Phyre2

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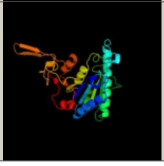
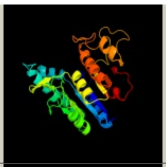
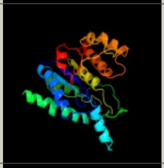
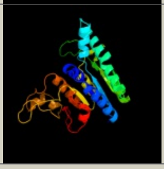
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j5tF_	Alignment		100.0	99	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** glutamate 5-kinase from escherichia coli complexed with2 glutamate
2	c2w21A_	Alignment		100.0	97	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** crystal structure of the aminoacid kinase domain of the2 glutamate 5 kinase of escherichia coli.
3	d2akoa1	Alignment		100.0	34	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
4	d1z9da1	Alignment		100.0	18	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
5	d1ybda1	Alignment		100.0	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
6	c2jjxC_	Alignment		100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridylate kinase; **PDBTitle:** the crystal structure of ump kinase from bacillus anthracis2 (ba1797)
7	d1e19a_	Alignment		100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase
8	c3nwyB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridylate kinase; **PDBTitle:** structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
9	c2rd5A_	Alignment		100.0	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**acetylglutamate kinase-like protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
10	c2v5hB_	Alignment		100.0	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** controlling the storage of nitrogen as arginine: the2 complex of pii and acetylglutamate kinase from3 synechococcus elongatus pcc 7942
11	c3ek5A_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridylate kinase; **PDBTitle:** unique gtp-binding pocket and allostery of ump kinase from a gram-2 negative phytopathogen bacterium

12	d2ap9a1	Alignment		100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
13	c2e9yA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbamate kinase; **PDBTitle:** crystal structure of project ape1968 from aeropyrum pernix k1
14	d2bnea1	Alignment		100.0	17	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
15	d2bufa1	Alignment		100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
16	d1b7ba_	Alignment		100.0	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase
17	c2ogxB_	Alignment		100.0	21	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**molybdenum storage protein subunit beta; **PDBTitle:** the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
18	c3kzfC_	Alignment		100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**carbamate kinase; **PDBTitle:** structure of giardia carbamate kinase
19	d2a1fa1	Alignment		100.0	18	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
20	d2btya1	Alignment		100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
21	d2brxa1	Alignment	not modelled	100.0	23	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
22	d1gs5a_	Alignment	not modelled	100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
23	c2egxA_	Alignment	not modelled	100.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acetylglutamate kinase; **PDBTitle:** crystal structure of the putative acetylglutamate kinase from thermus2 thermophilus
24	c2r98A_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetylglutamate synthase; **PDBTitle:** crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
25	c3ll9A_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** x-ray structures of isopentenyl phosphate kinase
26	c3ll5C_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**gamma-glutamyl kinase related protein; **PDBTitle:** crystal structure of t. acidophilum isopentenyl phosphate kinase2 product complex
27	c3d40A_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**foma protein; **PDBTitle:** crystal structure of fosfomycin resistance kinase foma from2 streptomyces wedmorensis complexed with diphosphate
28	c2va1A_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of ump kinase from ureaplasma parvum
						PDB header:metal binding protein

29	c2ogxA_	Alignment	not modelled	100.0	24	**Chain:** A: **PDB Molecule:**molybdenum storage protein subunit alpha; **PDBTitle:** the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
30	c2j4kC_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of uridylate kinase from sulfolobus2 solfataricus in complex with ump to 2.2 angstrom3 resolution
31	c3k4yB_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** crystal structure of isopentenyl phosphate kinase from m. jannaschii2 in complex with ipp
32	d2ij9a1	Alignment	not modelled	100.0	24	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
33	c3l86A_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** the crystal structure of smu.665 from streptococcus mutans ua159
34	c3l76B_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
35	d2hmfa1	Alignment	not modelled	100.0	26	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
36	c3ab4K_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** K: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
37	d2j0wa1	Alignment	not modelled	100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
38	c3c1nA_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartokinase; **PDBTitle:** crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
39	d2cdqa1	Alignment	not modelled	100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
40	c2j0wA_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lysine-sensitive aspartokinase 3; **PDBTitle:** crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
41	c2cdqB_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
42	d2cx1a1	Alignment	not modelled	99.5	33	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
43	c3zv0D_	Alignment	not modelled	99.4	17	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1p-cbf5p complex
44	d1iq8a3	Alignment	not modelled	99.4	12	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
45	d1q7ha1	Alignment	not modelled	99.3	31	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
46	d2as0a1	Alignment	not modelled	99.2	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
47	d1r3ea1	Alignment	not modelled	99.2	28	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
48	d2ey4a1	Alignment	not modelled	99.2	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
49	d2apoa1	Alignment	not modelled	99.2	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
50	c1q7hA_	Alignment	not modelled	99.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of a conserved pua domain protein from thermoplasma2 acidophilum
51	c3d79A_	Alignment	not modelled	99.0	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph0734; **PDBTitle:** crystal structure of hypothetical protein ph0734.1 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
52	c1zs7A_	Alignment	not modelled	98.9	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ape0525; **PDBTitle:** the structure of gene product ape0525 from aeropyrum pernix
53	c3uaiA_	Alignment	not modelled	98.4	20	**PDB header:**isomerase/chaperone **Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
54	c3r90E_	Alignment	not modelled	97.9	18	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**malignant t cell-amplified sequence 1; **PDBTitle:** crystal structure of malignant t cell-amplified sequence 1 protein

55	c2ey4A_	Alignment	not modelled	97.9	23	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
56	c1iq8B_	Alignment	not modelled	97.9	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**archaeosine trna-guanine transglycosylase; **PDBTitle:** crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii
57	c2apoA_	Alignment	not modelled	97.5	23	**PDB header:**isomerase/rna binding protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of the methanococcus jannaschii cbf52 nop10 complex
58	d1sqwa1	Alignment	not modelled	96.5	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
59	c2as0A_	Alignment	not modelled	95.1	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ph1915; **PDBTitle:** crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase
60	c1sqwA_	Alignment	not modelled	95.1	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**saccharomyces cerevisiae nip7p homolog; **PDBTitle:** crystal structure of kd93, a novel protein expressed in the2 human pro
61	d2q07a1	Alignment	not modelled	94.6	12	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
62	c3c0kB_	Alignment	not modelled	93.5	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0064 protein yccw; **PDBTitle:** crystal structure of a ribosomal rna methyltranferase
63	c3mn1B_	Alignment	not modelled	92.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable yrbi family phosphatase; **PDBTitle:** crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
64	c2q07A_	Alignment	not modelled	92.0	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af0587; **PDBTitle:** crystal structure of af0587, a protein of unknown function
65	d1k1ea_	Alignment	not modelled	90.8	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Probable phosphatase YrbI
66	c3e8mD_	Alignment	not modelled	89.7	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acylneuraminate cytidylyltransferase; **PDBTitle:** structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
67	c2b78A_	Alignment	not modelled	89.1	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein smu.776; **PDBTitle:** a putative sam-dependent methyltransferase from2 streptococcus mutans
68	c3mmzA_	Alignment	not modelled	86.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative had family hydrolase; **PDBTitle:** crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
69	c3n07B_	Alignment	not modelled	85.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; **PDBTitle:** structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae
70	c2p9jH_	Alignment	not modelled	84.8	18	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**hypothetical protein aq2171; **PDBTitle:** crystal structure of aq2171 from aquifex aeolicus
71	c1ze2B_	Alignment	not modelled	84.0	31	**PDB header:**lyase/rna **Chain:** B: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
72	c2r8zC_	Alignment	not modelled	83.7	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; **PDBTitle:** crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
73	c3dnpA_	Alignment	not modelled	81.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**stress response protein yhax; **PDBTitle:** crystal structure of stress response protein yhax from bacillus2 subtilis
74	c3niwA_	Alignment	not modelled	80.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
75	c3ewiB_	Alignment	not modelled	78.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**n-acylneuraminate cytidylyltransferase; **PDBTitle:** structural analysis of the c-terminal domain of murine cmp-2 sialic acid synthetase
76	c3n1uA_	Alignment	not modelled	77.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, had superfamily, subfamily iii a; **PDBTitle:** structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
77	c1xviA_	Alignment	not modelled	76.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative mannosyl-3-phosphoglycerate phosphatase; **PDBTitle:** crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
78	d1xvia_	Alignment	not modelled	76.4	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
79	c2gvhD_	Alignment	not modelled	72.8	24	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical conserved protein, gk1056;

79	c2qyhD_	Alignment	not modelled	72.8	24	**PDBTitle:** crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
80	d1s2oa1	Alignment	not modelled	72.1	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
81	d1xpja_	Alignment	not modelled	58.7	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
82	c3bq9A_	Alignment	not modelled	54.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
83	d1u02a_	Alignment	not modelled	54.4	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Trehalose-phosphatase
84	d2b78a1	Alignment	not modelled	54.0	16	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
85	d1sgva1	Alignment	not modelled	50.5	34	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
86	d2obba1	Alignment	not modelled	49.1	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
87	d2rbka1	Alignment	not modelled	45.3	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
88	d1ovma1	Alignment	not modelled	44.1	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
89	c2i55C_	Alignment	not modelled	43.9	25	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphomannomutase; **PDBTitle:** complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
90	c4a26B_	Alignment	not modelled	40.4	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
91	d1rlma_	Alignment	not modelled	39.5	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
92	d1vpea_	Alignment	not modelled	36.0	7	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
93	c1f5nA_	Alignment	not modelled	35.7	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**interferon-induced guanylate-binding protein 1; **PDBTitle:** human guanylate binding protein-1 in complex with the gtp2 analogue, gmppnp.
94	c2hx1D_	Alignment	not modelled	35.1	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted sugar phosphatases of the had **PDBTitle:** crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution
95	d2b30a1	Alignment	not modelled	33.8	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
96	c2p38A_	Alignment	not modelled	31.4	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**protein involved in ribosomal biogenesis; **PDBTitle:** crystal structure of pyrococcus abyssi protein homologue of2 saccharomyces cerevisiae nip7p
97	c1zmrA_	Alignment	not modelled	29.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of the e. coli phosphoglycerate kinase
98	c3pgvB_	Alignment	not modelled	29.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
99	d1g2ba_	Alignment	not modelled	28.7	13	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
100	c2dbkA_	Alignment	not modelled	27.9	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** solution structures of the sh3 domain of human crk-like2 protein
101	c3q3vA_	Alignment	not modelled	27.7	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
102	c2cunA_	Alignment	not modelled	26.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
103	c3gh1A_	Alignment	not modelled	25.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted nucleotide-binding protein; **PDBTitle:** crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae
104	d1phpa_	Alignment	not modelled	24.7	9	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase

105	d1v6sa_	Alignment	not modelled	24.2	17	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
106	d1wmaa1	Alignment	not modelled	24.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
107	d1f5na2	Alignment	not modelled	22.6	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
108	c3mpoD_	Alignment	not modelled	22.2	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
109	d1tksa_	Alignment	not modelled	22.1	13	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
110	d1nrwa_	Alignment	not modelled	21.9	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
111	d1vjda_	Alignment	not modelled	21.5	13	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
112	c1b0aA_	Alignment	not modelled	21.4	20	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
113	d16pka_	Alignment	not modelled	20.3	11	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
114	d1zq1a2	Alignment	not modelled	20.2	12	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase