled	100.0	14	<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
61	<a href="#">c4atpD_</a>	Alignment	not modelled	100.0	20	<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 aureus in2 complex with plp
62	<a href="#">c3wgcB_</a>	Alignment	not modelled	100.0	21	<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
63	<a href="#">c4a6tA_</a>	Alignment	not modelled	100.0	15	<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
64	<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
65	<a href="#">c4ppmB_</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 pige: a transaminase involved in the biosynthesis2 of 2-methyl-3-n-amy-l-pyrrole (map) from serratia sp. fs14
66	<a href="#">c6io1B_</a>	Alignment	not modelled	100.0	18	<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
67	<a href="#">c3bv0A_</a>	Alignment	not modelled	100.0	21	<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
68	<a href="#">d2gsaa_</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
69	<a href="#">d1b5pa_</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
70	<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
71	<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
72	<a href="#">c5h7dl_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase, immune system/metal binding <b>Chain:</b> I: <b>PDB Molecule:</b> putrescine aminotransferase,immunoglobulin g-binding <b>PDBTitle:</b> crystal structure of the ygjg-protein a-zpa963-calmodulin complex
73	<a href="#">c6g4dB_</a>	Alignment	not modelled	100.0	16	<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
74	<a href="#">c5ti8A_</a>	Alignment	not modelled	100.0	11	<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
75	<a href="#">c3i4jC_</a>	Alignment	not modelled	100.0	18	<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
76	<a href="#">c5d95A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase class-iii; <b>PDBTitle:</b> structure of thermostable omega-transaminase
77	<a href="#">d1ohwa_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
78	<a href="#">c3nraA_</a>	Alignment	not modelled	100.0	17	<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
79	<a href="#">c4r8dB_</a>	Alignment	not modelled	100.0	19	<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
80	<a href="#">d1lc5a_</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
81	<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
82	<a href="#">d1o4sa_</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
83	<a href="#">c4my5C_</a>	Alignment	not modelled	100.0	12	<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
84	<a href="#">c6gioB_</a>	Alignment	not modelled	100.0	23	<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
85	<a href="#">c3kaxB_</a>	Alignment	not modelled	100.0	10	<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
86	<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
87	<a href="#">d1xi9a_</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
88	<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
89	<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
90	<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
91	<a href="#">c3dodA_</a>	Alignment	not modelled	100.0	16	<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 bacillus subtilis
92	<a href="#">c2o0rA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rv0858c (n-succinylidiaminopimelate aminotransferase); <b>PDBTitle:</b> the three-dimensional structure of n-succinylidiaminopimelate2 aminotransferase from mycobacterium tuberculosis
93	<a href="#">c2x5dD_</a>	Alignment	not modelled	100.0	13	<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
94	<a href="#">d1vp4a_</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
95	<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
96	<a href="#">c3l8aB_</a>	Alignment	not modelled	100.0	14	<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
97	<a href="#">c3g0tA_</a>	Alignment	not modelled	100.0	12	<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
98	<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 hemI-1, glutamate semialdehyde2 aminotransferase
99	<a href="#">c6gwiA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putrescine aminotransferase; <b>PDBTitle:</b> the crystal structure of halomonas elongata amino-transferase
						<b>PDB header:</b> transferase



100	<a href="#">c3i5tB_</a>	Alignment	not modelled	100.0	12	<b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
101	<a href="#">c3bcxA_</a>	Alignment	not modelled	100.0	16	<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
102	<a href="#">c6cboB_</a>	Alignment	not modelled	100.0	19	<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)
103	<a href="#">c3pj0D_</a>	Alignment	not modelled	100.0	17	<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
104	<a href="#">c5lhaC_</a>	Alignment	not modelled	100.0	19	<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
105	<a href="#">c4zm3C_</a>	Alignment	not modelled	100.0	19	<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
106	<a href="#">c3b46B_</a>	Alignment	not modelled	100.0	13	<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
107	<a href="#">c3dzzB_</a>	Alignment	not modelled	100.0	14	<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
108	<a href="#">c3ftbA_</a>	Alignment	not modelled	100.0	12	<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="#">c5ykrB_</a>	Alignment	not modelled	100.0	22	<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
110	<a href="#">c2po3B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-dehydrase; <b>PDBTitle:</b> crystal structure analysis of desi in the presence of its2 tdp-sugar product
111	<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 )
112	<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
113	<a href="#">c4lnjA_</a>	Alignment	not modelled	100.0	19	<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
114	<a href="#">c3b1dD_</a>	Alignment	not modelled	100.0	13	<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
115	<a href="#">c3e2yB_</a>	Alignment	not modelled	100.0	13	<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
116	<a href="#">d1w7la_</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
117	<a href="#">c3qguB_</a>	Alignment	not modelled	100.0	16	<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
118	<a href="#">c4fl0A_</a>	Alignment	not modelled	100.0	12	<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
119	<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
120	<a href="#">d1j32a_</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