

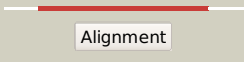

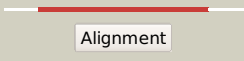

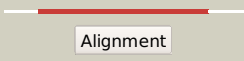

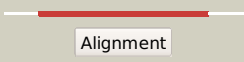

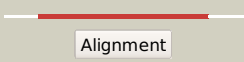

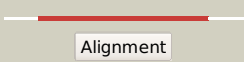

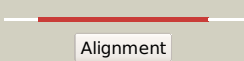

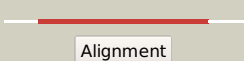

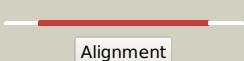

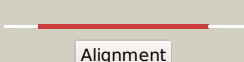












Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0620_(galK)_712719_713810
 Date Fri Jul 26 01:50:18 BST 2019
 Unique Job ID 0285b64a439ebc7e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1pieA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: galactokinase; PDBTitle: crystal structure of lactococcus lactis galactokinase2 complexed with galactose
2	c2aj4B_	 Alignment		100.0	31	PDB header: transferase Chain: B: PDB Molecule: galactokinase; PDBTitle: crystal structure of saccharomyces cerevisiae galactokinase2 in complex with galactose and mg:amppnp
3	c3v2uC_	 Alignment		100.0	27	PDB header: transcription Chain: C: PDB Molecule: protein gal3; PDBTitle: crystal structure of the yeast gal regulon complex of the repressor,2 gal80p, and the transducer, gal3p, with galactose and atp
4	c1wuuA_	 Alignment		100.0	35	PDB header: transferase Chain: A: PDB Molecule: galactokinase; PDBTitle: crystal structure of human galactokinase complexed with2 mgamppnp and galactose
5	c2a2cA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: n-acetylgalactosamine kinase; PDBTitle: x-ray structure of human n-acetyl galactosamine kinase2 complexed with mg-ADP and n-acetyl galactosamine 1-3 phosphate
6	c2cz9A_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: probable galactokinase; PDBTitle: crystal structure of galactokinase from pyrococcus horikoshi
7	c4ut4B_	 Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: putative sugar kinase; PDBTitle: burkholderia pseudomallei heptokinase wcbI, d-mannose complex.
8	c2r42A_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: the biochemical and structural basis for feedback2 inhibition of mevalonate kinase and isoprenoid metabolism
9	c2hfuB_	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: mevalonate kinase, putative; PDBTitle: crystal structure of l. major mevalonate kinase in complex2 with r-mevalonate
10	c3k17A_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: lin0012 protein; PDBTitle: crystal structure of a lin0012 protein from listeria innocua
11	c5yysC_	 Alignment		100.0	17	PDB header: transferase Chain: C: PDB Molecule: l-fucokinase, l-fucose-1-p guanylyltransferase; PDBTitle: cryo-em structure of l-fucokinase, gdp-fucose pyrophosphorylase (fkp)2 in bacteroides fragilis

12	c4n3oB_	Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: putative d-glycero-d-manno-heptose 7-phosphate kinase; PDBTitle: 2.4 angstrom resolution crystal structure of putative sugar kinase2 from campylobacter jejuni.
13	c4hacA_	Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: crystal structure of the mevalonate kinase from an archaeon2 methanosarcina maezi
14	c1kkhA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: crystal structure of the methanococcus jannaschii2 mevalonate kinase
15	c2x7iA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: crystal structure of mevalonate kinase from methicillin-2 resistant staphylococcus aureus mrsa252
16	c1k47F_	Alignment		100.0	16	PDB header: transferase Chain: F: PDB Molecule: phosphomevalonate kinase; PDBTitle: crystal structure of the streptococcus pneumoniae2 phosphomevalonate kinase (pmk)
17	c2oi2A_	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: streptococcus pneumoniae mevalonate kinase in complex with2 diphosphomevalonate
18	c3k85B_	Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: d-glycero-d-manno-heptose 1-phosphate kinase; PDBTitle: crystal structure of a d-glycero-d-manno-heptose 1-phosphate2 kinase from bacteriodes thetaiotaomicron
19	c3pygA_	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: 4-diphosphocytidyl-2-c-methyl-d-erythritol kinase; PDBTitle: mycobacterium tuberculosis 4-diphosphocytidyl-2-c-methyl-d-erythritol2 kinase (ispe) in complex with adp
20	c4p52A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase from cytophaga hutchinsonii2 atcc 33406, nysgrc target 032717.
21	d1piea1	Alignment	not modelled	100.0	33	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
22	c1fwID_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: D: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase
23	c4rpfA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase from yersinia pestis nepal516,2 nysgrc target 032715
24	d1wuua1	Alignment	not modelled	100.0	35	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
25	c4z7cA_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: diphosphomevalonate decarboxylase from the sulfobolbus solfataricus,2 space group h32
26	c6n0yB_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: crystal structure of anaerolinea thermophila mevalonate 5-phosphate2 decarboxylase complexed with (r)-mvapp PDB header: lyase Chain: A: PDB Molecule: mevalonate diphosphate decarboxylase; PDBTitle: mevalonate diphosphate mediated atp binding mechanism of the2 mevalonate diphosphate decarboxylase from enterococcus faecalis
27	c5v2lA_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: mevalonate diphosphate decarboxylase; PDBTitle: mevalonate diphosphate mediated atp binding mechanism of the2 mevalonate diphosphate decarboxylase from enterococcus faecalis
28	d1piea2	Alignment	not modelled	100.0	30	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
						PDB header: lyase Chain: A: PDB Molecule: mevalonate pyrophosphate

29	c2qs8A_	Alignment	not modelled	100.0	16	decarboxylase; PDBTitle: structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes
30	d1s4ea2	Alignment	not modelled	100.0	30	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
31	c2hk3A_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: crystal structure of mevalonate diphosphate decarboxylase2 from staphylococcus aureus (orthorhombic form)
32	c3hulA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: structure of putative homoserine kinase thrb from listeria2 monocytogenes
33	d1s4ea1	Alignment	not modelled	100.0	35	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
34	d1wuua2	Alignment	not modelled	100.0	37	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
35	d1kkha1	Alignment	not modelled	100.0	21	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
36	c6cyzA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: mycobacterial homoserine kinase thrb in complex with amppnp
37	c2v34B_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: 4-diphosphocytidyl-2c-methyl-d-erythritol kinase; PDBTitle: ispe in complex with cytidine and ligand
38	d1kvka1	Alignment	not modelled	100.0	23	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
39	c5watB_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: homoserine kinase; PDBTitle: corynebacterium glutamicum full length homoserine kinase
40	c1uekA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: 4-(cytidine 5'-diphospho)-2c-methyl-d-erythritol PDBTitle: crystal structure of 4-(cytidine 5'-diphospho)-2c-methyl-d-2 erythritol kinase
41	c1oj4B_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: 4-diphosphocytidyl-2-c-methyl-d-erythritol PDBTitle: ternary complex of 2 4-diphosphocytidyl-2-c-methyl-d-erythritol kinase
42	d1k47a1	Alignment	not modelled	100.0	17	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
43	c3ltoB_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: B: PDB Molecule: mevalonate diphosphate decarboxylase; PDBTitle: crystal structure of a mevalonate diphosphate decarboxylase2 from legionella pneumophila
44	d1h72c1	Alignment	not modelled	99.9	20	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
45	d1oj4a1	Alignment	not modelled	99.9	21	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
46	d1kvka2	Alignment	not modelled	99.9	16	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate kinase
47	d1k47a2	Alignment	not modelled	99.8	15	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Phosphomevalonate kinase (PMK)
48	c2hkeB_	Alignment	not modelled	99.8	15	PDB header: lyase Chain: B: PDB Molecule: diphosphomevalonate decarboxylase, putative; PDBTitle: mevalonate diphosphate decarboxylase from trypanosoma brucei
49	d1ueka1	Alignment	not modelled	99.8	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
50	d1kkha2	Alignment	not modelled	99.8	23	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate kinase
51	c1fi4A_	Alignment	not modelled	99.7	16	PDB header: lyase Chain: A: PDB Molecule: mevalonate 5-diphosphate decarboxylase; PDBTitle: the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
52	c6n10A_	Alignment	not modelled	99.6	17	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase mvd1, peroxisomal; PDBTitle: crystal structure of arabidopsis thaliana mevalonate 5-diphosphate2 decarboxylase 1 complexed with (r)-mvapp
53	d1fi4a1	Alignment	not modelled	99.5	18	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
54	c3f0nB_	Alignment	not modelled	99.3	20	PDB header: lyase Chain: B: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: mus musculus mevalonate pyrophosphate decarboxylase PDB header: transferase

55	c4rksB	Alignment	not modelled	99.3	11	Chain: B; PDB Molecule: putative uncharacterized protein ta1305; PDBTitle: crystal structure of mevalonate-3-kinase from thermoplasma acidophilum2 (mevalonate bound)
56	d1h72c2	Alignment	not modelled	99.1	18	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Homoserine kinase
57	d1ueka2	Alignment	not modelled	98.0	21	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: 4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
58	d1oj4a2	Alignment	not modelled	96.6	24	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: 4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
59	d1fi4a2	Alignment	not modelled	93.7	13	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate 5-diphosphate decarboxylase
60	c3c7bA	Alignment	not modelled	58.7	14	PDB header: oxidoreductase Chain: A; PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
61	d2cz4a1	Alignment	not modelled	53.2	16	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
62	d2ns1b1	Alignment	not modelled	45.1	21	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
63	c2v4jA	Alignment	not modelled	41.4	12	PDB header: oxidoreductase Chain: A; PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
64	c5d4pA	Alignment	not modelled	41.0	18	PDB header: signaling protein Chain: A; PDB Molecule: putative nitrogen regulatory protein p-ii glnb; PDBTitle: structure of cpII bound to adp and bicarbonate, from thiomonas2 intermedia k12
65	c4rleA	Alignment	not modelled	39.9	10	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein yaaq; PDBTitle: crystal structure of the c-di-amp binding pII-like protein dara
66	c2y9jt	Alignment	not modelled	39.1	12	PDB header: protein transport Chain: T; PDB Molecule: protein prgh; PDBTitle: three-dimensional model of salmonella's needle complex at subnanometer2 resolution
67	c3bzqA	Alignment	not modelled	38.6	21	PDB header: signaling protein/transcription Chain: A; PDB Molecule: nitrogen regulatory protein p-ii; PDBTitle: high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
68	c4w8yA	Alignment	not modelled	38.1	25	PDB header: rna binding protein Chain: A; PDB Molecule: crispr system cmr subunit cmr2; PDBTitle: structure of full length cmr2 from pyrococcus furiosus (manganese2 bound form)
69	c4rwwB	Alignment	not modelled	36.6	10	PDB header: protein binding Chain: B; PDB Molecule: lmo2692 protein; PDBTitle: crystal structure of l. monocytogenes psta in complex with cyclic-di-2 amp
70	d1vfja	Alignment	not modelled	34.4	12	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
71	d2piia	Alignment	not modelled	33.3	23	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
72	c2j9dG	Alignment	not modelled	32.2	13	PDB header: membrane transport Chain: G; PDB Molecule: hypothetical nitrogen regulatory pII-like PDBTitle: structure of glnK1 with bound effectors indicates2 regulatory mechanism for ammonia uptake
73	d3c7bb2	Alignment	not modelled	30.7	10	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
74	c3ncpD	Alignment	not modelled	29.1	14	PDB header: signaling protein Chain: D; PDB Molecule: nitrogen regulatory protein p-ii (glnb-2); PDBTitle: glnK2 from archaeoglobus fulgidus
75	d1mg7a1	Alignment	not modelled	27.9	13	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Early switch protein XOL-1, N-terminal domain
76	c3o8wA	Alignment	not modelled	25.8	19	PDB header: signaling protein Chain: A; PDB Molecule: nitrogen regulatory protein p-ii (glnb-1); PDBTitle: archaeoglobus fulgidus glnK1
77	c3mhyC	Alignment	not modelled	25.3	22	PDB header: signaling protein Chain: C; PDB Molecule: pII-like protein pz; PDBTitle: a new pII protein structure
78	c4r25A	Alignment	not modelled	25.0	12	PDB header: transcription Chain: A; PDB Molecule: nitrogen regulatory pII-like protein; PDBTitle: structure of b. subtilis glnK
79	c4ozlA	Alignment	not modelled	25.0	21	PDB header: signaling protein Chain: A; PDB Molecule: nitrogen regulatory protein p-ii; PDBTitle: glnK2 from haloferax mediterranei complexed with amp
80	d1qy7a	Alignment	not modelled	24.8	20	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
						PDB header: signaling protein

81	c4wk1A_	Alignment	not modelled	23.8	14	Chain: A; PDB Molecule: psta; PDBTitle: crystal structure of staphylococcus aureus psta in complex with c-di-2 amp
82	c3m05A_	Alignment	not modelled	22.8	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein pepe_1480; PDBTitle: the crystal structure of a functionally unknown protein pepe_1480 from <i>pediococcus pentosaceus</i> atcc 25745
83	c4usiC_	Alignment	not modelled	22.8	16	PDB header: signaling protein Chain: C; PDB Molecule: nitrogen regulatory protein pii; PDBTitle: nitrogen regulatory protein pii from <i>chlamydomonas2 reinhardtii</i> in complex with mgatp and 2-oxoglutarate
84	d2cp9a1	Alignment	not modelled	22.0	21	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
85	d2pv7a1	Alignment	not modelled	21.2	12	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
86	d1ul3a_	Alignment	not modelled	21.1	21	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
87	d1zj8a1	Alignment	not modelled	21.0	21	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
88	d1hwua_	Alignment	not modelled	20.6	18	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
89	d2bv3a3	Alignment	not modelled	19.9	20	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
90	d2cl5a1	Alignment	not modelled	19.7	10	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: COMT-like
91	c1yj7A_	Alignment	not modelled	19.3	8	PDB header: protein transport Chain: A; PDB Molecule: escj; PDBTitle: crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
92	d1lb2b_	Alignment	not modelled	18.0	13	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
93	c5j2dA_	Alignment	not modelled	16.5	15	PDB header: transcription/dna/rna Chain: A; PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: crystal structure of t. thermophilus tthb099 class ii transcription2 activation complex: tap-rpo
94	d1cooa_	Alignment	not modelled	15.9	13	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
95	d1xd7a_	Alignment	not modelled	14.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
96	d1z3eb1	Alignment	not modelled	14.1	11	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
97	c3wz2C_	Alignment	not modelled	13.2	13	PDB header: chaperone Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pyrococcus furiosus pbaa, an archaeal homolog of 2 proteasome-assembly chaperone
98	d2p90a1	Alignment	not modelled	13.1	16	Fold: Phosphorylase/hydrolase-like Superfamily: Cgl1923-like Family: Cgl1923-like
99	d1a6qa1	Alignment	not modelled	12.3	26	Fold: Another 3-helical bundle Superfamily: Protein serine/threonine phosphatase 2C, C-terminal domain Family: Protein serine/threonine phosphatase 2C, C-terminal domain