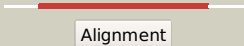

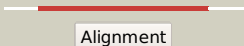

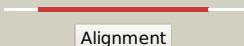







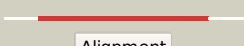











Phyre2

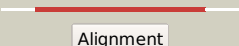




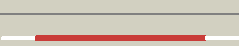

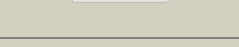
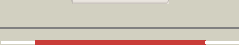



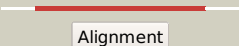
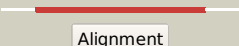
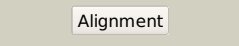
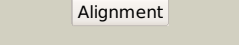
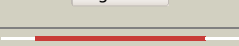


Email	mdejesus@rockefeller.edu
Description	RVBD3290c_(lat)_3670442_3671791
Date	Thu Aug 8 16:20:49 BST 2019
Unique Job ID	aab39089144397ca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2cjdA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: l-lysine-epsilon aminotransferase; PDBTitle: lysine aminotransferase from m. tuberculosis in external aldimine form
2	c5h7dI_	 Alignment		100.0	29	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
3	d1ohwA_	 Alignment		100.0	26	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
4	c4a0rB_	 Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: adenosylmethionine-8-amino-7-oxonanoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana bound to dethiobiotin (dtb).
5	c3n5mD_	 Alignment		100.0	23	PDB header: transferase Chain: D: PDB Molecule: adenosylmethionine-8-amino-7-oxonanoate aminotransferase; PDBTitle: crystals structure of a bacillus anthracis aminotransferase
6	c3hmuA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of a class iii aminotransferase from silicibacter2 pomeroyi
7	c3fcrA_	 Alignment		100.0	21	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
8	c4ysnD_	 Alignment		100.0	22	PDB header: isomerase Chain: D: PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in complex with plp
9	c5lhaC_	 Alignment		100.0	26	PDB header: transferase Chain: C: PDB Molecule: omega transaminase; PDBTitle: amine transaminase crystal structure from an uncultivated pseudomonas2 species in the pmp-bound form
10	c5ddwD_	 Alignment		100.0	27	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
11	c4a6tA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: omega transaminase; PDBTitle: crystal structure of the omega transaminase from chromobacterium2 violaceum in complex with plp

12	c5kqwD_	Alignment		100.0	20	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: directed evolution of transaminases by ancestral reconstruction. using2 old proteins for new chemistries
13	c3i5tB_	Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
14	c6gioB_	Alignment		100.0	25	PDB header: isomerase Chain: B: PDB Molecule: amino acid amide racemase; PDBTitle: structure of amino acid amide racemase from ochrobactrum anthropi
15	c3oksB_	Alignment		100.0	26	PDB header: transferase Chain: B: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis
16	c6gwiA_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: putrescine aminotransferase; PDBTitle: the crystal structure of halomonas elongata amino-transferase
17	c6io1B_	Alignment		100.0	28	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
18	c4e3rC_	Alignment		100.0	22	PDB header: transferase Chain: C: PDB Molecule: pyruvate transaminase; PDBTitle: plp-bound aminotransferase mutant crystal structure from vibrio2 fluvialis
19	c4atpD_	Alignment		100.0	25	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: structure of gaba-transaminase a1r958 from arthrobacter aurescens in2 complex with plp
20	c3lv2A_	Alignment		100.0	22	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
21	c4uoxB_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: B: PDB Molecule: putrescine aminotransferase; PDBTitle: crystal structure of ygjg in complex with pyridoxal-5'-phosphate2 and putrescine
22	c6g4dB_	Alignment	not modelled	100.0	22	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
23	c3bv0A_	Alignment	not modelled	100.0	22	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
24	c4ffcD_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate aminotransferase (gabt); PDBTitle: crystal structure of a 4-aminobutyrate aminotransferase (gabt) from2 mycobacterium abscessus
25	c5g2pA_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: transaminase; PDBTitle: the crystal structure of a s-selective transaminase from2 arthrobacter sp.
26	d1s0aa_	Alignment	not modelled	100.0	23	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
27	c3a8uX_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: X: PDB Molecule: omega-amino acid--pyruvate aminotransferase; PDBTitle: crystal structure of omega-amino acid:pyruvate aminotransferase
						PDB header: transferase

28	c5ghfB_	Alignment	not modelled	100.0	24	Chain: B: PDB Molecule: aminotransferase class-iii; PDBTitle: transaminase with l-ala
29	d1zoda1	Alignment	not modelled	100.0	25	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
30	c2eo5A_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: 419aa long hypothetical aminotransferase; PDBTitle: crystal structure of 4-aminobutyrate aminotransferase from sulfolobus2 tokodaii strain7
31	c4nogB_	Alignment	not modelled	100.0	24	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
32	c5g4iA_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: phosphorylase; PDBTitle: plp-dependent phosphorylase a1rdf1 from arthrobacter aurescens tc1
33	c3dxvA_	Alignment	not modelled	100.0	23	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	c4a0gC_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: C: PDB Molecule: adenosylmethionine-8-amino-7- oxononoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana in its apo form.
35	c3bs8A_	Alignment	not modelled	100.0	19	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
36	d1sffa_	Alignment	not modelled	100.0	29	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
37	c2e7uA_	Alignment	not modelled	100.0	23	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
38	c6erkB_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of diaminopelargonic acid aminotransferase from2 psychrobacter cryohalolentis
39	d2byla1	Alignment	not modelled	100.0	27	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
40	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
41	d2gsaa_	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
42	c4ppmB_	Alignment	not modelled	100.0	28	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
43	c1oatB_	Alignment	not modelled	100.0	26	PDB header: aminotransferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase
44	c5ykrB_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a glutamate-1-semialdehyde- aminomutase from2 pseudomonas aeruginosa pao1
45	c5d95A_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class-iii; PDBTitle: structure of thermostable omega-transaminase
46	c2ykyB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: structural determinants of the beta-selectivity of a bacterial2 aminotransferase
47	c4e77A_	Alignment	not modelled	100.0	23	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
48	c4addD_	Alignment	not modelled	100.0	27	PDB header: transferase Chain: D: PDB Molecule: succinylornithine transaminase; PDBTitle: structural and functional study of succinyl-ornithine transaminase2 from e. coli
49	c4zm4B_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: complex structure of pctv k276r mutant with pmp and 3- dehydroshkimate
50	c3ruyB_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis
51	c6fyqA_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: amine transaminase; PDBTitle: the crystal structure of a new transaminase from the marine bacterium2 virgibacillus

52	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
53	c2ordA	 Alignment	not modelled	100.0	28	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
54	c4ysvA	 Alignment	not modelled	100.0	24	PDB header: isomerase Chain: A: PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in apo-form
55	c2pb2B	 Alignment	not modelled	100.0	27	PDB header: transferase Chain: B: PDB Molecule: acetylornithine/succinyl diaminopimelate aminotransferase; PDBTitle: structure of biosynthetic n-acetylornithine aminotransferase from salmonella typhimurium: studies on substrate specificity and inhibitor binding
56	c5viuB	 Alignment	not modelled	100.0	23	PDB header: transferase Chain: B: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from elizabethkingia anophelis
57	c6cbnA	 Alignment	not modelled	100.0	17	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
58	c3dodA	 Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in bacillus subtilis
59	c3l44A	 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 hemI-1, glutamate semialdehyde2 aminotransferase
60	c6iz9B	 Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: crystal structure of the apo form of a beta-transaminase from mesorhizobium sp. strain luk
61	c3nx3A	 Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (argd) from campylobacter jejuni
62	d1z7da1	 Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
63	d1vefa1	 Alignment	not modelled	100.0	27	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
64	c4aooA	 Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: beta-phenylalanine aminotransferase; PDBTitle: biochemical properties and crystal structure of a novel beta-phenylalanine aminotransferase from variovorax3 paradoxus
65	c1z7dE	 Alignment	not modelled	100.0	22	PDB header: transferase Chain: E: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase py00104 from plasmodium yoelii
66	c5i92E	 Alignment	not modelled	100.0	18	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
67	c6cboB	 Alignment	not modelled	100.0	17	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)
68	c5ti8A	 Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aspartate aminotransferase from pseudomonas
69	c2cy8A	 Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: d-phenylglycine aminotransferase; PDBTitle: crystal structure of d-phenylglycine aminotransferase (d-phgat) from pseudomonas strutzeri st-201
70	c3i4jC	 Alignment	not modelled	100.0	26	PDB header: transferase Chain: C: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of aminotransferase, class iii from deinococcus2 radiodurans
71	c2eh6A	 Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
72	c4zm3C	 Alignment	not modelled	100.0	21	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of plp-dependent 3-aminobenzoate synthase pctx wild-2 type
73	d2cfba1	 Alignment	not modelled	100.0	23	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
74	c2w8wA	 Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
75	d1fc4a	 Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like

76	c3a2bA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
77	d1bs0a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
78	c3tqxA_	Alignment	not modelled	100.0	10	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	d2bwna1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
80	c6hrhA_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 5-aminolevulinate synthase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
81	c5txtA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinate synthase, mitochondrial; PDBTitle: structure of asymmetric apo/holo alas dimer from s. cerevisiae
82	c5jayB_	Alignment	not modelled	100.0	19	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
83	c3hqtB_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqa
84	c3wy7D_	Alignment	not modelled	100.0	17	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
85	c4iw7A_	Alignment	not modelled	100.0	14	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.
86	c3pj0D_	Alignment	not modelled	100.0	13	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
87	d1wsta1	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
88	c3ke3A_	Alignment	not modelled	100.0	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
89	c3wgcB_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: B: PDB Molecule: l-allo-threonine aldolase; PDBTitle: aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
90	d1m6sa_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
91	d1x0ma1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
92	d1qz9a_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
93	d1c7ga_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
94	d2v1pa1	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
95	c2zc0C_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
96	c3f9tB_	Alignment	not modelled	99.9	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
97	c3lwsF_	Alignment	not modelled	99.9	15	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
98	d1svva_	Alignment	not modelled	99.9	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
99	d1v72a1	Alignment	not modelled	99.9	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
100	c4lbia	Alignment	not modelled	99.9	13	PDB header: lyase Chain: A: PDB Molecule: low-specificity l-threonine aldolase;

100	c4mjA_	Alignment	not modelled	99.9	13	PDBTitle: structure of escherichia coli threonine aldolase in unliganded form
101	c2hzpA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
102	d1wyub1	Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
103	c3e9kA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
104	d1ax4a_	Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
105	c5wt2A_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase iscs; PDBTitle: nifs from helicobacter pylori
106	c4q76B_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase 2, chloroplastic; PDBTitle: crystal structure of nfs2 c384s mutant, the plastidial cysteine2 desulfurase from arabidopsis thaliana
107	c3mafB_	Alignment	not modelled	99.9	15	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
108	c4isyB_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of iscs from mycobacterium tuberculosis
109	d1tpla_	Alignment	not modelled	99.9	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
110	c5vyeA_	Alignment	not modelled	99.9	17	PDB header: lyase Chain: A: PDB Molecule: l-threonine aldolase; PDBTitle: crystal structure of l-threonine aldolase from pseudomonas putida
111	c4w91C_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp
112	c5yvhA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
113	d1c7na_	Alignment	not modelled	99.9	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
114	d1vp4a_	Alignment	not modelled	99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
115	c6c9eB_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
116	d1b5pa_	Alignment	not modelled	99.9	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
117	d1wyua1	Alignment	not modelled	99.9	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
118	d1xi9a_	Alignment	not modelled	99.9	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
119	d1j32a_	Alignment	not modelled	99.9	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
120	c3l8aB_	Alignment	not modelled	99.9	12	PDB header: lyase Chain: B: PDB Molecule: putative aminotransferase, probable beta-cystathionase; PDBTitle: crystal structure of metc from streptococcus mutans