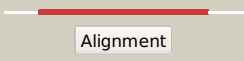

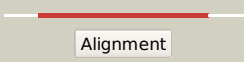

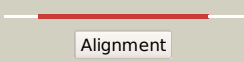

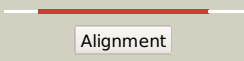

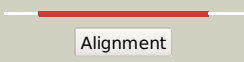

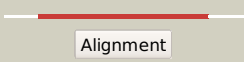

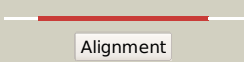

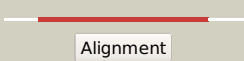

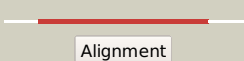

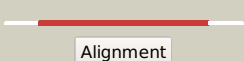

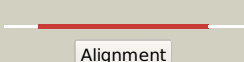



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0091_(mtn)_99681_100448
Date	Tue Jul 23 14:50:12 BST 2019
Unique Job ID	6a54504e191bbae9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6aytD_			100.0	29	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
2	c4jwta_			100.0	27	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)
3	c1zosE_			100.0	32	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
4	c4kn5A_			100.0	30	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)
5	c5dk6A_			100.0	33	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
6	c6po4A_			100.0	26	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 (mtan) from haemophilus influenzae3 pittii.
7	c3dp9A_			100.0	32	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
8	c3eeiA_			100.0	30	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
9	c3bl6A_			100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase/s-adenosylhomocysteine PDBTitle: crystal structure of staphylococcus aureus 5'-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase in3 complex with formycin a
10	c4g41A_			100.0	32	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
11	c3nm5B_			100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: mta/sah nucleosidase; PDBTitle: helicobacter pylori mtan complexed with formycin a

12	c4josA_	Alignment		100.0	28	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)
13	c4qezC_	Alignment		100.0	34	PDB header: hydrolase Chain: C: PDB Molecule: 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; PDBTitle: crystal structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from bacillus anthracis
14	c4l0mA_	Alignment		100.0	25	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)
15	c6if8D_	Alignment		100.0	32	PDB header: hydrolase Chain: D: PDB Molecule: 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; PDBTitle: aeromonas hydrophila mtan-2 complexed with adenine
16	d1jysa_	Alignment		100.0	32	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
17	c5b7pB_	Alignment		100.0	24	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
18	c2h8gA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase; PDBTitle: 5'-methylthioadenosine nucleosidase from arabidopsis2 thaliana
19	c3bsfB_	Alignment		100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: at4g34840; PDBTitle: crystal structure of the mta/sah nucleosidase
20	d1rxya_	Alignment		100.0	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
21	c4tymA_	Alignment	not modelled	100.0	19	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
22	c1z34A_	Alignment	not modelled	100.0	17	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
23	c5mx6C_	Alignment	not modelled	100.0	17	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
24	d1je0a_	Alignment	not modelled	100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
25	c1nw4C_	Alignment	not modelled	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
26	d1vhwa_	Alignment	not modelled	100.0	15	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
27	d1q1ga_	Alignment	not modelled	100.0	19	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
28	c4m7wA_	Alignment	not modelled	100.0	17	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.
29	d2ac7a1	Alignment	not modelled	100.0	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
30	d1k9sa	Alignment	not modelled	100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
31	d1odka	Alignment	not modelled	100.0	21	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
32	c4m3nA	Alignment	not modelled	100.0	20	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.
33	c4d98A	Alignment	not modelled	100.0	14	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
34	c4ldnA	Alignment	not modelled	100.0	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)
35	c4qasB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: ct263; PDBTitle: 1.27 a resolution structure of ct263-d161n (mtan) from chlamydia2 trachomatis
36	c3mb8A	Alignment	not modelled	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
37	c3tl6B	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
38	c3qpB	Alignment	not modelled	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
39	c4lkrA	Alignment	not modelled	100.0	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
40	c4r31A	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of a putative uridine phosphorylase from2 actinobacillus succinogenes 130z (target nysgrc-029667)
41	c4lnhA	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of uridine phosphorylase from vibrio fischeri es114,2 nysgrc target 29520.
42	c4pr3A	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase / s- PDBTitle: crystal structure of brucella melitensis 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase
43	d1t8sa	Alignment	not modelled	100.0	20	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
44	d1ybfa	Alignment	not modelled	100.0	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
45	c6k5gC	Alignment	not modelled	100.0	16	PDB header: transferase Chain: C: PDB Molecule: uridine phosphorylase; PDBTitle: structural and catalytic analysis of two diverse uridine2 phosphorylases in the oomycete phytophthora capsici
46	c3khsB	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
47	d1v4na	Alignment	not modelled	100.0	12	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
48	c1wtaA	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: 5'-methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
49	d1vmka	Alignment	not modelled	100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
50	c3ozbF	Alignment	not modelled	99.9	14	PDB header: transferase Chain: F: PDB Molecule: methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
51	c1tcvB	Alignment	not modelled	99.9	16	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
52	c2p4sA	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
53	c3bjeA	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: nucleoside phosphorylase, putative; PDBTitle: crystal structure of trypanosoma brucei nucleoside

						phosphorylase shows2 uridine phosphorylase activity
54	c2xrfA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase 2; PDBTitle: crystal structure of human uridine phosphorylase 2
55	c4txjD_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: D: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of uridine phosphorylase from schistosoma mansoni in2 complex with thymidine
56	d1cb0a_	Alignment	not modelled	99.9	18	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
57	c5cxsA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of isoform 2 of purine nucleoside phosphorylase2 complexed with mes
58	c3la8A_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: putative purine nucleoside phosphorylase; PDBTitle: the crystal structure of smu.1229 from streptococcus mutans ua159
59	c1yr3A_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: xanthosine phosphorylase; PDBTitle: escherichia coli purine nucleoside phosphorylase ii, the product of2 the xapa gene
60	d3bgsa1	Alignment	not modelled	99.9	18	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
61	c3eufC_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: C: PDB Molecule: uridine phosphorylase 1; PDBTitle: crystal structure of bau-bound human uridine phosphorylase 1
62	d1g2oa_	Alignment	not modelled	99.9	18	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
63	c3ggsA_	Alignment	not modelled	99.9	18	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
64	d3pnpa_	Alignment	not modelled	99.9	18	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
65	c4qlfA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: rsfp; PDBTitle: crystal structure of methylthioadenosine phosphorylase sourced from an2 antarctic soil metagenomic library
66	c5ifkC_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: purine nucleoside phosphorylase
67	d1qe5a_	Alignment	not modelled	99.8	17	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
68	c4lnaA_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from spiroso2a2 linguale dsm 74, nysgrc target 029362
69	c4m1eC_	Alignment	not modelled	99.7	16	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.
70	c4nsnC_	Alignment	not modelled	99.6	14	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
71	c4uc0A_	Alignment	not modelled	99.5	13	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
72	c4l5cE_	Alignment	not modelled	99.5	13	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
73	d1a2za_	Alignment	not modelled	74.7	9	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
74	c3giuA_	Alignment	not modelled	73.2	11	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus
75	c5z47A_	Alignment	not modelled	56.5	21	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of pyrrolidone carboxylate peptidase i with2 disordered loop a from deinococcus radiodurans r1
76	c4gxhC_	Alignment	not modelled	56.0	13	PDB header: hydrolase Chain: C: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of a pyrrolidone-carboxylate peptidase 1 (target id2 nysgrc-012831) from xenorhabdus bovienii ss-2004
77	c3lacA_	Alignment	not modelled	55.4	11	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of bacillus anthracis pyrrolidone-carboxylate2 peptidase, pcp
78	d1iofa_	Alignment	not modelled	55.0	9	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
						Fold: Phosphorylase/hydrolase-like

79	d1auga_	Alignment	not modelled	41.5	13	Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
80	c3sc6F_	Alignment	not modelled	28.9	12	PDB header: oxidoreductase Chain: F: PDB Molecule: dtdp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
81	c2d0iC_	Alignment	not modelled	23.4	15	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase; PDBTitle: crystal structure ph0520 protein from pyrococcus horikoshii ot3
82	c3peiA_	Alignment	not modelled	18.7	19	PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from francisella2 tularensis
83	c4h3zA_	Alignment	not modelled	16.0	22	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of a symmetric dimer of a trna (guanine-(n(1)-)-2 methyltransferase from burkholderia phymatum bound to s-adenosyl3 homocystein in both half-sites
84	c5wyrA_	Alignment	not modelled	15.9	26	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure and catalytic mechanism of the essential m1g37 trna2 methyltransferase trmd from pseudomonas aeruginosa
85	c1oy5B_	Alignment	not modelled	15.2	21	PDB header: transferase Chain: B: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
86	d1oy5a_	Alignment	not modelled	15.2	21	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
87	c2ebjB_	Alignment	not modelled	14.7	15	PDB header: hydrolase Chain: B: PDB Molecule: pyrrolidone carboxyl peptidase; PDBTitle: crystal structure of pyrrolidone carboxyl peptidase from thermus2 thermophilus
88	d1p9pa_	Alignment	not modelled	14.7	28	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
89	c3nhzA_	Alignment	not modelled	14.6	16	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
90	c1olsB_	Alignment	not modelled	13.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: roles of his291-alpha and his146-beta' in the reductive acylation2 reaction catalyzed by human branched-chain alpha-ketoacid3 dehydrogenase
91	c1tvmA_	Alignment	not modelled	13.6	4	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
92	c2p4qA_	Alignment	not modelled	13.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae
93	d1iu8a_	Alignment	not modelled	13.5	15	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
94	d1iowa1	Alignment	not modelled	13.4	22	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
95	c3knuD_	Alignment	not modelled	12.7	23	PDB header: transferase Chain: D: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
96	d1gl9b1	Alignment	not modelled	12.3	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
97	d1uala_	Alignment	not modelled	11.0	30	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
98	c3iefA_	Alignment	not modelled	10.8	26	PDB header: transferase, rna binding protein Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna guanine-n1-methyltransferase from bartonella2 henselae using mpccs.
99	c6fxwA_	Alignment	not modelled	10.7	19	PDB header: isomerase Chain: A: PDB Molecule: putative ribose 5-phosphate isomerase; PDBTitle: structure of leishmania infantum type b ribose 5-phosphate isomerase