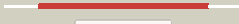



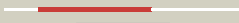







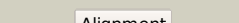









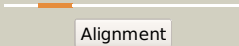
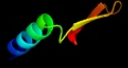
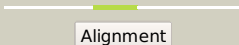

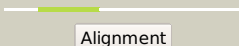
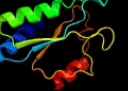
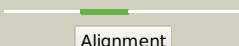

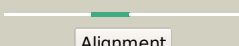
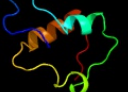
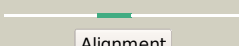

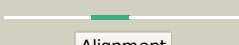






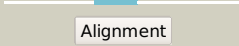

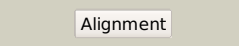

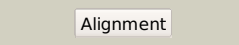
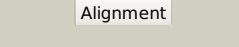



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1940_(ribA1)_2192613_2193674
Date	Mon Aug 5 13:25:03 BST 2019
Unique Job ID	7de09fef8a40ca6d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4i14B_</a>	 Alignment		100.0	51	<b>PDB header:</b> hydrolase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribba; <b>PDBTitle:</b> crystal structure of mtb-riba2 (rv1415)
2	<a href="#">c6mnzB_</a>	 Alignment		100.0	33	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase; <b>PDBTitle:</b> crystal structure of ribbx, a two domain 3,4-dihydroxy-2-butanone 4-2 phosphate synthase from a. baumannii.
3	<a href="#">c4ffjA_</a>	 Alignment		100.0	33	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribba; <b>PDBTitle:</b> the crystal structure of spdhbps from s.pneumoniae
4	<a href="#">d1k4ia_</a>	 Alignment		100.0	38	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
5	<a href="#">d1g57a_</a>	 Alignment		100.0	38	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
6	<a href="#">d1snaa_</a>	 Alignment		100.0	30	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
7	<a href="#">d1tksa_</a>	 Alignment		100.0	36	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
8	<a href="#">c3mioA_</a>	 Alignment		100.0	56	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase; <b>PDBTitle:</b> crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
9	<a href="#">c4p6dA_</a>	 Alignment		100.0	38	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase; <b>PDBTitle:</b> structure of ribb complexed with po4 ion
10	<a href="#">d2bz1a1</a>	 Alignment		100.0	32	<b>Fold:</b> RibA-like <b>Superfamily:</b> RibA-like <b>Family:</b> RibA-like
11	<a href="#">c4ri4B_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gtp cyclohydrolase-2; <b>PDBTitle:</b> crystal structure of gtp cyclohydrolase ii from helicobacter pylori2 26695

12	<a href="#">d1y0na_</a>	 Alignment		82.4	38	<b>Fold:</b> YehU-like <b>Superfamily:</b> YehU-like <b>Family:</b> YehU-like
13	<a href="#">d1lh0a_</a>	 Alignment		67.4	12	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
14	<a href="#">c5f56A_</a>	 Alignment		63.3	19	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded-dna-specific exonuclease; <b>PDBTitle:</b> structure of recj complexed with dna and ssb-ct
15	<a href="#">d1ko7a1</a>	 Alignment		52.8	13	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> HprK N-terminal domain-like <b>Family:</b> HPr kinase/phoshatase HprK N-terminal domain
16	<a href="#">c4gijC_</a>	 Alignment		49.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> pseudouridine-5'-phosphate glycosidase; <b>PDBTitle:</b> crystal structure of pseudouridine monophosphate glycosidase complexed2 with sulfate
17	<a href="#">d1js3a_</a>	 Alignment		43.6	11	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Pyridoxal-dependent decarboxylase
18	<a href="#">d1vkma_</a>	 Alignment		43.5	18	<b>Fold:</b> Indigoidine synthase A-like <b>Superfamily:</b> Indigoidine synthase A-like <b>Family:</b> Indigoidine synthase A-like
19	<a href="#">d1oi2a_</a>	 Alignment		42.5	11	<b>Fold:</b> DAK1/DegV-like <b>Superfamily:</b> DAK1/DegV-like <b>Family:</b> DAK1
20	<a href="#">c6eeiA_</a>	 Alignment		38.1	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
21	<a href="#">d1oeyj_</a>	 Alignment	not modelled	37.6	31	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
22	<a href="#">c3n2IA_</a>	 Alignment	not modelled	35.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
23	<a href="#">c1un9B_</a>	 Alignment	not modelled	33.5	20	<b>PDB header:</b> kinase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroxyacetone kinase; <b>PDBTitle:</b> crystal structure of the dihydroxyacetone kinase from c.2 freundii in complex with amp-pnp and mg2+
24	<a href="#">c6eeqA_</a>	 Alignment	not modelled	32.2	17	<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
25	<a href="#">c4obuG_</a>	 Alignment	not modelled	31.1	13	<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)
26	<a href="#">d1un8a4</a>	 Alignment	not modelled	27.8	20	<b>Fold:</b> DAK1/DegV-like <b>Superfamily:</b> DAK1/DegV-like <b>Family:</b> DAK1
27	<a href="#">c3ct4B_</a>	 Alignment	not modelled	27.4	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pts-dependent dihydroxyacetone kinase, dihydroxyacetone- <b>PDBTitle:</b> structure of dha-kinase subunit dhak from l. lactis
28	<a href="#">c3p04A_</a>	 Alignment	not modelled	26.4	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized bcr; <b>PDBTitle:</b> crystal structure of the bcr protein from corynebacterium

						glutamicum.2 northeast structural genomics consortium target cgr8
29	<a href="#">c6eewC</a>	Alignment	not modelled	26.3	15	<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
30	<a href="#">c2zxrA</a>	Alignment	not modelled	25.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna specific exonuclease recj; <b>PDBTitle:</b> crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8
31	<a href="#">c3zihB</a>	Alignment	not modelled	25.3	14	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein sepf; <b>PDBTitle:</b> bacillus subtilis sepf, c-terminal domain
32	<a href="#">c4ritB</a>	Alignment	not modelled	25.1	28	<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
33	<a href="#">d1wd5a</a>	Alignment	not modelled	23.5	27	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
34	<a href="#">d1hrua</a>	Alignment	not modelled	22.6	7	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> YrdC-like
35	<a href="#">c5o5cD</a>	Alignment	not modelled	22.4	15	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative decarboxylase involved in desferrioxamine <b>PDBTitle:</b> the crystal structure of dfoj, the desferrioxamine biosynthetic2 pathway lysine decarboxylase from the fire blight disease pathogen3 erwinia amylovora
36	<a href="#">c3p04B</a>	Alignment	not modelled	22.1	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized bcr; <b>PDBTitle:</b> crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
37	<a href="#">c1xr4B</a>	Alignment	not modelled	22.0	24	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative citrate lyase alpha chain/citrate-acp transferase; <b>PDBTitle:</b> x-ray crystal structure of putative citrate lyase alpha chain/citrate-2 acp transferase [salmonella typhimurium]
38	<a href="#">c6eemB</a>	Alignment	not modelled	21.2	9	<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
39	<a href="#">c2iu6B</a>	Alignment	not modelled	21.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroxyacetone kinase; <b>PDBTitle:</b> regulation of the dha operon of lactococcus lactis
40	<a href="#">c5j84A</a>	Alignment	not modelled	19.3	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase; <b>PDBTitle:</b> crystal structure of l-arabinonate dehydratase in holo-form
41	<a href="#">d1jcua</a>	Alignment	not modelled	18.5	22	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> YrdC-like
42	<a href="#">c1ko7B</a>	Alignment	not modelled	18.3	13	<b>PDB header:</b> transferase,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hpr kinase/phosphatase; <b>PDBTitle:</b> x-ray structure of the hpr kinase/phosphatase from staphylococcus2 xylofus at 1.95 a resolution
43	<a href="#">c5g4iA</a>	Alignment	not modelled	17.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphorylase; <b>PDBTitle:</b> plp-dependent phosphorylase a1rdf1 from arthrobacter aurescens tc1
44	<a href="#">c2mdtA</a>	Alignment	not modelled	17.6	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> a pilt n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfolobus solfataricus p2
45	<a href="#">d1pj5a3</a>	Alignment	not modelled	17.5	31	<b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> L-aminoacid/polyamine oxidase
46	<a href="#">c2gp4B</a>	Alignment	not modelled	17.3	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydratase; <b>PDBTitle:</b> structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
47	<a href="#">d2coba1</a>	Alignment	not modelled	17.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
48	<a href="#">c5yh1A</a>	Alignment	not modelled	16.8	16	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> member of s1p family of ribosomal proteins; <b>PDBTitle:</b> member of s1p family of ribosomal proteins pf0399 dhh domain
49	<a href="#">c4ex8A</a>	Alignment	not modelled	16.6	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alna; <b>PDBTitle:</b> crystal structure of the prealuminum c-glycosynthase alna
50	<a href="#">c1pixB</a>	Alignment	not modelled	16.3	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaconyl-coa decarboxylase a subunit; <b>PDBTitle:</b> crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase
51	<a href="#">c3mjdA</a>	Alignment	not modelled	16.1	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
52	<a href="#">c3jszA</a>	Alignment	not modelled	15.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> legionella pneumophila glucosyltransferase lgt1 n293a with udp-glc
53	<a href="#">d1knxa1</a>	Alignment	not modelled	15.3	14	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> HprK N-terminal domain-like <b>Family:</b> HPr kinase/phosphatase HprK N-terminal domain

54	<a href="#">c3cf4G</a>	Alignment	not modelled	15.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase epsilon subunit; <b>PDBTitle:</b> structure of the codh component of the m. barkeri acids complex
55	<a href="#">c2okkA</a>	Alignment	not modelled	15.0	9	<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)
56	<a href="#">c2kg4A</a>	Alignment	not modelled	14.8	19	<b>PDB header:</b> :cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> growth arrest and dna-damage-inducible protein gadd45 <b>PDBTitle:</b> three-dimensional structure of human gadd45alpha in solution by nmr
57	<a href="#">c4e1oC</a>	Alignment	not modelled	14.7	11	<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)
58	<a href="#">d1ohwa</a>	Alignment	not modelled	14.4	15	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
59	<a href="#">c4efzB</a>	Alignment	not modelled	14.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> metallo-beta-lactamase family protein; <b>PDBTitle:</b> crystal structure of a hypothetical metallo-beta-lactamase from2 burkholderia pseudomallei
60	<a href="#">d1pixa3</a>	Alignment	not modelled	14.2	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
61	<a href="#">c6jrlA</a>	Alignment	not modelled	14.1	11	<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
62	<a href="#">c5ze4A</a>	Alignment	not modelled	13.9	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase, chloroplastic; <b>PDBTitle:</b> the structure of holo- structure of dhad complex with [2fe-2s] cluster
63	<a href="#">d1qh5a</a>	Alignment	not modelled	13.8	16	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Glyoxalase II (hydroxyacylglutathione hydrolase)
64	<a href="#">c2k89A</a>	Alignment	not modelled	13.5	7	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a-2-activating protein; <b>PDBTitle:</b> solution structure of a novel ubiquitin-binding domain from2 human plaa (pfuc, gly76-pro77 cis isomer)
65	<a href="#">c5ikID</a>	Alignment	not modelled	13.4	10	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> geranyl-coa carboxylase, beta-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa geranyl-coa carboxylase (gcc), beta2 subunit
66	<a href="#">d2ji7a1</a>	Alignment	not modelled	13.3	26	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
67	<a href="#">c5h7dl</a>	Alignment	not modelled	13.3	17	<b>PDB header:</b> transferase, immune system/metal binding <b>Chain:</b> I: <b>PDB Molecule:</b> putrescine aminotransferase,immunoglobulin g-binding <b>PDBTitle:</b> crystal structure of the ygjg-protein a-zpa963-calmodulin complex
68	<a href="#">d1k7ja</a>	Alignment	not modelled	13.1	11	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> YrdC-like
69	<a href="#">c6f87C</a>	Alignment	not modelled	12.1	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> threonylcarbamoyl-amp synthase; <b>PDBTitle:</b> crystal structure of p. abyssi sua5 complexed with l-threonine and ppi
70	<a href="#">d1lj8a4</a>	Alignment	not modelled	12.0	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
71	<a href="#">c1on3E</a>	Alignment	not modelled	11.9	21	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> methylmalonyl-coa carboxyltransferase 12s <b>PDBTitle:</b> transcaboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methylmalonyl-coenzyme a and methylmalonic acid bound)
72	<a href="#">c4rcnA</a>	Alignment	not modelled	11.9	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> long-chain acyl-coa carboxylase; <b>PDBTitle:</b> structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase
73	<a href="#">d1fvpa</a>	Alignment	not modelled	11.8	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (luxF, FP390)
74	<a href="#">d2hqva1</a>	Alignment	not modelled	11.8	19	<b>Fold:</b> Heme iron utilization protein-like <b>Superfamily:</b> Heme iron utilization protein-like <b>Family:</b> ChuX-like
75	<a href="#">c2qmaB</a>	Alignment	not modelled	11.5	13	<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
76	<a href="#">c2przB</a>	Alignment	not modelled	11.5	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> orotate phosphoribosyltransferase 1; <b>PDBTitle:</b> s. cerevisiae orotate phosphoribosyltransferase complexed with omp
77	<a href="#">d1k3ra1</a>	Alignment	not modelled	11.3	13	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Hypothetical protein MTH1 (MT0001), insert domain
						<b>PDB header:</b> transferase

78	<a href="#">c4uoxB_</a>	Alignment	not modelled	11.0	16	<b>Chain:</b> B: <b>PDB Molecule:</b> putrescine aminotransferase; <b>PDBTitle:</b> crystal structure of ygjg in complex with pyridoxal-5'-phosphate2 and putrescine
79	<a href="#">c5vnyA_</a>	Alignment	not modelled	11.0	27	<b>PDB header:</b> endocytosis, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> lethal (2) giant discs 1, isoform b; <b>PDBTitle:</b> crystal structure of dm14-3 domain of Igd
80	<a href="#">c1t3mA_</a>	Alignment	not modelled	10.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative l-asparaginase; <b>PDBTitle:</b> structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
81	<a href="#">c3vthA_</a>	Alignment	not modelled	10.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
82	<a href="#">d1ea0a2</a>	Alignment	not modelled	10.6	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
83	<a href="#">c2I09A_</a>	Alignment	not modelled	10.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> asr4154 protein; <b>PDBTitle:</b> solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
84	<a href="#">d1ovma1</a>	Alignment	not modelled	10.5	19	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
85	<a href="#">c2gezE_</a>	Alignment	not modelled	10.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> l-asparaginase alpha subunit; <b>PDBTitle:</b> crystal structure of potassium-independent plant asparaginase
86	<a href="#">c3k40B_</a>	Alignment	not modelled	10.4	17	<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
87	<a href="#">d1xm8a_</a>	Alignment	not modelled	10.2	14	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Glyoxalase II (hydroxyacylglutathione hydrolase)
88	<a href="#">c2gp4A_</a>	Alignment	not modelled	10.2	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydratase; <b>PDBTitle:</b> structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
89	<a href="#">d1w8ia_</a>	Alignment	not modelled	10.1	18	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
90	<a href="#">c2wnsB_</a>	Alignment	not modelled	10.1	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> human orotate phosphoribosyltransferase (oprta) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
91	<a href="#">d1tifa_</a>	Alignment	not modelled	10.0	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Translation initiation factor IF3, N-terminal domain <b>Family:</b> Translation initiation factor IF3, N-terminal domain
92	<a href="#">c3u54B_</a>	Alignment	not modelled	9.9	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole-succinocarboxamide synthase; <b>PDBTitle:</b> crystal structure (type-1) of saicar synthetase from pyrococcus2 horikoshii ot3
93	<a href="#">c4gduB_</a>	Alignment	not modelled	9.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of sulfate-bound human l-asparaginase protein
94	<a href="#">c1e0cA_</a>	Alignment	not modelled	9.8	21	<b>PDB header:</b> sulfurtransferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfurtransferase; <b>PDBTitle:</b> sulfurtransferase from azotobacter vinelandii
95	<a href="#">c3ervA_</a>	Alignment	not modelled	9.8	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative c39-like peptidase; <b>PDBTitle:</b> crystal structure of an putative c39-like peptidase from bacillus2 anthracis
96	<a href="#">c3nx3A_</a>	Alignment	not modelled	9.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylornithine aminotransferase; <b>PDBTitle:</b> crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
97	<a href="#">c3g8gA_</a>	Alignment	not modelled	9.7	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> predicted rna-binding protein, contains thump <b>PDBTitle:</b> a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
98	<a href="#">c2jisA_</a>	Alignment	not modelled	9.6	13	<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.
99	<a href="#">c4nogB_</a>	Alignment	not modelled	9.5	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative ornithine aminotransferase, mitochondrial; <b>PDBTitle:</b> crystal structure of a putative ornithine aminotransferase from2 toxoplasma gondii me49 in complex with pyrodoxal-5'-phosphate