Phyre^2

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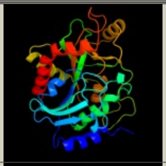
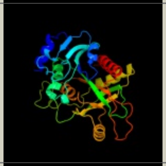
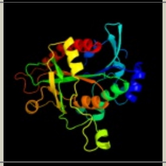
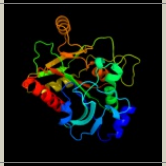
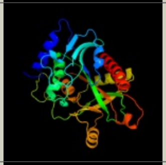
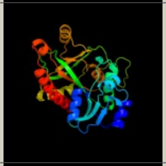
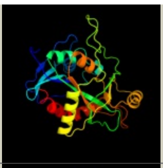
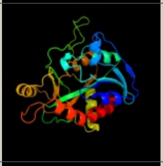
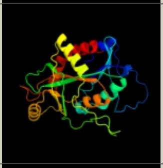
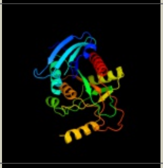
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yr3A_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xanthosine phosphorylase; **PDBTitle:** escherichia coli purine nucleoside phosphorylase ii, the2 product of the xapa gene
2	d3bgsa1	Alignment		100.0	41	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
3	c2p4sA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
4	c3ggsA_	Alignment		100.0	41	**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
5	d1g2oa_	Alignment		100.0	37	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
6	c1tcvB_	Alignment		100.0	40	**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
7	d1qe5a_	Alignment		100.0	35	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
8	d3pnpa_	Alignment		100.0	43	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
9	c3khsB_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
10	d1vmka_	Alignment		100.0	36	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
11	c3la8A_	Alignment		100.0	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative purine nucleoside phosphorylase; **PDBTitle:** the crystal structure of smu.1229 from streptococcus mutans ua159

12	c1wtaA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
13	d1cb0a_	Alignment		100.0	25	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
14	d1v4na_	Alignment		100.0	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
15	c3ozbF_	Alignment		100.0	25	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
16	d1rxya_	Alignment		100.0	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
17	c3nm5B_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mta/sah nucleosidase; **PDBTitle:** helicobacter pylori mtan complexed with formycin a
18	c3qpbB_	Alignment		100.0	17	**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
19	c1nw4C_	Alignment		100.0	15	**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
20	d1q1ga_	Alignment		100.0	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
21	c3mb8A_	Alignment	not modelled	100.0	17	**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
22	d1je0a_	Alignment	not modelled	100.0	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
23	d1vhwa_	Alignment	not modelled	100.0	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
24	c1z34A_	Alignment	not modelled	99.9	14	**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
25	d1odka_	Alignment	not modelled	99.9	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
26	c3bl6A_	Alignment	not modelled	99.9	14	**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
27	d2ac7a1	Alignment	not modelled	99.9	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
28	c1zosE_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**5'-methylthioadenosine / s-adenosylhomocysteine **PDBTitle:** structure of 5'-methylthionadenosine/s-

						adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state3 inhibitor mt-imma
29	c3eeiA_	Alignment	not modelled	99.9	17	**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
30	d1k9sa_	Alignment	not modelled	99.9	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
31	d1jysa_	Alignment	not modelled	99.9	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
32	d1ybfa_	Alignment	not modelled	99.9	9	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
33	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
34	c3dp9A_	Alignment	not modelled	99.9	14	**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
35	c2h8gA_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine nucleosidase; **PDBTitle:** 5'-methylthioadenosine nucleosidase from arabidopsis2 thaliana
36	c3bsfB_	Alignment	not modelled	99.9	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**at4g34840; **PDBTitle:** crystal structure of the mta/sah nucleosidase
37	d1t8sa_	Alignment	not modelled	99.8	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
38	c2xrfA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridine phosphorylase 2; **PDBTitle:** crystal structure of human uridine phosphorylase 2
39	c3eufC_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridine phosphorylase 1; **PDBTitle:** crystal structure of bau-bound human uridine phosphorylase 1
40	c3bjeA_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside phosphorylase, putative; **PDBTitle:** crystal structure of trypanosoma brucei nucleoside phosphorylase shows2 uridine phosphorylase activity
41	d1oy0a_	Alignment	not modelled	85.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
42	c2vdcF_	Alignment	not modelled	83.6	9	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glutamate synthase [nadph] large chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
43	c1llm1A_	Alignment	not modelled	79.2	13	**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
44	d1y0ya2	Alignment	not modelled	77.1	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
45	d1ea0a2	Alignment	not modelled	58.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
46	c2greC_	Alignment	not modelled	57.6	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deblocking aminopeptidase; **PDBTitle:** crystal structure of deblocking aminopeptidase from bacillus cereus
47	d1o1xa_	Alignment	not modelled	56.9	21	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
48	d1tg7a5	Alignment	not modelled	55.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Glycosyl hydrolases family 35 catalytic domain
49	c3fhkF_	Alignment	not modelled	53.3	20	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**upf0403 protein yphp; **PDBTitle:** crystal structure of apc1446, b.subtilis yphp disulfide2 isomerase
50	c3qd5B_	Alignment	not modelled	52.9	29	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
51	c2rjoA_	Alignment	not modelled	52.3	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
52	d1vixa1	Alignment	not modelled	49.5	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
53	c2vk2A_	Alignment	not modelled	46.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq;

						PDBTitle: crystal structure of a galactofuranose binding protein
54	c3he8A_	Alignment	not modelled	43.5	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
55	d1twda_	Alignment	not modelled	41.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
56	d1nn4a_	Alignment	not modelled	40.3	18	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
57	d2vvpa1	Alignment	not modelled	35.6	32	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
58	c3czcA_	Alignment	not modelled	34.6	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
59	c3thdD_	Alignment	not modelled	33.1	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
60	d2cx1a2	Alignment	not modelled	31.6	25	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**Hypothetical protein APE0525, N-terminal domain
61	c3k9cA_	Alignment	not modelled	31.5	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family protein; **PDBTitle:** crystal structure of laci transcriptional regulator from rhodococcus2 species.
62	c3s81A_	Alignment	not modelled	30.6	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium
63	d2dria_	Alignment	not modelled	30.3	18	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
64	c3onoA_	Alignment	not modelled	30.3	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
65	d1u9ya1	Alignment	not modelled	29.6	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
66	c3d3aA_	Alignment	not modelled	29.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
67	c3fokH_	Alignment	not modelled	29.3	16	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**uncharacterized protein cgl0159; **PDBTitle:** crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
68	c1tvmA_	Alignment	not modelled	28.5	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
69	c3d3qB_	Alignment	not modelled	28.4	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
70	d1on3a2	Alignment	not modelled	28.0	15	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
71	c3iwpK_	Alignment	not modelled	27.6	26	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
72	d1xnya2	Alignment	not modelled	27.6	23	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
73	c3kl9F_	Alignment	not modelled	27.4	13	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**glutamyl aminopeptidase; **PDBTitle:** crystal structure of pepa from streptococcus pneumoniae
74	d8abpa_	Alignment	not modelled	27.2	19	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
75	d2pv7a2	Alignment	not modelled	27.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
76	d1fvia1	Alignment	not modelled	24.0	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
77	d1a9xa4	Alignment	not modelled	23.2	9	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
78	c3ctpB_	Alignment	not modelled	23.0	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**periplasmic binding protein/laci transcriptional regulator; **PDBTitle:** crystal structure of periplasmic binding protein/laci

						transcriptional2 regulator from alkaliphilus metalliredigens qymf complexed with d-3 xylulofuranose
79	d1dkua1	Alignment	not modelled	22.4	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
80	d1sv6a_	Alignment	not modelled	21.8	26	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
81	c3k7pA_	Alignment	not modelled	21.8	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
82	c3m1pA_	Alignment	not modelled	21.8	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
83	c2ppwA_	Alignment	not modelled	21.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
84	d2a0ua1	Alignment	not modelled	20.7	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
85	c1vkrA_	Alignment	not modelled	20.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components; **PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii
86	d1vkra_	Alignment	not modelled	20.6	17	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
87	c2glfB_	Alignment	not modelled	20.5	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** crystal structure of aminipeptidase (m18 family) from thermotoga2 maritima
88	d2f9ya1	Alignment	not modelled	19.6	14	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
89	c3exaD_	Alignment	not modelled	19.5	28	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of the full-length trna2 isopentenylpyrophosphate transferase (bh2366) from3 bacillus halodurans, northeast structural genomics4 consortium target bhr41.
90	d2gpfa1	Alignment	not modelled	19.4	24	**Fold:**MbtH/L9 domain-like **Superfamily:**MbtH-like **Family:**MbtH-like
91	d2pstx1	Alignment	not modelled	19.4	24	**Fold:**MbtH/L9 domain-like **Superfamily:**MbtH-like **Family:**MbtH-like
92	d1jhda2	Alignment	not modelled	19.1	40	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
93	c2hjsA_	Alignment	not modelled	18.9	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**usg-1 protein homolog; **PDBTitle:** the structure of a probable aspartate-semialdehyde dehydrogenase from2 pseudomonas aeruginosa
94	c3u7vA_	Alignment	not modelled	18.7	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
95	c2ioyB_	Alignment	not modelled	18.2	18	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**periplasmic sugar-binding protein; **PDBTitle:** crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
96	c2qz9B_	Alignment	not modelled	18.0	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 ii from vibrio cholerae
97	c2zskA_	Alignment	not modelled	17.4	18	**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
98	d1umua_	Alignment	not modelled	17.4	20	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**LexA-related
99	c2gaaA_	Alignment	not modelled	17.3	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical 39.9 kda protein; **PDBTitle:** crystal structure of yfh7 from saccharomyces cerevisiae: a2 putative p-loop containing kinase with a circular3 permutation.