
























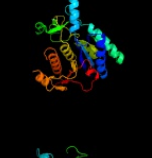
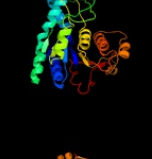



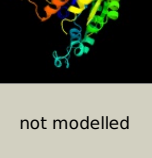


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1654_(argB)_1867849_1868733
Date	Fri Aug 2 13:30:25 BST 2019
Unique Job ID	58291b570d138b3d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2ap9a1</a>	 Alignment		100.0	97	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> N-acetyl-l-glutamate kinase
2	<a href="#">c2r98A_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetylglutamate synthase; <b>PDBTitle:</b> crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
3	<a href="#">d2bufa1</a>	 Alignment		100.0	48	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> N-acetyl-l-glutamate kinase
4	<a href="#">c2rd5A_</a>	 Alignment		100.0	42	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> acetylglutamate kinase-like protein; <b>PDBTitle:</b> structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
5	<a href="#">c2v5hB_</a>	 Alignment		100.0	45	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> acetylglutamate kinase; <b>PDBTitle:</b> controlling the storage of nitrogen as arginine: the2 complex of pii and acetylglutamate kinase from3 synechococcus elongatus pcc 7942
6	<a href="#">d2btya1</a>	 Alignment		100.0	42	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> N-acetyl-l-glutamate kinase
7	<a href="#">c3zqzC_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetylglutamate kinase; <b>PDBTitle:</b> crystal structure of the amino acid kinase domain from saccharomyces2 cerevisiae acetylglutamate kinase without ligands
8	<a href="#">c4ab7C_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> protein arg5,6, mitochondrial; <b>PDBTitle:</b> crystal structure of a tetrameric acetylglutamate kinase from2 saccharomyces cerevisiae complexed with its substrate n-3 acetylglutamate
9	<a href="#">c3s7yX_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> n-acetylglutamate kinase / n-acetylglutamate synthase; <b>PDBTitle:</b> crystal structure of mmnags in space group p3121 at 4.3 a resolution
10	<a href="#">d1gs5a_</a>	 Alignment		100.0	26	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> N-acetyl-l-glutamate kinase
11	<a href="#">c3s6kA_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylglutamate kinase; <b>PDBTitle:</b> crystal structure of xcngas

12	<a href="#">c2egxA</a>	Alignment		100.0	34	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative acetylglutamate kinase; <b>PDBTitle:</b> crystal structure of the putative acetylglutamate kinase from thermus2 thermophilus
13	<a href="#">c3l86A</a>	Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> acetylglutamate kinase; <b>PDBTitle:</b> the crystal structure of smu.665 from streptococcus mutans ua159
14	<a href="#">d1e19a</a>	Alignment		100.0	23	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> Carbamate kinase
15	<a href="#">d1b7ba</a>	Alignment		100.0	22	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> Carbamate kinase
16	<a href="#">c4axsA</a>	Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> carbamate kinase; <b>PDBTitle:</b> structure of carbamate kinase from mycoplasma penetrans
17	<a href="#">c2e9yA</a>	Alignment		100.0	21	<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
18	<a href="#">c3kzfC</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> carbamate kinase; <b>PDBTitle:</b> structure of giardia carbamate kinase
19	<a href="#">c2j5tF</a>	Alignment		100.0	21	<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
20	<a href="#">c2w21A</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate 5-kinase; <b>PDBTitle:</b> crystal structure of the aminoacid kinase domain of the2 glutamate 5 kinase of escherichia coli.
21	<a href="#">c5yeiG</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> G; <b>PDB Molecule:</b> aspartokinase; <b>PDBTitle:</b> mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
22	<a href="#">d2hmfA1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
23	<a href="#">d2bnea1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
24	<a href="#">d1ybda1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
25	<a href="#">c3ek5A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> uridylyate kinase; <b>PDBTitle:</b> unique gtp-binding pocket and allostery of ump kinase from a gram-2 negative phytopathogen bacterium
26	<a href="#">c3l19A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> isopentenyl phosphate kinase; <b>PDBTitle:</b> x-ray structures of isopentenyl phosphate kinase
27	<a href="#">d2akoa1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
28	<a href="#">c4a7xF</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> uridylyate kinase; <b>PDBTitle:</b> crystal structure of uridylyate kinase from helicobacter pylori
29	<a href="#">c3nwyB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> uridylyate kinase;

29	<a href="#">c3lwyB_</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
30	<a href="#">d1z9da1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
31	<a href="#">c3l5C_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> gamma-glutamyl kinase related protein; <b>PDBTitle:</b> crystal structure of t. acidophilum isopentenyl phosphate kinase2 product complex
32	<a href="#">c2jxcC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> uridylyate kinase; <b>PDBTitle:</b> the crystal structure of ump kinase from bacillus anthracis (ba1797)
33	<a href="#">c3d40A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> foma protein; <b>PDBTitle:</b> crystal structure of fosfomycin resistance kinase foma from2 streptomyces wedmorensis complexed with diphosphate
34	<a href="#">c3k4yB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> isopentenyl phosphate kinase; <b>PDBTitle:</b> crystal structure of isopentenyl phosphate kinase from m. jannaschii2 in complex with ipp
35	<a href="#">c3l76B_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartokinase; <b>PDBTitle:</b> crystal structure of aspartate kinase from synechocystis
36	<a href="#">c4q1tD_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glutamate 5-kinase; <b>PDBTitle:</b> crystal structure of a glutamate 5-kinase from burkholderia2 thailandensis
37	<a href="#">c3c1nA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aspartokinase; <b>PDBTitle:</b> crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
38	<a href="#">d2a1fa1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
39	<a href="#">d2j0wa1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
40	<a href="#">c2va1A_</a>	Alignment	not modelled	100.0	16	<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
41	<a href="#">c2ogxA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum storage protein subunit alpha; <b>PDBTitle:</b> the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
42	<a href="#">d2cdqa1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
43	<a href="#">c2ogxB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> molybdenum storage protein subunit beta; <b>PDBTitle:</b> the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
44	<a href="#">c4f6tA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum storage protein subunit alpha; <b>PDBTitle:</b> the crystal structure of the molybdenum storage protein (mosto) from2 azotobacter vinelandii loaded with various polyoxometalates
45	<a href="#">c3ab4K_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> K: <b>PDB Molecule:</b> aspartokinase; <b>PDBTitle:</b> crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
46	<a href="#">c3tviD_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> aspartokinase; <b>PDBTitle:</b> crystal structure of clostridium acetobutylicum aspartate kinase2 (caak): an important allosteric enzyme for industrial amino acids3 production
47	<a href="#">d2brxa1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
48	<a href="#">c2j4kC_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> uridylyate kinase; <b>PDBTitle:</b> crystal structure of uridylyate kinase from sulfolobus solfataricus in2 complex with ump to 2.2 angstrom resolution
49	<a href="#">c2cdqB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartokinase; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
50	<a href="#">d2j9a1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like
51	<a href="#">c2j0wA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-sensitive aspartokinase 3; <b>PDBTitle:</b> crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
52	<a href="#">c3bq9A_</a>	Alignment	not modelled	64.1	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted rossmann fold nucleotide-binding domain- <b>PDBTitle:</b> crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
53	<a href="#">d1xpja_</a>	Alignment	not modelled	62.8	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Hypothetical protein VC0232

54	<a href="#">d1qwga_</a>	Alignment	not modelled	60.9	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (2r)-phospho-3-sulfolactate synthase ComA <b>Family:</b> (2r)-phospho-3-sulfolactate synthase ComA
55	<a href="#">c3menC_</a>	Alignment	not modelled	59.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> acetylpolyamine aminohydrolase; <b>PDBTitle:</b> crystal structure of acetylpolyamine aminohydrolase from burkholderia2 pseudomallei, iodide soak
56	<a href="#">c3ew8A_</a>	Alignment	not modelled	58.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histone deacetylase 8; <b>PDBTitle:</b> crystal structure analysis of human hdac8 d101l variant
57	<a href="#">c3q9cF_</a>	Alignment	not modelled	50.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> acetylpolyamine amidohydrolase; <b>PDBTitle:</b> crystal structure of h159a apah complexed with n8-acetylspermidine
58	<a href="#">c2vy9A_</a>	Alignment	not modelled	47.5	18	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> anti-sigma-factor antagonist; <b>PDBTitle:</b> molecular architecture of the stressosome, a signal2 integration and transduction hub
59	<a href="#">d2obba1</a>	Alignment	not modelled	46.3	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> BT0820-like
60	<a href="#">c2hx1D_</a>	Alignment	not modelled	45.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> predicted sugar phosphatases of the had superfamily; <b>PDBTitle:</b> crystal structure of possible sugar phosphatase, had superfamily2 (zp_00311070.1) from cytophaga hutchinsonii atcc 33406 at 2.10 a3 resolution
61	<a href="#">d1t64a_</a>	Alignment	not modelled	43.8	14	<b>Fold:</b> Arginase/deacetylase <b>Superfamily:</b> Arginase/deacetylase <b>Family:</b> Histone deacetylase, HDAC
62	<a href="#">c3zlbA_</a>	Alignment	not modelled	42.1	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> crystal structure of phosphoglycerate kinase from streptococcus2 pneumoniae
63	<a href="#">c3maxB_</a>	Alignment	not modelled	40.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> histone deacetylase 2; <b>PDBTitle:</b> crystal structure of human hdac2 complexed with an n-(2-aminophenyl)2 benzamide
64	<a href="#">c6jddA_</a>	Alignment	not modelled	39.1	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cypemycin cysteine dehydrogenase (decarboxylating); <b>PDBTitle:</b> crystal structure of the cypemycin decarboxylase cypd.
65	<a href="#">d1vjda_</a>	Alignment	not modelled	38.3	28	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
66	<a href="#">c4bz7A_</a>	Alignment	not modelled	38.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histone deacetylase 8; <b>PDBTitle:</b> crystal structure of schistosoma mansoni hdac8 complexed with m344
67	<a href="#">c4zexA_</a>	Alignment	not modelled	37.9	15	<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
68	<a href="#">c3pgvB_</a>	Alignment	not modelled	37.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
69	<a href="#">c5dmxC_</a>	Alignment	not modelled	36.4	23	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from acinetobacter2 baumannii, space group p212121
70	<a href="#">c2i55C_</a>	Alignment	not modelled	35.3	15	<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
71	<a href="#">d1hdia_</a>	Alignment	not modelled	34.3	35	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
72	<a href="#">c3dnpA_</a>	Alignment	not modelled	32.8	13	<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
73	<a href="#">c2d6fA_</a>	Alignment	not modelled	32.7	23	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit d; <b>PDBTitle:</b> crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
74	<a href="#">c6gfmA_</a>	Alignment	not modelled	32.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine/purine nucleotide 5'-monophosphate nucleosidase; <b>PDBTitle:</b> crystal structure of the escherichia coli nucleosidase ppnn (pppgpp-2 form)
75	<a href="#">d1phpa_</a>	Alignment	not modelled	31.3	29	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
76	<a href="#">d1xbta1</a>	Alignment	not modelled	29.4	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Type II thymidine kinase
77	<a href="#">c2cunA_</a>	Alignment	not modelled	28.4	21	<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
78	<a href="#">d1wmaa1</a>	Alignment	not modelled	27.3	40	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
						<b>Fold:</b> HAD-like

79	<a href="#">d1yv9a1</a>	Alignment	not modelled	27.3	10	<b>Superfamily:</b> HAD-like <b>Family:</b> NagD-like
80	<a href="#">c3ecsD</a>	Alignment	not modelled	27.3	14	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit alpha; <b>PDBTitle:</b> crystal structure of human eif2b alpha
81	<a href="#">c3zg6A</a>	Alignment	not modelled	27.2	15	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent protein deacetylase sirtuin-6; <b>PDBTitle:</b> the novel de-long chain fatty acid function of human sirt6
82	<a href="#">c3f43A</a>	Alignment	not modelled	26.6	7	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative anti-sigma factor antagonist tm1081; <b>PDBTitle:</b> crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
83	<a href="#">d1qpga</a>	Alignment	not modelled	26.4	22	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
84	<a href="#">c4gxtA</a>	Alignment	not modelled	26.1	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> a conserved functionally unknown protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548
85	<a href="#">d1ltka</a>	Alignment	not modelled	25.2	24	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
86	<a href="#">c3zupB</a>	Alignment	not modelled	24.7	18	<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.
87	<a href="#">c4fu0B</a>	Alignment	not modelled	24.6	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanine--d-alanine ligase 7; <b>PDBTitle:</b> crystal structure of vang d-ala:d-ser ligase from enterococcus2 faecalis
88	<a href="#">c1zmrA</a>	Alignment	not modelled	24.4	24	<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
89	<a href="#">d1p3y1</a>	Alignment	not modelled	24.3	13	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
90	<a href="#">c3mcf</a>	Alignment	not modelled	23.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dipicolinate synthase, b chain; <b>PDBTitle:</b> crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.
91	<a href="#">c4xs5D</a>	Alignment	not modelled	23.5	16	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> sulfate transporter/antisigma-factor antagonist stas; <b>PDBTitle:</b> crystal structure of sulfate transporter/antisigma-factor antagonist2 stas from dyadobacter fermentans dsm 18053
92	<a href="#">d1vpea</a>	Alignment	not modelled	22.9	26	<b>Fold:</b> Phosphoglycerate kinase <b>Superfamily:</b> Phosphoglycerate kinase <b>Family:</b> Phosphoglycerate kinase
93	<a href="#">d1gp1a</a>	Alignment	not modelled	22.6	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
94	<a href="#">c5bt8D</a>	Alignment	not modelled	22.4	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> x-ray crystal structure of phosphoglycerate kinase from acinetobacter2 baumannii
95	<a href="#">c3lkB</a>	Alignment	not modelled	22.3	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> antisigma-factor antagonist stas; <b>PDBTitle:</b> crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
96	<a href="#">d1wpga2</a>	Alignment	not modelled	22.0	25	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
97	<a href="#">c3lqkA</a>	Alignment	not modelled	21.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit b; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
98	<a href="#">c4ehjA</a>	Alignment	not modelled	20.9	19	<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
99	<a href="#">c3e5nA</a>	Alignment	not modelled	20.5	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine-d-alanine ligase a; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331