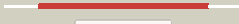



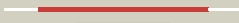



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2589_(gabT)_2916370_2917719
Date	Wed Aug 7 12:50:23 BST 2019
Unique Job ID	41a15a42c76d4008

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3oksB_</a>	 Alignment		100.0	78	<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="#">c4atpD_</a>	 Alignment		100.0	63	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> 4-aminobutyrate transaminase; <b>PDBTitle:</b> crystal structure of gaba-transaminase a1r958 from arthrobacter aurescens in2 complex with plp
3	<a href="#">c4ffcD_</a>	 Alignment		100.0	65	<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
4	<a href="#">c5h7dI_</a>	 Alignment		100.0	33	<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 ygig-protein a-zpa963-calmodulin complex
5	<a href="#">c4ysnD_</a>	 Alignment		100.0	31	<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
6	<a href="#">c3n5mD_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxonanoate aminotransferase; <b>PDBTitle:</b> crystals structure of a bacillus anthracis aminotransferase
7	<a href="#">c3fcrA_</a>	 Alignment		100.0	23	<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
8	<a href="#">d1ohwa_</a>	 Alignment		100.0	28	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
9	<a href="#">c6gioB_</a>	 Alignment		100.0	32	<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
10	<a href="#">c4a0rB_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxonanoate <b>PDBTitle:</b> structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana bound to dethiobiotin (dtb).
11	<a href="#">c3hmuA_</a>	 Alignment		100.0	24	<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

12	<a href="#">c5lhaC_</a>	Alignment		100.0	32	<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
13	<a href="#">c5kqwD_</a>	Alignment		100.0	26	<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
14	<a href="#">c4a6tA_</a>	Alignment		100.0	28	<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
15	<a href="#">c5ddwD_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> crmg; <b>PDBTitle:</b> crystal structure of aminotransferase crmg from actinoalloteichus sp.2 wh1-2216-6 in complex with the pmp external aldimine adduct with3 caerulomycin m
16	<a href="#">c6gwiA_</a>	Alignment		100.0	28	<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
17	<a href="#">c6g4dB_</a>	Alignment		100.0	27	<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
18	<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
19	<a href="#">c4e3rC_</a>	Alignment		100.0	29	<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
20	<a href="#">c6io1B_</a>	Alignment		100.0	30	<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
21	<a href="#">d1sffa_</a>	Alignment	not modelled	100.0	43	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
22	<a href="#">d1zoda1</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
23	<a href="#">c2cjdA_</a>	Alignment	not modelled	100.0	26	<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
24	<a href="#">c3a8uX_</a>	Alignment	not modelled	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
25	<a href="#">c2eo5A_</a>	Alignment	not modelled	100.0	30	<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
26	<a href="#">c3dxvA_</a>	Alignment	not modelled	100.0	34	<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
27	<a href="#">c4uoxB_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putrescine aminotransferase; <b>PDBTitle:</b> crystal structure of ygjg in complex with pyridoxal-5'-phosphate2 and putrescine
28	<a href="#">c5g2nA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transaminase;

28	<a href="#">c3g2pA</a>	Alignment	not modelled	100.0	28	<b>PDBTitle:</b> the crystal structure of a s-selective transaminase from2 arthrobacter sp.
29	<a href="#">c5ghfB</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase class-iii; <b>PDBTitle:</b> transaminase with l-ala
30	<a href="#">c2e7uA</a>	Alignment	not modelled	100.0	28	<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
31	<a href="#">c3bv0A</a>	Alignment	not modelled	100.0	28	<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
32	<a href="#">c3lv2A</a>	Alignment	not modelled	100.0	28	<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
33	<a href="#">c5g4iA</a>	Alignment	not modelled	100.0	27	<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
34	<a href="#">d1s0aa</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="#">c4nogB</a>	Alignment	not modelled	100.0	31	<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
36	<a href="#">c5ykrB</a>	Alignment	not modelled	100.0	23	<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
37	<a href="#">d2gsaa</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
38	<a href="#">c5d95A</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase class-iii; <b>PDBTitle:</b> structure of thermostable omega-transaminase
39	<a href="#">c3bs8A</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; <b>PDBTitle:</b> crystal structure of glutamate 1-semialdehyde aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
40	<a href="#">c4ppmB</a>	Alignment	not modelled	100.0	29	<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-amylyl-pyrrole (map) from serratia sp. fs14
41	<a href="#">c2ykyB</a>	Alignment	not modelled	100.0	23	<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
42	<a href="#">c2zsmA</a>	Alignment	not modelled	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
43	<a href="#">c3nuiA</a>	Alignment	not modelled	100.0	30	<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
44	<a href="#">c4a0gC</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate <b>PDBTitle:</b> structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana in its apo form.
45	<a href="#">c4zm4B</a>	Alignment	not modelled	100.0	27	<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
46	<a href="#">d2byla1</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
47	<a href="#">c4e77A</a>	Alignment	not modelled	100.0	27	<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
48	<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 hemI-1, glutamate semialdehyde2 aminotransferase
49	<a href="#">c6fyqA</a>	Alignment	not modelled	100.0	27	<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
50	<a href="#">c4ysvA</a>	Alignment	not modelled	100.0	34	<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> aminotransferase

51	<a href="#">c1oatB_</a>	Alignment	not modelled	100.0	31	<b>Chain:</b> B: <b>PDB Molecule:</b> ornithine aminotransferase; <b>PDBTitle:</b> ornithine aminotransferase
52	<a href="#">c4addD_</a>	Alignment	not modelled	100.0	33	<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
53	<a href="#">c4aoaA_</a>	Alignment	not modelled	100.0	24	<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
54	<a href="#">c6erkB_</a>	Alignment	not modelled	100.0	26	<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
55	<a href="#">c3ruyB_</a>	Alignment	not modelled	100.0	33	<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
56	<a href="#">c6iz9B_</a>	Alignment	not modelled	100.0	22	<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
57	<a href="#">c2pb2B_</a>	Alignment	not modelled	100.0	32	<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
58	<a href="#">d1z7da1</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
59	<a href="#">c5viuB_</a>	Alignment	not modelled	100.0	35	<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
60	<a href="#">d1vefa1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
61	<a href="#">c6cbnA_</a>	Alignment	not modelled	100.0	25	<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
62	<a href="#">c5i92E_</a>	Alignment	not modelled	100.0	26	<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
63	<a href="#">c3dodA_</a>	Alignment	not modelled	100.0	29	<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
64	<a href="#">c1z7dE_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> ornithine aminotransferase; <b>PDBTitle:</b> ornithine aminotransferase py00104 from plasmodium yoelii
65	<a href="#">c2ordA_</a>	Alignment	not modelled	100.0	30	<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
66	<a href="#">c2cy8A_</a>	Alignment	not modelled	100.0	25	<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
67	<a href="#">c3nx3A_</a>	Alignment	not modelled	100.0	29	<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
68	<a href="#">c5ti8A_</a>	Alignment	not modelled	100.0	28	<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
69	<a href="#">c6cboB_</a>	Alignment	not modelled	100.0	21	<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)
70	<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 from deinococcus2 radiodurans
71	<a href="#">c4zm3C_</a>	Alignment	not modelled	100.0	26	<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
72	<a href="#">c2eh6A_</a>	Alignment	not modelled	100.0	34	<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
73	<a href="#">d2cfba1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
74	<a href="#">c2w8wA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser
75	<a href="#">d1fc4a_</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

76	<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
77	<a href="#">c6hrhA</a>	Alignment	not modelled	100.0	14	<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
78	<a href="#">c5txtA</a>	Alignment	not modelled	100.0	15	<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
79	<a href="#">c3tqxA</a>	Alignment	not modelled	100.0	14	<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
80	<a href="#">d2bwna1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
81	<a href="#">d1bs0a</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
82	<a href="#">c5jayB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 8-amino-7-oxonanoate synthase; <b>PDBTitle:</b> crystal structure of an 8-amino-7-oxonanoate synthase from2 burkholderia xenovorans
83	<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 cgsa
84	<a href="#">c3wy7D</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 8-amino-7-oxonanoate synthase; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
85	<a href="#">c4iw7A</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-amino-7-oxonanoate synthase; <b>PDBTitle:</b> crystal structure of 8-amino-7-oxonanoate synthase (biof) from2 francisella tularensis.
86	<a href="#">d1wsta1</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
87	<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
88	<a href="#">c3wgcB</a>	Alignment	not modelled	100.0	14	<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
89	<a href="#">c3ke3A</a>	Alignment	not modelled	100.0	12	<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
90	<a href="#">d1m6sa</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
91	<a href="#">d1x0ma1</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
92	<a href="#">d1c7ga</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
93	<a href="#">c5yhvA</a>	Alignment	not modelled	100.0	16	<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
94	<a href="#">c3lwsF</a>	Alignment	not modelled	100.0	14	<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
95	<a href="#">d1tpla</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
96	<a href="#">d1xi9a</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
97	<a href="#">c2zc0C</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> alanine glyoxylate transaminase; <b>PDBTitle:</b> crystal structure of an archaean alanine:glyoxylate aminotransferase
98	<a href="#">d1c7na</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
99	<a href="#">c4lnjA</a>	Alignment	not modelled	100.0	17	<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
100	<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

101	<a href="#">d1b5pa_</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
102	<a href="#">d1j32a_</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
103	<a href="#">d1vp4a_</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
104	<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
105	<a href="#">c3jtxB_</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 (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
106	<a href="#">c2douA_</a>	Alignment	not modelled	99.9	17	<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
107	<a href="#">d1qz9a_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
108	<a href="#">c3op7A_</a>	Alignment	not modelled	99.9	14	<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
109	<a href="#">c3kaxB_</a>	Alignment	not modelled	99.9	13	<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
110	<a href="#">d1svva_</a>	Alignment	not modelled	99.9	9	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
111	<a href="#">c3f9tB_</a>	Alignment	not modelled	99.9	13	<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
112	<a href="#">c6c3aB_</a>	Alignment	not modelled	99.9	10	<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
113	<a href="#">d1v72a1</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
114	<a href="#">c3b1dD_</a>	Alignment	not modelled	99.9	14	<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="#">c3l8aB_</a>	Alignment	not modelled	99.9	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
116	<a href="#">c2x5dD_</a>	Alignment	not modelled	99.9	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 from pseudomonas2 aeruginosa
117	<a href="#">c4my5C_</a>	Alignment	not modelled	99.9	14	<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
118	<a href="#">d2v1pa1</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
119	<a href="#">c6hndA_</a>	Alignment	not modelled	99.9	12	<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
120	<a href="#">c3ftbA_</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> the crystal structure of the histidinol-phosphate aminotransferase2 from clostridium acetobutylicum