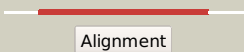

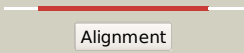

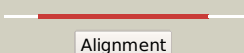

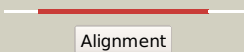

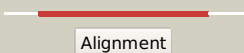



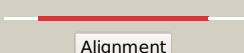

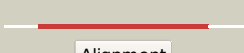

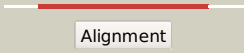
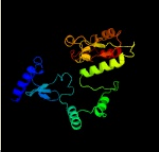


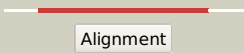



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2322c_(rocD1)_2594709_2595374
 Date Mon Aug 5 13:25:47 BST 2019
 Unique Job ID 47b0e532a58e12fe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5h7dl_			100.0	27	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	c3n5mD_			100.0	26	PDB header: transferase Chain: D: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystals structure of a bacillus anthracis aminotransferase
3	c3hmuA_			100.0	25	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of a class iii aminotransferase from silicibacter2 pomeroyi
4	c4a0rB_			100.0	15	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).
5	c4nogB_			100.0	35	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
6	c3fcrA_			100.0	18	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
7	c4a6tA_			100.0	24	PDB header: transferase Chain: A: PDB Molecule: omega transaminase; PDBTitle: crystal structure of the omega transaminase from chromobacterium2 violaceum in complex with plp
8	c6gwiA_			100.0	28	PDB header: transferase Chain: A: PDB Molecule: putrescine aminotransferase; PDBTitle: the crystal structure of halomonas elongata amino-transferase
9	c4uoxB_			100.0	25	PDB header: transferase Chain: B: PDB Molecule: putrescine aminotransferase; PDBTitle: crystal structure of ygjg in complex with pyridoxal-5'-phosphate2 and putrescine
10	c6io1B_			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
11	c6g4dB_			100.0	21	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

12	c5ykrB_	Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a glutamate-1-semialdehyde-aminomutase from2 pseudomonas aeruginosa pao1
13	c3ruyB_	Alignment		100.0	44	PDB header: transferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis
14	c5kqwD_	Alignment		100.0	18	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: directed evolution of transaminases by ancestral reconstruction. using2 old proteins for new chemistries
15	c4ysnD_	Alignment		100.0	25	PDB header: isomerase Chain: D: PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in complex with plp
16	c3i5tB_	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
17	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
18	c4e3rC_	Alignment		100.0	24	PDB header: transferase Chain: C: PDB Molecule: pyruvate transaminase; PDBTitle: plp-bound aminotransferase mutant crystal structure from vibrio2 fluvialis
19	c3a8uX_	Alignment		100.0	21	PDB header: transferase Chain: X: PDB Molecule: omega-amino acid--pyruvate aminotransferase; PDBTitle: crystal structure of omega-amino acid:pyruvate aminotransferase
20	d1ohwa_	Alignment		100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
21	d2byla1	Alignment	not modelled	100.0	35	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
22	c1oatB_	Alignment	not modelled	100.0	36	PDB header: aminotransferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase
23	c3bs8A_	Alignment	not modelled	100.0	22	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
24	c5ddwD_	Alignment	not modelled	100.0	23	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
25	c2ykyB_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: structural determinants of the beta-selectivity of a bacterial2 aminotransferase
26	c3l44A_	Alignment	not modelled	100.0	25	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
27	c2e7uA_	Alignment	not modelled	100.0	27	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

28	d1s0aa_	Alignment	not modelled	100.0	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
29	d1zoda1	Alignment	not modelled	100.0	26	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
30	d2gsaa_	Alignment	not modelled	100.0	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
31	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
32	c3oksB_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: B: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis
33	c4zm4B_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: complex structure of pctv k276r mutant with pmp and 3-dehydroshikimate
34	c2cjdA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: l-lysine-epsilon aminotransferase; PDBTitle: lysine aminotransferase from m. tuberculosis in external aldimine form
35	c3lv2A_	Alignment	not modelled	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
36	c5d95A_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class-iii; PDBTitle: structure of thermostable omega-transaminase
37	c4ppmB_	Alignment	not modelled	100.0	26	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
38	c4atpD_	Alignment	not modelled	100.0	27	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: structure of gaba-transaminase a1r958 from arthrobacter aureescens in2 complex with plp
39	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 from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
40	c4addD_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: D: PDB Molecule: succinylornithine transaminase; PDBTitle: structural and functional study of succinyl-ornithine transaminase2 from e. coli
41	c6gioB_	Alignment	not modelled	100.0	22	PDB header: isomerase Chain: B: PDB Molecule: amino acid amide racemase; PDBTitle: structure of amino acid amide racemase from ochrobactrum anthropi
42	c4ffcD_	Alignment	not modelled	100.0	27	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate aminotransferase (gabt); PDBTitle: crystal structure of a 4-aminobutyrate aminotransferase (gabt) from2 mycobacterium abscessus
43	c5g2pA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: transaminase; PDBTitle: the crystal structure of a s-selective transaminase from2 arthrobacter sp.
44	d1vefa1	Alignment	not modelled	100.0	26	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
45	c6fyqA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: amine transaminase; PDBTitle: the crystal structure of a new transaminase from the marine bacterium2 virgibacillus
46	c6iz9B_	Alignment	not modelled	100.0	23	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
47	c2eo5A_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: 419aa long hypothetical aminotransferase; PDBTitle: crystal structure of 4-aminobutyrate aminotransferase from sulfobolbus2 tokodaii strain7
48	c4aoaA_	Alignment	not modelled	100.0	26	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
49	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
50	c4e77A_	Alignment	not modelled	100.0	24	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
51	c2zsmA_	Alignment	not modelled	100.0	22	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

52	c5ghfB_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: aminotransferase class-iii; PDBTitle: transaminase with l-ala
53	c2ordA_	Alignment	not modelled	100.0	25	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	c4a0gC_	Alignment	not modelled	100.0	16	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.
55	c3nx3A_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
56	d1sffa_	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
57	c5i92E_	Alignment	not modelled	100.0	22	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
58	d1z7da1	Alignment	not modelled	100.0	35	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
59	c2cy8A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: d-phenylglycine aminotransferase; PDBTitle: crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201
60	c5viuB_	Alignment	not modelled	100.0	39	PDB header: transferase Chain: B: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from2 elizabethkingia anophelis
61	c5g4iA_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: phosphorylase; PDBTitle: plp-dependent phosphorylase a1rdf1 from arthrobacter aureusens tc1
62	c3nuia_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: pyruvate transaminase; PDBTitle: crystal structure of omega-transferase from vibrio fluvialis js17
63	c3dodA_	Alignment	not modelled	100.0	20	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
64	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
65	c3dxvA_	Alignment	not modelled	100.0	20	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
66	c6cbnA_	Alignment	not modelled	100.0	21	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
67	c1z7dE_	Alignment	not modelled	100.0	36	PDB header: transferase Chain: E: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase py00104 from plasmodium yoelii
68	c4zm3C_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of plp-dependent 3-aminobenzoate synthase pctv wild-2 type
69	c4ysvA_	Alignment	not modelled	100.0	27	PDB header: isomerase Chain: A: PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in apo-form
70	c6cboB_	Alignment	not modelled	100.0	22	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)
71	c5ti8A_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aspartate aminotransferase from pseudomonas
72	d2cfba1	Alignment	not modelled	100.0	28	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
73	c3i4jC_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: C: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of aminotransferase, class iii from deinococcus2 radiodurans
74	c2w8wA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
75	c3a2bA_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
76	d1fc4a_	Alianment	not modelled	99.9	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

						Family: GABA-aminotransferase-like
77	c3tqxA_	Alignment	not modelled	99.9	16	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
78	d1bs0a_	Alignment	not modelled	99.9	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
79	c6hrhA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 5-aminolevulinate synthase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
80	c5jayB_	Alignment	not modelled	99.9	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
81	d2bwna1	Alignment	not modelled	99.9	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
82	c3hqtB_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
83	c5txtA_	Alignment	not modelled	99.5	16	PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinate synthase, mitochondrial; PDBTitle: structure of asymmetric apo/holo alas dimer from s. cerevisiae
84	c3ke3A_	Alignment	not modelled	99.5	18	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
85	c4iw7A_	Alignment	not modelled	99.5	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.
86	d1wyub1	Alignment	not modelled	99.4	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
87	c3wy7D_	Alignment	not modelled	99.4	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
88	d1ax4a_	Alignment	not modelled	99.3	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
89	c3pj0D_	Alignment	not modelled	99.3	12	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	d2v1pa1	Alignment	not modelled	99.2	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
91	c3wgcB_	Alignment	not modelled	99.2	16	PDB header: lyase Chain: B: PDB Molecule: l-allo-threonine aldolase; PDBTitle: aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
92	c3w1hB_	Alignment	not modelled	99.1	15	PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) selenium transferase; PDBTitle: crystal structure of the selenocysteine synthase sela from aquifex2 aeolicus
93	d1c7ga_	Alignment	not modelled	99.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
94	d1m6sa_	Alignment	not modelled	99.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
95	d1qz9a_	Alignment	not modelled	98.9	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
96	c3lwsF_	Alignment	not modelled	98.9	14	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
97	d1v72a1	Alignment	not modelled	98.8	9	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
98	d1tpla_	Alignment	not modelled	98.8	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
99	c4q76B_	Alignment	not modelled	98.8	10	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
100	c4lnjA_	Alignment	not modelled	98.7	13	PDB header: lyase Chain: A: PDB Molecule: low-specificity l-threonine aldolase; PDBTitle: structure of escherichia coli threonine aldolase in unliganded form
101	c5wv0A_	Alignment	not modelled	98.6	13	PDB header: lyase Chain: A: PDB Molecule: l-threonine aldolase;

101	c3vyvA_	Alignment	not modelled	98.5	15	PDBTitle: crystal structure of l-threonine aldolase from pseudomonas putida
102	c4isyB_	Alignment	not modelled	98.5	18	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of iscs from mycobacterium tuberculosis
103	d1svva_	Alignment	not modelled	98.5	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
104	c4qgrA_	Alignment	not modelled	98.5	15	PDB header: transferase Chain: A: PDB Molecule: degt/dnrj/eryc1/strs aminotransferase; PDBTitle: crystal structure of a degt dnrj eryc1 strs aminotransferase from2 brucella abortus
105	c3mafB_	Alignment	not modelled	98.5	15	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
106	c6c9eB_	Alignment	not modelled	98.5	11	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
107	c4w91C_	Alignment	not modelled	98.4	9	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp
108	c2hdyA_	Alignment	not modelled	98.4	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
109	c3f9tB_	Alignment	not modelled	98.4	13	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
110	d1wyua1	Alignment	not modelled	98.4	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
111	c4lw2C_	Alignment	not modelled	98.3	14	PDB header: lyase Chain: C: PDB Molecule: cysteine sulfinate desulfinase; PDBTitle: structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration
112	c4ytjC_	Alignment	not modelled	98.3	15	PDB header: transferase Chain: C: PDB Molecule: cals13; PDBTitle: crystal structure of sugar aminotransferase cals13 from micromonospora2 echinospora
113	c4xauG_	Alignment	not modelled	98.3	15	PDB header: transferase Chain: G: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of ats13 from actinomadura melliura
114	c5k1rB_	Alignment	not modelled	98.3	16	PDB header: lyase Chain: B: PDB Molecule: burkholderia pseudomallei sphingosine-1-phosphate lyase PDBTitle: structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021
115	c3fdbA_	Alignment	not modelled	98.3	10	PDB header: transferase Chain: A: PDB Molecule: putative plp-dependent beta-cystathionase; PDBTitle: crystal structure of a putative plp-dependent beta-cystathionase2 (aecd, dip1736) from corynebacterium diphtheriae at 1.99 a resolution
116	c5j8qA_	Alignment	not modelled	98.2	11	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase sufs; PDBTitle: crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis
117	d1c7na_	Alignment	not modelled	98.2	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
118	d1t3ia_	Alignment	not modelled	98.2	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
119	c5zsqA_	Alignment	not modelled	98.2	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: cysteine desulfurase; PDBTitle: nifs from hydrogenimonas thermophila, soaked with l-cysteine for 4 min
120	c5dx5B_	Alignment	not modelled	98.2	12	PDB header: lyase Chain: B: PDB Molecule: methionine gamma-lyase; PDBTitle: crystal structure of methionine gamma-lyase from clostridium2 sporogenes