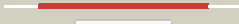



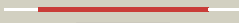

















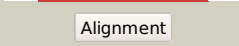

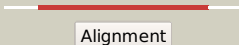

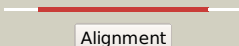


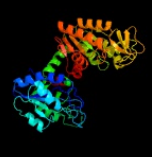
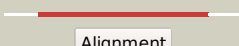

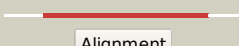

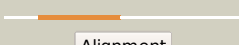




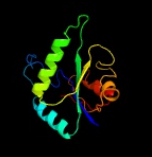


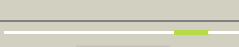
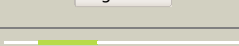
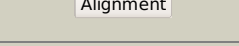
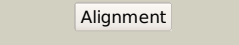

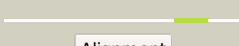


# Phyre2

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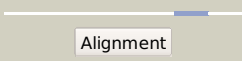
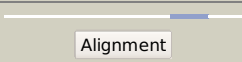


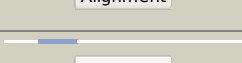
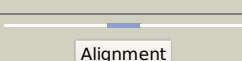
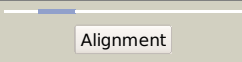
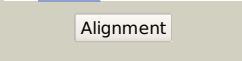
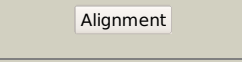
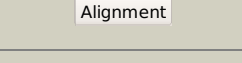
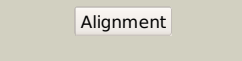
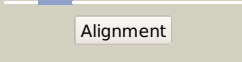
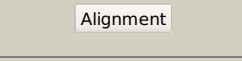
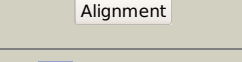
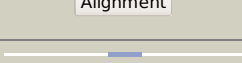
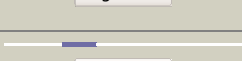
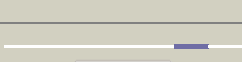

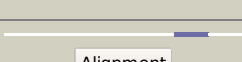
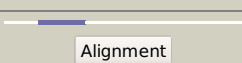

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1phpa_</a>	 Alignment		100.0	44	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
2	<a href="#">d1vpea_</a>	 Alignment		100.0	47	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
3	<a href="#">c4dg5A_</a>	 Alignment		100.0	42	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> crystal structure of staphylococcal phosphoglycerate kinase
4	<a href="#">c3zlbA_</a>	 Alignment		100.0	44	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> crystal structure of phosphoglycerate kinase from streptococcus2 pneumoniae
5	<a href="#">c3q3vA_</a>	 Alignment		100.0	42	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
6	<a href="#">d16pka_</a>	 Alignment		100.0	41	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
7	<a href="#">d1v6sa_</a>	 Alignment		100.0	49	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
8	<a href="#">d1vjda_</a>	 Alignment		100.0	39	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
9	<a href="#">d1qpqa_</a>	 Alignment		100.0	38	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
10	<a href="#">c5bt8D_</a>	 Alignment		100.0	42	<b>PDB header:</b> transferase <b>Chain: D: PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> x-ray crystal structure of phosphoglycerate kinase from acinetobacter2 baumannii
11	<a href="#">d1ltka_</a>	 Alignment		100.0	37	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase

12	<a href="#">c2cunA</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
13	<a href="#">c4ng4B</a>	 Alignment		100.0	39	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> structure of phosphoglycerate kinase (cbu_1782) from coxiella burnetii
14	<a href="#">c1zmrA</a>	 Alignment		100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> crystal structure of the e. coli phosphoglycerate kinase
15	<a href="#">d1hdia</a>	 Alignment		100.0	38	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
16	<a href="#">c4ehjA</a>	 Alignment		100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> an x-ray structure of a putative phosphoglycerate kinase from2 francisella tularensis subsp. tularensis schu s4
17	<a href="#">d1fw8a</a>	 Alignment		100.0	38	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
18	<a href="#">c3zvmA</a>	 Alignment		89.1	22	<b>PDB header:</b> hydrolase/transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional polynucleotide phosphatase/kinase; <b>PDBTitle:</b> the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
19	<a href="#">d1vj5a1</a>	 Alignment		88.5	21	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> phosphatase domain of polynucleotide kinase
20	<a href="#">c1vj5B</a>	 Alignment		87.3	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5' polynucleotide kinase-3' phosphatase catalytic domain; <b>PDBTitle:</b> molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
21	<a href="#">c3rfoA</a>	 Alignment	not modelled	72.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> crystal structure of methionyl-trna formyltransferase from bacillus2 anthracis
22	<a href="#">c3ek5A</a>	 Alignment	not modelled	67.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uridylyate kinase; <b>PDBTitle:</b> unique gtp-binding pocket and allosterism of ump kinase from a gram-2 negative phytopathogen bacterium
23	<a href="#">d2pjuA1</a>	 Alignment	not modelled	66.5	14	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> PrpR receptor domain-like <b>Family:</b> PrpR receptor domain-like
24	<a href="#">c3uagA</a>	 Alignment	not modelled	62.8	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (udp-n-acetylmuramoyl-l-alanine:d- <b>PDBTitle:</b> udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
25	<a href="#">c3kc2A</a>	 Alignment	not modelled	61.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ykr070w; <b>PDBTitle:</b> crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
26	<a href="#">d1ybdA1</a>	 Alignment	not modelled	61.8	10	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
27	<a href="#">c2pjuD</a>	 Alignment	not modelled	61.6	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> propionate catabolism operon regulatory protein; <b>PDBTitle:</b> crystal structure of propionate catabolism operon regulatory protein2 prpr
28	<a href="#">c5uaiA</a>	 Alignment	not modelled	54.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> crystal structure of methionyl-trna formyltransferase from pseudomonas2 aeruginosa

29	<a href="#">c5ajtA</a>	Alignment	not modelled	51.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribohydrolase lonely guy; <b>PDBTitle:</b> crystal structure of ligand-free phosphoribohydrolase lonely guy from2 claviceps purpurea
30	<a href="#">c3obaA</a>	Alignment	not modelled	50.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> structure of the beta-galactosidase from kluyveromyces lactis
31	<a href="#">c2j5tF</a>	Alignment	not modelled	50.3	13	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate 5-kinase; <b>PDBTitle:</b> glutamate 5-kinase from escherichia coli complexed with2 glutamate
32	<a href="#">c2wdfA</a>	Alignment	not modelled	48.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfur oxidation protein soxb; <b>PDBTitle:</b> termus thermophilus sulfate thiohydrolase soxb
33	<a href="#">c4zexA</a>	Alignment	not modelled	43.8	28	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pfhad1; <b>PDBTitle:</b> crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
34	<a href="#">c4jyrG</a>	Alignment	not modelled	41.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> d,d-heptose 1,7-bisphosphate phosphatase; <b>PDBTitle:</b> crystal structure of d,d-heptose 1,7-bisphosphate phosphatase from2 burkholderia thailandensis
35	<a href="#">d2b30a1</a>	Alignment	not modelled	41.4	22	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
36	<a href="#">d2a1fa1</a>	Alignment	not modelled	39.2	22	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
37	<a href="#">d1kfa1</a>	Alignment	not modelled	38.1	15	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
38	<a href="#">c5ykaA</a>	Alignment	not modelled	37.0	26	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein kdoo; <b>PDBTitle:</b> crystal structure of the kdo hydroxylase kdoo, a non-heme fe(ii)2 alphaketoglutarate dependent dioxygenase in complex with cobalt(ii)
39	<a href="#">c3n5IA</a>	Alignment	not modelled	34.3	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> binding protein component of abc phosphonate transporter; <b>PDBTitle:</b> crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
40	<a href="#">c4zkjA</a>	Alignment	not modelled	33.5	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated protein cas1; <b>PDBTitle:</b> crystal structure of crispr-associated protein
41	<a href="#">c2yybA</a>	Alignment	not modelled	33.3	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha1606; <b>PDBTitle:</b> crystal structure of ttha1606 from thermus thermophilus hb8
42	<a href="#">c2i55C</a>	Alignment	not modelled	33.3	26	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphomannomutase; <b>PDBTitle:</b> complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
43	<a href="#">c2va1A</a>	Alignment	not modelled	33.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uridylyate kinase; <b>PDBTitle:</b> crystal structure of ump kinase from ureaplasma parvum
44	<a href="#">d1rkqa</a>	Alignment	not modelled	31.6	33	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
45	<a href="#">c4rapD</a>	Alignment	not modelled	30.1	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycosyltransferase tbc; <b>PDBTitle:</b> crystal structure of bacterial iron-containing dodecameric2 glycosyltransferase tbc from enterotoxigenic e.coli h10407
46	<a href="#">d1dkua2</a>	Alignment	not modelled	29.9	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
47	<a href="#">d2btya1</a>	Alignment	not modelled	29.2	10	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> N-acetyl-l-glutamate kinase
48	<a href="#">d1z9da1</a>	Alignment	not modelled	28.1	14	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
49	<a href="#">c5xvnL</a>	Alignment	not modelled	28.0	18	<b>PDB header:</b> immune system <b>Chain:</b> L: <b>PDB Molecule:</b> crispr-associated endonuclease cas1; <b>PDBTitle:</b> e. far cas1-cas2/prespacer binary complex
50	<a href="#">d2ji7a1</a>	Alignment	not modelled	27.8	18	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
51	<a href="#">d2z1aa2</a>	Alignment	not modelled	27.4	32	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
52	<a href="#">d1mv8a3</a>	Alignment	not modelled	27.3	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> UDP-glucose/GDP-mannose dehydrogenase C-terminal domain <b>Family:</b> UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
53	<a href="#">c3r4cA</a>	Alignment	not modelled	27.2	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily;

						analysis of bt1666 from3 bacteroides thetaiotaomicron
54	<a href="#">c3p7iA_</a>	Alignment	not modelled	26.7	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phnd, subunit of alkylphosphonate abc transporter; <b>PDBTitle:</b> crystal structure of escherichia coli phnd in complex with 2-2 aminoethyl phosphonate
55	<a href="#">c4qjbB_</a>	Alignment	not modelled	26.4	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
56	<a href="#">d1wzca1</a>	Alignment	not modelled	26.1	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
57	<a href="#">c2e9yA_</a>	Alignment	not modelled	25.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamate kinase; <b>PDBTitle:</b> crystal structure of project ape1968 from aeropyrum pernix k1
58	<a href="#">c2ohoA_</a>	Alignment	not modelled	25.6	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> structural basis for glutamate racemase inhibitor
59	<a href="#">c6hz4B_</a>	Alignment	not modelled	25.3	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> 5-methylcytosine-specific restriction enzyme b; <b>PDBTitle:</b> structure of mcrcb without dna binding domains (one half of the full2 complex)
60	<a href="#">d1sm4a2</a>	Alignment	not modelled	25.2	4	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
61	<a href="#">d1vhna_</a>	Alignment	not modelled	25.1	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
62	<a href="#">c1pkIB_</a>	Alignment	not modelled	25.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (pyruvate kinase); <b>PDBTitle:</b> the structure of leishmania pyruvate kinase
63	<a href="#">d1xpja_</a>	Alignment	not modelled	24.9	8	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Hypothetical protein VC0232
64	<a href="#">c4a7xF_</a>	Alignment	not modelled	24.7	20	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> uridylate kinase; <b>PDBTitle:</b> crystal structure of uridylate kinase from helicobacter pylori
65	<a href="#">c2kxhB_</a>	Alignment	not modelled	24.6	33	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> peptide of far upstream element-binding protein 1; <b>PDBTitle:</b> solution structure of the first two rrm domains of fir in the complex2 with fbp nbx peptide
66	<a href="#">d1c8ba_</a>	Alignment	not modelled	24.6	19	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> HybD-like <b>Family:</b> Germination protease
67	<a href="#">c2iz6A_</a>	Alignment	not modelled	24.2	23	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum cofactor carrier protein; <b>PDBTitle:</b> structure of the chlamydomonas reinhardtii moco carrier2 protein
68	<a href="#">c3prjB_</a>	Alignment	not modelled	24.1	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
69	<a href="#">c5fclD_</a>	Alignment	not modelled	23.8	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> crisp-associated endonuclease cas1; <b>PDBTitle:</b> crystal structure of cas1 from pectobacterium atrosepticum
70	<a href="#">d1krha2</a>	Alignment	not modelled	23.7	23	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Aromatic dioxygenase reductase-like
71	<a href="#">d1vh0a_</a>	Alignment	not modelled	23.4	17	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YbeA-like
72	<a href="#">c3nkdB_</a>	Alignment	not modelled	23.4	15	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> crisp-associated protein cas1; <b>PDBTitle:</b> structure of crisp-associated protein cas1 from escherichia coli str.2 k-12
73	<a href="#">d2bmwa2</a>	Alignment	not modelled	23.1	7	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
74	<a href="#">d2obba1</a>	Alignment	not modelled	22.9	23	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> BT0820-like
75	<a href="#">c5htxA_</a>	Alignment	not modelled	22.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative xylulose kinase; <b>PDBTitle:</b> putative sugar kinases from arabidopsis thaliana in complex with adp
76	<a href="#">d1h5ya_</a>	Alignment	not modelled	22.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
77	<a href="#">c3zupB_</a>	Alignment	not modelled	22.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mannosyl-3-phosphoglycerate phosphatase; <b>PDBTitle:</b> the 3-dimensional structure of mpgp from thermus2 thermophilus hb27, in complex with the alpha-3 mannosylglycerate and orthophosphate reaction products.
78	<a href="#">c5dmnA_</a>	Alignment	not modelled	22.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homocysteine s-methyltransferase; <b>PDBTitle:</b> crystal structure of the homocysteine methyltransferase mmum from2 escherichia coli, apo form

79	<a href="#">c5zbfA</a>	 Alignment	not modelled	22.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytokinin riboside 5'-monophosphate <b>PDBTitle:</b> crystal structure of type-i log from pseudomonas aeruginosa pao1
80	<a href="#">c5ynfA</a>	 Alignment	not modelled	22.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> arginase; <b>PDBTitle:</b> crystal structure of a cold-adapted arginase from psychrophilic yeast,2 glaciozyma antarctica
81	<a href="#">c3jyfB</a>	 Alignment	not modelled	22.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- <b>PDBTitle:</b> the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
82	<a href="#">c4edfC</a>	 Alignment	not modelled	22.3	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> dimeric hugdh, k94e
83	<a href="#">d2b8ea1</a>	 Alignment	not modelled	22.3	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
84	<a href="#">c1zdrB</a>	 Alignment	not modelled	22.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrofolate reductase; <b>PDBTitle:</b> dhfr from bacillus stearothermophilus
85	<a href="#">c2ek8A</a>	 Alignment	not modelled	22.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase; <b>PDBTitle:</b> aminopeptidase from aneurinibacillus sp. strain am-1
86	<a href="#">c3t07D</a>	 Alignment	not modelled	21.9	13	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
87	<a href="#">c4pu6A</a>	 Alignment	not modelled	21.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-asparaginase alpha subunit; <b>PDBTitle:</b> crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with k+ cations
88	<a href="#">c2vx6A</a>	 Alignment	not modelled	21.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellvibrio japonicus mannanase cjman26c; <b>PDBTitle:</b> cellvibrio japonicus mannanase cjman26c gal1man4-bound form
89	<a href="#">c3dg8B</a>	 Alignment	not modelled	21.3	29	<b>PDB header:</b> oxidoreductase, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional dihydrofolate reductase-thymidylate synthase; <b>PDBTitle:</b> quadruple mutant (n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase (pdfhfr-ts) complexed3 with rjf670, nadph, and dump
90	<a href="#">c6igmH</a>	 Alignment	not modelled	21.0	19	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> helicase srcap; <b>PDBTitle:</b> cryo-em structure of human srcap complex
91	<a href="#">c4f4fB</a>	 Alignment	not modelled	20.9	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> x-ray crystal structure of plp bound threonine synthase from brucella2 melitensis
92	<a href="#">c3dnpA</a>	 Alignment	not modelled	20.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> stress response protein yhax; <b>PDBTitle:</b> crystal structure of stress response protein yhax from bacillus2 subtilis
93	<a href="#">c3gveB</a>	 Alignment	not modelled	20.2	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> yfkn protein; <b>PDBTitle:</b> crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
94	<a href="#">d1gawa2</a>	 Alignment	not modelled	20.2	3	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
95	<a href="#">c3g7uA</a>	 Alignment	not modelled	19.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosine-specific methyltransferase; <b>PDBTitle:</b> crystal structure of putative dna modification methyltransferase2 encoded within prophage cp-933r (e.coli)
96	<a href="#">d1vb3a1</a>	 Alignment	not modelled	19.7	29	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
97	<a href="#">d1p3da2</a>	 Alignment	not modelled	19.7	10	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
98	<a href="#">c5wqlC</a>	 Alignment	not modelled	19.6	24	<b>PDB header:</b> protein binding/signaling protein/hydrol <b>Chain:</b> C: <b>PDB Molecule:</b> tail-specific protease; <b>PDBTitle:</b> structure of a pdz-protease bound to a substrate-binding adaptor
99	<a href="#">d1tr9a</a>	 Alignment	not modelled	19.6	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> NagZ-like