Phyre2

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Description	RVBD2439c_(proB)_2737127_2738257
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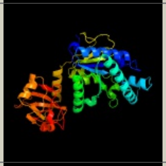
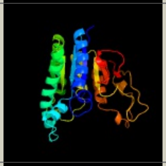
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j5tF_	Alignment		100.0	39	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** glutamate 5-kinase from escherichia coli complexed with2 glutamate
2	c4q1tD_	Alignment		100.0	41	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** crystal structure of a glutamate 5-kinase from burkholderia2 thailandensis
3	c2w21A_	Alignment		100.0	42	**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.
4	d2akoa1	Alignment		100.0	35	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
5	d1e19a_	Alignment		100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase
6	c2e9yA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbamate kinase; **PDBTitle:** crystal structure of project ape1968 from aeropyrum pernix k1
7	d1ybda1	Alignment		100.0	17	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
8	c4axsA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbamate kinase; **PDBTitle:** structure of carbamate kinase from mycoplasma penetrans
9	c3kzfC_	Alignment		100.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**carbamate kinase; **PDBTitle:** structure of giardia carbamate kinase
10	d1z9da1	Alignment		100.0	18	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
11	c2rd5A_	Alignment		100.0	18	**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

12	d1b7ba_	Alignment		100.0	23	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase
13	c2jjxC_	Alignment		100.0	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridylate kinase; **PDBTitle:** the crystal structure of ump kinase from bacillus anthracis (ba1797)
14	c2v5hB_	Alignment		100.0	16	**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
15	d2ap9a1	Alignment		100.0	23	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
16	d2bufa1	Alignment		100.0	23	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
17	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
18	c3ek5A_	Alignment		100.0	26	**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
19	d2btya1	Alignment		100.0	20	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
20	d2bnea1	Alignment		100.0	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
21	d1gs5a_	Alignment	not modelled	100.0	22	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
22	d2brxa1	Alignment	not modelled	100.0	20	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
23	c2r98A_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetylglutamate synthase; **PDBTitle:** crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
24	d2a1fa1	Alignment	not modelled	100.0	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
25	c2ogxB_	Alignment	not modelled	100.0	18	**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)
26	c3d40A_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**foma protein; **PDBTitle:** crystal structure of fosfomycin resistance kinase foma from2 streptomyces wedmorensis complexed with diphosphate
27	c4a7xF_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** F: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of uridylate kinase from helicobacter pylori
28	c2egxA_	Alignment	not modelled	100.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acetylglutamate kinase; **PDBTitle:** crystal structure of the putative acetylglutamate kinase from thermus2 thermophilus
						PDB header:transferase

29	c3zzgC_	Alignment	not modelled	100.0	13	**Chain:** C: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** crystal structure of the amino acid kinase domain from saccharomyces2 cerevisiae acetylglutamate kinase without ligands
30	c3ll9A_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** x-ray structures of isopentenyl phosphate kinase
31	c3ll5C_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**gamma-glutamyl kinase related protein; **PDBTitle:** crystal structure of t. acidophilum isopentenyl phosphate kinase2 product complex
32	c3l86A_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** the crystal structure of smu.665 from streptococcus mutans ua159
33	c5yeiG_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** G: **PDB Molecule:**aspartokinase; **PDBTitle:** mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
34	c4f6tA_	Alignment	not modelled	100.0	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**molybdenum storage protein subunit alpha; **PDBTitle:** the crystal structure of the molybdenum storage protein (mosto) from2 azotobacter vinelandii loaded with various polyoxometalates
35	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
36	c2ogxA_	Alignment	not modelled	100.0	18	**PDB header:**metal binding protein **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)
37	c2j4kC_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of uridylate kinase from sulfolobus solfataricus in2 complex with ump to 2.2 angstrom resolution
38	d2ij9a1	Alignment	not modelled	100.0	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
39	d2hmfa1	Alignment	not modelled	100.0	25	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
40	c3l76B_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
41	c3k4yB_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** crystal structure of isopentenyl phosphate kinase from m. jannaschii2 in complex with ipp
42	c3ab4K_	Alignment	not modelled	100.0	23	**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
43	d2j0wa1	Alignment	not modelled	100.0	18	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
44	c3c1nA_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartokinase; **PDBTitle:** crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
45	d2cdqa1	Alignment	not modelled	100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
46	c3tviD_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of clostridium acetobutylicum aspartate kinase2 (caak): an important allosteric enzyme for industrial amino acids3 production
47	c2j0wA_	Alignment	not modelled	100.0	23	**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)
48	c2cdqB_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
49	c4ab7C_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**protein arg5,6, mitochondrial; **PDBTitle:** crystal structure of a tetrameric acetylglutamate kinase from2 saccharomyces cerevisiae complexed with its substrate n-3 acetylglutamate
50	c3s7yX_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** X: **PDB Molecule:**n-acetylglutamate kinase / n-acetylglutamate synthase; **PDBTitle:** crystal structure of mmnags in space group p3121 at 4.3 a resolution
51	c3s6kA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** crystal structure of xcnags
52	c3zv0D_	Alignment	not modelled	99.5	16	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1p-cbf5p complex
53	d2cx1a1	Alignment	not modelled	99.5	32	**Fold:**PUA domain-like **Superfamily:**PUA domain-like

						Family:PUA domain
54	d1iq8a3	Alignment	not modelled	99.4	12	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
55	d1q7ha1	Alignment	not modelled	99.4	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
56	d1r3ea1	Alignment	not modelled	99.3	14	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
57	d2ey4a1	Alignment	not modelled	99.3	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
58	d2apoa1	Alignment	not modelled	99.2	16	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
59	d2as0a1	Alignment	not modelled	99.2	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
60	c1q7hA_	Alignment	not modelled	99.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of a conserved pua domain protein from thermoplasma2 acidophilum
61	c3d79A_	Alignment	not modelled	99.1	16	**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
62	c1zs7A_	Alignment	not modelled	99.0	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ape0525; **PDBTitle:** the structure of gene product ape0525 from aeropyrum pernix
63	c3uaiA_	Alignment	not modelled	98.7	16	**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
64	c6em5l_	Alignment	not modelled	98.4	17	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**60s ribosomal protein l13-a; **PDBTitle:** state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
65	c3r90E_	Alignment	not modelled	98.3	16	**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
66	c1iq8B_	Alignment	not modelled	98.3	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**archaeosine trna-guanine transglycosylase; **PDBTitle:** crystal structure of archaeosine trna-guanine transglycosylase from2 pyrococcus horikoshii
67	c2ey4A_	Alignment	not modelled	98.2	25	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
68	c5oa30_	Alignment	not modelled	97.9	26	**PDB header:**translation **Chain:** 0: **PDB Molecule:**eukaryotic translation initiation factor 2d; **PDBTitle:** human 40s-eif2d-re-initiation complex
69	c2apoA_	Alignment	not modelled	97.8	19	**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
70	d1sqwa1	Alignment	not modelled	97.0	13	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
71	d2q07a1	Alignment	not modelled	96.6	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
72	c1sqwA_	Alignment	not modelled	96.3	14	**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
73	c2q07A_	Alignment	not modelled	96.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af0587; **PDBTitle:** crystal structure of af0587, a protein of unknown function
74	c2as0A_	Alignment	not modelled	96.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ph1915; **PDBTitle:** crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase
75	c3c0kB_	Alignment	not modelled	94.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0064 protein yccw; **PDBTitle:** crystal structure of a ribosomal rna methyltranferase
76	c3vseA_	Alignment	not modelled	92.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of methyltransferase
77	c2b78A_	Alignment	not modelled	92.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein smu.776; **PDBTitle:** a putative sam-dependent methyltransferase from streptococcus mutans
78	c1ze2B_	Alignment	not modelled	91.0	10	**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
79	c5wwrA_	Alignment	not modelled	82.6	21	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**putative methyltransferase nsun6; **PDBTitle:** crystal structure of human nsun6/trna/sfg

80	c4dmgA_	Alignment	not modelled	75.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1493; **PDBTitle:** thermus thermophilus m5c1942 methyltransferase rlmo
81	c2p38A_	Alignment	not modelled	67.9	8	**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
82	c2hx1D_	Alignment	not modelled	64.9	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted sugar phosphatases of the had superfamily; **PDBTitle:** crystal structure of possible sugar phosphatase, had superfamily2 (zp_00311070.1) from cytophaga hutchinsonii atcc 33406 at 2.10 a3 resolution
83	d2b78a1	Alignment	not modelled	64.4	14	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
84	d1xpja_	Alignment	not modelled	64.1	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
85	c4gxtA_	Alignment	not modelled	62.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**a conserved functionally unknown protein; **PDBTitle:** the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548
86	c3zupB_	Alignment	not modelled	60.2	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mannosyl-3-phosphoglycerate phosphatase; **PDBTitle:** the 3-dimensional structure of mpgp from thermus2 thermophilus hb27, in complex with the alpha-3 mannosylglycerate and orthophosphate reaction products.
87	c6gfmA_	Alignment	not modelled	59.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrimidine/purine nucleotide 5'-monophosphate nucleosidase; **PDBTitle:** crystal structure of the escherichia coli nucleosidase ppnn (pppgpp-2 form)
88	d1ovma1	Alignment	not modelled	58.8	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
89	c5gvxA_	Alignment	not modelled	57.4	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trehalose-phosphate phosphatase; **PDBTitle:** structural insight into dephosphorylation by trehalose 6-phosphate2 phosphatase (otsb2) from mycobacterium tuberculosis
90	d1s2oa1	Alignment	not modelled	56.4	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
91	c4m4xA_	Alignment	not modelled	51.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**aryl hydrocarbon receptor; **PDBTitle:** structure and dimerization properties of the aryl hydrocarbon receptor2 (ahr) pas-a domain
92	c3bq9A_	Alignment	not modelled	50.2	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
93	d1vpea_	Alignment	not modelled	46.9	13	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
94	d1u02a_	Alignment	not modelled	45.5	8	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Trehalose-phosphatase
95	d1sgva1	Alignment	not modelled	44.1	32	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
96	c3zlbA_	Alignment	not modelled	44.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from streptococcus2 pneumoniae
97	c2p9jH_	Alignment	not modelled	43.0	15	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**hypothetical protein aq2171; **PDBTitle:** crystal structure of aq2171 from aquifex aeolicus
98	c1zmrA_	Alignment	not modelled	40.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of the e. coli phosphoglycerate kinase
99	c5dxlA_	Alignment	not modelled	40.3	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trehalose-6-phosphate phosphatase; **PDBTitle:** structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
100	c5zvdB_	Alignment	not modelled	40.0	28	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**389aa long hypothetical nucleolar protein; **PDBTitle:** the crystal structure of nsun6 from pyrococcus horikoshii
101	c4ehjA_	Alignment	not modelled	39.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** an x-ray structure of a putative phosphogylcerate kinase from2 francisella tularensis subsp. tularensis schu s4
102	d2obba1	Alignment	not modelled	39.0	9	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
103	c4ng4B_	Alignment	not modelled	38.6	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** structure of phosphoglycerate kinase (cbu_1782) from coxiella burnetii
104	c4he5A_	Alignment	not modelled	38.5	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**peptidase family u32; **PDBTitle:** crystal structure of the selenomethionine variant of the c-terminal2 domain of geobacillus thermoleovorans putative u32

						peptidase
105	c2cunA_	Alignment	not modelled	38.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
106	c3q3vA_	Alignment	not modelled	37.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
107	d1xvia_	Alignment	not modelled	37.2	30	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
108	c1xviA_	Alignment	not modelled	37.2	30	**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
109	c5bt8D_	Alignment	not modelled	37.1	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** x-ray crystal structure of phosphoglycerate kinase from acinetobacter2 baumannii
110	c3zg6A_	Alignment	not modelled	37.0	19	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**nad-dependent protein deacetylase sirtuin-6; **PDBTitle:** the novel de-long chain fatty acid function of human sirt6
111	d1v6sa_	Alignment	not modelled	36.9	15	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
112	d1phpa_	Alignment	not modelled	36.8	13	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
113	d1k1ea_	Alignment	not modelled	36.0	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Probable phosphatase YrbI
114	c4dg5A_	Alignment	not modelled	35.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of staphylococcal phosphoglycerate kinase
115	c3mmzA_	Alignment	not modelled	34.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative had family hydrolase; **PDBTitle:** crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
116	c2vlgD_	Alignment	not modelled	34.3	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sporulation kinase a; **PDBTitle:** kina pas-a domain, homodimer
117	d1rq2a1	Alignment	not modelled	34.0	14	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
118	c2zakB_	Alignment	not modelled	33.7	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-asparaginase precursor; **PDBTitle:** orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
119	d2zdra2	Alignment	not modelled	33.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
120	d2rbka1	Alignment	not modelled	33.1	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof