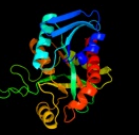


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bl6A_	 Alignment		100.0	55	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase/s- PDBTitle: crystal structure of staphylococcus aureus 5'-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase in3 complex with formycin a
2	c1zosE_	 Alignment		100.0	41	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
3	dljysa_	 Alignment		100.0	100	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
4	c3eeiA_	 Alignment		100.0	49	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
5	c3dp9A_	 Alignment		100.0	61	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
6	c3nm5B_	 Alignment		100.0	35	PDB header: hydrolase Chain: B: PDB Molecule: mta/sah nucleosidase; PDBTitle: helicobacter pylori mtan complexed with formycin a
7	c2h8gA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase; PDBTitle: 5'-methylthioadenosine nucleosidase from arabidopsis2 thaliana
8	c3bsfB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: at4g34840; PDBTitle: crystal structure of the mta/sah nucleosidase
9	c1z34A_	 Alignment		100.0	21	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
10	dlrxya_	 Alignment		100.0	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
11	dlje0a_	 Alignment		100.0	21	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases

12	dlvhwa_	Alignment		100.0	18	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
13	c1nw4C_	Alignment		100.0	19	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
14	dlodka_	Alignment		100.0	22	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
15	dlqlga_	Alignment		100.0	19	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
16	d2ac7a1	Alignment		100.0	19	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
17	dlk9sa_	Alignment		100.0	18	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
18	c3mb8A_	Alignment		100.0	18	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
19	c3tl6B_	Alignment		100.0	27	PDB header: transferase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
20	c3qpbB_	Alignment		100.0	19	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
21	d1ybfa_	Alignment	not modelled	100.0	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
22	d1t8sa_	Alignment	not modelled	100.0	19	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
23	d1v4na_	Alignment	not modelled	100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
24	c3khsB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
25	c2xrfa_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase 2; PDBTitle: crystal structure of human uridine phosphorylase 2
26	c1wtaA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: 5'-methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
27	c3ozbF_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: F: PDB Molecule: methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
28	c1tcvB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: purine-nucleoside phosphorylase; PDBTitle: crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansonii in complex with non-detergent3 sulfobetaine 195 and acetate

29	d1cb0a_	Alignment	not modelled	100.0	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
30	c3eufC_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: C: PDB Molecule: uridine phosphorylase 1; PDBTitle: crystal structure of bau-bound human uridine phosphorylase 1
31	d1vmka_	Alignment	not modelled	100.0	14	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
32	c3bjcA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: nucleoside phosphorylase, putative; PDBTitle: crystal structure of trypanosoma brucei nucleoside phosphorylase shows2 uridine phosphorylase activity
33	c2p4sA_	Alignment	not modelled	100.0	16	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	c3la8A_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: putative purine nucleoside phosphorylase; PDBTitle: the crystal structure of smu.1229 from streptococcus mutans ua159
35	c1yr3A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: xanthosine phosphorylase; PDBTitle: escherichia coli purine nucleoside phosphorylase ii, the2 product of the xpa gene
36	d3bgsa1	Alignment	not modelled	100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
37	d1g2oa_	Alignment	not modelled	99.9	13	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
38	c3ggsA_	Alignment	not modelled	99.9	19	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
39	d3pnpa_	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
40	d1qe5a_	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
41	d1a2za_	Alignment	not modelled	60.9	24	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
42	c3giuA_	Alignment	not modelled	50.7	19	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus
43	c3lacA_	Alignment	not modelled	39.8	17	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of bacillus anthracis pyrrolidone-carboxylate2 peptidase, pcp
44	d1iofa_	Alignment	not modelled	35.0	24	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
45	d1auga_	Alignment	not modelled	22.7	17	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
46	c2ywjA_	Alignment	not modelled	20.5	21	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
47	d1vb5a_	Alignment	not modelled	16.6	33	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
48	d2nv0a1	Alignment	not modelled	15.6	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
49	d1t9ka_	Alignment	not modelled	15.2	28	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
50	c2equA_	Alignment	not modelled	14.8	30	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
51	c2yvkA_	Alignment	not modelled	14.7	28	PDB header: isomerase Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
52	d2a0ua1	Alignment	not modelled	14.1	17	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
53	d1fdra2	Alignment	not modelled	13.9	10	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
54	d1t5oa_	Alignment	not modelled	12.8	28	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like

					Family:IF2B-like
55	c1yt5A_	Alignment	not modelled	12.2	22 PDB header: transferase Chain: A: PDB Molecule: inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of nad kinase from thermotoga maritima
56	c3cwcB_	Alignment	not modelled	12.1	14 PDB header: transferase Chain: B: PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
57	d1txga2	Alignment	not modelled	11.1	50 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
58	d2f1ka2	Alignment	not modelled	10.2	63 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
59	c1tvmA_	Alignment	not modelled	9.9	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
60	c3a11D_	Alignment	not modelled	9.4	17 PDB header: isomerase Chain: D: PDB Molecule: translation initiation factor eif-2b, delta PDBTitle: crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
61	d1jfla1	Alignment	not modelled	9.3	42 Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
62	c1w2wj_	Alignment	not modelled	9.1	26 PDB header: isomerase Chain: J: PDB Molecule: 5-methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of yeast ypr118w, a methylthioribose-1-2 phosphate isomerase related to regulatory eif2b subunits
63	c2pjka_	Alignment	not modelled	8.7	17 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 178aa long hypothetical molybdenum cofactor PDBTitle: structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
64	d1eola_	Alignment	not modelled	8.7	10 Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
65	d1vola1	Alignment	not modelled	8.4	15 Fold: Cyclin-like Superfamily: Cyclin-like Family: Transcription factor IIB (TFIIB), core domain
66	c2qneA_	Alignment	not modelled	7.9	22 PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase (zp_00558420.1) from2 desulfitobacterium hafniense y51 at 2.30 a resolution
67	d1cqxa3	Alignment	not modelled	7.7	18 Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavo-hemoglobin, C-terminal domain
68	d1gkub3	Alignment	not modelled	7.7	13 Fold: Prokaryotic type I DNA topoisomerase Superfamily: Prokaryotic type I DNA topoisomerase Family: Prokaryotic type I DNA topoisomerase
69	c3peiA_	Alignment	not modelled	7.7	27 PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from francisella2 tularensis
70	d2bm8a1	Alignment	not modelled	7.6	22 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Cmcl-like
71	c2wfbA_	Alignment	not modelled	7.3	10 PDB header: biosynthetic protein Chain: A: PDB Molecule: putative uncharacterized protein orp; PDBTitle: high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
72	d1gvha3	Alignment	not modelled	7.2	16 Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Flavo-hemoglobin, C-terminal domain
73	d1dxya2	Alignment	not modelled	7.2	29 Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
74	d1iu8a_	Alignment	not modelled	7.1	25 Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
75	d1o6ca_	Alignment	not modelled	6.8	17 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
76	d2fug61	Alignment	not modelled	6.6	17 Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nqo6-like
77	d1sqsa_	Alignment	not modelled	6.5	11 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein SP1951
78	d1rdua_	Alignment	not modelled	6.4	8 Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
79	d1l5xa_	Alignment	not modelled	6.3	12 Fold: SurE-like Superfamily: SurE-like

						Family: SurE-like
80	d1ks9a2	Alignment	not modelled	6.0	50	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
81	d1a8pa2	Alignment	not modelled	5.9	10	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
82	c2f1kD	Alignment	not modelled	5.9	63	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
83	d1wd5a	Alignment	not modelled	5.8	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
84	d1mv8a2	Alignment	not modelled	5.8	50	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
85	c1olsB	Alignment	not modelled	5.8	11	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: roles of his291-alpha and his146-beta' in the reductive2 acylation reaction catalyzed by human branched-chain3 alpha-ketoacid dehydrogenase
86	d1j0aa	Alignment	not modelled	5.7	11	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
87	d1a5za1	Alignment	not modelled	5.7	75	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
88	d1gv0a1	Alignment	not modelled	5.6	75	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
89	d1pvda2	Alignment	not modelled	5.4	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
90	d1zpa2	Alignment	not modelled	5.4	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
91	d1ojua1	Alignment	not modelled	5.3	63	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
92	c3snrA	Alignment	not modelled	5.3	22	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
93	c3ecsD	Alignment	not modelled	5.3	26	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit PDBTitle: crystal structure of human eif2b alpha
94	c3fysA	Alignment	not modelled	5.2	29	PDB header: fatty acid-binding protein Chain: A: PDB Molecule: protein degv; PDBTitle: crystal structure of degv, a fatty acid binding protein2 from bacillus subtilis
95	c2gf2B	Alignment	not modelled	5.1	50	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
96	d2bfdb1	Alignment	not modelled	5.1	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module