























Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4jwA_	 Alignment		100.0	19	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)
2	c6aytD_	 Alignment		100.0	20	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
3	c4josA_	 Alignment		100.0	19	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)
4	c5dk6A_	 Alignment		100.0	17	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
5	c3nm5B_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: mta/sah nucleosidase; PDBTitle: helicobacter pylori mtan complexed with formycin a
6	c4kn5A_	 Alignment		100.0	21	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)
7	c4l0mA_	 Alignment		100.0	23	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)
8	c3dp9A_	 Alignment		100.0	19	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
9	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-state inhibitor mt-3 imma
10	c4g41A_	 Alignment		100.0	22	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	c6if8D_	 Alignment		100.0	21	PDB header: hydrolase Chain: D: PDB Molecule: 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; PDBTitle: aeromonas hydrophila mtan-2 complexed with adenine

12	c4qezC_	Alignment		100.0	23	PDB header: hydrolase Chain: C: PDB Molecule: 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; PDBTitle: crystal structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from bacillus anthracis
13	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
14	d1jysa_	Alignment		100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
15	c6po4A_	Alignment		100.0	18	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.
16	c2h8gA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase; PDBTitle: 5'-methylthioadenosine nucleosidase from arabidopsis2 thaliana
17	c3bl6A_	Alignment		100.0	20	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
18	c3eeiA_	Alignment		100.0	24	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
19	c3bsfB_	Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: at4g34840; PDBTitle: crystal structure of the mta/sah nucleosidase
20	c1z34A_	Alignment		100.0	13	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
21	c5mx6C_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of h. pylori purine nucleoside phosphorylase from2 clinical isolate hppnp-2
22	c4tymA_	Alignment	not modelled	100.0	10	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of purine nucleoside phosphorylase from2 streptococcus agalactiae 2603v/r, nysgrc target 030935
23	d1vhwa_	Alignment	not modelled	99.9	10	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
24	d1k9sa_	Alignment	not modelled	99.9	15	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
25	c4qasB_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: ct263; PDBTitle: 1.27 a resolution structure of ct263-d161n (mtan) from chlamydia2 trachomatis
26	c4m3nA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of purine nucleoside phosphorylase from meiothermus2 ruber dsm 1279, nysgrc target 029804.
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	d1rxya_	Alignment	not modelled	99.9	13	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases

29	d1q1ga_	Alignment	not modelled	99.9	13	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
30	c4d98A_	Alignment	not modelled	99.9	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
31	c4pr3A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase / s- PDBTitle: crystal structure of brucella melitensis 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase
32	d2ac7a1	Alignment	not modelled	99.9	14	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
33	d1je0a_	Alignment	not modelled	99.9	14	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
34	c4m7wA_	Alignment	not modelled	99.9	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.
35	c3tl6B_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
36	c4lnhA_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of uridine phosphorylase from vibrio fischeri es114,2 nysgrc target 29520.
37	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)
38	d1lodka_	Alignment	not modelled	99.9	15	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
39	c3mb8A_	Alignment	not modelled	99.9	14	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
40	d1t8sa_	Alignment	not modelled	99.9	14	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
41	c3qpbB_	Alignment	not modelled	99.9	21	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
42	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
43	d1ybfa_	Alignment	not modelled	99.9	14	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
44	c4r31A_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of a putative uridine phosphorylase from2 actinobacillus succinogenes 130z (target nysgrc-029667)
45	c6k5gC_	Alignment	not modelled	99.9	18	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	d1v4na_	Alignment	not modelled	99.8	10	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
47	c3ozbF_	Alignment	not modelled	99.7	12	PDB header: transferase Chain: F: PDB Molecule: methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
48	c1wtaA_	Alignment	not modelled	99.7	10	PDB header: transferase Chain: A: PDB Molecule: 5'-methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
49	c3bjeA_	Alignment	not modelled	99.6	14	PDB header: transferase Chain: A: PDB Molecule: nucleoside phosphorylase, putative; PDBTitle: crystal structure of trypanosoma brucei nucleoside phosphorylase shows2 uridine phosphorylase activity
50	c3khsB_	Alignment	not modelled	99.6	9	PDB header: hydrolase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
51	d1vmka_	Alignment	not modelled	99.6	13	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
52	c2xrfA_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase 2; PDBTitle: crystal structure of human uridine phosphorylase 2
53	c4txjD_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: D: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of uridine phosphorylase from schistosoma mansoni in2 complex with thymidine
54	c3l8A_	Alignment	not modelled	99.5	12	PDB header: transferase Chain: A: PDB Molecule: putative purine nucleoside phosphorylase;

54	c3iaaA	Alignment	not modelled	99.3	12	PDBTitle: the crystal structure of smu.1229 from streptococcus mutans ua159 PDB header: transferase
55	c3eufC	Alignment	not modelled	99.4	14	Chain: C; PDB Molecule: uridine phosphorylase 1; PDBTitle: crystal structure of bau-bound human uridine phosphorylase 1
56	d1cb0a	Alignment	not modelled	99.4	12	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
57	c1ctvB	Alignment	not modelled	99.2	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
58	d1g2oa	Alignment	not modelled	99.2	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
59	c2p4sA	Alignment	not modelled	99.2	12	PDB header: transferase Chain: A; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
60	c5cxsA	Alignment	not modelled	99.1	15	PDB header: transferase Chain: A; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of isoform 2 of purine nucleoside phosphorylase2 complexed with mes
61	d3pnpa	Alignment	not modelled	99.1	13	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
62	c1yr3A	Alignment	not modelled	99.0	11	PDB header: transferase Chain: A; PDB Molecule: xanthosine phosphorylase; PDBTitle: escherichia coli purine nucleoside phosphorylase ii, the product of2 the xpa gene
63	c3ggsA	Alignment	not modelled	98.9	12	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	d3bgsa1	Alignment	not modelled	98.9	12	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
65	d1qe5a	Alignment	not modelled	98.4	13	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
66	c4glfA	Alignment	not modelled	98.0	12	PDB header: transferase Chain: A; PDB Molecule: rsfp; PDBTitle: crystal structure of methylthioadenosine phosphorylase sourced from an2 antarctic soil metagenomic library
67	c5ifkC	Alignment	not modelled	97.6	17	PDB header: transferase Chain: C; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: purine nucleoside phosphorylase
68	c4lnaA	Alignment	not modelled	96.6	17	PDB header: transferase Chain: A; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from spirosoa2 linguale dsm 74, nysgrc target 029362
69	c4m1eC	Alignment	not modelled	96.5	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.
70	c4nsnC	Alignment	not modelled	96.4	17	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	95.9	17	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	c4I5cE	Alignment	not modelled	92.1	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	c3giuA	Alignment	not modelled	46.1	16	PDB header: hydrolase Chain: A; PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus
74	d1a2za	Alignment	not modelled	38.4	15	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
75	c4maqB	Alignment	not modelled	25.9	27	PDB header: hydrolase Chain: B; PDB Molecule: putative fumarylpyruvate hydrolase; PDBTitle: crystal structure of a putative fumarylpyruvate hydrolase from2 burkholderia cenocepacia
76	c4gxhC	Alignment	not modelled	23.7	14	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	d1gtta2	Alignment	not modelled	22.5	18	Fold: FAH Superfamily: FAH Family: FAH
78	d2aioa1	Alignment	not modelled	21.6	8	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
79	c3dclC	Alignment	not modelled	21.2	16	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: tm1086; PDBTitle: crystal structure of tm1086

80	d1hyoa2	Alignment	not modelled	21.1	31	Fold: FAH Superfamily: FAH Family: FAH
81	c3lacA	Alignment	not modelled	21.0	16	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of bacillus anthracis pyrrolidone-carboxylate2 peptidase, pcp
82	c2lqkA	Alignment	not modelled	20.8	29	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: nmr solution structure of the n-terminal domain of the cdnl protein2 from thermus thermophilus
83	c4dbhA	Alignment	not modelled	20.4	23	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of cg1458 with inhibitor
84	d1iofa	Alignment	not modelled	20.3	18	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
85	d2gdtA1	Alignment	not modelled	19.5	30	Fold: SARS Nsp1-like Superfamily: SARS Nsp1-like Family: SARS Nsp1-like
86	c4q51A	Alignment	not modelled	19.5	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative molybdenum cofactor biosynthesis2 protein f from burkholderia cenocepacia j2315
87	c5z47A	Alignment	not modelled	18.7	20	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
88	c3qdfA	Alignment	not modelled	16.4	23	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from mycobacterium marinum
89	d1sawa	Alignment	not modelled	15.7	18	Fold: FAH Superfamily: FAH Family: FAH
90	d1gtta1	Alignment	not modelled	14.7	14	Fold: FAH Superfamily: FAH Family: FAH
91	d1sv6a	Alignment	not modelled	14.7	13	Fold: FAH Superfamily: FAH Family: FAH
92	d1auga	Alignment	not modelled	13.9	13	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
93	c6jvwA	Alignment	not modelled	13.2	23	PDB header: hydrolase Chain: A: PDB Molecule: maley pyruvate hydrolase; PDBTitle: crystal structure of maley pyruvate hydrolase from sphingobium sp.2 syk-6 in complex with manganese (ii) ion and pyruvate
94	c3zvrA	Alignment	not modelled	12.3	45	PDB header: hydrolase Chain: A: PDB Molecule: dynamin-1; PDBTitle: crystal structure of dynamin
95	c4xd9A	Alignment	not modelled	10.9	10	PDB header: translation Chain: A: PDB Molecule: ribosome biogenesis protein, putative (afu_orthologue) PDBTitle: structure of rpf2-rrs1 complex involved in ribosome biogenesis
96	c4xd9C	Alignment	not modelled	10.7	10	PDB header: translation Chain: C: PDB Molecule: ribosome biogenesis protein, putative (afu_orthologue) PDBTitle: structure of rpf2-rrs1 complex involved in ribosome biogenesis
97	c4qkuC	Alignment	not modelled	10.5	30	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase; PDBTitle: crystal structure of a putative hydrolase from burkholderia2 cenocepacia
98	c1wzoC	Alignment	not modelled	9.8	15	PDB header: isomerase Chain: C: PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8
99	c3vqzA	Alignment	not modelled	9.3	16	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of metallo-beta-lactamase, smb-1, in a complex with2 mercaptoacetic acid