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Description	RVBD1093_(glyA)_1220579_1221859
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3h7fB_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> serine hydroxymethyltransferase 1; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
2	<a href="#">d1ejia_</a>	 Alignment		100.0	47	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
3	<a href="#">d1bj4a_</a>	 Alignment		100.0	48	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
4	<a href="#">c3n0lA_</a>	 Alignment		100.0	49	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
5	<a href="#">c6cd1A_</a>	 Alignment		100.0	49	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of medicago truncatula serine2 hydroxymethyltransferase 3 (mtshmt3), complexes with reaction3 intermediates
6	<a href="#">d1rv3a_</a>	 Alignment		100.0	48	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
7	<a href="#">c2a7vA_</a>	 Alignment		100.0	53	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> human mitochondrial serine hydroxymethyltransferase 2
8	<a href="#">d2a7va1</a>	 Alignment		100.0	53	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
9	<a href="#">c4n0wA_</a>	 Alignment		100.0	53	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> x-ray crystal structure of a serine hydroxymethyltransferase from2 burkholderia cenocepacia with covalently attached pyridoxal phosphate
10	<a href="#">c4j5uB_</a>	 Alignment		100.0	48	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> x-ray crystal structure of a serine hydroxymethyltransferase with2 covalently bound plp from rickettsia rickettsii str. sheila smith
11	<a href="#">c4o6zC_</a>	 Alignment		100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase with covalently2 bound plp schiff-base from plasmodium falciparum

12	<a href="#">c4wxfC_</a>	Alignment		100.0	52	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of l-serine hydroxymethyltransferase in complex with 2 glycine
13	<a href="#">c5vc2A_</a>	Alignment		100.0	46	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of a serine hydroxymethyltransferase from <i>Helicobacter pylori</i>
14	<a href="#">c3eccC_</a>	Alignment		100.0	53	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> serine hydroxymethyltransferase 2; <b>PDBTitle:</b> crystal structure of serine hydroxymethyltransferase from <i>Burkholderia pseudomallei</i>
15	<a href="#">d1dfoa_</a>	Alignment		100.0	55	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
16	<a href="#">c4bhel_</a>	Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> I; <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> methanococcus jannaschii serine hydroxymethyltransferase 2 in complex with plp
17	<a href="#">d1kl1a_</a>	Alignment		100.0	58	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
18	<a href="#">c2dkjB_</a>	Alignment		100.0	61	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of t.th.hb8 serine hydroxymethyltransferase
19	<a href="#">c5z0yA_</a>	Alignment		100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystallization and structure determination of cytoplasmic serine 2 hydroxymethyltransferase (shmt) from <i>Pichia pastoris</i>
20	<a href="#">c5txtA_</a>	Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> 5-aminolevulinic acid synthase, mitochondrial; <b>PDBTitle:</b> structure of asymmetric apo/holo <i>Alas</i> dimer from <i>Saccharomyces cerevisiae</i>
21	<a href="#">c6hrhA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 5-aminolevulinic acid synthase, erythroid-specific; <b>PDBTitle:</b> structure of human erythroid-specific 5'-aminolevulinic acid synthase, 2 <i>Alas2</i>
22	<a href="#">d1c4ka2</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Ornithine decarboxylase major domain
23	<a href="#">c3bcxA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydratase; <b>PDBTitle:</b> e1 dehydratase
24	<a href="#">c1c4kA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (ornithine decarboxylase); <b>PDBTitle:</b> ornithine decarboxylase mutant (gly121tyr)
25	<a href="#">c2vycA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> biodegradative arginine decarboxylase; <b>PDBTitle:</b> crystal structure of acid induced arginine decarboxylase 2 from <i>E. coli</i>
26	<a href="#">c5w70B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> l-glutamine:2-deoxy-scylo-inosose aminotransferase; <b>PDBTitle:</b> x-ray structure of rbmb from <i>Streptomyces ribosidificus</i>
27	<a href="#">c5fkzE_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> E; <b>PDB Molecule:</b> lysine decarboxylase, constitutive; <b>PDBTitle:</b> structure of <i>E. coli</i> constitutive lysine decarboxylase
28	<a href="#">c2w8wA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser

29	<a href="#">c3hqtB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cai-1 autoinducer synthase; <b>PDBTitle:</b> plp-dependent acyl-coa transferase cqsa
30	<a href="#">c3n75E_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> lysine decarboxylase, inducible; <b>PDBTitle:</b> x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldci
31	<a href="#">c2c7tA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine-2-deoxy-scylo-inosose aminotransferase; <b>PDBTitle:</b> crystal structure of the plp-bound form of btrr, a dual functional2 aminotransferase involved in butirosin biosynthesis.
32	<a href="#">c4k2bA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ntd biosynthesis operon protein ntda; <b>PDBTitle:</b> crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
33	<a href="#">c5k8bA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-amino-3,8-dideoxy-alpha-d-manno-octulosonate <b>PDBTitle:</b> x-ray structure of kdna, 8-amino-3,8-dideoxy-alpha-d-manno-2 octulosonate transaminase, from shewanella oneidensis in the presence3 of the external aldimine with plp and glutamate
34	<a href="#">c2ogeC_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> transaminase; <b>PDBTitle:</b> x-ray structure of s. venezuelae desv in its internal2 aldimine form
35	<a href="#">c4q6rB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase 1; <b>PDBTitle:</b> crystal structure of human sphingosine-1-phosphate lyase in complex2 with inhibitor 6-[(2r)-4-(4-benzyl-7-chlorophthalazin-1-yl)-2-3 methylpiperazin-1-yl]pyridine-3-carbonitrile
36	<a href="#">c3wy7D_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 8-amino-7-oxononanoate synthase; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
37	<a href="#">d1b9ha_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
38	<a href="#">c5k1rB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> burkholderia pseudomallei sphingosine-1-phosphate lyase <b>PDBTitle:</b> structure of burkholderia pseudomallei k96243 sphingosine-1-phosphate2 lyase bpss2021
39	<a href="#">c2r0tA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5-phosphate-dependent dehydrase; <b>PDBTitle:</b> crystal structure of gdp-4-keto-6-deoxymannose-3-dehydratase with a2 trapped plp-glutamate geminal diamine
40	<a href="#">d1o69a_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
41	<a href="#">c2po3B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-dehydrase; <b>PDBTitle:</b> crystal structure analysis of desi in the presence of its2 tdp-sugar product
42	<a href="#">d1bs0a_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
43	<a href="#">d1c7ga_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
44	<a href="#">c3tqxA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-3-ketobutyrate coenzyme a ligase; <b>PDBTitle:</b> structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii
45	<a href="#">d1vjoa_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
46	<a href="#">c4qgrA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> degt/dnrj/eryc1/strs aminotransferase; <b>PDBTitle:</b> crystal structure of a degt dnrj eryc1 strs aminotransferase from2 brucella abortus
47	<a href="#">d1mdoa_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
48	<a href="#">c3a2bA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
49	<a href="#">d2bwna1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
50	<a href="#">d1qgna_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
51	<a href="#">d1jf9a_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
52	<a href="#">c3nnkC_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ureidoglycine-glyoxylate aminotransferase; <b>PDBTitle:</b> biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
						<b>Fold:</b> PLP-dependent transferase-like

53	<a href="#">d2fnua1</a>	Alignment	not modelled	100.0	12	<b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
54	<a href="#">d2v1pa1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
55	<a href="#">d1wyub1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Glycine dehydrogenase subunits (GDC-P)
56	<a href="#">d1tpla_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Beta-eliminating lyases
57	<a href="#">c3hbxB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate decarboxylase 1; <b>PDBTitle:</b> crystal structure of gad1 from arabidopsis thaliana
58	<a href="#">c3nysA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase wbpe; <b>PDBTitle:</b> x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution
59	<a href="#">c5kz5M_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase/oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> cysteine desulfurase, mitochondrial; <b>PDBTitle:</b> architecture of the human mitochondrial iron-sulfur cluster assembly2 machinery: the complex formed by the iron donor, the sulfur donor,3 and the scaffold
60	<a href="#">c2cb1A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> o-acetyl homoserine sulfhydrylase; <b>PDBTitle:</b> crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8, oah2.
61	<a href="#">c3mafB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of stspl (asymmetric form)
62	<a href="#">c3frkB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> qdtb; <b>PDBTitle:</b> x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine
63	<a href="#">c4j8IA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yhfs; <b>PDBTitle:</b> crystal structure of the pyridoxal-5'-phosphate dependent protein yhfs2 from escherichia coli
64	<a href="#">d1fc4a_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
65	<a href="#">c3wgcB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> l-allo-threonine aldolase; <b>PDBTitle:</b> aeromonas jandaei l-allo-threonine aldolase h128y/s292r double mutant
66	<a href="#">c2z9wA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate aminotransferase; <b>PDBTitle:</b> crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
67	<a href="#">c4oc9N_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> N: <b>PDB Molecule:</b> putative o-acetylhomoserine (thiol)-lyase; <b>PDBTitle:</b> 2.35 angstrom resolution crystal structure of putative o-2 acetylhomoserine (thiol)-lyase (mety) from campylobacter jejuni3 subsp. jejuni nctc 11168 with n'-pyridoxyl-lysine-5'-monophosphate at4 position 205
68	<a href="#">c3dr4B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative perosamine synthetase; <b>PDBTitle:</b> gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
69	<a href="#">c3zrrB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine-pyruvate aminotransferase (agxt); <b>PDBTitle:</b> crystal structure and substrate specificity of a thermophilic2 archaeal serine : pyruvate aminotransferase from sulfobolus3 solfataricus
70	<a href="#">c3isIA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine catabolism protein pucg; <b>PDBTitle:</b> crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
71	<a href="#">d2ctza1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
72	<a href="#">c3madA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of stspl (symmetric form)
73	<a href="#">c5gp4C_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate decarboxylase; <b>PDBTitle:</b> lactobacillus brevis cgmcc 1306 glutamate decarboxylase
74	<a href="#">c4obuG_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> pyridoxal-dependent decarboxylase domain protein; <b>PDBTitle:</b> ruminococcus gnavus tryptophan decarboxylase rumgna_01526 (apo)
75	<a href="#">c4ritB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxal-dependent decarboxylase; <b>PDBTitle:</b> the yellow crystal structure of pyridoxal-dependent decarboxylase from2 sphaerobacter thermophilus dsm 20745
76	<a href="#">c3e9kA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
77	<a href="#">c3uwcA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotide-sugar aminotransferase; <b>PDBTitle:</b> structure of an aminotransferase (degt-dnrj-eryc1-strs family) from2 coxiella burnetii in complex with pmp
						<b>PDB header:</b> lyase

78	<a href="#">c1i41J_</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> J; <b>PDB Molecule:</b> cystathionine gamma-synthase; <b>PDBTitle:</b> cystathionine gamma-synthase in complex with the inhibitor2 appa
79	<a href="#">c2jisA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> cysteine sulfinic acid decarboxylase; <b>PDBTitle:</b> human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
80	<a href="#">c3hvyC_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> cystathionine beta-lyase family protein, ynbb b.subtilis <b>PDBTitle:</b> crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_348457.1) from clostridium acetobutylicum at3 2.00 a resolution
81	<a href="#">c3fd0B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> putative cystathionine beta-lyase involved in aluminum <b>PDBTitle:</b> crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
82	<a href="#">c3f9tB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> l-tyrosine decarboxylase mfna; <b>PDBTitle:</b> crystal structure of l-tyrosine decarboxylase mfna (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution
83	<a href="#">c5dx5B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> methionine gamma-lyase; <b>PDBTitle:</b> crystal structure of methionine gamma-lyase from clostridium2 sporogenes
84	<a href="#">d1m6sa_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
85	<a href="#">c6ewqA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative capsular polysaccharide biosynthesis protein; <b>PDBTitle:</b> putative sugar aminotransferase spr1654 from streptococcus pneumoniae,2 plp-form
86	<a href="#">d2c0ra1</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
87	<a href="#">d2ch1a1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
88	<a href="#">c3ndnC_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> o-succinylhomoserine sulfhydrylase; <b>PDBTitle:</b> crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
89	<a href="#">c4lc3B_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> putative udp-4-amino-4-deoxy-l-arabinose-oxoglutarate <b>PDBTitle:</b> x-ray crystal structure of a putative udp-4-amino-4-deoxy-l-arabinose-2-oxoglutarate aminotransferase from burkholderia cenocepacia
90	<a href="#">c5j8qA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> cysteine desulfurase sufs; <b>PDBTitle:</b> crystal structure of the cysteine desulfurase sufs of bacillus2 subtilis
91	<a href="#">c5u20C_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> x-ray structure of the wlarg aminotransferase from campylobacter2 jejuni, internal plp-aldimine
92	<a href="#">d1pmma_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Pyridoxal-dependent decarboxylase
93	<a href="#">d1wyua1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Glycine dehydrogenase subunits (GDC-P)
94	<a href="#">c4xauG_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> G; <b>PDB Molecule:</b> putative aminotransferase; <b>PDBTitle:</b> crystal structure of ats13 from actinomadura melliura
95	<a href="#">c4xk1A_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> crystal structure of a phosphoserine/phosphohydroxythreonine2 aminotransferase (psat) from pseudomonas aeruginosa with cofactor3 pyridoxal phosphate and bound glutamate
96	<a href="#">c4lnjA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> low-specificity l-threonine aldolase; <b>PDBTitle:</b> structure of escherichia coli threonine aldolase in unliganded form
97	<a href="#">c2okkA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate decarboxylase 2; <b>PDBTitle:</b> the x-ray crystal structure of the 65kda isoform of glutamic acid2 decarboxylase (gad65)
98	<a href="#">c5ijgB_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> cys/met metabolism pyridoxal-phosphate-dependent enzyme; <b>PDBTitle:</b> crystal structure of o-acetylhomoserine sulfhydrylase from brucella2 melitensis at 2.0 a resolution
99	<a href="#">d1h0ca_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
100	<a href="#">c6c9eB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of cysteine desulfurase from legionella pneumophila2 philadelphia 1
						<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> methionine gamma-lyase;



101	<a href="#">c3aemD_</a>	Alignment	not modelled	99.9	17	<b>PDBTitle:</b> reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate
102	<a href="#">c3mc6C_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of scdpl1
103	<a href="#">c6enzA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> acidic amino acid decarboxylase gad11; <b>PDBTitle:</b> crystal structure of mouse gad11
104	<a href="#">d1js3a_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Pyridoxal-dependent decarboxylase
105	<a href="#">c4e1oC_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> histidine decarboxylase; <b>PDBTitle:</b> human histidine decarboxylase complex with histidine methyl ester2 (hme)
106	<a href="#">c2dr1A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 386aa long hypothetical serine aminotransferase; <b>PDBTitle:</b> crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
107	<a href="#">d1qz9a_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
108	<a href="#">c3caiA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> possible aminotransferase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv3778c2 protein
109	<a href="#">c3f0hA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
110	<a href="#">d1y4ia1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
111	<a href="#">c6jrlA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,4-dihydroxyphenylacetaldehyde synthase; <b>PDBTitle:</b> crystal structure of drosophila alpha methyl-dopa-resistant protein/3,2 4-dihydroxyphenylacetaldehyde synthase
112	<a href="#">d3bc8a1</a>	Alignment	not modelled	99.9	8	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SepSecS-like
113	<a href="#">c6eewC_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> aromatic-l-amino-acid decarboxylase; <b>PDBTitle:</b> crystal structure of catharanthus roseus tryptophan decarboxylase in2 complex with l-tryptophan
114	<a href="#">c2gqnB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cystathionine beta-lyase; <b>PDBTitle:</b> cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
115	<a href="#">c2x3lA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> orn/lys/arg decarboxylase family protein; <b>PDBTitle:</b> crystal structure of the orn_lys_arg decarboxylase family2 protein sar0482 from methicillin-resistant staphylococcus3 aureus
116	<a href="#">d1cl1a_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
117	<a href="#">c5uidC_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aminotransferase tlmj; <b>PDBTitle:</b> the crystal structure of an aminotransferase tlmj from2 streptoalloteichus hindustanus
118	<a href="#">c4lw2C_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cysteine sulfinate desulfinate; <b>PDBTitle:</b> structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration
119	<a href="#">d1t3ia_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
120	<a href="#">c3ju7B_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative plp-dependent aminotransferase; <b>PDBTitle:</b> crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution