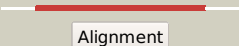



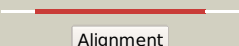





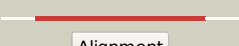













Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2321c_(rocD2)_2594164_2594709
Date	Mon Aug 5 13:25:47 BST 2019
Unique Job ID	3abd2dcb3a6d0f72

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5h7dL_	 Alignment		100.0	33	PDB header: transferase, immune system/metal binding Chain: I: PDB Molecule: putrescine aminotransferase,immunoglobulin g-binding PDBTitle: crystal structure of the ygjg-protein a-zpa963-calmodulin complex
2	c4a0rB_	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana bound to dethiobiotin (dtb).
3	c3n5mD_	 Alignment		100.0	30	PDB header: transferase Chain: D: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystals structure of a bacillus anthracis aminotransferase
4	c3fcrA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of putative aminotransferase (yp_614685.1) from2 silicibacter sp. tm1040 at 1.80 a resolution
5	c5ddwD_	 Alignment		100.0	30	PDB header: transferase Chain: D: PDB Molecule: crmg; PDBTitle: crystal structure of aminotransferase crmg from actinoalloteichus sp.2 wh1-2216-6 in complex with the pmp external aldimine adduct with3 caerulomycin m
6	c4a0gC_	 Alignment		100.0	20	PDB header: transferase Chain: C: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana in its apo form.
7	c3hmuA_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of a class iii aminotransferase from silicibacter2 pomeroyi
8	c5lhaC_	 Alignment		100.0	31	PDB header: transferase Chain: C: PDB Molecule: omega transaminase; PDBTitle: amine transaminase crystal structure from an uncultivated pseudomonas2 species in the pmp-bound form
9	c3lv2A_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
10	c2cjdA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: l-lysine-epsilon aminotransferase; PDBTitle: lysine aminotransferase from m. tuberculosis in external aldimine form
11	c4ysnD_	 Alignment		100.0	27	PDB header: isomerase Chain: D: PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in complex with plp

12	c4a6tA_	Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: omega transaminase; PDBTitle: crystal structure of the omega transaminase from chromobacterium2 violaceum in complex with plp
13	c3i5tB_	Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
14	c6gioB_	Alignment		100.0	32	PDB header: isomerase Chain: B: PDB Molecule: amino acid amide racemase; PDBTitle: structure of amino acid amide racemase from ochrobactrum anthropi
15	c6g4dB_	Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase family protein; PDBTitle: crystal structure of the omega transaminase from pseudomonas jessenii2 in complex with plp
16	c5kqwD_	Alignment		100.0	31	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: directed evolution of transaminases by ancestral reconstruction. using2 old proteins for new chemistries
17	c5g2pA_	Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: transaminase; PDBTitle: the crystal structure of a s-selective transaminase from2 arthrobacter sp.
18	c5ghfB_	Alignment		100.0	28	PDB header: transferase Chain: B: PDB Molecule: aminotransferase class-iii; PDBTitle: transaminase with l-ala
19	c4atpD_	Alignment		100.0	32	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: structure of gaba-transaminase a1r958 from arthrobacter aurescens in2 complex with plp
20	c4nogB_	Alignment		100.0	39	PDB header: transferase Chain: B: PDB Molecule: putative ornithine aminotransferase, mitochondrial; PDBTitle: crystal structure of a putative ornithine aminotransferase from2 toxoplasma gondii me49 in complex with pyrodoxal-5'-phosphate
21	d1ohwa_	Alignment	not modelled	100.0	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
22	c6gwiA_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: putrescine aminotransferase; PDBTitle: the crystal structure of halomonas elongata amino-transferase
23	c3oksB_	Alignment	not modelled	100.0	30	PDB header: transferase Chain: B: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis
24	c4e3rC_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: C: PDB Molecule: pyruvate transaminase; PDBTitle: plp-bound aminotransferase mutant crystal structure from vibrio2 fluvialis
25	c3bv0A_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 mycobacterium tuberculosis
26	c6io1B_	Alignment	not modelled	100.0	30	PDB header: transferase Chain: B: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of a novel thermostable (s)-enantioselective omega-2 transaminase from thermomicrobium roseum
27	d1z7da1	Alignment	not modelled	100.0	34	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
28	c3a8uX_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: X: PDB Molecule: omega-amino acid--pyruvate aminotransferase;

						PDBTitle: crystal structure of omega-amino acid:pyruvate aminotransferase
29	c4uoxB_	Alignment	not modelled	100.0	33	PDB header: transferase Chain: B: PDB Molecule: putrescine aminotransferase; PDBTitle: crystal structure of yggj in complex with pyridoxal-5'-phosphate2 and putrescine
30	c1z7dE_	Alignment	not modelled	100.0	34	PDB header: transferase Chain: E: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase py00104 from plasmodium yoelii
31	d2byla1	Alignment	not modelled	100.0	39	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
32	c5viuB_	Alignment	not modelled	100.0	38	PDB header: transferase Chain: B: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from2 elizabethkingia anophelis
33	c3dxvA_	Alignment	not modelled	100.0	32	PDB header: isomerase Chain: A: PDB Molecule: alpha-amino-epsilon-caprolactam racemase; PDBTitle: the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
34	c1oatB_	Alignment	not modelled	100.0	40	PDB header: aminotransferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase
35	c4ffcD_	Alignment	not modelled	100.0	31	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate aminotransferase (gabt); PDBTitle: crystal structure of a 4-aminobutyrate aminotransferase (gabt) from2 mycobacterium abscessus
36	d1s0aa_	Alignment	not modelled	100.0	28	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
37	c6erkB_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of diaminopelargonic acid aminotransferase from2 psychrobacter cryohalolentis
38	c2eo5A_	Alignment	not modelled	100.0	30	PDB header: transferase Chain: A: PDB Molecule: 419aa long hypothetical aminotransferase; PDBTitle: crystal structure of 4-aminobutyrate aminotransferase from sulfolobus2 tokodaii strain7
39	c3nuiA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: pyruvate transaminase; PDBTitle: crystal structure of omega-transferase from vibrio fluvialis js17
40	d1zoda1	Alignment	not modelled	100.0	33	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
41	c4addD_	Alignment	not modelled	100.0	31	PDB header: transferase Chain: D: PDB Molecule: succinylornithine transaminase; PDBTitle: structural and functional study of succinyl-ornithine transaminase2 from e. coli
42	c3ruyB_	Alignment	not modelled	100.0	38	PDB header: transferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis
43	c3dodA_	Alignment	not modelled	100.0	31	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
44	c6cbnA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: neamine transaminase neon; PDBTitle: x-ray structure of neob from streptomyces fradiae in complex with plp2 and neomycin (as the external aldimine) at ph 7.5
45	c5g4iA_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A: PDB Molecule: phosphorylase; PDBTitle: plp-dependent phosphorylase a1rdf1 from arthrobacter aureus tc1
46	c2e7uA_	Alignment	not modelled	100.0	26	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate-1-semialdehyde 2,1-aminomutase from2 thermus thermophilus hb8
47	c4ppmB_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of pige: a transaminase involved in the biosynthesis2 of 2-methyl-3-n-amy-l-pyrrole (map) from serratia sp. fs14
48	d1sffa_	Alignment	not modelled	100.0	29	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
49	c2pb2B_	Alignment	not modelled	100.0	31	PDB header: transferase Chain: B: PDB Molecule: acetylornithine/succinyl-diaminopimelate aminotransferase; PDBTitle: structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
50	c3bs8A_	Alignment	not modelled	100.0	25	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate 1-semialdehyde aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
51	d2gsaa_	Alignment	not modelled	100.0	23	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
						Fold: PLP-dependent transferase-like

52	d1vefa1	Alignment	not modelled	100.0	34	Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
53	c6fyqA	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: amine transaminase; PDBTitle: the crystal structure of a new transaminase from the marine bacterium2 virgibacillus
54	c3nx3A	Alignment	not modelled	100.0	29	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
55	c2ykyB	Alignment	not modelled	100.0	24	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: structural determinants of the beta-selectivity of a bacterial2 aminotransferase
56	c2zsmA	Alignment	not modelled	100.0	20	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form
57	c4e77A	Alignment	not modelled	100.0	22	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: 2.0a crystal structure of a glutamate-1-semialdehyde aminotransferase2 from yersinia pestis co92
58	c5ti8A	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aspartate aminotransferase from pseudomonas
59	c3i4jC	Alignment	not modelled	100.0	31	PDB header: transferase Chain: C: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of aminotransferase, class iii from deinococcus2 radiodurans
60	c2ordA	Alignment	not modelled	100.0	31	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution
61	c6cboB	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: c-6' aminotransferase; PDBTitle: x-ray structure of genb1 from micromonospora echinospora in complex2 with neamine and plp (as the external aldimine)
62	c4ysvA	Alignment	not modelled	100.0	28	PDB header: isomerase Chain: A: PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in apo-form
63	c4zm4B	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: complex structure of pctv k276r mutant with pmp and 3-dehydroshkimate
64	c5ykrB	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a glutamate-1-semialdehyde-aminomutase from2 pseudomonas aeruginosa pao1
65	c5d95A	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class-iii; PDBTitle: structure of thermostable omega-transaminase
66	c4aooA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: beta-phenylalanine aminotransferase; PDBTitle: biochemical properties and crystal structure of a novel2 beta-phenylalanine aminotransferase from variovorax3 paradoxus
67	c3i44A	Alignment	not modelled	100.0	22	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase 1; PDBTitle: crystal structure of bacillus anthracis heml-1, glutamate semialdehyde2 aminotransferase
68	c2cy8A	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: d-phenylglycine aminotransferase; PDBTitle: crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201
69	c2eh6A	Alignment	not modelled	100.0	38	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
70	c6iz9B	Alignment	not modelled	99.9	19	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: crystal structure of the apo form of a beta-transaminase from2 mesorhizobium sp. strain luk
71	c5i92E	Alignment	not modelled	99.9	21	PDB header: isomerase Chain: E: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate-1-semialdehyde 2,1-aminomutase (gsa)2 from pseudomonas aeruginosa
72	d2cfba1	Alignment	not modelled	99.9	23	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
73	c4zm3C	Alignment	not modelled	99.9	19	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of plp-dependent 3-aminobenzoate synthase pctv wild-2 type
74	c5txtA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinate synthase, mitochondrial; PDBTitle: structure of asymmetric apo/holo alas dimer from s. cerevisiae
75	c6hrhA	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 5-aminolevulinate synthase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
						Fold: PLP-dependent transferase-like

76	d2bwna1	Alignment	not modelled	99.7	19	Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
77	d1fc4a	Alignment	not modelled	99.7	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
78	c3tqxA	Alignment	not modelled	99.7	14	PDB header: transferase Chain: A: PDB Molecule: 2-amino-3-ketobutyrate coenzyme a ligase; PDBTitle: structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii
79	d1wsta1	Alignment	not modelled	99.6	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
80	c2w8wA	Alignment	not modelled	99.6	16	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
81	c3hqtB	Alignment	not modelled	99.6	10	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
82	d1m6sa	Alignment	not modelled	99.6	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
83	d1bs0a	Alignment	not modelled	99.6	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
84	c3a2bA	Alignment	not modelled	99.5	17	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
85	c5jayB	Alignment	not modelled	99.5	13	PDB header: transferase Chain: B: PDB Molecule: 8-amino-7-oxononanoate synthase; PDBTitle: crystal structure of an 8-amino-7-oxononanoate synthase from2 burkholderia xenovorans
86	d1wyua1	Alignment	not modelled	99.5	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
87	d1x0ma1	Alignment	not modelled	99.5	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
88	c3wgcB	Alignment	not modelled	99.5	15	PDB header: lyase Chain: B: PDB Molecule: l-allo-threonine aldolase; PDBTitle: aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
89	c3pj0D	Alignment	not modelled	99.5	14	PDB header: lyase Chain: D: PDB Molecule: lmo0305 protein; PDBTitle: crystal structure of a putative l-allo-threonine aldolase (lmo0305)2 from listeria monocytogenes egd-e at 1.80 a resolution
90	d1svva	Alignment	not modelled	99.4	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
91	c3zrrB	Alignment	not modelled	99.4	13	PDB header: transferase Chain: B: PDB Molecule: serine-pyruvate aminotransferase (agxt); PDBTitle: crystal structure and substrate specificity of a thermophilic2 archael serine : pyruvate aminotransferase from sulfolobus3 solfataricus
92	c3wy7D	Alignment	not modelled	99.4	19	PDB header: transferase Chain: D: PDB Molecule: 8-amino-7-oxononanoate synthase; PDBTitle: crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
93	d1qz9a	Alignment	not modelled	99.4	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
94	c4iw7A	Alignment	not modelled	99.4	15	PDB header: transferase Chain: A: PDB Molecule: 8-amino-7-oxononanoate synthase; PDBTitle: crystal structure of 8-amino-7-oxononanoate synthase (biof) from2 francisella tularensis.
95	c5vprA	Alignment	not modelled	99.3	15	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from elizabethkingia2 anophelis with covalently bound pyridoxal phosphate
96	c3mafB	Alignment	not modelled	99.3	16	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
97	c3op7A	Alignment	not modelled	99.3	10	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of a plp-dependent aminotransferase (zp_03625122.1)2 from streptococcus suis 89-1591 at 1.70 a resolution
98	c5dj3B	Alignment	not modelled	99.3	15	PDB header: transferase Chain: B: PDB Molecule: plp-dependent l-arginine hydroxylase mppp; PDBTitle: structure of the plp-dependent l-arginine hydroxylase mppp with d-2 arginine bound
99	c3f9tB	Alignment	not modelled	99.3	14	PDB header: lyase Chain: B: PDB Molecule: l-tyrosine decarboxylase mfna; PDBTitle: crystal structure of l-tyrosine decarboxylase mfna (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution
100	c2douA	Alignment	not modelled	99.3	16	PDB header: transferase Chain: A: PDB Molecule: probable n-succinyldiaminopimelate aminotransferase; PDBTitle: probable n-succinyldiaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8 PDB header: transferase

101	c5yhvA_	Alignment	not modelled	99.3	19	Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
102	c4lnjA_	Alignment	not modelled	99.3	13	PDB header: lyase Chain: A: PDB Molecule: low-specificity l-threonine aldolase; PDBTitle: structure of escherichia coli threonine aldolase in unliganded form
103	c5wt2A_	Alignment	not modelled	99.3	14	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase iscs; PDBTitle: nifs from helicobacter pylori
104	d1wyub1_	Alignment	not modelled	99.3	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
105	d1tpla_	Alignment	not modelled	99.2	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
106	c5b87B_	Alignment	not modelled	99.2	13	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of a cysteine desulfurase from thermococcus2 onnurineus na1 in complex with alanine at 2.3 angstrom resolution
107	d1c7ga_	Alignment	not modelled	99.2	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
108	c3ke3A_	Alignment	not modelled	99.2	13	PDB header: transferase Chain: A: PDB Molecule: putative serine-pyruvate aminotransferase; PDBTitle: crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution
109	c3dc1A_	Alignment	not modelled	99.2	11	PDB header: transferase Chain: A: PDB Molecule: kynurenine/alpha-aminoadipate aminotransferase PDBTitle: crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
110	c5vyeA_	Alignment	not modelled	99.2	12	PDB header: lyase Chain: A: PDB Molecule: l-threonine aldolase; PDBTitle: crystal structure of l-threonine aldolase from pseudomonas putida
111	c4fl0A_	Alignment	not modelled	99.2	16	PDB header: transferase Chain: A: PDB Molecule: aminotransferase ald1; PDBTitle: crystal structure of ald1 from arabidopsis thaliana
112	d1o4sa_	Alignment	not modelled	99.2	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
113	d1kl1a_	Alignment	not modelled	99.2	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
114	d1v72a1_	Alignment	not modelled	99.1	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
115	d1vp4a_	Alignment	not modelled	99.1	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
116	c3cbfA_	Alignment	not modelled	99.1	15	PDB header: transferase Chain: A: PDB Molecule: alpha-aminodipate aminotransferase; PDBTitle: crystal structure of lysn, alpha-aminoadipate2 aminotransferase, from thermus thermophilus hb27
117	c5usrC_	Alignment	not modelled	99.1	17	PDB header: transferase Chain: C: PDB Molecule: cysteine desulfurase, mitochondrial; PDBTitle: crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
118	c3lwsF_	Alignment	not modelled	99.1	10	PDB header: lyase Chain: F: PDB Molecule: aromatic amino acid beta-eliminating lyase/threonine PDBTitle: 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
119	c2zc0C_	Alignment	not modelled	99.1	14	PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
120	c2hzpA_	Alignment	not modelled	99.1	16	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase