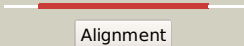

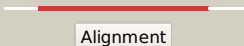

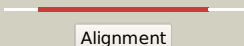







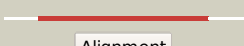











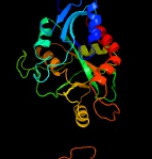


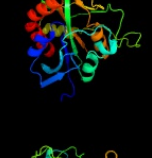

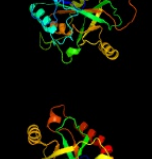



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0535_(pnp)_626460_627254
Date	Fri Jul 26 01:50:08 BST 2019
Unique Job ID	c50734dd53afb9fe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4l5cE_			100.0	36	PDB header: transferase Chain: E; PDB Molecule: s-methyl-5'-thioadenosine phosphorylase; PDBTitle: methylthioadenosine phosphorylase from schistosoma mansoni in complex2 with adenine in space group p212121
2	c4glfA_			100.0	37	PDB header: transferase Chain: A; PDB Molecule: rsfp; PDBTitle: crystal structure of methylthioadenosine phosphorylase sourced from an2 antarctic soil metagenomic library
3	d1cb0a_			100.0	38	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
4	c1wtaA_			100.0	41	PDB header: transferase Chain: A; PDB Molecule: 5'-methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
5	c4m1eC_			100.0	20	PDB header: transferase Chain: C; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from2 planctomyces limnophilus dsm 3776, nysgrc target 029364.
6	c4lnaA_			100.0	22	PDB header: transferase Chain: A; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from spirosoxa2 linguale dsm 74, nysgrc target 029362
7	c4uc0A_			100.0	22	PDB header: transferase Chain: A; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of a purine nucleoside phosphorylase (psi-nysgrc-2 029736) from agrobacterium vitis
8	d1v4na_			100.0	41	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
9	c5cxsA_			100.0	20	PDB header: transferase Chain: A; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of isoform 2 of purine nucleoside phosphorylase2 complexed with mes
10	c4nsnC_			100.0	20	PDB header: transferase Chain: C; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from2 porphyromonas gingivalis atcc 33277, nysgrc target 030972,3 orthorhombic symmetry
11	c5ifkC_			100.0	21	PDB header: transferase Chain: C; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: purine nucleoside phosphorylase

12	d3bgsa1	Alignment		100.0	22	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
13	c1ctcvB	Alignment		100.0	26	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
14	c1yr3A	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: xanthosine phosphorylase; PDBTitle: escherichia coli purine nucleoside phosphorylase ii, the product of2 the xapa gene
15	c3ggsA	Alignment		100.0	23	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
16	c2p4sA	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
17	d1g2oa	Alignment		100.0	25	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
18	c3la8A	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: putative purine nucleoside phosphorylase; PDBTitle: the crystal structure of smu.1229 from streptococcus mutans ua159
19	c3khsB	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
20	d1qe5a	Alignment		100.0	22	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
21	c3ozbF	Alignment	not modelled	100.0	37	PDB header: transferase Chain: F: PDB Molecule: methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
22	d3pnpa	Alignment	not modelled	100.0	24	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
23	d1vmka	Alignment	not modelled	100.0	21	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
24	c4r31A	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of a putative uridine phosphorylase from2 actinobacillus succinogenes 130z (target nysgrc-029667)
25	c3nm5B	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: mta/sah nucleosidase; PDBTitle: helicobacter pylori mtan complexed with formycin a
26	d1rxya	Alignment	not modelled	99.9	13	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
27	c1nw4C	Alignment	not modelled	99.9	13	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
28	c6aytD	Alignment	not modelled	99.9	11	PDB header: hydrolase, transferase Chain: D: PDB Molecule: 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; PDBTitle: crystal structure of campylobacter jejuni 5'-methylthioadenosine/s-2 adenosyl homocysteine nucleosidase (mtan) complexed with3 pyrazinylthio-dadme-immucillin-a

29	c4g41A_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: mta/sah nucleosidase; PDBTitle: crystal structure of s-adenosylhomocysteine nucleosidase from2 streptococcus pyogenes in complex with 5-methylthiotubericidin
30	d1q1ga_	Alignment	not modelled	99.9	13	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
31	c4jwA_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: methylthioadenosine nucleosidase; PDBTitle: crystal structure of a putative 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from sulfurimonas denitrificans dsm3 1251 (target nysgrc-029304)
32	c6if8D_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: D: PDB Molecule: 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; PDBTitle: aeromonas hydrophila mtan-2 complexed with adenine
33	c3bl6A_	Alignment	not modelled	99.9	16	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
34	c3qpbB_	Alignment	not modelled	99.9	14	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
35	c3mb8A_	Alignment	not modelled	99.9	15	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
36	d1vhwa_	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
37	c1zosE_	Alignment	not modelled	99.9	16	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-state inhibitor mt-3 imma
38	c4tymA_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deod-type; PDBTitle: crystal structure of purine nucleoside phosphorylase from2 streptococcus agalactiae 2603v/r, nysgrc target 030935
39	c4ldnA_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deod-type; PDBTitle: crystal structure of a putative purine nucleoside phosphorylase from2 vibrio fischeri es114 (target nysgrc-029521)
40	c6po4A_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; PDBTitle: 2.1 angstrom resolution crystal structure of 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase (mtnn) from haemophilus influenzae3 pittii.
41	d1je0a_	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
42	d1lodka_	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
43	c4m7wA_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deod-type; PDBTitle: crystal structure of purine nucleoside phosphorylase from leptotrichia2 buccalis c-1013-b, nysgrc target 029767.
44	c3eeiA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: 5-methylthioadenosine nucleosidase/s-adenosylhomocysteine PDBTitle: crystal structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from neisseria meningitidis in complex with methylthio-3 immucillin-a
45	c4kn5A_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: methylthioadenosine nucleosidase; PDBTitle: crystal structure of a putative methylthioadenosine nucleosidase from2 weissella paramesenteroides atcc 33313 (target nysgrc-029342)
46	c1z34A_	Alignment	not modelled	99.9	12	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
47	c4josA_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteine nucleosidase; PDBTitle: crystal structure of a putative 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from francisella philomiragia atcc3 25017 (target nysgrc-029335)
48	c4qezC_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: C: PDB Molecule: 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; PDBTitle: crystal structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from bacillus anthracis
49	d2ac7a1	Alignment	not modelled	99.9	13	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
50	c4lkrA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deod-type; PDBTitle: crystal structure of deod-3 gene product from shewanella

						oneidensis2 mr-1, nysgrc target 029437
51	c5mx6C_	Alignment	not modelled	99.9	10	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase deod-type; PDBTitle: crystal structure of h. pylori purine nucleoside phosphorylase from2 clinical isolate hppnp-2
52	d1k9sa_	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
53	d1jysa_	Alignment	not modelled	99.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
54	c4m3nA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deod-type; PDBTitle: crystal structure of purine nucleoside phosphorylase from meiothermus2 ruber dsm 1279, nysgrc target 029804.
55	c4d98A_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deod-type; PDBTitle: crystal structure of the hexameric purine nucleoside phosphorylase2 from bacillus subtilis in space group h32 at ph 7.5
56	c5dk6A_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; PDBTitle: 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
57	c3dp9A_	Alignment	not modelled	99.8	16	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
58	c2h8gA_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase; PDBTitle: 5'-methylthioadenosine nucleosidase from arabidopsis2 thaliana
59	c5b7pB_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: mta/sah nucleosidase; PDBTitle: structures and functional analysis of periplasmic 5-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase from3 aeromonas hydrophila
60	c4lnhA_	Alignment	not modelled	99.8	12	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of uridine phosphorylase from vibrio fischeri es114.2 nysgrc target 29520.
61	d1ybfa_	Alignment	not modelled	99.8	11	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
62	c3tl6B_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
63	c4l0mA_	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: A: PDB Molecule: putative 5'-methylthioadenosine/s-adenosylhomocysteine PDBTitle: crystal structure of a putative 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from borrelia burgdorferi b31 bound3 to adenine (target nysgrc-029268)
64	c3bsfB_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: B: PDB Molecule: at4g34840; PDBTitle: crystal structure of the mta/sah nucleosidase
65	d1t8sa_	Alignment	not modelled	99.7	14	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
66	c6k5gC_	Alignment	not modelled	99.5	20	PDB header: transferase Chain: C: PDB Molecule: uridine phosphorylase; PDBTitle: structural and catalytic analysis of two diverse uridine2 phosphorylases in the oomycete phytophthora capsici
67	c3eufC_	Alignment	not modelled	99.4	17	PDB header: transferase Chain: C: PDB Molecule: uridine phosphorylase 1; PDBTitle: crystal structure of bau-bound human uridine phosphorylase 1
68	c3bjeA_	Alignment	not modelled	99.3	15	PDB header: transferase Chain: A: PDB Molecule: nucleoside phosphorylase, putative; PDBTitle: crystal structure of trypanosoma brucei nucleoside phosphorylase shows2 uridine phosphorylase activity
69	c2xrfA_	Alignment	not modelled	99.3	15	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase 2; PDBTitle: crystal structure of human uridine phosphorylase 2
70	c4pr3A_	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase / s- PDBTitle: crystal structure of brucella melitensis 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase
71	c4txjD_	Alignment	not modelled	99.3	13	PDB header: transferase Chain: D: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of uridine phosphorylase from schistosoma mansoni in2 complex with thymidine
72	c4qasB_	Alignment	not modelled	99.1	12	PDB header: hydrolase Chain: B: PDB Molecule: ct263; PDBTitle: 1.27 a resolution structure of ct263-d161n (mtan) from chlamydia2 trachomatis
73	c5c4nD_	Alignment	not modelled	87.1	22	PDB header: oxidoreductase Chain: D: PDB Molecule: precorrin-6a reductase; PDBTitle: cobk precorrin-6a reductase
74	c5w70B_	Alignment	not modelled	64.5	15	PDB header: transferase Chain: B: PDB Molecule: l-glutamine:2-deoxy-scylo-inosose

74	c3w70B	Alignment	not modelled	49.3	13	aminotransferase; PDBTitle: x-ray structure of rbmb from streptomyces ribosidificus
75	c4r9xB	Alignment	not modelled	49.0	15	PDB header: metal transport Chain: B: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of putative copper homeostasis protein cutc from2 bacillus anthracis
76	c5wxzA	Alignment	not modelled	48.4	60	PDB header: isomerase Chain: A: PDB Molecule: mcyf; PDBTitle: crystal structure of microcystis aeruginosa pcc 7806 aspartate2 racemase in complex with d-aspartate
77	c3s81A	Alignment	not modelled	45.6	36	PDB header: isomerase Chain: A: PDB Molecule: putative aspartate racemase; PDBTitle: crystal structure of putative aspartate racemase from salmonella2 typhimurium
78	c3hm8D	Alignment	not modelled	44.9	22	PDB header: transferase Chain: D: PDB Molecule: hexokinase-3; PDBTitle: crystal structure of the c-terminal hexokinase domain of human hk3
79	d1bdga2	Alignment	not modelled	44.7	30	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
80	d1jfla1	Alignment	not modelled	42.2	40	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
81	c1bdgA	Alignment	not modelled	41.9	28	PDB header: hexokinase Chain: A: PDB Molecule: hexokinase; PDBTitle: hexokinase from schistosoma mansoni complexed with glucose
82	d1t57a	Alignment	not modelled	41.7	19	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
83	d1bg3a4	Alignment	not modelled	41.2	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
84	c5b19B	Alignment	not modelled	41.1	50	PDB header: isomerase Chain: B: PDB Molecule: aspartate racemase; PDBTitle: picrophilus torridus aspartate racemase
85	c5zqtA	Alignment	not modelled	39.1	19	PDB header: transferase Chain: A: PDB Molecule: hexokinase-6; PDBTitle: crystal structure of oryza sativa hexokinase 6
86	c4qs9A	Alignment	not modelled	38.8	19	PDB header: transferase Chain: A: PDB Molecule: hexokinase-1; PDBTitle: arabidopsis hexokinase 1 (athxk1) mutant s177a structure in glucose-2 bound form
87	c2zskA	Alignment	not modelled	37.9	40	PDB header: unknown function Chain: A: PDB Molecule: 226aa long hypothetical aspartate racemase; PDBTitle: crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
88	c3ojcD	Alignment	not modelled	37.6	45	PDB header: isomerase Chain: D: PDB Molecule: putative aspartate/glutamate racemase; PDBTitle: crystal structure of a putative asp/glu racemase from yersinia pestis
89	d2pv7a2	Alignment	not modelled	37.4	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
90	c5exkG	Alignment	not modelled	35.9	16	PDB header: transferase Chain: G: PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
91	c3t72o	Alignment	not modelled	35.7	11	PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
92	d1czan2	Alignment	not modelled	35.5	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
93	d1czan4	Alignment	not modelled	35.2	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
94	c5b19A	Alignment	not modelled	33.4	50	PDB header: isomerase Chain: A: PDB Molecule: aspartate racemase; PDBTitle: picrophilus torridus aspartate racemase
95	c3ju7B	Alignment	not modelled	32.8	7	PDB header: transferase Chain: B: PDB Molecule: putative plp-dependent aminotransferase; PDBTitle: crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
96	d1bg3a2	Alignment	not modelled	32.5	25	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
97	d1ea0a2	Alignment	not modelled	32.2	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
98	c2dx7B	Alignment	not modelled	31.8	40	PDB header: isomerase Chain: B: PDB Molecule: aspartate racemase; PDBTitle: crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
99	c5elmB	Alignment	not modelled	31.3	30	PDB header: isomerase Chain: B: PDB Molecule: asp/glu_racemase family protein; PDBTitle: crystal structure of l-aspartate/glutamate specific racemase in2 complex with l-glutamate
100	c1hkgA	Alianment	not modelled	31.2	25	PDB header: transferase Chain: A: PDB Molecule: hexokinase a;

						PDBTitle: structural dynamics of yeast hexokinase during catalysis
101	c2hwgA_	Alignment	not modelled	31.2	33	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
102	c5gsmB_	Alignment	not modelled	30.7	18	PDB header: hydrolase Chain: B: PDB Molecule: exo-beta-d-glucosaminidase; PDBTitle: glycoside hydrolase b with product
103	c2vdcF_	Alignment	not modelled	30.2	11	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadh] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
104	c1v4sA_	Alignment	not modelled	29.6	25	PDB header: transferase Chain: A: PDB Molecule: glucokinase isoform 2; PDBTitle: crystal structure of human glucokinase
105	c6aphA_	Alignment	not modelled	29.5	18	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
106	c5n2iC_	Alignment	not modelled	28.8	36	PDB header: oxidoreductase Chain: C: PDB Molecule: reduced coenzyme f420:nadp oxidoreductase; PDBTitle: f420:nadph oxidoreductase from thermobifida fusca with nadp+ bound
107	c1lm1A_	Alignment	not modelled	28.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-dependent glutamate synthase; PDBTitle: structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
108	c3oixA_	Alignment	not modelled	28.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dihydroorotate dehydrogenase; dihydroorotate PDBTitle: crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
109	c2i3aD_	Alignment	not modelled	27.7	36	PDB header: oxidoreductase Chain: D: PDB Molecule: n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (rv1652) from mycobacterium tuberculosis
110	c3x2fA_	Alignment	not modelled	27.4	14	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
111	d1v4sa2	Alignment	not modelled	27.3	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
112	c1tvmA_	Alignment	not modelled	27.3	20	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
113	c1qhaA_	Alignment	not modelled	27.1	16	PDB header: transferase Chain: A: PDB Molecule: protein (hexokinase); PDBTitle: human hexokinase type i complexed with atp analogue amp-pnp
114	d2p7vb1	Alignment	not modelled	27.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
115	c5gslB_	Alignment	not modelled	26.8	8	PDB header: hydrolase Chain: B: PDB Molecule: 778aa long hypothetical beta-galactosidase; PDBTitle: glycoside hydrolase a
116	c2c7tA_	Alignment	not modelled	26.5	10	PDB header: transferase Chain: A: PDB Molecule: glutamine-2-deoxy-scylo-inosose aminotransferase; PDBTitle: crystal structure of the plp-bound form of btrr, a dual functional2 aminotransferase involved in butirosin biosynthesis.
117	c2hcuA_	Alignment	not modelled	26.4	25	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: crystal structure of smu.1381 (or leud) from streptococcus mutans
118	c3ki9F_	Alignment	not modelled	26.4	13	PDB header: hydrolase Chain: F: PDB Molecule: glutamyl aminopeptidase; PDBTitle: crystal structure of pepa from streptococcus pneumoniae
119	d1ku3a_	Alignment	not modelled	26.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
120	d1ku7a_	Alignment	not modelled	26.0	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain