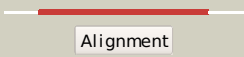
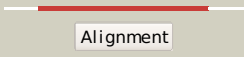
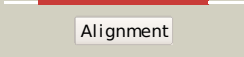
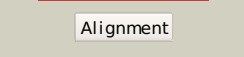
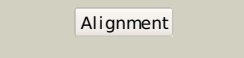
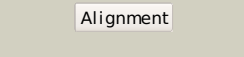
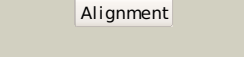
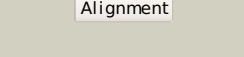
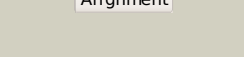
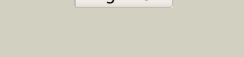
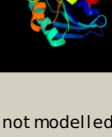
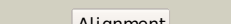
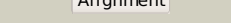
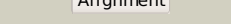
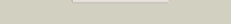
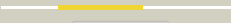
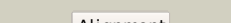
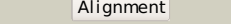
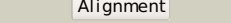
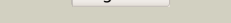
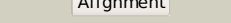
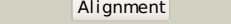
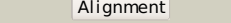


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k9sa_	 Alignment		100.0	100	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
2	d1vhwa_	 Alignment		100.0	80	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
3	c1z34A_	 Alignment		100.0	59	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
4	d1odka_	 Alignment		100.0	36	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
5	c3bjeA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: nucleoside phosphorylase, putative; PDBTitle: crystal structure of trypanosoma brucei nucleoside phosphorylase shows2 uridine phosphorylase activity
6	c3tl6B_	 Alignment		100.0	48	PDB header: transferase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
7	d2ac7a1	 Alignment		100.0	58	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
8	d1je0a_	 Alignment		100.0	33	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
9	c3mb8A_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from toxoplasma2 gondii in complex with immucillin-h
10	d1rxya_	 Alignment		100.0	28	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
11	c3qpbB_	 Alignment		100.0	31	PDB header: transferase Chain: B: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily

12	c1nw4C_	Alignment		100.0	27	PDB header: transferase Chain: C: PDB Molecule: uridine phosphorylase, putative; PDBTitle: crystal structure of plasmodium falciparum purine nucleoside2 phosphorylase in complex with immh and sulfate
13	dlq1ga_	Alignment		100.0	27	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
14	c2xrfA_	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase 2; PDBTitle: crystal structure of human uridine phosphorylase 2
15	c3eufC_	Alignment		100.0	22	PDB header: transferase Chain: C: PDB Molecule: uridine phosphorylase 1; PDBTitle: crystal structure of bau-bound human uridine phosphorylase 1
16	dl1yba_	Alignment		100.0	15	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
17	c3nm5B_	Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: mta/sah nucleosidase; PDBTitle: helicobacter pylori mtan complexed with formycin a
18	dl1t8sa_	Alignment		100.0	19	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
19	c1zosE_	Alignment		100.0	20	PDB header: hydrolase Chain: E: PDB Molecule: 5'-methylthioadenosine / s-adenosylhomocysteine PDBTitle: structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state3 inhibitor mt-imma
20	c3bl6A_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase/s- PDBTitle: crystal structure of staphylococcus aureus 5'-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase in3 complex with formycin a
21	c3eeiA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: 5-methylthioadenosine nucleosidase/s- PDBTitle: crystal structure of 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from neisseria3 meningitidis in complex with methylthio-immucillin-a
22	c3dp9A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: mta/sah nucleosidase; PDBTitle: crystal structure of vibrio cholerae 5'-methylthioadenosine/s-adenosyl2 homocysteine nucleosidase (mtan) complexed with butylthio-dadme-3 immucillin a
23	dl1ysa_	Alignment	not modelled	100.0	18	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
24	c2h8gA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase; PDBTitle: 5'-methylthioadenosine nucleosidase from arabidopsis2 thaliana
25	c3bsfB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: at4g34840; PDBTitle: crystal structure of the mta/sah nucleosidase
26	c3ozbF_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: F: PDB Molecule: methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
27	c3khsB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
28	dlv4na_	Alignment	not modelled	99.9	19	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases

29	c1wtaA	 Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: 5'-methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
30	c3la8A	 Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: putative purine nucleoside phosphorylase; PDBTitle: the crystal structure of smu.1229 from streptococcus mutans ua159
31	d1g2oa	 Alignment	not modelled	99.9	12	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
32	d1cb0a	 Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
33	c2p4sA	 Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
34	d1vmka	 Alignment	not modelled	99.9	17	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
35	c1yr3A	 Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: xanthosine phosphorylase; PDBTitle: escherichia coli purine nucleoside phosphorylase ii, the2 product of the xapa gene
36	c1ctvB	 Alignment	not modelled	99.9	19	PDB header: transferase Chain: B: PDB Molecule: purine-nucleoside phosphorylase; PDBTitle: crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate
37	d3bgsa1	 Alignment	not modelled	99.9	17	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
38	d1qe5a	 Alignment	not modelled	99.9	11	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
39	c3ggsA	 Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
40	d3pnpa	 Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
41	c1tvmA	 Alignment	not modelled	71.7	8	PDB header: transferase Chain: A: PDB Molecule: pts system, galactitol-specific iib component; PDBTitle: nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
42	c3czcA	 Alignment	not modelled	45.7	16	PDB header: transferase Chain: A: PDB Molecule: rmpb; PDBTitle: the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
43	c3efhB	 Alignment	not modelled	43.7	16	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
44	d2c4ka2	 Alignment	not modelled	40.8	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
45	c1vkrA	 Alignment	not modelled	40.7	25	PDB header: transferase Chain: A: PDB Molecule: mannitol-specific pts system enzyme iiaabc components; PDBTitle: structure of iib domain of the mannitol-specific permease enzyme ii
46	d1vkra	 Alignment	not modelled	40.7	25	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
47	c2q1yB	 Alignment	not modelled	40.5	18	PDB header: cell cycle, signaling protein Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
48	d1v58a2	 Alignment	not modelled	37.3	20	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
49	c2f9iD	 Alignment	not modelled	29.6	19	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl PDBTitle: crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
50	d2csba3	 Alignment	not modelled	27.7	46	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
51	d1ea9c1	 Alignment	not modelled	26.0	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
52	c1ii0A	 Alignment	not modelled	24.6	35	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
53	d1a4ia1	Alignment	not modelled	23.5	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
54	d2a7sa2	Alignment	not modelled	22.4	18	Fold: ClpP/crotonase Superfamily: ClpP/crotonase

						Family: Biotin dependent carboxylase carboxyltransferase domain
55	d2bm8a1	Alignment	not modelled	21.1	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Cmcl-like PDB header: isomerase Chain: A: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase lacab_rpb from2 vibrio parahaemolyticus
56	c3onoA	Alignment	not modelled	20.4	21	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of cytosol aminopeptidase from francisella2 tularensis
57	c3peiA	Alignment	not modelled	20.3	17	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus
58	c3giuA	Alignment	not modelled	20.2	7	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
59	c3o38D	Alignment	not modelled	20.2	36	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
60	c1a4iB	Alignment	not modelled	20.0	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
61	d1dkua2	Alignment	not modelled	19.5	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
62	d1wzla1	Alignment	not modelled	19.4	22	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
63	c1dkrB	Alignment	not modelled	19.3	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Nickel responsive regulator NikR, C-terminal domain
64	d2bj7a2	Alignment	not modelled	19.3	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
65	d1gvia1	Alignment	not modelled	18.7	33	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
66	d1u9ya2	Alignment	not modelled	18.7	16	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
67	d1x94a	Alignment	not modelled	18.7	20	PDB header: cell division Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz, t7 mutated, domain swapped (t. maritima)
68	c1w5fA	Alignment	not modelled	18.6	22	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein radc homolog; PDBTitle: the crystal structure of dna repair protein radc from chlorobium2 tepidum t1s
69	c2qlcC	Alignment	not modelled	18.4	17	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
70	c2bj3D	Alignment	not modelled	18.1	19	PDB header: isomerase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpb from streptococcus pneumoniae
71	c2ppwA	Alignment	not modelled	18.1	21	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
72	c1q5vB	Alignment	not modelled	17.8	22	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid
73	c1e9yB	Alignment	not modelled	17.7	40	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
74	c3k7pA	Alignment	not modelled	17.7	21	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with alllose-6-phosphate
75	c3m1pA	Alignment	not modelled	17.7	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: Nickel responsive regulator NikR, C-terminal domain
76	d1q5ya	Alignment	not modelled	17.5	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
77	d1j0ha1	Alignment	not modelled	17.4	33	PDB header: transcriptional regulation Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
78	c2ca9B	Alignment	not modelled	17.3	13	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
79	d1id0a	Alignment	not modelled	17.2	19	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase;
80	c3e5nA	Alignment	not modelled	17.1	43	

80	c3s3pA	Alignment	not modelled	17.1	43	PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia PDB header: isomerase
81	c3he8A	Alignment	not modelled	16.9	36	Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
82	d2vvpa1	Alignment	not modelled	16.9	29	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
83	d1b0aa1	Alignment	not modelled	16.8	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
84	d1nn4a	Alignment	not modelled	16.6	36	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
85	d1sv6a	Alignment	not modelled	16.5	15	Fold: FAH Superfamily: FAH Family: FAH
86	c2y3yC	Alignment	not modelled	16.5	13	PDB header: transcription Chain: C: PDB Molecule: putative nickel-responsive regulator; PDBTitle: holo-ni(ii) hpnikr is a symmetric tetramer containing four2 canonic square-planar ni(ii) ions at physiological ph
87	d1b12a	Alignment	not modelled	16.5	14	Fold: LexA/Signal peptidase Superfamily: LexA/Signal peptidase Family: Type 1 signal peptidase
88	d1a2za	Alignment	not modelled	16.4	9	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
89	c2l2qA	Alignment	not modelled	16.3	18	PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
90	c2equA	Alignment	not modelled	15.3	25	PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1
91	c2c4kD	Alignment	not modelled	15.1	16	PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase- PDBTitle: crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
92	c2jyD	Alignment	not modelled	14.9	16	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of francisella tularensis enoyl reductase2 (fffabi) with bound nad
93	d1sqsa	Alignment	not modelled	14.8	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein SP1951
94	d2d1ya1	Alignment	not modelled	14.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
95	c2qmoA	Alignment	not modelled	14.3	21	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biob) from helicobacter2 pylori
96	d2h7ma1	Alignment	not modelled	14.2	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
97	d1fdra2	Alignment	not modelled	14.0	10	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
98	d1rq2a1	Alignment	not modelled	14.0	20	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
99	c3ngmB	Alignment	not modelled	13.8	21	PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae