

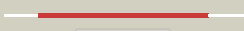














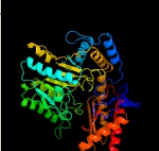



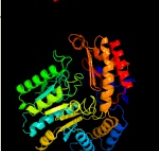


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3329 (-) _3714563_3715879
Date	Thu Aug 8 16:20:54 BST 2019
Unique Job ID	e667771e6fdb62d9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6io1B_	 Alignment		100.0	39	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
2	c3fcrA_	 Alignment		100.0	35	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
3	c3hmuA_	 Alignment		100.0	39	PDB header: transferase Chain: A; PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of a class iii aminotransferase from silicibacter2 pomeroyi
4	c3n5mD_	 Alignment		100.0	37	PDB header: transferase Chain: D; PDB Molecule: adenosylmethionine-8-amino-7-oxonanoate aminotransferase; PDBTitle: crystals structure of a bacillus anthracis aminotransferase
5	c6gwiA_	 Alignment		100.0	38	PDB header: transferase Chain: A; PDB Molecule: putrescine aminotransferase; PDBTitle: the crystal structure of halomonas elongata amino-transferase
6	c5kqwD_	 Alignment		100.0	37	PDB header: transferase Chain: D; PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: directed evolution of transaminases by ancestral reconstruction. using2 old proteins for new chemistries
7	c4a6tA_	 Alignment		100.0	35	PDB header: transferase Chain: A; PDB Molecule: omega transaminase; PDBTitle: crystal structure of the omega transaminase from chromobacterium2 violaceum in complex with plp
8	c5h7dl_	 Alignment		100.0	32	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
9	c3i5tB_	 Alignment		100.0	35	PDB header: transferase Chain: B; PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
10	c6g4dB_	 Alignment		100.0	36	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
11	c5lhaC_	 Alignment		100.0	35	PDB header: transferase Chain: C; PDB Molecule: omega transaminase; PDBTitle: amine transaminase crystal structure from an uncultivated pseudomonas2 species in the pmp-bound form

12	c4e3rC_	Alignment		100.0	33	PDB header: transferase Chain: C: PDB Molecule: pyruvate transaminase; PDBTitle: plp-bound aminotransferase mutant crystal structure from vibrio2 fluvialis
13	c3a8uX_	Alignment		100.0	35	PDB header: transferase Chain: X: PDB Molecule: omega-amino acid--pyruvate aminotransferase; PDBTitle: crystal structure of omega-amino acid:pyruvate aminotransferase
14	c5ghfB_	Alignment		100.0	35	PDB header: transferase Chain: B: PDB Molecule: aminotransferase class-iii; PDBTitle: transaminase with l-ala
15	c4ysnD_	Alignment		100.0	29	PDB header: isomerase Chain: D: PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in complex with plp
16	c4a0rB_	Alignment		100.0	24	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).
17	c3nuiA_	Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: pyruvate transaminase; PDBTitle: crystal structure of omega-transferase from vibrio fluvialis js17
18	c6gioB_	Alignment		100.0	27	PDB header: isomerase Chain: B: PDB Molecule: amino acid amide racemase; PDBTitle: structure of amino acid amide racemase from ochrobactrum anthropi
19	c3oksB_	Alignment		100.0	31	PDB header: transferase Chain: B: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis
20	d1zoda1	Alignment		100.0	29	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
21	c4ffcD_	Alignment	not modelled	100.0	30	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate aminotransferase (gabt); PDBTitle: crystal structure of a 4-aminobutyrate aminotransferase (gabt) from2 mycobacterium abscessus
22	c3lv2A_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxonanoate aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
23	c4atpD_	Alignment	not modelled	100.0	30	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: structure of gaba-transaminase a1r958 from arthrobacter aurescens in2 complex with plp
24	c4uoxB_	Alignment	not modelled	100.0	32	PDB header: transferase Chain: B: PDB Molecule: putrescine aminotransferase; PDBTitle: crystal structure of ygjg in complex with pyridoxal-5'-phosphate2 and putrescine
25	d1s0aa_	Alignment	not modelled	100.0	27	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
26	c5g2pA_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: transaminase; PDBTitle: the crystal structure of a s-selective transaminase from2 arthrobacter sp.
27	c6fyqA_	Alignment	not modelled	100.0	39	PDB header: transferase Chain: A: PDB Molecule: amine transaminase; PDBTitle: the crystal structure of a new transaminase from the marine bacterium2 virgibacillus
						PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-

28	c3bv0A_	Alignment	not modelled	100.0	29	oxonanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 mycobacterium tuberculosis PDB header: transferase Chain: D: PDB Molecule: crmg;
29	c5ddwD_	Alignment	not modelled	100.0	24	PDBTitle: crystal structure of aminotransferase crmg from actinoalloteichus sp.2 wh1-2216-6 in complex with the pmp external aldimine adduct with3 caerulomycin m PDB header: transferase
30	c6erkB_	Alignment	not modelled	100.0	28	Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of diaminopelargonic acid aminotransferase from2 psychrobacter cryohalolentis PDB header: transferase
31	c4ppmB_	Alignment	not modelled	100.0	29	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
32	d1ohwa_	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
33	d1sffa_	Alignment	not modelled	100.0	28	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
34	c2cjdA_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: l-lysine-epsilon aminotransferase; PDBTitle: lysine aminotransferase from m. tuberculosis in external aldimine form
35	c4nogB_	Alignment	not modelled	100.0	28	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
36	c3dxvA_	Alignment	not modelled	100.0	28	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
37	c5g4iA_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A: PDB Molecule: phosphorylase; PDBTitle: plp-dependent phosphorylase a1rdf1 from arthrobacter aureescens tc1
38	c3bs8A_	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 aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
39	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
40	c2eo5A_	Alignment	not modelled	100.0	33	PDB header: transferase Chain: A: PDB Molecule: 419aa long hypothetical aminotransferase; PDBTitle: crystal structure of 4-aminobutyrate aminotransferase from sulfobolus2 tokodaii strain7
41	d2gsaa_	Alignment	not modelled	100.0	22	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
42	c3dodA_	Alignment	not modelled	100.0	35	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxonanoate aminotransferase; PDBTitle: crystal structure of plp bound 7,8-diaminopelargonic acid synthase in2 bacillus subtilis
43	c2ykyB_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: structural determinants of the beta-selectivity of a bacterial2 aminotransferase
44	c5d95A_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class-iii; PDBTitle: structure of thermostable omega-transaminase
45	d2byla1	Alignment	not modelled	100.0	27	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
46	c4ysvA_	Alignment	not modelled	100.0	29	PDB header: isomerase Chain: A: PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in apo-form
47	c4addD_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: D: PDB Molecule: succinylornithine transaminase; PDBTitle: structural and functional study of succinyl-ornithine transaminase2 from e. coli
48	c5ykrB_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a glutamate-1-semialdehyde-aminomutase from2 pseudomonas aeruginosa pao1
49	c1oatB_	Alignment	not modelled	100.0	27	PDB header: aminotransferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase
50	c4zm4B_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: complex structure of pctv k276r mutant with pmp and 3-dehydroshkimate
51	c3ruyB_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis

52	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 from 2 salmonella typhimurium: studies on substrate specificity and 3 inhibitor binding
53	c5ti8A_	Alignment	not modelled	100.0	37	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aspartate aminotransferase from pseudomonas
54	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
55	c4aoaA_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: beta-phenylalanine aminotransferase; PDBTitle: biochemical properties and crystal structure of a novel 2 beta-phenylalanine aminotransferase from variovorax 3 paradoxus
56	c3i4jC_	Alignment	not modelled	100.0	38	PDB header: transferase Chain: C: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of aminotransferase, class iii from deinococcus 2 radiodurans
57	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 heml-1, glutamate semialdehyde 2 aminotransferase
58	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 aminotransferase 2 from yersinia pestis co92
59	c2ordA_	Alignment	not modelled	100.0	35	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
60	c4a0gC_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: C: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from 2 arabidopsis thaliana in its apo form.
61	d1vefa1	Alignment	not modelled	100.0	33	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
62	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 from 2 mesorhizobium sp. strain luk
63	c5viuB_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: B: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from 2 elizabethkingia anophelis
64	d1z7da1	Alignment	not modelled	100.0	26	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
65	c5i92E_	Alignment	not modelled	100.0	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
66	c3nx3A_	Alignment	not modelled	100.0	32	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (argd) from 2 campylobacter jejuni
67	c1z7dE_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: E: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase py00104 from plasmodium yoelii
68	c6cbnA_	Alignment	not modelled	100.0	23	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
69	c2cy8A_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: d-phenylglycine aminotransferase; PDBTitle: crystal structure of d-phenylglycine aminotransferase (d-phgat) from 2 pseudomonas strutzeri st-201
70	c2eh6A_	Alignment	not modelled	100.0	34	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from aquifex 2 aeolicus vf5
71	d2cfba1	Alignment	not modelled	100.0	26	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
72	c4zm3C_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: C: PDB Molecule: aminotransferase; PDBTitle: crystal structure of plp-dependent 3-aminobenzoate synthase pctv wild-2 type
73	c6cboB_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: c-6' aminotransferase; PDBTitle: x-ray structure of genb1 from micromonospora echinospora in complex 2 with neamine and plp (as the external aldimine)
74	c2w8wA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
75	c5txtA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinat synthase, mitochondrial;

						PDBTitle: structure of asymmetric apo/olo alas dimer from s. cerevisiae
76	c6hrhA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 5-aminolevulinate synthase, erythroid-specific, PDBTitle: structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
77	c3a2bA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
78	d1fc4a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
79	d2bwna1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
80	d1bs0a_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
81	c3tqxA_	Alignment	not modelled	100.0	17	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
82	c5jayB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: 8-amino-7-oxonanoate synthase; PDBTitle: crystal structure of an 8-amino-7-oxonanoate synthase from2 burkholderia xenovorans
83	c3hqtB_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
84	c3wy7D_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: D: PDB Molecule: 8-amino-7-oxonanoate 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-oxonanoate synthase; PDBTitle: crystal structure of 8-amino-7-oxonanoate synthase (biof) from2 francisella tularensis.
86	c3wgcB_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: B: PDB Molecule: l-allo-threonine aldolase; PDBTitle: aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
87	c3ke3A_	Alignment	not modelled	100.0	15	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
88	d1m6sa_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
89	d1tpla_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
90	d1qz9a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
91	c3pj0D_	Alignment	not modelled	100.0	11	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
92	d1c7ga_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
93	d1svva_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
94	d1v72a1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
95	d1wsta1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
96	c4lnjA_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: low-specificity l-threonine aldolase; PDBTitle: structure of escherichia coli threonine aldolase in unliganded form
97	c3f9tB_	Alignment	not modelled	100.0	18	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
98	c4q76B_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase 2, chloroplastic; PDBTitle: crystal structure of nfs2 c384s mutant, the plastidal cysteine2 desulfurase from arabidopsis thaliana
99	d1c7na_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
100	d1ax4a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases

101	c2hdyA_	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
102	d2v1pa1	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
103	c3mafB_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: B; PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
104	c4isyB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B; PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of iscs from mycobacterium tuberculosis
105	c6c9eB_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B; PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
106	d1c5a_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
107	d1jf9a_	Alignment	not modelled	100.0	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
108	c5yhvA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A; PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
109	d1wyub1	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
110	c3e9kA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
111	c5vyeA_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A; PDB Molecule: l-threonine aldolase; PDBTitle: crystal structure of l-threonine aldolase from pseudomonas putida
112	d1x0ma1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
113	c3lwsF_	Alignment	not modelled	100.0	12	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
114	c2hzpA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
115	c4w91C_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C; PDB Molecule: aminotransferase; PDBTitle: crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp
116	c5wt2A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A; PDB Molecule: cysteine desulfurase iscs; PDBTitle: nifs from helicobacter pylori
117	c5j8qA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A; PDB Molecule: cysteine desulfurase sufs; PDBTitle: crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis
118	c3b1dD_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: D; PDB Molecule: betac-s lyase; PDBTitle: crystal structure of betac-s lyase from streptococcus anginosus in2 complex with l-serine: external aldimine form
119	d1eg5a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
120	c3kaxB_	Alignment	not modelled	100.0	10	PDB header: lyase Chain: B; PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis