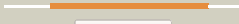
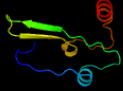
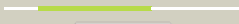
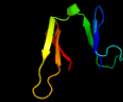
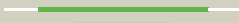


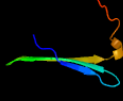



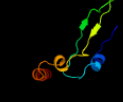



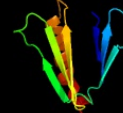








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3819 (- )_4284174_4284509
Date	Fri Aug 9 18:20:53 BST 2019
Unique Job ID	1c8c3a634c441d9d

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5a3gA_</a>	 Alignment		89.2	21	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> m50; <b>PDBTitle:</b> structure of herpesvirus nuclear egress complex subunit m50
2	<a href="#">c4tyzB_</a>	 Alignment		63.5	13	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of an unknown protein from2 leishmania infantum
3	<a href="#">d2hthb1</a>	 Alignment		58.8	20	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> VPS36 N-terminal domain-like
4	<a href="#">c4xuuD_</a>	 Alignment		57.9	12	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> phosphatidylinositide phosphatase sac2; <b>PDBTitle:</b> the hsac2 domain from human phosphoinositide phosphatase sac2
5	<a href="#">d1boba_</a>	 Alignment		51.2	24	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> N-acetyl transferase, NAT
6	<a href="#">c5d5nA_</a>	 Alignment		39.6	19	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> virion egress protein ul34 homolog; <b>PDBTitle:</b> crystal structure of the human cytomegalovirus pul50-pul53 complex
7	<a href="#">c2p0wB_</a>	 Alignment		39.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histone acetyltransferase type b catalytic subunit; <b>PDBTitle:</b> human histone acetyltransferase 1 (hat1)
8	<a href="#">d2rnrb1</a>	 Alignment		38.5	13	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> TFIIH domain
9	<a href="#">c3ffrA_</a>	 Alignment		34.5	12	<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
10	<a href="#">c5husA_</a>	 Alignment		32.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose synthase regulatory protein; <b>PDBTitle:</b> structure of candida albicans trehalose synthase regulatory protein c-2 terminal domain
11	<a href="#">c4r8gE_</a>	 Alignment		31.6	22	<b>PDB header:</b> protein binding/calcium-binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> unconventional myosin-1c; <b>PDBTitle:</b> crystal structure of myosin-1c tail in complex with calmodulin

12	<a href="#">c3f0hA_</a>	Alignment		29.7	8	<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
13	<a href="#">d1qz9a_</a>	Alignment		28.5	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
14	<a href="#">c3ftbA_</a>	Alignment		28.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> the crystal structure of the histidinol-phosphate aminotransferase2 from clostridium acetobutylicum
15	<a href="#">c3getA_</a>	Alignment		28.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution
16	<a href="#">c3ly1C_</a>	Alignment		26.9	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> putative histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution
17	<a href="#">c3lfxE_</a>	Alignment		26.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of tm1797, a cas1 protein from thermotoga maritima
18	<a href="#">c4r8dB_</a>	Alignment		26.5	4	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of rv1600 encoded aminotransferase in complex with2 plp-mes from mycobacterium tuberculosis
19	<a href="#">d1lc5a_</a>	Alignment		24.3	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
20	<a href="#">c3fkdC_</a>	Alignment		22.7	21	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> l-threonine-o-3-phosphate decarboxylase; <b>PDBTitle:</b> the crystal structure of l-threonine-o-3-phosphate decarboxylase from2 porphyromonas gingivalis
21	<a href="#">c4isyB_</a>	Alignment	not modelled	22.4	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of iscs from mycobacterium tuberculosis
22	<a href="#">c4wwrD_</a>	Alignment	not modelled	22.1	7	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> ubiquitin-like protein 4a; <b>PDBTitle:</b> crystal structure of bag6-ubl4a dimerization domain
23	<a href="#">d2caya1</a>	Alignment	not modelled	21.9	19	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> VPS36 N-terminal domain-like
24	<a href="#">d1vjoa_</a>	Alignment	not modelled	21.5	16	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
25	<a href="#">c6j5bC_</a>	Alignment	not modelled	21.5	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> protein phosphate starvation response 1; <b>PDBTitle:</b> structural basis for the target dna recognition and binding by the myb2 domain of phosphate starvation response regulator 1
26	<a href="#">c5vyeA_</a>	Alignment	not modelled	20.7	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-threonine aldolase; <b>PDBTitle:</b> crystal structure of l-threonine aldolase from pseudomonas putida
27	<a href="#">c4xk1A_</a>	Alignment	not modelled	20.5	12	<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
28	<a href="#">c5j90A_</a>	Alignment	not modelled	19.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pvdn; <b>PDBTitle:</b> crystal structure of pvdn from pseudomonas aeruginosa

29	<a href="#">d2q3la1</a>	Alignment	not modelled	19.3	17	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Sfri0576-like
30	<a href="#">c2yrrA</a>	Alignment	not modelled	19.2	24	<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
31	<a href="#">c3eucB</a>	Alignment	not modelled	19.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase 2; <b>PDBTitle:</b> crystal structure of histidinol-phosphate aminotransferase2 (yp_297314.1) from ralstonia eutropha jmp134 at 2.05 a resolution
32	<a href="#">c4wbtA</a>	Alignment	not modelled	19.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of histidinol-phosphate aminotransferase from2 sinorhizobium meliloti in complex with pyridoxal-5'-phosphate
33	<a href="#">c3lvmB</a>	Alignment	not modelled	18.8	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of e.coli iscs
34	<a href="#">c5yb0I</a>	Alignment	not modelled	18.7	9	<b>PDB header:</b> transferase <b>Chain:</b> I: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> crystal structure of wild type phosphoserine aminotransferase (psat)2 from e. histolytica
35	<a href="#">d1jf9a</a>	Alignment	not modelled	18.6	9	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
36	<a href="#">c5yqrA</a>	Alignment	not modelled	18.4	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> endolysin/membrane-anchored lipid-binding protein lam6 <b>PDBTitle:</b> crystal structure of the ph-like domain of lam6
37	<a href="#">c4wvrB</a>	Alignment	not modelled	17.8	7	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like protein 4a; <b>PDBTitle:</b> crystal structure of bag6-ubl4a dimerization domain
38	<a href="#">c3cq6E</a>	Alignment	not modelled	17.7	13	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound )
39	<a href="#">c4lnjA</a>	Alignment	not modelled	16.7	17	<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
40	<a href="#">d1f08a</a>	Alignment	not modelled	15.8	21	<b>Fold:</b> Origin of replication-binding domain, RBD-like <b>Superfamily:</b> Origin of replication-binding domain, RBD-like <b>Family:</b> Replication initiation protein E1
41	<a href="#">d1t3ia</a>	Alignment	not modelled	15.5	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
42	<a href="#">c3hdoB</a>	Alignment	not modelled	15.4	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
43	<a href="#">d1ug7a</a>	Alignment	not modelled	15.4	14	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Domain from hypothetical 2610208m17rik protein <b>Family:</b> Domain from hypothetical 2610208m17rik protein
44	<a href="#">d2ooka1</a>	Alignment	not modelled	15.2	22	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Sfri0576-like
45	<a href="#">c5usrG</a>	Alignment	not modelled	15.1	7	<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
46	<a href="#">d1rcqa2</a>	Alignment	not modelled	14.9	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
47	<a href="#">c4pw0A</a>	Alignment	not modelled	14.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> alpha/beta hydrolase fold protein from chitinophaga pinensis
48	<a href="#">c3r3xA</a>	Alignment	not modelled	14.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fluoroacetate dehalogenase; <b>PDBTitle:</b> crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
49	<a href="#">d2vj0a1</a>	Alignment	not modelled	14.3	9	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Clathrin adaptor appendage domain <b>Family:</b> Alpha-adaptin ear subdomain-like
50	<a href="#">c6f77D</a>	Alignment	not modelled	14.1	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> aspartate aminotransferase a; <b>PDBTitle:</b> crystal structure of the prephenate aminotransferase from rhizobium2 meliloti
51	<a href="#">d1fg7a</a>	Alignment	not modelled	14.0	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
52	<a href="#">d1p3wa</a>	Alignment	not modelled	13.7	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
53	<a href="#">d1iuga</a>	Alignment	not modelled	13.4	12	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
54	<a href="#">d1kyfa1</a>	Alignment	not modelled	13.2	9	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Clathrin adaptor appendage domain <b>Family:</b> Alpha-adaptin ear subdomain-like
						<b>PDB header:</b> transferase

55	<a href="#">c3ffhA_</a>	Alignment	not modelled	13.1	26	<b>Chain:</b> A: <b>PDB Molecule:</b> histidinol-phosphate aminotransferase; <b>PDBTitle:</b> the crystal structure of histidinol-phosphate aminotransferase from 2 listeria innocua clip11262.
56	<a href="#">d2d9ta1</a>	Alignment	not modelled	12.9	25	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Tudor/PWWP/MBT <b>Family:</b> Tudor domain
57	<a href="#">d1eg5a_</a>	Alignment	not modelled	12.8	21	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
58	<a href="#">c2huuA_</a>	Alignment	not modelled	12.5	17	<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
59	<a href="#">c2ju5A_</a>	Alignment	not modelled	12.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin disulfide isomerase; <b>PDBTitle:</b> dsbh oxidoreductase
60	<a href="#">c4q76B_</a>	Alignment	not modelled	12.3	16	<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
61	<a href="#">c5b0aA_</a>	Alignment	not modelled	12.2	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> olivetolic acid cyclase; <b>PDBTitle:</b> polyketide cyclase oac from cannabis sativa, h5q mutant
62	<a href="#">c4ql6A_</a>	Alignment	not modelled	12.1	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxy-terminal processing protease; <b>PDBTitle:</b> structure of c. trachomatis ct441
63	<a href="#">d1m32a_</a>	Alignment	not modelled	11.9	0	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
64	<a href="#">c5lxuA_</a>	Alignment	not modelled	11.9	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor lux; <b>PDBTitle:</b> structure of the dna-binding domain of lux arrhythmo
65	<a href="#">c5xqgC_</a>	Alignment	not modelled	11.9	21	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> pcrglx protein; <b>PDBTitle:</b> crystal structure of a pl 26 exo-rhamnogalacturonan lyase from 2 penicillium chrysogenum complexed with unsaturated galacturonosyl3 rhamnose
66	<a href="#">c2fyfB_</a>	Alignment	not modelled	11.8	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 from 2 mycobacterium tuberculosis
67	<a href="#">c3wgcB_</a>	Alignment	not modelled	11.8	17	<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
68	<a href="#">c3m cwA_</a>	Alignment	not modelled	11.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution
69	<a href="#">c5b87B_</a>	Alignment	not modelled	10.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of a cysteine desulfurase from thermococcus2 onnurineus na1 in complex with alanine at 2.3 angstrom resolution
70	<a href="#">d1h0ca_</a>	Alignment	not modelled	10.8	20	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
71	<a href="#">d2f69a1</a>	Alignment	not modelled	10.7	27	<b>Fold:</b> open-sided beta-meander <b>Superfamily:</b> Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain <b>Family:</b> Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain
72	<a href="#">d2qiya1</a>	Alignment	not modelled	10.6	4	<b>Fold:</b> immunoglobulin-like beta-sandwich <b>Superfamily:</b> immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
73	<a href="#">d1ogmx1</a>	Alignment	not modelled	10.4	29	<b>Fold:</b> Dextranase, N-terminal domain <b>Superfamily:</b> Dextranase, N-terminal domain <b>Family:</b> Dextranase, N-terminal domain
74	<a href="#">c5o9eB_</a>	Alignment	not modelled	10.2	17	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> putative u3 small nucleolar ribonucleoprotein protein; <b>PDBTitle:</b> crystal structure of the imp4-mpp10 complex from chaetomium2 thermophilum
75	<a href="#">c6c9eB_</a>	Alignment	not modelled	10.1	8	<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
76	<a href="#">c4aooA_</a>	Alignment	not modelled	10.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phenylalanine aminotransferase; <b>PDBTitle:</b> biochemical properties and crystal structure of a novel2 beta-phenylalanine aminotransferase from variovorax3 paradoxus
77	<a href="#">c5jm0A_</a>	Alignment	not modelled	10.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-mannosidase,alpha-mannosidase,alpha-mannosidase; <b>PDBTitle:</b> structure of the s. cerevisiae alpha-mannosidase 1
78	<a href="#">c5dxlA_</a>	Alignment	not modelled	9.8	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-6-phosphate phosphatase; <b>PDBTitle:</b> structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
79	<a href="#">c4eb5B_</a>	Alignment	not modelled	9.8	8	<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
80	<a href="#">d2f8ja1</a>	Alignment	not modelled	9.8	5	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases

						Family:AAT-like
81	<a href="#">c3ezsB_</a>	Alignment	not modelled	9.7	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase aspb; <b>PDBTitle:</b> crystal structure of aminotransferase aspb (np_207418.1) from2 helicobacter pylori 26695 at 2.19 a resolution
82	<a href="#">c4w91C_</a>	Alignment	not modelled	9.6	8	<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
83	<a href="#">c2z9fC_</a>	Alignment	not modelled	9.5	28	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> cellulose synthase operon protein d; <b>PDBTitle:</b> crystal structure of axcesd protein from acetobacter xylinum
84	<a href="#">c4r2nA_</a>	Alignment	not modelled	9.5	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phenylalanine aminotransferase; <b>PDBTitle:</b> crystal structure of rv3772 in complex with its substrate
85	<a href="#">c2qycA_</a>	Alignment	not modelled	9.4	0	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-like protein; <b>PDBTitle:</b> crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
86	<a href="#">d2bp3a1</a>	Alignment	not modelled	9.3	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)
87	<a href="#">c4a4fA_</a>	Alignment	not modelled	9.2	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> survival of motor neuron-related-splicing factor 30; <b>PDBTitle:</b> solution structure of spf30 tudor domain in complex with symmetrically2 dimethylated arginine
88	<a href="#">c3islA_</a>	Alignment	not modelled	9.2	19	<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
89	<a href="#">c3wy7D_</a>	Alignment	not modelled	9.1	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 8-amino-7-oxonanoate synthase; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis 7-keto-8-aminopelargonic2 acid (kapa) synthase biof
90	<a href="#">c4ps2A_</a>	Alignment	not modelled	9.1	30	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative type vi secretion protein; <b>PDBTitle:</b> structure of the c-terminal fragment (87-165) of e.coli eaec tssb2 molecule
91	<a href="#">c4chmB_</a>	Alignment	not modelled	9.0	38	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> imc sub-compartment protein isp1; <b>PDBTitle:</b> structure of inner membrane complex (imc) sub-compartment protein 12 (isp1) from toxoplasma gondii
92	<a href="#">d1lrza_</a>	Alignment	not modelled	9.0	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> GARP response regulators
93	<a href="#">c5zsqa_</a>	Alignment	not modelled	8.9	11	<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
94	<a href="#">d1j2ra_</a>	Alignment	not modelled	8.8	23	<b>Fold:</b> Isochorismatase-like hydrolases <b>Superfamily:</b> Isochorismatase-like hydrolases <b>Family:</b> Isochorismatase-like hydrolases
95	<a href="#">c4iw7A_</a>	Alignment	not modelled	8.7	4	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 8-amino-7-oxonanoate synthase; <b>PDBTitle:</b> crystal structure of 8-amino-7-oxonanoate synthase (biof) from2 francisella tularensis.
96	<a href="#">c3nuwC_</a>	Alignment	not modelled	8.6	60	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-oxo-3-deoxygalactonate kinase; <b>PDBTitle:</b> crystal structure of 2-oxo-3-deoxygalactonate kinase from klebsiella2 pneumoniae
97	<a href="#">c4ixoB_</a>	Alignment	not modelled	8.5	17	<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
98	<a href="#">d2ch1a1</a>	Alignment	not modelled	8.4	19	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
99	<a href="#">c4b9aA_</a>	Alignment	not modelled	8.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable epoxide hydrolase; <b>PDBTitle:</b> structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.