























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3307_(deoD)_3694225_3695031
Date	Thu Aug 8 16:20:51 BST 2019
Unique Job ID	4458225a1fab4fb6


























Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1g2oa_</a>	Alignment 		100.0	100	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
2	<a href="#">c4m1eC_</a>	Alignment 		100.0	34	<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 plantomyces limnophilus dsm 3776, nysgrc target 029364.
3	<a href="#">d1qe5a_</a>	Alignment 		100.0	58	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
4	<a href="#">c4nsnC_</a>	Alignment 		100.0	36	<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
5	<a href="#">d3bgsa1</a>	Alignment 		100.0	39	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
6	<a href="#">c1yr3A_</a>	Alignment 		100.0	37	<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
7	<a href="#">c5cxsa_</a>	Alignment 		100.0	37	<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
8	<a href="#">c4lnaA_</a>	Alignment 		100.0	35	<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 spirosoa2 linguale dsm 74, nysgrc target 029362
9	<a href="#">c3ggsA_</a>	Alignment 		100.0	38	<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
10	<a href="#">c2p4sA_</a>	Alignment 		100.0	35	<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
11	<a href="#">c5ifkC_</a>	Alignment 		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> purine nucleoside phosphorylase; <b>PDBTitle:</b> purine nucleoside phosphorylase

12	<a href="#">c1tcvB_</a>	Alignment		100.0	37	<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
13	<a href="#">d3pnpa_</a>	Alignment		100.0	39	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
14	<a href="#">c4uc0A_</a>	Alignment		100.0	40	<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
15	<a href="#">d1vmka_</a>	Alignment		100.0	39	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
16	<a href="#">c3khsB_</a>	Alignment		100.0	37	<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
17	<a href="#">c4glfA_</a>	Alignment		100.0	20	<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
18	<a href="#">c4l5cE_</a>	Alignment		100.0	24	<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
19	<a href="#">c3la8A_</a>	Alignment		100.0	40	<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
20	<a href="#">c1wtaA_</a>	Alignment		100.0	26	<b>PDB header:</b> transferase <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)
21	<a href="#">d1cb0a_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
22	<a href="#">d1v4na_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
23	<a href="#">c3ozbF_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> methylthioadenosine phosphorylase; <b>PDBTitle:</b> crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
24	<a href="#">c4r31A_</a>	Alignment	not modelled	100.0	15	<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 )
25	<a href="#">d1rxya_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
26	<a href="#">c1nw4C_</a>	Alignment	not modelled	99.9	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
27	<a href="#">c3mb8A_</a>	Alignment	not modelled	99.9	13	<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
28	<a href="#">d1q1ga_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
29	<a href="#">c3qpbB_</a>	Alignment	not modelled	99.9	16	<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
30	<a href="#">c3nm5B_</a>	Alignment	not modelled	99.9	16	<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
31	<a href="#">c6aytD_</a>	Alignment	not modelled	99.9	14	<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
32	<a href="#">d1vhwa_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
33	<a href="#">c4lkrA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase deod-type; <b>PDBTitle:</b> crystal structure of deod-3 gene product from shewanella oneidensis2 mr-1, nysgrc target 029437
34	<a href="#">c4ldnA_</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase deod-type; <b>PDBTitle:</b> crystal structure of a putative purine nucleoside phosphorylase from2 vibrio fischeri es114 (target nysgrc-029521)
35	<a href="#">d1je0a_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
36	<a href="#">c4jwta_</a>	Alignment	not modelled	99.9	13	<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 )
37	<a href="#">c4m7wA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase deod-type; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase from leptotrichia2 buccalis c-1013-b, nysgrc target 029767.
38	<a href="#">c4tymA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase deod-type; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase from2 streptococcus agalactiae 2603v/r, nysgrc target 030935
39	<a href="#">d1lodka_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
40	<a href="#">d2ac7a1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
41	<a href="#">c4g41A_</a>	Alignment	not modelled	99.9	15	<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 from2 streptococcus pyogenes in complex with 5-methylthiotubercidin
42	<a href="#">c6if8D_</a>	Alignment	not modelled	99.9	14	<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
43	<a href="#">c1z34A_</a>	Alignment	not modelled	99.9	10	<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
44	<a href="#">d1k9sa_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
45	<a href="#">c3bl6A_</a>	Alignment	not modelled	99.9	15	<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 in3 complex with formycin a
46	<a href="#">d1ybfa_</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
47	<a href="#">c5mx6C_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> purine nucleoside phosphorylase deod-type; <b>PDBTitle:</b> crystal structure of h. pylori purine nucleoside phosphorylase from2 clinical isolate hppnp-2
48	<a href="#">c4m3nA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase deod-type; <b>PDBTitle:</b> crystal structure of purine nucleoside phosphorylase from meiothermus2 ruber dsm 1279, nysgrc target 029804.
49	<a href="#">c4kn5A_</a>	Alignment	not modelled	99.9	15	<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 )
50	<a href="#">c4lnhA_</a>	Alignment	not modelled	99.9	12	<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.
51	<a href="#">c1zosE_</a>	Alignment	not modelled	99.9	14	<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
						<b>PDB header:</b> hydrolase

52	<a href="#">c3eeiA</a>	Alignment	not modelled	99.9	14	<b>Chain:</b> A; <b>PDB Molecule:</b> 5-methylthioadenosine nucleosidase/s-adenosylhomocysteine <b>PDBTitle:</b> crystal structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from neisseria meningitidis in complex with methylthio-3 immucillin-a
53	<a href="#">c4josA</a>	Alignment	not modelled	99.9	16	<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)
54	<a href="#">c6po4A</a>	Alignment	not modelled	99.9	17	<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.
55	<a href="#">c4qezC</a>	Alignment	not modelled	99.9	15	<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
56	<a href="#">c4d98A</a>	Alignment	not modelled	99.9	17	<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
57	<a href="#">c3tl6B</a>	Alignment	not modelled	99.9	13	<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
58	<a href="#">c3dp9A</a>	Alignment	not modelled	99.9	17	<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
59	<a href="#">d1jysa</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
60	<a href="#">c5dk6A</a>	Alignment	not modelled	99.9	14	<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
61	<a href="#">c2h8gA</a>	Alignment	not modelled	99.9	17	<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
62	<a href="#">c3bsfB</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> at4g34840; <b>PDBTitle:</b> crystal structure of the mta/sah nucleosidase
63	<a href="#">c4l0mA</a>	Alignment	not modelled	99.8	11	<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 )
64	<a href="#">c5b7pB</a>	Alignment	not modelled	99.8	17	<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 from3 aeromonas hydrophila
65	<a href="#">d1t8sa</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Purine and uridine phosphorylases <b>Family:</b> Purine and uridine phosphorylases
66	<a href="#">c6k5gC</a>	Alignment	not modelled	99.7	17	<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
67	<a href="#">c3eufC</a>	Alignment	not modelled	99.7	12	<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
68	<a href="#">c3bjcA</a>	Alignment	not modelled	99.7	15	<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
69	<a href="#">c2xrfA</a>	Alignment	not modelled	99.7	10	<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
70	<a href="#">c4txjD</a>	Alignment	not modelled	99.7	16	<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
71	<a href="#">c4qasB</a>	Alignment	not modelled	99.5	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
72	<a href="#">c4pr3A</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 5'-methylthioadenosine nucleosidase / s- <b>PDBTitle:</b> crystal structure of brucella melitensis 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase
73	<a href="#">c5c4nD</a>	Alignment	not modelled	89.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> precorrin-6a reductase; <b>PDBTitle:</b> cobk precorrin-6a reductase
74	<a href="#">c1lm1A</a>	Alignment	not modelled	88.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ferredoxin-dependent glutamate synthase; <b>PDBTitle:</b> structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme

75	<a href="#">c2vdcF_</a>	 Alignment	not modelled	88.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate synthase [nadh] large chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
76	<a href="#">d1ea0a2</a>	 Alignment	not modelled	87.5	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
77	<a href="#">d1ofda2</a>	 Alignment	not modelled	83.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
78	<a href="#">d2af4c1</a>	 Alignment	not modelled	77.9	21	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Phosphotransacetylase
79	<a href="#">c6ioxB_</a>	 Alignment	not modelled	73.3	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphotransacetylase; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis phosphotransacetylase in2 complex with acetyl-coa
80	<a href="#">c3fhkF_</a>	 Alignment	not modelled	68.7	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> upf0403 protein yphp; <b>PDBTitle:</b> crystal structure of apc1446, b.subtilis yphp disulfide isomerase
81	<a href="#">d2nqra3</a>	 Alignment	not modelled	66.2	14	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
82	<a href="#">d1tg7a5</a>	 Alignment	not modelled	65.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Glycosyl hydrolases family 35 catalytic domain
83	<a href="#">d1gtea2</a>	 Alignment	not modelled	65.3	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
84	<a href="#">c1vmiA_</a>	 Alignment	not modelled	65.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphate acetyltransferase; <b>PDBTitle:</b> crystal structure of putative phosphate acetyltransferase2 (np_416953.1) from escherichia coli k12 at 2.32 a resolution
85	<a href="#">d1vmia_</a>	 Alignment	not modelled	65.2	24	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Phosphotransacetylase
86	<a href="#">c2nqqa_</a>	 Alignment	not modelled	62.5	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein moea; <b>PDBTitle:</b> moea r137q
87	<a href="#">c3qd5B_</a>	 Alignment	not modelled	61.9	39	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative ribose-5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
88	<a href="#">d1r5ja_</a>	 Alignment	not modelled	61.3	23	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Phosphotransacetylase
89	<a href="#">c2yfvC_</a>	 Alignment	not modelled	57.0	21	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> scm3; <b>PDBTitle:</b> the heterotrimeric complex of kluyveromyces lactis scm3, cse4 and h4
90	<a href="#">d1t57a_</a>	 Alignment	not modelled	56.0	15	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> MTH1675-like
91	<a href="#">c5w70B_</a>	 Alignment	not modelled	54.7	15	<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
92	<a href="#">c6fxsA_</a>	 Alignment	not modelled	52.8	39	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase, putative; <b>PDBTitle:</b> structure of trypanosoma brucei type b ribose 5-phosphate isomerase
93	<a href="#">d1o1xa_</a>	 Alignment	not modelled	52.5	30	<b>Fold:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Superfamily:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Family:</b> Ribose/Galactose isomerase RpiB/AlsB
94	<a href="#">d1uz5a3</a>	 Alignment	not modelled	52.2	21	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
95	<a href="#">d1xcoa_</a>	 Alignment	not modelled	47.1	21	<b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like <b>Family:</b> Phosphotransacetylase
96	<a href="#">c4e8cA_</a>	 Alignment	not modelled	47.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase, family 35; <b>PDBTitle:</b> crystal structure of streptococcal beta-galactosidase in complex with2 galactose
97	<a href="#">d1p80a1</a>	 Alignment	not modelled	46.5	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Catalase, C-terminal domain
98	<a href="#">c3hbaA_</a>	 Alignment	not modelled	44.3	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
99	<a href="#">c3he8A_</a>	 Alignment	not modelled	42.7	30	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase; <b>PDBTitle:</b> structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
100	<a href="#">c3gaaB_</a>	Alignment	not modelled	42.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ta1441; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from2 thermoplasma acidophilum

101	<a href="#">c4s2uA</a>	Alignment	not modelled	41.2	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> crystal structure of the phosphorybosylpyrophosphate synthetase from2 e. coli
102	<a href="#">d1oy0a</a>	Alignment	not modelled	40.3	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
103	<a href="#">c4r9xB</a>	Alignment	not modelled	39.2	17	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> copper homeostasis protein cutc; <b>PDBTitle:</b> crystal structure of putative copper homeostasis protein cutc from2 bacillus anthracis
104	<a href="#">c3tngA</a>	Alignment	not modelled	39.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lmo1369 protein; <b>PDBTitle:</b> the crystal structure of a possible phosphate acetyl/butaryl2 transferase from listeria monocytogenes egd-e.
105	<a href="#">d1sy7a1</a>	Alignment	not modelled	38.6	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Catalase, C-terminal domain
106	<a href="#">d2fts3</a>	Alignment	not modelled	37.9	13	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
107	<a href="#">d2cx1a2</a>	Alignment	not modelled	35.9	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Pre-PUA domain <b>Family:</b> Hypothetical protein APE0525, N-terminal domain
108	<a href="#">c1ycoA</a>	Alignment	not modelled	35.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> branched-chain phosphotransacylase; <b>PDBTitle:</b> crystal structure of a branched-chain phosphotransacylase from2 enterococcus faecalis v583
109	<a href="#">d2vvp1</a>	Alignment	not modelled	35.7	24	<b>Fold:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Superfamily:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Family:</b> Ribose/Galactose isomerase RpiB/AlsB
110	<a href="#">c5gsmB</a>	Alignment	not modelled	35.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exo-beta-d-glucosaminidase; <b>PDBTitle:</b> glycoside hydrolase b with product
111	<a href="#">c6fxwA</a>	Alignment	not modelled	35.1	33	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ribose 5-phosphate isomerase; <b>PDBTitle:</b> structure of leishmania infantum type b ribose 5-phosphate isomerase
112	<a href="#">c5gslB</a>	Alignment	not modelled	34.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 778aa long hypothetical beta-galactosidase; <b>PDBTitle:</b> glycoside hydrolase a
113	<a href="#">c2fu3A</a>	Alignment	not modelled	34.3	13	<b>PDB header:</b> biosynthetic protein/structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> gephyrin; <b>PDBTitle:</b> crystal structure of gephyrin e-domain
114	<a href="#">c3thdD</a>	Alignment	not modelled	34.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
115	<a href="#">c3d3jA</a>	Alignment	not modelled	33.0	24	<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
116	<a href="#">c3d3aA</a>	Alignment	not modelled	32.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
117	<a href="#">d1jz8a5</a>	Alignment	not modelled	30.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
118	<a href="#">d1bg3a2</a>	Alignment	not modelled	30.6	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
119	<a href="#">c1uz5A</a>	Alignment	not modelled	30.5	16	<b>PDB header:</b> molybdopterin biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> 402aa long hypothetical molybdopterin <b>PDBTitle:</b> the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
120	<a href="#">c2pjkA</a>	Alignment	not modelled	30.1	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 178aa long hypothetical molybdenum cofactor <b>PDBTitle:</b> structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii