

Phyre2

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 Description RVBD1655_(argD)_1868730_1869932
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5h7dL_	Alignment		100.0	37	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_	Alignment		100.0	32	PDB header: transferase Chain: D; PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystals structure of a bacillus anthracis aminotransferase
3	c3fcrA_	Alignment		100.0	29	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
4	c4ysnD_	Alignment		100.0	32	PDB header: isomerase Chain: D; PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in complex with plp
5	c4nogB_	Alignment		100.0	33	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	c4addD_	Alignment		100.0	42	PDB header: transferase Chain: D; PDB Molecule: succinylornithine transaminase; PDBTitle: structural and functional study of succinyl-ornithine transaminase2 from e. coli
7	c4a0rB_	Alignment		100.0	22	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).
8	c3ruyB_	Alignment		100.0	37	PDB header: transferase Chain: B; PDB Molecule: ornithine aminotransferase; PDBTitle: crystal structure of the ornithine-oxo acid transaminase rocd from2 bacillus anthracis
9	dlvefa1	Alignment		100.0	44	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
10	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
11	c3hmuA_	Alignment		100.0	29	PDB header: transferase Chain: A; PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of a class iii aminotransferase from silicibacter2 pomeroyi

12	c4uoxB_	Alignment		100.0	37	PDB header: transferase Chain: B: PDB Molecule: putrescine aminotransferase; PDBTitle: crystal structure of ygjg in complex with pyridoxal-5'-phosphate2 and putrescine
13	c4a6tA_	Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: omega transaminase; PDBTitle: crystal structure of the omega transaminase from chromobacterium2 violaceum in complex with plp
14	c4e3rC_	Alignment		100.0	27	PDB header: transferase Chain: C: PDB Molecule: pyruvate transaminase; PDBTitle: plp-bound aminotransferase mutant crystal structure from vibrio2 fluvialis
15	c6g4dB_	Alignment		100.0	32	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	c4atpD_	Alignment		100.0	35	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: structure of gaba-transaminase a1r958 from arthrobacter aurescens in2 complex with plp
17	c6io1B_	Alignment		100.0	35	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	c3a8uX_	Alignment		100.0	30	PDB header: transferase Chain: X: PDB Molecule: omega-amino acid--pyruvate aminotransferase; PDBTitle: crystal structure of omega-amino acid:pyruvate aminotransferase
19	d2byla1	Alignment		100.0	35	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
20	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
21	c5kqwD_	Alignment	not modelled	100.0	30	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: directed evolution of transaminases by ancestral reconstruction. using2 old proteins for new chemistries
22	c1oatB_	Alignment	not modelled	100.0	35	PDB header: aminotransferase Chain: B: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase
23	c6gwiA_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: A: PDB Molecule: putrescine aminotransferase; PDBTitle: the crystal structure of halomonas elongata amino-transferase
24	c3i5tB_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
25	c2ordA_	Alignment	not modelled	100.0	40	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
26	c5g2pA_	Alignment	not modelled	100.0	27	PDB header: transferase Chain: A: PDB Molecule: transaminase; PDBTitle: the crystal structure of a s-selective transaminase from2 arthrobacter sp.
27	d1ohwa_	Alignment	not modelled	100.0	26	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
28	d1zoda1	Alignment	not modelled	100.0	34	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like

29	c3lv2A_	Alignment	not modelled	100.0	28	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
30	d1s0aa_	Alignment	not modelled	100.0	27	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
31	c3oksB_	Alignment	not modelled	100.0	35	PDB header: transferase Chain: B: PDB Molecule: 4-aminobutyrate transaminase; PDBTitle: crystal structure of 4-aminobutyrate transaminase from mycobacterium2 smegmatis
32	c2cjdA_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: l-lysine-epsilon aminotransferase; PDBTitle: lysine aminotransferase from m. tuberculosis in external aldimine form
33	c6erkB_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of diaminopelargonic acid aminotransferase from2 psychrobacter cryohalolentis
34	c4ffcD_	Alignment	not modelled	100.0	38	PDB header: transferase Chain: D: PDB Molecule: 4-aminobutyrate aminotransferase (gabt); PDBTitle: crystal structure of a 4-aminobutyrate aminotransferase (gabt) from2 mycobacterium abscessus
35	c3bv0A_	Alignment	not modelled	100.0	28	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
36	c2pb2B_	Alignment	not modelled	100.0	40	PDB header: transferase Chain: B: PDB Molecule: acetylornithine/succinyldiaminopimelate aminotransferase; PDBTitle: structure of biosynthetic n-acetylornithine aminotransferase from2 salmonella typhimurium: studies on substrate specificity and3 inhibitor binding
37	c5ddwD_	Alignment	not modelled	100.0	32	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
38	c2eo5A_	Alignment	not modelled	100.0	36	PDB header: transferase Chain: A: PDB Molecule: 419aa long hypothetical aminotransferase; PDBTitle: crystal structure of 4-aminobutyrate aminotransferase from sulfobolus2 tokodaii strain7
39	c4ppmB_	Alignment	not modelled	100.0	36	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
40	c3dxvA_	Alignment	not modelled	100.0	33	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
41	d1sffa_	Alignment	not modelled	100.0	33	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
42	c5ghfB_	Alignment	not modelled	100.0	35	PDB header: transferase Chain: B: PDB Molecule: aminotransferase class-iii; PDBTitle: transaminase with l-ala
43	c3nx3A_	Alignment	not modelled	100.0	33	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
44	c3bs8A_	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 aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
45	c2e7uA_	Alignment	not modelled	100.0	29	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
46	c2ykyB_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: structural determinants of the beta-selectivity of a bacterial2 aminotransferase
47	d2gsaa_	Alignment	not modelled	100.0	30	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
48	c2eh6A_	Alignment	not modelled	100.0	41	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
49	c5ykrB_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: B: PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a glutamate-1-semialdehyde-aminomutase from2 pseudomonas aeruginosa pao1
50	d1z7da1	Alignment	not modelled	100.0	34	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
51	c5viuB_	Alignment	not modelled	100.0	36	PDB header: transferase Chain: B: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from2 elizabethkingia anophelis

52	c5d95A_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: A: PDB Molecule: aminotransferase class-iii; PDBTitle: structure of thermostable omega-transaminase
53	c3nuia_	Alignment	not modelled	100.0	30	PDB header: transferase Chain: A: PDB Molecule: pyruvate transaminase; PDBTitle: crystal structure of omega-transferase from vibrio fluvialis js17
54	c2zsmA_	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 2,1-2 aminomutase from aeropyrum pernix, hexagonal form
55	c4zm4B_	Alignment	not modelled	100.0	29	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: complex structure of pctx k276r mutant with pmp and 3-dehydroshikimate
56	c6fyqA_	Alignment	not modelled	100.0	31	PDB header: transferase Chain: A: PDB Molecule: amine transaminase; PDBTitle: the crystal structure of a new transaminase from the marine bacterium2 virgibacillus
57	c3l44A_	Alignment	not modelled	100.0	28	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
58	c5g4iA_	Alignment	not modelled	100.0	30	PDB header: transferase Chain: A: PDB Molecule: phosphorylase; PDBTitle: plp-dependent phosphorylase a1rdf1 from arthrobacter aurescens tc1
59	c4e77A_	Alignment	not modelled	100.0	26	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
60	c1z7dE_	Alignment	not modelled	100.0	34	PDB header: transferase Chain: E: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase py00104 from plasmodium yoelii
61	c3dodA_	Alignment	not modelled	100.0	28	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
62	c4a0aA_	Alignment	not modelled	100.0	27	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
63	c4a0gC_	Alignment	not modelled	100.0	22	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.
64	c5i92E_	Alignment	not modelled	100.0	24	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
65	c6iz9B_	Alignment	not modelled	100.0	26	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
66	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
67	c4ysvA_	Alignment	not modelled	100.0	34	PDB header: isomerase Chain: A: PDB Molecule: putative 4-aminobutyrate aminotransferase; PDBTitle: structure of aminoacid racemase in apo-form
68	c5ti8A_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aspartate aminotransferase from pseudomonas
69	c3i4jC_	Alignment	not modelled	100.0	32	PDB header: transferase Chain: C: PDB Molecule: aminotransferase, class iii; PDBTitle: crystal structure of aminotransferase, class iii from deinococcus2 radiodurans
70	c2cy8A_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: d-phenylglycine aminotransferase; PDBTitle: crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201
71	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 complex2 with neamine and plp (as the external aldimine)
72	c4zm3C_	Alignment	not modelled	100.0	28	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	30	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
74	c2w8wA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: n100y spt with plp-ser
75	d1fc4a_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
						PDB header: oxidoreductase

76	c6hrhA_	Alignment	not modelled	100.0	18	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	18	PDB header: transferase Chain: A: PDB Molecule: serine palmitoyltransferase; PDBTitle: crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
78	d2bwna1	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
79	d1bs0a_	Alignment	not modelled	100.0	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
80	c5txtA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: 5-aminolevulinate synthase, mitochondrial; PDBTitle: structure of asymmetric apo/holo alas dimer from s. cerevisiae
81	c3tqxA_	Alignment	not modelled	100.0	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
82	c5jayB_	Alignment	not modelled	100.0	20	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	15	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	23	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	18	PDB header: lyase Chain: B: PDB Molecule: l-allo-threonine aldolase; PDBTitle: aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
87	d1wsta1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
88	c3ke3A_	Alignment	not modelled	100.0	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
89	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
90	d1qz9a_	Alignment	not modelled	100.0	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
91	d1m6sa_	Alignment	not modelled	100.0	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
92	d1o4sa_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
93	d1x0ma1	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
94	d1svva_	Alignment	not modelled	100.0	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
95	c4q76B_	Alignment	not modelled	100.0	16	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
96	c5yhvA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: aminotransferase; PDBTitle: crystal structure of an aminotransferase from mycobacterium2 tuberculosis
97	d1c7na_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
98	d1xi9a_	Alignment	not modelled	100.0	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
99	c3mafB_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
100	c6c9eB_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
101	d1j32a_	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

						Family: AAT-like
102	c3jtxB_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
103	d1lc5a_	Alignment	not modelled	100.0	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
104	c3h14A_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative aminotransferase from silicibacter2 pomeroyi
105	c3kaxB_	Alignment	not modelled	100.0	11	PDB header: lyase Chain: B: PDB Molecule: aminotransferase, classes i and ii; PDBTitle: crystal structure of a putative c-s lyase from bacillus anthracis
106	c4lnjA_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: A: PDB Molecule: low-specificity l-threonine aldolase; PDBTitle: structure of escherichia coli threonine aldolase in unliganded form
107	c3fdbA_	Alignment	not modelled	100.0	15	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
108	c2zc0C_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: C: PDB Molecule: alanine glyoxylate transaminase; PDBTitle: crystal structure of an archaeal alanine:glyoxylate aminotransferase
109	c3lwsF_	Alignment	not modelled	100.0	13	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
110	c3b1dD_	Alignment	not modelled	100.0	10	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
111	d1b5pa_	Alignment	not modelled	100.0	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
112	c5wt2A_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: cysteine desulfurase iscs; PDBTitle: nifs from helicobacter pylori
113	c3e9kA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
114	c2hzpA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
115	c4f10A_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: aminotransferase ald1; PDBTitle: crystal structure of ald1 from arabidopsis thaliana
116	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
117	d1v72a1	Alignment	not modelled	100.0	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
118	c3b46B_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: aminotransferase bna3; PDBTitle: crystal structure of bna3p, a putative kynurenine2 aminotransferase from saccharomyces cerevisiae
119	d1jf9a_	Alignment	not modelled	100.0	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
120	c3g0tA_	Alignment	not modelled	100.0	9	PDB header: transferase Chain: A: PDB Molecule: putative aminotransferase; PDBTitle: crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution