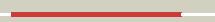
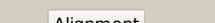
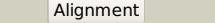
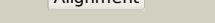
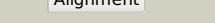
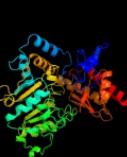
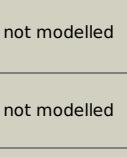


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD1655_(argD)_1868730_1869932
Date	Fri Aug 2 13:30:25 BST 2019
Unique Job ID	3ce61a395aa00636

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5h7dl</a>			100.0	37	<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
2	<a href="#">c3n5mD</a>			100.0	32	<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
3	<a href="#">c3fcra</a>			100.0	29	<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="#">c4ysnD</a>			100.0	32	<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
5	<a href="#">c4nogB</a>			100.0	33	<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 pyridoxal-5'-phosphate
6	<a href="#">c4addD</a>			100.0	42	<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
7	<a href="#">c4a0rB</a>			100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate <b>PDBTitle:</b> structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana bound to dethiobiotin (dtb).
8	<a href="#">c3ruyB</a>			100.0	37	<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
9	<a href="#">d1vefa1</a>			100.0	44	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
10	<a href="#">c5lhaC</a>			100.0	31	<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
11	<a href="#">c3hmuA</a>			100.0	29	<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="#">c4uoxB</a>	Alignment		100.0	37	<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
13	<a href="#">c4a6tA</a>	Alignment		100.0	31	<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
14	<a href="#">c4e3rC</a>	Alignment		100.0	27	<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
15	<a href="#">c6g4dB</a>	Alignment		100.0	32	<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
16	<a href="#">c4atpD</a>	Alignment		100.0	35	<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 aurescens in2 complex with plp
17	<a href="#">c6io1B</a>	Alignment		100.0	35	<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
18	<a href="#">c3a8uX</a>	Alignment		100.0	30	<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	35	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
20	<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
21	<a href="#">c5kqwD</a>	Alignment	not modelled	100.0	30	<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
22	<a href="#">c1oatB</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> aminotransferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine aminotransferase; <b>PDBTitle:</b> ornithine aminotransferase
23	<a href="#">c6gwiA</a>	Alignment	not modelled	100.0	29	<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
24	<a href="#">c3i5tB</a>	Alignment	not modelled	100.0	28	<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
25	<a href="#">c2ordA</a>	Alignment	not modelled	100.0	40	<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
26	<a href="#">c5g2pA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transaminase; <b>PDBTitle:</b> the crystal structure of a s-selective transaminase from2 arthrobacter sp.
27	<a href="#">d1ohwa</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
28	<a href="#">d1zoda1</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

29	<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-diaminopelargonic acid synthase in complex with substrate analog sinefungin
30	<a href="#">d1s0aa</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
31	<a href="#">c3oksB</a>	Alignment	not modelled	100.0	35	<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 mycobacterium smegmatis
32	<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
33	<a href="#">c6erkB</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of diaminopelargonic acid aminotransferase from psychrobacter cryohalolentis
34	<a href="#">c4ffcD</a>	Alignment	not modelled	100.0	38	<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) from mycobacterium abscessus
35	<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
36	<a href="#">c2pb2B</a>	Alignment	not modelled	100.0	40	<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 from salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
37	<a href="#">c5ddwD</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> crmg; <b>PDBTitle:</b> crystal structure of aminotransferase crmg from actinomycete sp.2 wh1-2216-6 in complex with the pmp external aldimine adduct with3 caerulomycin m
38	<a href="#">c2eo5A</a>	Alignment	not modelled	100.0	36	<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 sulfobolus2 tokodaii strain7
39	<a href="#">c4ppmB</a>	Alignment	not modelled	100.0	36	<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-amyl-pyrrole (map) from serratia sp. fs14
40	<a href="#">c3dxvA</a>	Alignment	not modelled	100.0	33	<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
41	<a href="#">d1sffa</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
42	<a href="#">c5ghfB</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase class-iii; <b>PDBTitle:</b> transaminase with l-alanine
43	<a href="#">c3nx3A</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 (argd) from2 campylobacter jejuni
44	<a href="#">c3bs8A</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> crystal structure of glutamate 1-semialdehyde aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
45	<a href="#">c2e7uA</a>	Alignment	not modelled	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
46	<a href="#">c2kykB</a>	Alignment	not modelled	100.0	28	<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
47	<a href="#">d2gsaa</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
48	<a href="#">c2eh6A</a>	Alignment	not modelled	100.0	41	<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
49	<a href="#">c5ykrB</a>	Alignment	not modelled	100.0	26	<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
50	<a href="#">d1z7da1</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
51	<a href="#">c5viuB</a>	Alignment	not modelled	100.0	36	<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

52	<a href="#">c5d95A</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase class-iii; <b>PDBTitle:</b> structure of thermostable omega-transaminase
53	<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
54	<a href="#">c2zsmA</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> crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form
55	<a href="#">c4zm4B</a>	Alignment	not modelled	100.0	29	<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-dehydroshikimate
56	<a href="#">c6fyqA</a>	Alignment	not modelled	100.0	31	<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
57	<a href="#">c3l44A</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 1; <b>PDBTitle:</b> crystal structure of bacillus anthracis heml-1, glutamate semialdehyde2 aminotransferase
58	<a href="#">c5g4iA</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholyase; <b>PDBTitle:</b> plp-dependent phospholyase a1rdf1 from arthrobacter aurescens tc1
59	<a href="#">c4e77A</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> 2.0a crystal structure of a glutamate-1-semialdehyde aminotransferase2 from yersinia pestis co92
60	<a href="#">c1z7dE</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> ornithine aminotransferase; <b>PDBTitle:</b> ornithine aminotransferase py00104 from plasmodium yoelii
61	<a href="#">c3dodA</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 bacillus subtilis
62	<a href="#">c4aoaA</a>	Alignment	not modelled	100.0	27	<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
63	<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.
64	<a href="#">c5i92E</a>	Alignment	not modelled	100.0	24	<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
65	<a href="#">c6iz9B</a>	Alignment	not modelled	100.0	26	<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
66	<a href="#">c6cbnA</a>	Alignment	not modelled	100.0	23	<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
67	<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
68	<a href="#">c5ti8A</a>	Alignment	not modelled	100.0	25	<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="#">c3i4jC</a>	Alignment	not modelled	100.0	32	<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
70	<a href="#">c2cy8A</a>	Alignment	not modelled	100.0	26	<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-phgt) from2 pseudomonas strutzeri st-201
71	<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)
72	<a href="#">c4zm3C</a>	Alignment	not modelled	100.0	28	<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
73	<a href="#">d2cfba1</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
74	<a href="#">c2w8wA</a>	Alignment	not modelled	100.0	18	<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	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
						<b>PDB header:</b> oxidoreductase

76	<a href="#">c6hrhA</a>	Alignment	not modelled	100.0	18	<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
77	<a href="#">c3a2bA</a>	Alignment	not modelled	100.0	18	<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
78	<a href="#">d2bwna1</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
79	<a href="#">d1bs0a</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
80	<a href="#">c5txtA</a>	Alignment	not modelled	100.0	18	<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
81	<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
82	<a href="#">c5jayB</a>	Alignment	not modelled	100.0	20	<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
83	<a href="#">c3hqtB</a>	Alignment	not modelled	100.0	15	<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
84	<a href="#">c3wy7D</a>	Alignment	not modelled	100.0	23	<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
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-oxononanoate synthase; <b>PDBTitle:</b> crystal structure of 8-amino-7-oxononanoate synthase (biof) from2 francisella tularensis.
86	<a href="#">c3wgcB</a>	Alignment	not modelled	100.0	18	<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
87	<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
88	<a href="#">c3ke3A</a>	Alignment	not modelled	100.0	18	<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
89	<a href="#">c3pj0D</a>	Alignment	not modelled	100.0	13	<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
90	<a href="#">d1gq9a</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
91	<a href="#">d1m6sa</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
92	<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
93	<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
94	<a href="#">d1svva</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
95	<a href="#">c4q76B</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase 2, chloroplastic; <b>PDBTitle:</b> crystal structure of nfs2 c384s mutant, the plastidial cysteine2 desulfurase from arabidopsis thaliana
96	<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
97	<a href="#">d1c7na</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
98	<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
99	<a href="#">c3mafB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of stspl (asymmetric form)
100	<a href="#">c6c9eB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
101	<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
102	<a href="#">c3jtxB_</a>	Alignment	not modelled	100.0	<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
103	<a href="#">d1lc5a_</a>	Alignment	not modelled	100.0	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
104	<a href="#">c3h14A_</a>	Alignment	not modelled	100.0	<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
105	<a href="#">c3kaxB_</a>	Alignment	not modelled	100.0	<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
106	<a href="#">c4InjA_</a>	Alignment	not modelled	100.0	<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
107	<a href="#">c3fdbA_</a>	Alignment	not modelled	100.0	<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
108	<a href="#">c2zc0C_</a>	Alignment	not modelled	100.0	<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
109	<a href="#">c3lwsF_</a>	Alignment	not modelled	100.0	<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
110	<a href="#">c3b1dD_</a>	Alignment	not modelled	100.0	<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 in complex with l-serine: external aldimine form
111	<a href="#">d1b5pa_</a>	Alignment	not modelled	100.0	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
112	<a href="#">c5wt2A_</a>	Alignment	not modelled	100.0	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine desulfurase iscs; <b>PDBTitle:</b> nifs from helicobacter pylori
113	<a href="#">c3e9kA_</a>	Alignment	not modelled	100.0	<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
114	<a href="#">c2hzpA_</a>	Alignment	not modelled	100.0	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase
115	<a href="#">c4fl0A_</a>	Alignment	not modelled	100.0	<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
116	<a href="#">c4w91C_</a>	Alignment	not modelled	100.0	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp
117	<a href="#">d1v72a1</a>	Alignment	not modelled	100.0	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
118	<a href="#">c3b46B_</a>	Alignment	not modelled	100.0	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase bna3; <b>PDBTitle:</b> crystal structure of bna3p, a putative kynurene2 aminotransferase from saccharomyces cerevisiae
119	<a href="#">d1jf9a_</a>	Alignment	not modelled	100.0	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
120	<a href="#">c3g0tA_</a>	Alignment	not modelled	100.0	<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