

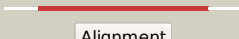

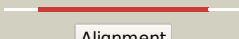






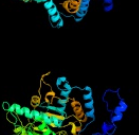

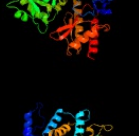
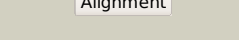

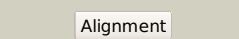













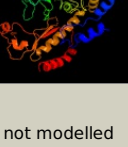


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3432c_gadB_3850552_3851934
Date	Fri Aug 9 18:20:10 BST 2019
Unique Job ID	e8cba44ff2db7c23

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5gp4C_</a>	 Alignment		100.0	45	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate decarboxylase; <b>PDBTitle:</b> lactobacillus brevis cgmc 1306 glutamate decarboxylase
2	<a href="#">d1pmma_</a>	 Alignment		100.0	47	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Pyridoxal-dependent decarboxylase
3	<a href="#">c3hbxB_</a>	 Alignment		100.0	49	<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
4	<a href="#">c6eemB_</a>	 Alignment		100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine/dopa decarboxylase; <b>PDBTitle:</b> crystal structure of papaver somniferum tyrosine decarboxylase in2 complex with l-tyrosine
5	<a href="#">c2qmaB_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminobutyrate-pyruvate transaminase and l-2,4- <b>PDBTitle:</b> crystal structure of glutamate decarboxylase domain of2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus
6	<a href="#">c4e1oC_</a>	 Alignment		100.0	17	<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)
7	<a href="#">c6eeiA_</a>	 Alignment		100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine decarboxylase 1; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana phenylacetaldehyde synthase2 in complex with l-phenylalanine
8	<a href="#">d1js3a_</a>	 Alignment		100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Pyridoxal-dependent decarboxylase
9	<a href="#">c6jrlA_</a>	 Alignment		100.0	18	<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
10	<a href="#">c6enzA_</a>	 Alignment		100.0	15	<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
11	<a href="#">c6eeqA_</a>	 Alignment		100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylacetaldehyde synthase; <b>PDBTitle:</b> crystal structure of rhodiola rosea 4-hydroxyphenylacetaldehyde2 synthase

12	<a href="#">c2jisA_</a>	Alignment		100.0	16	<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.
13	<a href="#">c3madA_</a>	Alignment		100.0	22	<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)
14	<a href="#">c3k40B_</a>	Alignment		100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> aromatic-l-amino-acid decarboxylase; <b>PDBTitle:</b> crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
15	<a href="#">c2okkA_</a>	Alignment		100.0	15	<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)
16	<a href="#">c6eewC_</a>	Alignment		100.0	17	<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
17	<a href="#">c5k1rB_</a>	Alignment		100.0	23	<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
18	<a href="#">c5o5cD_</a>	Alignment		100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative decarboxylase involved in desferrioxamine biosynthesis2 pathway lysine decarboxylase from the fire blight disease pathogen3 erwinia amylovora
19	<a href="#">c4q6rB_</a>	Alignment		100.0	21	<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
20	<a href="#">c5hsjB_</a>	Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative decarboxylase; <b>PDBTitle:</b> structure of tyrosine decarboxylase complex with plp at 1.9 angstroms2 resolution
21	<a href="#">c4obuG_</a>	Alignment	not modelled	100.0	17	<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)
22	<a href="#">c4ritB_</a>	Alignment	not modelled	100.0	19	<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
23	<a href="#">c3mafB_</a>	Alignment	not modelled	100.0	23	<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)
24	<a href="#">c6ebnB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> non canonical aromatic amino acid decarboxylase; <b>PDBTitle:</b> crystal structure of psilocybe cubensis noncanonical aromatic amino2 acid decarboxylase
25	<a href="#">c3mc6C_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of scdpl1
26	<a href="#">c4w8iB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> probable sphingosine-1-phosphate lyase; <b>PDBTitle:</b> crystal structure of lpspl/pp2128, legionella pneumophila2 sphingosine-1 phosphate lyase
27	<a href="#">c3hl2D_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> o-phosphoseryl-trna(sec) selenium transferase; <b>PDBTitle:</b> the crystal structure of the human sepsecs-trnasec complex
						<b>Fold:</b> PLP-dependent transferase-like

28	<a href="#">d3bc8a1</a>	Alignment	not modelled	100.0	14	<b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SepSecS-like
29	<a href="#">c3f9tB</a>	Alignment	not modelled	100.0	22	<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
30	<a href="#">d2z67a1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SepSecS-like
31	<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)
32	<a href="#">d1wyua1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Glycine dehydrogenase subunits (GDC-P)
33	<a href="#">d1jf9a</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
34	<a href="#">c3bcxA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; <b>PDBTitle:</b> e1 dehydrase
35	<a href="#">c3caiA</a>	Alignment	not modelled	100.0	16	<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
36	<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
37	<a href="#">c4lw2C</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cysteine sulfinatase desulfurase; <b>PDBTitle:</b> structural changes during cysteine desulfurase csda and sulfur-2 acceptor csde interactions provide insight into the trans-3 persulfuration
38	<a href="#">d1kl1a</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
39	<a href="#">c5j8qA</a>	Alignment	not modelled	100.0	16	<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
40	<a href="#">c3nnkC</a>	Alignment	not modelled	100.0	15	<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
41	<a href="#">c6c9eB</a>	Alignment	not modelled	100.0	14	<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
42	<a href="#">c4wxfC</a>	Alignment	not modelled	100.0	13	<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 with2 glycine
43	<a href="#">d1vjoa</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
44	<a href="#">c4k2bA</a>	Alignment	not modelled	100.0	13	<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
45	<a href="#">c4q76B</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase 2, chloroplastic; <b>PDBTitle:</b> crystal structure of nfs2 c384s mutant, the plastidial cysteine2 desulfurase from arabidopsis thaliana
46	<a href="#">c4lhdB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycine dehydrogenase [decarboxylating]; <b>PDBTitle:</b> crystal structure of synechocystis sp. pcc 6803 glycine decarboxylase2 (p-protein), holo form with pyridoxal-5'-phosphate and glycine,3 closed flexible loop
47	<a href="#">d1b9ha</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="#">c4w91C</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aminotransferase; <b>PDBTitle:</b> crystal structure of a cysteine desulfurase sufs from brucella suis2 bound to plp
49	<a href="#">c3e9kA</a>	Alignment	not modelled	100.0	14	<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
50	<a href="#">c6hrhA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-aminolevulinate synthase, erythroid-specific, <b>PDBTitle:</b> structure of human erythroid-specific 5'-aminolevulinate synthase,2 alas2
51	<a href="#">c5utsC</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> c-s lyase egt2; <b>PDBTitle:</b> carbon sulfoxide lyase, egt2 in the ergothioneine biosynthesis pathway
52	<a href="#">c2r0tA</a>	Alignment	not modelled	100.0	15	<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

53	<a href="#">c5zsqA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> nifs from hydrogenimonas thermophila, soaked with l-cysteine for 4 min
54	<a href="#">d1qz9a</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
55	<a href="#">c3ffrA</a>	Alignment	not modelled	100.0	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase serc; <b>PDBTitle:</b> crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
56	<a href="#">c2hzpA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> kynureninase; <b>PDBTitle:</b> crystal structure of homo sapiens kynureninase
57	<a href="#">c2dr1A</a>	Alignment	not modelled	100.0	14	<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
58	<a href="#">d1t3ia</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
59	<a href="#">c2hdyA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine lyase; <b>PDBTitle:</b> structure of human selenocysteine lyase
60	<a href="#">c2c7tA</a>	Alignment	not modelled	100.0	17	<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.
61	<a href="#">c3f0hA</a>	Alignment	not modelled	100.0	13	<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
62	<a href="#">c5i90A</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pvdn; <b>PDBTitle:</b> crystal structure of pvdn from pseudomonas aeruginosa
63	<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
64	<a href="#">c2w8wA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine palmitoyltransferase; <b>PDBTitle:</b> n100y spt with plp-ser
65	<a href="#">d1dfoa</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
66	<a href="#">c3e77A</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> human phosphoserine aminotransferase in complex with plp
67	<a href="#">c4j5uB</a>	Alignment	not modelled	100.0	15	<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
68	<a href="#">c3isiA</a>	Alignment	not modelled	100.0	13	<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
69	<a href="#">c4eb5B</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase/metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable cysteine desulfurase 2; <b>PDBTitle:</b> a. fulgidus iscs-iscu complex structure
70	<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
71	<a href="#">c2dkjB</a>	Alignment	not modelled	100.0	16	<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
72	<a href="#">c2po3B</a>	Alignment	not modelled	100.0	17	<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
73	<a href="#">c5vprA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of cysteine desulfurase from elizabethkingia2 anophelis with covalently bound pyridoxal phosphate
74	<a href="#">c5w70B</a>	Alignment	not modelled	100.0	16	<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 streptomyces ribosidificus
75	<a href="#">c2fyfB</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
76	<a href="#">c5usrG</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> cysteine desulfurase, mitochondrial; <b>PDBTitle:</b> crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
77	<a href="#">c5k8bA</a>	Alignment	not modelled	100.0	14	<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
78	<a href="#">c4xk1A_</a>	Alignment	not modelled	100.0	14	<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
79	<a href="#">c5uidC_</a>	Alignment	not modelled	100.0	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
80	<a href="#">c2ogeC_</a>	Alignment	not modelled	100.0	17	<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
81	<a href="#">d2c0ra1</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
82	<a href="#">c3lvmB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of e.coli iscs
83	<a href="#">d1h0ca_</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
84	<a href="#">c5vc2A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of a serine hydroxymethyltransferase from2 helicobacter pylori
85	<a href="#">c2huuA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine glyoxylate aminotransferase; <b>PDBTitle:</b> crystal structure of aedes aegypti alanine glyoxylate aminotransferase2 in complex with alanine
86	<a href="#">c3ecdC_</a>	Alignment	not modelled	100.0	18	<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 burkholderia2 pseudomallei
87	<a href="#">c5txtA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-aminolevulinate synthase, mitochondrial; <b>PDBTitle:</b> structure of asymmetric apo/holo alas dimer from s. cerevisiae
88	<a href="#">c2yrrA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminotransferase, class v; <b>PDBTitle:</b> hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
89	<a href="#">c4ytjC_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> cals13; <b>PDBTitle:</b> crystal structure of sugar aminotransferase cals13 from micromonospora2 echinospora
90	<a href="#">c3uwcA_</a>	Alignment	not modelled	100.0	13	<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
91	<a href="#">d2bwua1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
92	<a href="#">c5kz5M_</a>	Alignment	not modelled	100.0	17	<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
93	<a href="#">c6czyA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase 1, chloroplastic; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana phosphoserine2 aminotransferase isoform 1 (atpsat1) in complex with pyridoxamine-5'-3 phosphate (pmp)
94	<a href="#">d2fnua1</a>	Alignment	not modelled	100.0	10	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
95	<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
96	<a href="#">d2bkwa1</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
97	<a href="#">c4xauG_</a>	Alignment	not modelled	100.0	12	<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
98	<a href="#">c3vaxA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein dnda; <b>PDBTitle:</b> crystal structure of dnda from streptomyces lividans
99	<a href="#">c5jayB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 8-amino-7-oxononoate synthase; <b>PDBTitle:</b> crystal structure of an 8-amino-7-oxononoate synthase from2 burkholderia xenovorans
100	<a href="#">d1w23a_</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
101	<a href="#">d1v72a1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
102	<a href="#">d1m32a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases

					<b>Family:</b> Cystathionine synthase-like
103	<a href="#">d1mdoa_</a>	Alignment	not modelled	100.0	15 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
104	<a href="#">c2z9wA_</a>	Alignment	not modelled	100.0	14 <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
105	<a href="#">c4ixoB_</a>	Alignment	not modelled	100.0	13 <b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nifs-like protein; <b>PDBTitle:</b> x-ray structure of nifs-like protein from rickettsia africae esf-5
106	<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
107	<a href="#">c6cd1A_</a>	Alignment	not modelled	100.0	14 <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
108	<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
109	<a href="#">d1p3wa_</a>	Alignment	not modelled	100.0	17 <b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
110	<a href="#">d1elua_</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
111	<a href="#">d1eg5a_</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
112	<a href="#">c3dr4B_</a>	Alignment	not modelled	100.0	14 <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
113	<a href="#">c3m5uA_</a>	Alignment	not modelled	100.0	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
114	<a href="#">c3wgcB_</a>	Alignment	not modelled	100.0	19 <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
115	<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
116	<a href="#">c4n0wA_</a>	Alignment	not modelled	100.0	14 <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
117	<a href="#">c3hqtB_</a>	Alignment	not modelled	100.0	13 <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
118	<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
119	<a href="#">c3wy7D_</a>	Alignment	not modelled	100.0	17 <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
120	<a href="#">c3a2bA_</a>	Alignment	not modelled	100.0	12 <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