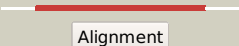



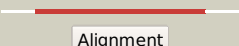





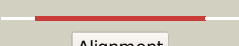
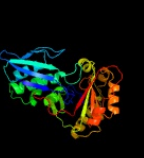












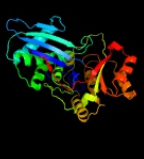








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1011_(ispE)_1130195_1131115
Date	Wed Jul 31 22:05:08 BST 2019
Unique Job ID	32e98e01c5da133a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pygA_	 Alignment		100.0	100	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
2	c1uekA_	 Alignment		100.0	35	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
3	c2v34B_	 Alignment		100.0	28	PDB header: transferase Chain: B: PDB Molecule: 4-diphosphocytidyl-2c-methyl-d-erythritol kinase; PDBTitle: ispe in complex with cytidine and ligand
4	c1oj4B_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: 4-diphosphocytidyl-2-c-methyl-d-erythritol PDBTitle: ternary complex of2 4-diphosphocytidyl-2-c-methyl-d-erythritol kinase
5	c4rpfA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase from yersinia pestis nepal516,2 nysgrc target 032715
6	c4p52A_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase from cytophaga hutchinsonii2 atcc 33406, nysgrc target 032717.
7	c1fwlD_	 Alignment		100.0	20	PDB header: transferase Chain: D: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase
8	c6cyzA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: mycobacterial homoserine kinase thrb in complex with amppnp
9	c3hulA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: structure of putative homoserine kinase thrb from listeria2 monocytogenes
10	c2cz9A_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: probable galactokinase; PDBTitle: crystal structure of galactokinase from pyrococcus horikoshi
11	c5watB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: homoserine kinase; PDBTitle: corynebacterium glutamicum full length homoserine kinase

12	c4z7cA_	Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: diphosphomevalonate decarboxylase from the sulfobolus solfataricus,2 space group h32
13	c4hacA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: crystal structure of the mevalonate kinase from an archaeon2 methanosarcina mazei
14	c2hk3A_	Alignment		100.0	16	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: crystal structure of mevalonate diphosphate decarboxylase2 from staphylococcus aureus (orthorhombic form)
15	c2hfuB_	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: mevalonate kinase, putative; PDBTitle: crystal structure of l. major mevalonate kinase in complex2 with r-mevalonate
16	c5v2IA_	Alignment		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
17	c2x7iA_	Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: crystal structure of mevalonate kinase from methicillin-2 resistant staphylococcus aureus mrsa252
18	c4ut4B_	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: putative sugar kinase; PDBTitle: burkholderia pseudomallei heptokinase wcbl, d-mannose complex.
19	c1pieA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: galactokinase; PDBTitle: crystal structure of lactococcus lactis galactokinase2 complexed with galactose
20	c2a2cA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: n-acetyl galactosamine kinase; PDBTitle: x-ray structure of human n-acetyl galactosamine kinase2 complexed with mg-ADP and n-acetyl galactosamine 1-3 phosphate
21	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
22	c2oi2A_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: streptococcus pneumoniae mevalonate kinase in complex with2 diphosphomevalonate
23	c1wuUa_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: galactokinase; PDBTitle: crystal structure of human galactokinase complexed with2 mgampnp and galactose
24	c2qs8A_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes
25	c4n3oB_	Alignment	not modelled	100.0	17	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.
26	c1kkhA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: crystal structure of the methanococcus jannaschii2 mevalonate kinase
27	c2aj4B_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: galactokinase; PDBTitle: crystal structure of saccharomyces cerevisiae galactokinase2 in complex with galactose and mg:ampnp
28	c2r42A_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase;

28	c1h4a	Alignment	not modelled	100.0	20	PDBTitle: the biochemical and structural basis for feedback2 inhibition of mevalonate kinase and isoprenoid metabolism
29	c3k17A	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: lin0012 protein; PDBTitle: crystal structure of a lin0012 protein from listeria innocua
30	c1k47F	Alignment	not modelled	100.0	16	PDB header: transferase Chain: F: PDB Molecule: phosphomevalonate kinase; PDBTitle: crystal structure of the streptococcus pneumoniae2 phosphomevalonate kinase (pmk)
31	c3v2uC	Alignment	not modelled	100.0	19	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
32	c3k85B	Alignment	not modelled	100.0	18	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
33	c5yysC	Alignment	not modelled	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 bacterioides fragilis
34	d1oj4a1	Alignment	not modelled	100.0	34	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
35	c3ltoB	Alignment	not modelled	100.0	12	PDB header: lyase Chain: B: PDB Molecule: mevalonate diphosphate decarboxylase; PDBTitle: crystal structure of a mevalonate diphosphate decarboxylase2 from legionella pneumophila
36	d1ueka1	Alignment	not modelled	100.0	43	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
37	d1h72c1	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
38	c2hkeB	Alignment	not modelled	99.9	16	PDB header: lyase Chain: B: PDB Molecule: diphosphomevalonate decarboxylase, putative; PDBTitle: mevalonate diphosphate decarboxylase from trypanosoma brucei
39	d1kkha1	Alignment	not modelled	99.9	12	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
40	d1piea1	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
41	d1wuua1	Alignment	not modelled	99.9	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
42	d1k47a1	Alignment	not modelled	99.9	15	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
43	d1s4ea1	Alignment	not modelled	99.9	16	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
44	d1fi4a1	Alignment	not modelled	99.9	15	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
45	c6n10A	Alignment	not modelled	99.9	15	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
46	d1kvka1	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
47	d1h72c2	Alignment	not modelled	99.8	18	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Homoserine kinase
48	c1fi4A	Alignment	not modelled	99.8	13	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.
49	d1ueka2	Alignment	not modelled	99.8	23	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: 4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
50	c4rksB	Alignment	not modelled	99.7	12	PDB header: transferase Chain: B: PDB Molecule: putative uncharacterized protein ta1305; PDBTitle: crystal structure of mevalonate-3-kinase from thermoplasma acidophilum2 (mevalonate bound)
51	c3f0nB	Alignment	not modelled	99.7	15	PDB header: lyase Chain: B: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: mus musculus mevalonate pyrophosphate decarboxylase
52	d1oj4a2	Alignment	not modelled	99.6	13	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: 4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
53	d1kvka2	Alignment	not modelled	99.6	17	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate kinase

54	d1k47a2	Alignment	not modelled	99.6	12	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Phosphomevalonate kinase (PMK)
55	d1wuua2	Alignment	not modelled	99.5	17	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
56	d1piea2	Alignment	not modelled	99.4	17	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
57	d1s4ea2	Alignment	not modelled	99.4	15	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
58	d1kkha2	Alignment	not modelled	99.3	14	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate kinase
59	d1fi4a2	Alignment	not modelled	75.0	13	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate 5-diphosphate decarboxylase
60	d1wgl1a	Alignment	not modelled	69.1	9	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
61	c5wasB	Alignment	not modelled	65.7	19	PDB header: transferase Chain: B: PDB Molecule: homoserine kinase; PDBTitle: corynebacterium glutamicum hydrolyzed homoserine kinase
62	c5jvoA	Alignment	not modelled	32.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the arginine repressor from the pathogenic2 bacterium corynebacterium pseudotuberculosis
63	c4rleA	Alignment	not modelled	27.5	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yaaq; PDBTitle: crystal structure of the c-di-amp binding pii-like protein dara
64	d1klpa	Alignment	not modelled	23.0	21	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
65	c3m05A	Alignment	not modelled	20.5	18	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 from2 pediococcus pentosaceus atcc 25745
66	c4hhuA	Alignment	not modelled	19.9	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: or280; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
67	c1k98A	Alignment	not modelled	19.7	18	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
68	c2qnwA	Alignment	not modelled	18.8	16	PDB header: signaling protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: toxoplasma gondii apicoplast-targeted acyl carrier protein
69	c4rwwB	Alignment	not modelled	17.1	20	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	d1b4ba	Alignment	not modelled	15.6	23	Fold: DcoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
71	d1a1va2	Alignment	not modelled	15.4	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
72	c4pxhF	Alignment	not modelled	15.2	23	PDB header: oxidoreductase/protein binding Chain: F: PDB Molecule: peptide synthetase; PDBTitle: structure of p450sky (cyp163b3), a cytochrome p450 from skyllamycin2 biosynthesis in complex with a peptidyl carrier protein domain
73	d2p5ma1	Alignment	not modelled	14.0	14	Fold: DcoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
74	c3cagF	Alignment	not modelled	13.8	11	PDB header: dna binding protein Chain: F: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
75	c2l26A	Alignment	not modelled	13.3	20	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein rv0899/mt0922; PDBTitle: rv0899 from mycobacterium tuberculosis contains two separated domains
76	c3s6eB	Alignment	not modelled	12.8	21	PDB header: rna binding protein Chain: B: PDB Molecule: rna-binding protein 39; PDBTitle: crystal structure of a rna binding motif protein 39 (rbm39) from mus2 musculus at 0.95 a resolution
77	c2n2uA	Alignment	not modelled	12.6	14	PDB header: unknown function, structural genomics Chain: A: PDB Molecule: or358; PDBTitle: solution nmr structure of de novo designed ferredoxin fold protein2 sfr3, northeast structural genomics consortium (nesg) target or358
78	c3mcqA	Alignment	not modelled	12.4	9	PDB header: transferase Chain: A: PDB Molecule: thiamine-monophosphate kinase; PDBTitle: crystal structure of thiamine-monophosphate kinase (mfla_0573) from2 methylobacillus flagellatus kt at 1.91 a resolution
79	c2zauB	Alignment	not modelled	11.7	12	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase; PDBTitle: crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus

80	c2cqyA_	Alignment	not modelled	11.7	18	PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, PDBTitle: solution structure of b domain from human propionyl-coa2 carboxylase alpha subunit
81	d1xxaa_	Alignment	not modelled	11.2	10	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
82	d1mlaa2	Alignment	not modelled	11.0	18	Fold: Ferredoxin-like Superfamily: Probable ACP-binding domain of malonyl-CoA ACP transacylase Family: Probable ACP-binding domain of malonyl-CoA ACP transacylase
83	c2dnwA_	Alignment	not modelled	10.9	13	PDB header: transport protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
84	c1x3oA_	Alignment	not modelled	10.9	9	PDB header: lipid transport Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: crystal structure of the acyl carrier protein from thermus2 thermophilus hb8
85	c2mr7A_	Alignment	not modelled	10.9	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: apo structure of the peptidyl carrier protein domain 7 of the2 teicoplanin producing non-ribosomal peptide synthetase
86	c4wk1A_	Alignment	not modelled	10.8	9	PDB header: signaling protein Chain: A: PDB Molecule: psta; PDBTitle: crystal structure of staphylococcus aureus psta in complex with c-di-2 amp
87	c3vr0D_	Alignment	not modelled	10.8	20	PDB header: protein binding Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pyrococcus furiosus pbab, an archaeal proteasome2 activator
88	c1vkrA_	Alignment	not modelled	10.6	14	PDB header: transferase Chain: A: PDB Molecule: mannitol-specific pts system enzyme iiabc components; PDBTitle: structure of iib domain of the mannitol-specific permease enzyme ii
89	d1vkra_	Alignment	not modelled	10.6	14	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
90	c2lo1A_	Alignment	not modelled	10.3	13	PDB header: lipid transport Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: nmr structure of an acyl-carrier protein from rickettsia prowazekii,2 seattle structural genomics center for infectious disease (ssgcid)
91	d7reqb2	Alignment	not modelled	10.2	34	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
92	d1yqga1	Alignment	not modelled	9.8	26	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
93	d1o51a_	Alignment	not modelled	9.6	15	Fold: Ferredoxin-like Superfamily: GlnB-like Family: DUF190/COG1993
94	c5wtlB_	Alignment	not modelled	9.6	17	PDB header: membrane protein Chain: B: PDB Molecule: ompa family protein; PDBTitle: crystal structure of the periplasmic portion of outer membrane protein2 a (ompa) from capnocytophaga gingivalis
95	c4r2nA_	Alignment	not modelled	8.5	23	PDB header: transferase Chain: A: PDB Molecule: putative phenylalanine aminotransferase; PDBTitle: crystal structure of rv3772 in complex with its substrate
96	c3wz2C_	Alignment	not modelled	8.1	20	PDB header: chaperone Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pyrococcus furiosus pbaa, an archaeal homolog of2 proteasome-assembly chaperone
97	c2cq8A_	Alignment	not modelled	8.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 10-formyltetrahydrofolate dehydrogenase; PDBTitle: solution structure of rsgi ruh-033, a pp-binding domain of2 10-fthfdh from human cdna
98	c2m5rA_	Alignment	not modelled	7.7	15	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of holo-acyl carrier protein of leishmania major
99	c2kw1A_	Alignment	not modelled	7.6	12	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of acyl carrier protein from borrelia burgdorferi