
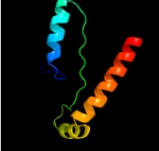






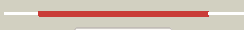




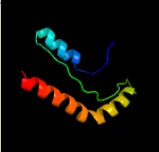

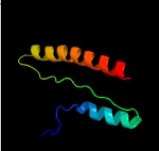



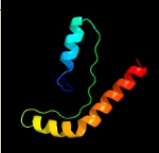




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2292c (-) _2564039_2564263
Date	Mon Aug 5 13:25:43 BST 2019
Unique Job ID	dc2e2091f7e4796a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4kn5A_</a>	 Alignment		99.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methylthioadenosine nucleosidase; <b>PDBTitle:</b> crystal structure of a putative methylthioadenosine nucleosidase from2 weissella paramesenteroides atcc 33313 (target nysgrc-029342 )
2	<a href="#">c5dk6A_</a>	 Alignment		99.6	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> crystal structure of a 5'-methylthioadenosine/s-adenosylhomocysteine2 (mta/sah) nucleosidase (mtan) from colwellia psychrerythraea 34h3 (cps_4743, target psi-029300) in complex with adenine at 2.27 a4 resolution
3	<a href="#">c4l0mA_</a>	 Alignment		99.6	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 5'-methylthioadenosine/s-adenosylhomocysteine <b>PDBTitle:</b> crystal structure of a putative 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from borrelia burgdorferi b31 bound3 to adenine (target nysgrc-029268 )
4	<a href="#">c4jwTA_</a>	 Alignment		99.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methylthioadenosine nucleosidase; <b>PDBTitle:</b> crystal structure of a putative 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from sulfurimonas denitrificans dsm3 1251 (target nysgrc-029304 )
5	<a href="#">c4josA_</a>	 Alignment		99.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> crystal structure of a putative 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from francisella philomiragia atcc3 25017 (target nysgrc-029335)
6	<a href="#">c6aytD_</a>	 Alignment		99.6	26	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> crystal structure of campylobacter jejuni 5'-methylthioadenosine/s-2 adenosyl homocysteine nucleosidase (mtan) complexed with3 pyrazinylthio-dadme-immucillin-a
7	<a href="#">c3nm5B_</a>	 Alignment		99.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mta/sah nucleosidase; <b>PDBTitle:</b> helicobacter pylori mtan complexed with formycin a
8	<a href="#">c4pr3A_</a>	 Alignment		99.6	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-methylthioadenosine nucleosidase / s-adenosylhomocysteine <b>PDBTitle:</b> crystal structure of brucella melitensis 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase
9	<a href="#">c6if8D_</a>	 Alignment		99.6	31	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> aeromonas hydrophila mtan-2 complexed with adenine
10	<a href="#">c1zosE_</a>	 Alignment		99.6	32	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> 5'-methylthioadenosine / s-adenosylhomocysteine <b>PDBTitle:</b> structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state inhibitor mt-3 imma
11	<a href="#">c3dp9A_</a>	 Alignment		99.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mta/sah nucleosidase; <b>PDBTitle:</b> crystal structure of vibrio cholerae 5'-methylthioadenosine/s-adenosyl2 homocysteine nucleosidase (mtan) complexed with butylthio-dadme-3 immucillin a

12	<a href="#">c4g41A_</a>	Alignment		99.6	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> mta/sah nucleosidase; <b>PDBTitle:</b> crystal structure of s-adenosylhomocysteine nucleosidase from streptococcus pyogenes in complex with 5-methylthiotubercidin
13	<a href="#">c3bl6A_</a>	Alignment		99.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 5'-methylthioadenosine nucleosidase/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus 5'-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase in complex with formycin a
14	<a href="#">c6po4A_</a>	Alignment		99.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase (mtnn) from haemophilus influenzae3 pittii.
15	<a href="#">d1jysa_</a>	Alignment		99.6	30	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
16	<a href="#">c4qezC_</a>	Alignment		99.5	29	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> crystal structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from bacillus anthracis
17	<a href="#">c2h8gA_</a>	Alignment		99.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 5'-methylthioadenosine nucleosidase; <b>PDBTitle:</b> 5'-methylthioadenosine nucleosidase from arabidopsis2 thaliana
18	<a href="#">c3eeiA_</a>	Alignment		99.5	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 5-methylthioadenosine nucleosidase/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> crystal structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from neisseria meningitidis in complex with methylthio-3 immucillin-a
19	<a href="#">c3bsfB_</a>	Alignment		99.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> at4g34840; <b>PDBTitle:</b> crystal structure of the mta/sah nucleosidase
20	<a href="#">c4qasB_</a>	Alignment		99.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> ct263; <b>PDBTitle:</b> 1.27 a resolution structure of ct263-d161n (mtan) from chlamydia2 trachomatis
21	<a href="#">c5b7pB_</a>	Alignment	not modelled	99.3	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> mta/sah nucleosidase; <b>PDBTitle:</b> structures and functional analysis of periplasmic 5-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase from aeromonas hydrophila
22	<a href="#">c3khsB_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
23	<a href="#">d1rxya_</a>	Alignment	not modelled	99.1	10	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
24	<a href="#">d1vmka_</a>	Alignment	not modelled	99.1	13	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
25	<a href="#">c1tcbB_</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> purine-nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate
26	<a href="#">d1v4na_</a>	Alignment	not modelled	99.1	7	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
27	<a href="#">d1ybfa_</a>	Alignment	not modelled	99.0	22	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
28	<a href="#">c3ozbF_</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> methylthioadenosine phosphorylase; <b>PDBTitle:</b> crystal structure of 5'-methylthioinosine phosphorylase from pseudomonas aeruginosa in complex with hypoxanthine
						<b>PDB header:</b> transferase

29	<a href="#">c1wtaA</a>	Alignment	not modelled	99.0	11	<b>Chain:</b> A; <b>PDB Molecule:</b> 5'-methylthioadenosine phosphorylase; <b>PDBTitle:</b> crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
30	<a href="#">d1t8sa</a>	Alignment	not modelled	99.0	18	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
31	<a href="#">c4ldnA</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> purine nucleoside phosphorylase deo-type; <b>PDBTitle:</b> crystal structure of a putative purine nucleoside phosphorylase from2 vibrio fischeri es114 (target nysgrc-029521)
32	<a href="#">c1nw4C</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> uridine phosphorylase, putative; <b>PDBTitle:</b> crystal structure of plasmodium falciparum purine nucleoside2 phosphorylase in complex with immh and sulfate
33	<a href="#">d1q1ga</a>	Alignment	not modelled	98.9	13	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
34	<a href="#">c5cxsA</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of isoform 2 of purine nucleoside phosphorylase2 complexed with mes
35	<a href="#">c3mb8A</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase from toxoplasma2 gondii in complex with immucillin-h
36	<a href="#">c4tymA</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> purine nucleoside phosphorylase deo-type; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase from2 streptococcus agalactiae 2603v/r, nysgrc target 030935
37	<a href="#">c4m7wA</a>	Alignment	not modelled	98.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> purine nucleoside phosphorylase deo-type; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase from leptotrichia2 buccalis c-1013-b, nysgrc target 029767.
38	<a href="#">c1z34A</a>	Alignment	not modelled	98.9	26	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
39	<a href="#">d1je0a</a>	Alignment	not modelled	98.9	17	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
40	<a href="#">c3tl6B</a>	Alignment	not modelled	98.9	28	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
41	<a href="#">d3bgsa1</a>	Alignment	not modelled	98.9	18	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
42	<a href="#">d1g2oa</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
43	<a href="#">d1odka</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
44	<a href="#">d1vhwa</a>	Alignment	not modelled	98.9	19	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
45	<a href="#">c5mx6C</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> purine nucleoside phosphorylase deo-type; <b>PDBTitle:</b> crystal structure of h. pylori purine nucleoside phosphorylase from2 clinical isolate hppnp-2
46	<a href="#">c3qpbB</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> uridine phosphorylase; <b>PDBTitle:</b> crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
47	<a href="#">c2p4sA</a>	Alignment	not modelled	98.8	9	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
48	<a href="#">d2ac7a1</a>	Alignment	not modelled	98.8	33	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
49	<a href="#">c4m3nA</a>	Alignment	not modelled	98.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> purine nucleoside phosphorylase deo-type; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase from meiothermus2 ruber dsm 1279, nysgrc target 029804.
50	<a href="#">c1yr3A</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> xanthosine phosphorylase; <b>PDBTitle:</b> escherichia coli purine nucleoside phosphorylase ii, the product of2 the xapa gene
51	<a href="#">c4r31A</a>	Alignment	not modelled	98.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> uridine phosphorylase; <b>PDBTitle:</b> crystal structure of a putative uridine phosphorylase from2 actinobacillus succinogenes 130z (target nysgrc-029667 )
52	<a href="#">d1qe5a</a>	Alignment	not modelled	98.7	16	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
53	<a href="#">c4d98A</a>	Alignment	not modelled	98.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> purine nucleoside phosphorylase deo-type; <b>PDBTitle:</b> crystal structure of the hexameric purine nucleoside phosphorylase2 from bacillus subtilis in space group h32 at ph 7.5

54	<a href="#">c4lkrA</a>	Alignment	not modelled	98.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase deo- type; <b>PDBTitle:</b> crystal structure of deod-3 gene product from shewanella oneidensis2 mr-1, nysgrc target 029437
55	<a href="#">d1cb0a</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
56	<a href="#">d1k9sa</a>	Alignment	not modelled	98.7	21	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
57	<a href="#">c3ggsA</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> human purine nucleoside phosphorylase double mutant e201q.n243d2 complexed with 2-fluoro-2'-deoxyadenosine
58	<a href="#">c3la8A</a>	Alignment	not modelled	98.7	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative purine nucleoside phosphorylase; <b>PDBTitle:</b> the crystal structure of smu.1229 from streptococcus mutans ua159
59	<a href="#">c4lnhA</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uridine phosphorylase; <b>PDBTitle:</b> crystal structure of uridine phosphorylase from vibrio fischeri es114,2 nysgrc target 29520.
60	<a href="#">c2xrfA</a>	Alignment	not modelled	98.1	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uridine phosphorylase 2; <b>PDBTitle:</b> crystal structure of human uridine phosphorylase 2
61	<a href="#">d3pnpa</a>	Alignment	not modelled	98.0	23	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
62	<a href="#">c4txjD</a>	Alignment	not modelled	98.0	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uridine phosphorylase; <b>PDBTitle:</b> crystal structure of uridine phosphorylase from schistosoma mansoni in2 complex with thymidine
63	<a href="#">c4glfA</a>	Alignment	not modelled	97.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rsfp; <b>PDBTitle:</b> crystal structure of methylthioadenosine phosphorylase sourced from an2 antarctic soil metagenomic library
64	<a href="#">c6k5gC</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> uridine phosphorylase; <b>PDBTitle:</b> structural and catalytic analysis of two diverse uridine2 phosphorylases in the oomycete phytophthora capsici
65	<a href="#">c5ifkC</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> purine nucleoside phosphorylase
66	<a href="#">c3eufC</a>	Alignment	not modelled	97.5	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> uridine phosphorylase 1; <b>PDBTitle:</b> crystal structure of bau-bound human uridine phosphorylase 1
67	<a href="#">c3bjeA</a>	Alignment	not modelled	96.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside phosphorylase, putative; <b>PDBTitle:</b> crystal structure of trypanosoma brucei nucleoside phosphorylase shows2 uridine phosphorylase activity
68	<a href="#">c4m1eC</a>	Alignment	not modelled	96.2	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase i from2 planctomyces limnophilus dsm 3776, nysgrc target 029364.
69	<a href="#">c4lnaA</a>	Alignment	not modelled	96.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase i from spirosona2 linguale dsm 74, nysgrc target 029362
70	<a href="#">c4l5cE</a>	Alignment	not modelled	95.5	10	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> s-methyl-5'-thioadenosine phosphorylase; <b>PDBTitle:</b> methylthioadenosine phosphorylase from schistosoma mansoni in complex2 with adenine in space group p212121
71	<a href="#">c4nsnC</a>	Alignment	not modelled	94.9	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase from2 porphyromonas gingivalis atcc 33277, nysgrc target 030972,3 orthorhombic symmetry
72	<a href="#">c4uc0A</a>	Alignment	not modelled	88.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of a purine nucleoside phosphorylase (psi-nysgrc-2 029736) from agrobacterium vitis
73	<a href="#">c3j39G</a>	Alignment	not modelled	56.7	21	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l7a; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
74	<a href="#">c3u5iG</a>	Alignment	not modelled	53.5	18	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l8-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome b
75	<a href="#">c3zf7x</a>	Alignment	not modelled	51.3	13	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> 60s ribosomal protein l23a; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
76	<a href="#">c3j3bG</a>	Alignment	not modelled	37.2	18	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein l7a; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
77	<a href="#">c6qq0G</a>	Alignment	not modelled	29.5	27	<b>PDB header:</b> translation <b>Chain:</b> G: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit delta; <b>PDBTitle:</b> structure of eif2b-eif2 (phosphorylated at ser51) complex (model 1)
78	<a href="#">c4a1eF</a>	Alignment	not modelled	28.9	15	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> rpl7a; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1

79	<a href="#">c6i7tB_</a>	Alignment	not modelled	26.6	22	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit alpha; <b>PDBTitle:</b> eif2b:eif2 complex
80	<a href="#">c3cwcB_</a>	Alignment	not modelled	26.4	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative glycerate kinase 2; <b>PDBTitle:</b> crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
81	<a href="#">c1w2wj_</a>	Alignment	not modelled	26.2	19	<b>PDB header:</b> isomerase <b>Chain:</b> J: <b>PDB Molecule:</b> 5-methylthioribose-1-phosphate isomerase; <b>PDBTitle:</b> crystal structure of yeast ypr118w, a methylthioribose-1-phosphate2 isomerase related to regulatory eif2b subunits
82	<a href="#">c6j3mD_</a>	Alignment	not modelled	25.7	27	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit delta; <b>PDBTitle:</b> eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
83	<a href="#">c6j3mF_</a>	Alignment	not modelled	24.7	11	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit beta; <b>PDBTitle:</b> eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
84	<a href="#">c3iz5H_</a>	Alignment	not modelled	24.6	17	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 60s ribosomal protein l7a (l7ae); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
85	<a href="#">c5b04B_</a>	Alignment	not modelled	23.6	19	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit alpha; <b>PDBTitle:</b> crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
86	<a href="#">c5dboA_</a>	Alignment	not modelled	22.4	19	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor eif-2b-like protein; <b>PDBTitle:</b> crystal structure of the tetrameric eif2b-beta2-delta2 complex from c.2 thermophilum
87	<a href="#">d1t5oa_</a>	Alignment	not modelled	20.2	23	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> lF2B-like
88	<a href="#">d1vb5a_</a>	Alignment	not modelled	19.8	15	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> lF2B-like
89	<a href="#">c5b04G_</a>	Alignment	not modelled	18.5	15	<b>PDB header:</b> translation <b>Chain:</b> G: <b>PDB Molecule:</b> probable translation initiation factor eif-2b subunit <b>PDBTitle:</b> crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
90	<a href="#">c4zeoH_</a>	Alignment	not modelled	18.2	19	<b>PDB header:</b> translation <b>Chain:</b> H: <b>PDB Molecule:</b> translation initiation factor eif-2b-like protein; <b>PDBTitle:</b> crystal structure of eif2b delta from chaetomium thermophilum
91	<a href="#">c3d3jA_</a>	Alignment	not modelled	18.0	10	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
92	<a href="#">d1j0aa_</a>	Alignment	not modelled	17.7	11	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
93	<a href="#">c4ldrA_</a>	Alignment	not modelled	16.3	35	<b>PDB header:</b> isomerase, cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> methylthioribose-1-phosphate isomerase; <b>PDBTitle:</b> structure of the s283y mutant of mrdi
94	<a href="#">c5kstA_</a>	Alignment	not modelled	16.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-nucleotidase sure; <b>PDBTitle:</b> stationary phase survival protein e (sure) from xylella fastidiosa-2 xfsure-tsamp (tetramer smaller - crystallization with 3'amp).
95	<a href="#">c3ecsd_</a>	Alignment	not modelled	15.7	23	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit alpha; <b>PDBTitle:</b> crystal structure of human eif2b alpha
96	<a href="#">c6ezoD_</a>	Alignment	not modelled	15.7	19	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit beta; <b>PDBTitle:</b> eukaryotic initiation factor eif2b in complex with isrib
97	<a href="#">c5tpwB_</a>	Alignment	not modelled	15.5	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate receptor ionotropic, nmda 2a; <b>PDBTitle:</b> crystal structure of amino terminal domains of the nmda receptor2 subunit glun1 and glun2a in complex with zinc at the glun2a
98	<a href="#">c4l8lA_</a>	Alignment	not modelled	15.4	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase 1; <b>PDBTitle:</b> crystal structure of the type ii dehydroquinase from pseudomonas2 aeruginosa
99	<a href="#">d2z67a1</a>	Alignment	not modelled	15.4	7	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SepSecS-like