Phyre2

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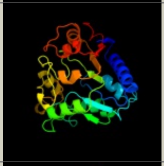
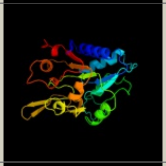
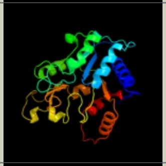
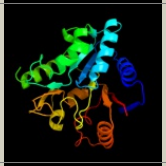
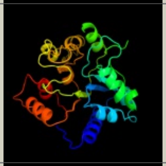
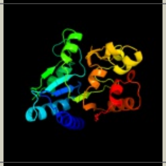
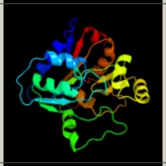
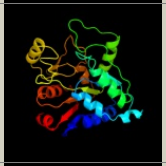
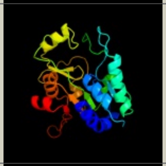
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ne7a_	Alignment		100.0	29	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
2	c2bkxB_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily
3	c3hn6D_	Alignment		100.0	32	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
4	d1fsfa_	Alignment		100.0	28	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
5	c2ri0B_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans
6	c3icoA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from2 mycobacterium tuberculosis
7	c2j0eA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
8	c3oc6A_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
9	c1y89B_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**devb protein; **PDBTitle:** crystal structure of devb protein
10	c3e15D_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** 6-phosphogluconolactonase from plasmodium vivax
11	c3cssA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from leishmania2 guyanensis

12	d1vl1a_	Alignment		100.0	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
13	c1pbtA_	Alignment		100.0	19	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
14	c3lhiA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative 6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
15	c3lwdA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
16	c3nwpA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
17	d2gnpa1	Alignment		100.0	12	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
18	c2w48D_	Alignment		100.0	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
19	c3nzeB_	Alignment		100.0	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator, sugar-binding family; **PDBTitle:** the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aurescens tc1.
20	c3kv1A_	Alignment		100.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor; **PDBTitle:** crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
21	c2o0mA_	Alignment	not modelled	100.0	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, sorc family; **PDBTitle:** the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
22	d2o0ma1	Alignment	not modelled	100.0	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
23	d2okga1	Alignment	not modelled	100.0	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
24	d3efba1	Alignment	not modelled	100.0	12	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
25	d2r5fa1	Alignment	not modelled	100.0	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
26	c3u7jA_	Alignment	not modelled	95.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
27	c3hheA_	Alignment	not modelled	93.3	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
28	c1uj6A_	Alignment	not modelled	91.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
						PDB header:isomerase

29	c1lk5C_	Alignment	not modelled	90.8	18	**Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
30	d1uj4a1	Alignment	not modelled	89.4	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
31	c2f8mB_	Alignment	not modelled	89.0	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** ribose 5-phosphate isomerase from plasmodium falciparum
32	c1xtzA_	Alignment	not modelled	89.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
33	c1m0sA_	Alignment	not modelled	87.8	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
34	c2pjmA_	Alignment	not modelled	87.6	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
35	c3kwmC_	Alignment	not modelled	86.3	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
36	c3l7oB_	Alignment	not modelled	85.9	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
37	c1lkzB_	Alignment	not modelled	85.7	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
38	d1lk5a1	Alignment	not modelled	83.5	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
39	d1m0sa1	Alignment	not modelled	80.7	30	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
40	d1o8bb1	Alignment	not modelled	78.1	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
41	c2i2aA_	Alignment	not modelled	59.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase 1; **PDBTitle:** crystal structure of lmnadk1 from listeria monocytogenes
42	d1ni5a1	Alignment	not modelled	59.2	8	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
43	d1wxia1	Alignment	not modelled	54.7	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
44	c1ni5A_	Alignment	not modelled	37.8	8	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
45	d1xnga1	Alignment	not modelled	36.8	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
46	c3p52B_	Alignment	not modelled	35.8	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
47	c3tqcB_	Alignment	not modelled	32.2	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pantothenate kinase; **PDBTitle:** structure of the pantothenate kinase (coaa) from coxiella burnetii
48	d1zuna1	Alignment	not modelled	31.2	7	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
49	c1zunA_	Alignment	not modelled	31.1	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2; **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
50	c2hfqA_	Alignment	not modelled	28.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** nmr structure of protein ne1680 from nitrosomonas europaea:2 northeast structural genomics consortium target net5
51	d2hfqa1	Alignment	not modelled	28.0	14	**Fold:**NE1680-like **Superfamily:**NE1680-like **Family:**NE1680-like
52	d1kqpa_	Alignment	not modelled	25.0	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
53	c3dpiA_	Alignment	not modelled	24.6	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nad+ synthetase; **PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei
54	c2gaaA_	Alignment	not modelled	24.1	23	**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.
55	c2c40B_	Alignment	not modelled	20.2	5	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inosine-uridine preferring nucleoside hydrolase family

						PDBTitle: crystal structure of inosine-uridine preferring nucleoside2 hydrolase from bacillus anthracis at 2.2a resolution
56	c3clhA_	Alignment	not modelled	19.7	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of 3-dehydroquinate synthase (dhqs)from2 helicobacter pylori
57	c1xahA_	Alignment	not modelled	19.2	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of staphlyococcus aureus 3-dehydroquinate2 synthase (dhqs) in complex with zn2+ and nad+
58	c1yqtA_	Alignment	not modelled	18.5	17	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
59	d1wy5a1	Alignment	not modelled	17.6	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
60	c3fiuD_	Alignment	not modelled	17.6	10	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
61	c3c7tB_	Alignment	not modelled	17.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ecdysteroid-phosphate phosphatase; **PDBTitle:** crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
62	d1xhoa_	Alignment	not modelled	16.6	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
63	d3bzka5	Alignment	not modelled	15.7	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
64	c3ozxA_	Alignment	not modelled	15.6	17	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
65	c3hjgB_	Alignment	not modelled	14.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-ribazole-5'-phosphate phosphatase **PDBTitle:** crystal structure of putative alpha-ribazole-5'-phosphate2 phosphatase cobc from vibrio parahaemolyticus
66	d1v43a3	Alignment	not modelled	14.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
67	c3q4gA_	Alignment	not modelled	14.2	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad synthetase from vibrio cholerae
68	d1pjqa3	Alignment	not modelled	13.9	19	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
69	c2p4sA_	Alignment	not modelled	13.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
70	c3ju3A_	Alignment	not modelled	13.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; **PDBTitle:** crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
71	d1ujna_	Alignment	not modelled	13.0	9	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Dehydroquinate synthase, DHQS
72	d1k6da_	Alignment	not modelled	12.3	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
73	c2gruB_	Alignment	not modelled	12.0	6	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-deoxy-scyllo-inosose synthase; **PDBTitle:** crystal structure of 2-deoxy-scyllo-inosose synthase2 complexed with carbaglucose-6-phosphate, nad+ and co2+
74	d2hhja1	Alignment	not modelled	11.5	10	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
75	c2ghiD_	Alignment	not modelled	11.5	22	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**transport protein; **PDBTitle:** crystal structure of plasmodium yoelii multidrug resistance2 protein 2
76	d3dhwc1	Alignment	not modelled	11.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
77	c3dqqB_	Alignment	not modelled	11.3	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative trna synthase; **PDBTitle:** the crystal structure of the putative trna synthase from salmonella2 typhimurium lt2
78	c3dl2A_	Alignment	not modelled	11.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquitin-conjugating enzyme e2 variant 3; **PDBTitle:** hexagonal structure of the ldh domain of human ubiquitin-2 conjugating enzyme e2-like isoform a
79	c3d4iD_	Alignment	not modelled	11.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sts-2 protein; **PDBTitle:** crystal structure of the 2h-phosphatase domain of sts-2
80	d1k6ma2	Alignment	not modelled	10.7	13	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
						PDB header:lyase

81	c3okfA_	Alignment	not modelled	10.6	14	**Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** 2.5 angstrom resolution crystal structure of 3-dehydroquinate synthase2 (arob) from vibrio cholerae
82	c3bk7A_	Alignment	not modelled	10.6	21	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
83	d1bifa2	Alignment	not modelled	10.4	13	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
84	d3d31a2	Alignment	not modelled	10.3	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
85	d1dbfa_	Alignment	not modelled	10.2	12	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
86	c2pcjB_	Alignment	not modelled	10.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipoprotein-releasing system atp-binding protein lold; **PDBTitle:** crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
87	d1g2912	Alignment	not modelled	9.9	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
88	c3fvqB_	Alignment	not modelled	9.9	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fe(3+) ions import atp-binding protein fbpc; **PDBTitle:** crystal structure of the nucleotide binding domain fbpc2 complexed with atp
89	c2i55C_	Alignment	not modelled	9.7	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphomannomutase; **PDBTitle:** complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
90	d1oxxk2	Alignment	not modelled	9.6	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
91	d2gnoa2	Alignment	not modelled	9.2	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
92	d1gpma1	Alignment	not modelled	9.2	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
93	c2e21A_	Alignment	not modelled	8.8	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
94	c3fzqA_	Alignment	not modelled	8.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
95	c1tcvB_	Alignment	not modelled	8.6	21	**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
96	c3c6kC_	Alignment	not modelled	8.5	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**spermine synthase; **PDBTitle:** crystal structure of human spermine synthase in complex2 with spermidine and 5-methylthioadenosine
97	d1sgwa_	Alignment	not modelled	8.5	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
98	c2cbzA_	Alignment	not modelled	8.2	14	**PDB header:**transport **Chain:** A: **PDB Molecule:**multidrug resistance-associated protein 1; **PDBTitle:** structure of the human multidrug resistance protein 12 nucleotide binding domain 1
99	d2g39a2	Alignment	not modelled	8.1	11	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like