
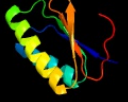

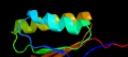

















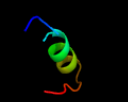


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2147c (-) _2406126_2406851
Date	Mon Aug 5 13:25:27 BST 2019
Unique Job ID	41fad7dcf658a13b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zihB_	 Alignment		100.0	32	PDB header: cell cycle Chain: B: PDB Molecule: cell division protein sepf; PDBTitle: bacillus subtilis sepf, c-terminal domain
2	c3p04A_	 Alignment		100.0	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
3	c3p04B_	 Alignment		99.9	37	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
4	c3zigA_	 Alignment		98.0	15	PDB header: cell cycle Chain: A: PDB Molecule: sepf-like protein; PDBTitle: sepf-like protein from pyrococcus furiosus
5	c3zieC_	 Alignment		97.3	19	PDB header: cell cycle Chain: C: PDB Molecule: sepf-like protein; PDBTitle: sepf-like protein from archaeoglobus fulgidus
6	c3mioA_	 Alignment		50.7	16	PDB header: lyase Chain: A: PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
7	c4p6dA_	 Alignment		46.8	17	PDB header: lyase Chain: A: PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: structure of ribb complexed with po4 ion
8	d1tksa_	 Alignment		42.2	19	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
9	d1k4ia_	 Alignment		39.9	24	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
10	c4i14B_	 Alignment		38.7	20	PDB header: hydrolase, lyase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribba; PDBTitle: crystal structure of mtb-riba2 (rv1415)
11	c4ffjA_	 Alignment		34.2	20	PDB header: lyase Chain: A: PDB Molecule: riboflavin biosynthesis protein ribba; PDBTitle: the crystal structure of spdhbps from s.pneumoniae

12	d1snaa_	Alignment		31.1	11	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
13	c6nhlB_	Alignment		29.4	13	PDB header: lyase Chain: B: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from escherichia coli
14	c4p3xA_	Alignment		28.9	14	PDB header: transferase Chain: A: PDB Molecule: quinolinate synthase a; PDBTitle: structure of the fe4s4 quinolinate synthase nada from thermotoga2 maritima
15	c3b6bF_	Alignment		28.4	17	PDB header: transferase Chain: F: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: crystal structure of acanthamoeba polyphaga mimivirus2 nucleoside diphosphate kinase complexed with dgdp
16	c2qs0A_	Alignment		28.4	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: quinolinate synthetase a; PDBTitle: quinolinate synthase from pyrococcus furiosus
17	c3od9B_	Alignment		26.9	24	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: putative exported protein; PDBTitle: crystal structure of plii-ah, periplasmic lysozyme inhibitor of i-type2 lysozyme from aeromonas hydrophyla
18	c2k8vA_	Alignment		26.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin domain-containing protein 12; PDBTitle: solution structure of oxidised erp18
19	c3crw1_	Alignment		25.2	19	PDB header: hydrolase Chain: 1: PDB Molecule: xpd/rad3 related dna helicase; PDBTitle: xpd_apo
20	c2nu9E_	Alignment		24.9	16	PDB header: ligase Chain: E: PDB Molecule: succinyl-coa synthetase beta chain; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
21	c5lklB_	Alignment	not modelled	23.4	43	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of full-length csfv ns3/4a
22	d1g57a_	Alignment	not modelled	22.9	16	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
23	c5cpcA_	Alignment	not modelled	22.7	36	PDB header: cell invasion Chain: A: PDB Molecule: secreted effector protein sopd; PDBTitle: crystal structure of sopd, a type iii secreted virulence effector from2 salmonella enterica
24	d1pkua1	Alignment	not modelled	22.6	19	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
25	d1wzua1	Alignment	not modelled	21.8	18	Fold: NadA-like Superfamily: NadA-like Family: NadA-like
26	c6mnzB_	Alignment	not modelled	21.7	23	PDB header: lyase Chain: B: PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: crystal structure of ribbx, a two domain 3,4-dihydroxy-2-butanone 4-2 phosphate synthase from a. baumannii.
27	c1senA_	Alignment	not modelled	21.5	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: thioredoxin-like protein p19; PDBTitle: endoplasmic reticulum protein rp19 o95881
28	d1sena_	Alignment	not modelled	21.5	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase PDB header: ligase

29	c6g4qB_	Alignment	not modelled	20.9	24	Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta, PDBTitle: structure of human adp-forming succinyl-coa ligase complex suclg1-2 sucla2
30	d1wu7a1	Alignment	not modelled	20.7	18	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
31	d1w7wa_	Alignment	not modelled	19.5	20	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
32	d1be4a_	Alignment	not modelled	18.7	21	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
33	c5x00A_	Alignment	not modelled	18.3	17	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: nucleoside diphosphate kinase from vibrio cholerae is a thermolabile2 type ii tetramer
34	c2opiB_	Alignment	not modelled	17.7	30	PDB header: lyase Chain: B: PDB Molecule: l-fucose-1-phosphate aldolase; PDBTitle: crystal structure of l-fucose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
35	c2pgsA_	Alignment	not modelled	17.4	43	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyguanosinetriphosphate triphosphohydrolase; PDBTitle: crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
36	d1q40b_	Alignment	not modelled	17.3	26	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
37	c3m1rF_	Alignment	not modelled	16.6	20	PDB header: hydrolase Chain: F: PDB Molecule: formimidoylglutamase; PDBTitle: the crystal structure of formimidoylglutamase from bacillus2 subtilis subsp. subtilis str. 168
38	c6hxqB_	Alignment	not modelled	16.2	10	PDB header: lyase Chain: B: PDB Molecule: citryl-coa synthetase large subunit; PDBTitle: structure of citryl-coa synthetase from hydrogenobacter thermophilus
39	c2irpA_	Alignment	not modelled	16.0	17	PDB header: lyase Chain: A: PDB Molecule: putative aldolase class 2 protein aq_1979; PDBTitle: crystal structure of the l-fucose-1-phosphate aldolase (aq_1979)2 from aquifex aeolicus vf5
40	d1nb2a_	Alignment	not modelled	15.9	20	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
41	c5gvdB_	Alignment	not modelled	15.7	22	PDB header: protein binding Chain: B: PDB Molecule: tudor domain-containing protein 3; PDBTitle: human tdrd3 duf1767-ob domains
42	d2b8qa1	Alignment	not modelled	15.7	17	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
43	d1s57a_	Alignment	not modelled	15.2	17	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
44	d1eucb1	Alignment	not modelled	14.9	15	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
45	c5chlA_	Alignment	not modelled	14.4	22	PDB header: chaperone Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 72 homolog; PDBTitle: structural basis of h2a.z recognition by y11 histone chaperone2 component of srcap/swr1 chromatin remodeling complex
46	d1ehwa_	Alignment	not modelled	14.3	8	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
47	c6melB_	Alignment	not modelled	14.3	29	PDB header: ligase Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta; PDBTitle: succinyl-coa synthase from campylobacter jejuni
48	c1vj5B_	Alignment	not modelled	13.8	21	PDB header: transferase Chain: B: PDB Molecule: 5' polynucleotide kinase-3' phosphatase catalytic domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
49	c1x1qA_	Alignment	not modelled	13.5	13	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
50	c1ezeA_	Alignment	not modelled	13.1	44	PDB header: transferase inhibitor Chain: A: PDB Molecule: cholesteryl ester transferase inhibitor protein; PDBTitle: structural studies of a baboon (papio sp.) plasma protein2 inhibitor of cholesteryl ester transferase.
51	c1w7wF_	Alignment	not modelled	12.6	20	PDB header: transferase Chain: F: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: structure and mutational analysis of a plant mitochondrial nucleoside2 diphosphate kinase: identification of residues involved in serine3 phosphorylation and oligomerization.
52	c5v6dH_	Alignment	not modelled	12.4	15	PDB header: transferase Chain: H: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: crystal structure of nucleoside diphosphate kinase from neisseria2 gonorrhoeae in complex with citrate
53	c5iolC_	Alignment	not modelled	11.8	8	PDB header: transferase Chain: C: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: crystal structure of nucleoside diphosphate kinase from

						schistosoma2 mansoni
54	c1eucB_	Alignment	not modelled	11.6	19	PDB header: ligase Chain: B: PDB Molecule: succinyl-coa synthetase, beta chain; PDBTitle: crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
55	c3bg2A_	Alignment	not modelled	11.2	0	PDB header: hydrolase Chain: A: PDB Molecule: dgtp triphosphohydrolase; PDBTitle: crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
56	c3js9A_	Alignment	not modelled	11.0	17	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate kinase family protein; PDBTitle: crystal structure of nucleoside diphosphate kinase family protein from2 babesia bovis
57	d1jo0a_	Alignment	not modelled	10.7	6	Fold: IF3-like Superfamily: YhbY-like Family: YhbY-like
58	c4ezbA_	Alignment	not modelled	10.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of the conserved hypothetical protein from2 sinorhizobium meliloti 1021
59	c3f9uA_	Alignment	not modelled	10.4	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported cytochrome c biogenesis-related protein; PDBTitle: crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
60	c3zvmA_	Alignment	not modelled	10.4	21	PDB header: hydrolase/transferase/dna Chain: A: PDB Molecule: bifunctional polynucleotide phosphatase/kinase; PDBTitle: the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
61	c6b2zS_	Alignment	not modelled	10.3	44	PDB header: membrane protein Chain: S: PDB Molecule: atp synthase subunit j, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
62	c6b2zi_	Alignment	not modelled	10.3	44	PDB header: membrane protein Chain: I: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
63	d3bzka2	Alignment	not modelled	10.1	19	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
64	c3x38B_	Alignment	not modelled	10.0	6	PDB header: replication regulator Chain: B: PDB Molecule: mitochondrial morphogenesis protein sld7; PDBTitle: crystal structure of the c-terminal domain of sld7
65	c3nbiA_	Alignment	not modelled	10.0	27	PDB header: protein binding Chain: A: PDB Molecule: recq-mediated genome instability protein 1; PDBTitle: crystal structure of human rmi1 n-terminus
66	c4rulA_	Alignment	not modelled	10.0	18	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of full-length e.coli topoisomerase i in complex2 with ssdna
67	c6btdA_	Alignment	not modelled	9.8	14	PDB header: lyase Chain: A: PDB Molecule: fuculose phosphate aldolase; PDBTitle: crystal structure of deoxyribose-phosphate aldolase from bacillus2 thuringiensis involved in dispatching the ubiquitous radical sam3 enzyme byproduct 5-deoxyribose
68	d2nu7b1	Alignment	not modelled	9.3	10	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
69	c2w31A_	Alignment	not modelled	9.3	24	PDB header: oxygen transport Chain: A: PDB Molecule: globin; PDBTitle: globin domain of geobacter sulfurreducens globin-coupled sensor
70	d1wkja1	Alignment	not modelled	9.2	19	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
71	c1oftC_	Alignment	not modelled	9.1	33	PDB header: bacterial cell division inhibitor Chain: C: PDB Molecule: hypothetical protein pa3008; PDBTitle: crystal structure of sula from pseudomonas aeruginosa
72	d1ofux_	Alignment	not modelled	8.9	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Bacterial cell division inhibitor Sula
73	c2fk5B_	Alignment	not modelled	8.8	30	PDB header: lyase Chain: B: PDB Molecule: fuculose-1-phosphate aldolase; PDBTitle: crystal structure of l-fuculose-1-phosphate aldolase from thermus2 thermophilus hb8
74	d2j01d2	Alignment	not modelled	8.7	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
75	c4xdsE_	Alignment	not modelled	8.6	25	PDB header: hydrolase/dna Chain: E: PDB Molecule: deoxyguanosinetriphosphate triphosphohydrolase; PDBTitle: deoxyguanosinetriphosphate triphosphohydrolase from escherichia coli2 with nickel
76	c4ar0A_	Alignment	not modelled	8.4	21	PDB header: transport Chain: A: PDB Molecule: type iv pilus biogenesis and competence protein pilq; PDBTitle: n0 domain of neisseria meningitidis pilus assembly protein pilq
77	c4o0nA_	Alignment	not modelled	8.3	15	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: 2.4 angstrom resolution crystal structure of putative nucleoside2 diphosphate kinase from toxoplasma gondii. PDB header: cell cycle

78	c3ghfA_	Alignment	not modelled	8.0	19	Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from 2 salmonella typhimurium
79	c5j4aA_	Alignment	not modelled	8.0	15	PDB header: toxin Chain: A: PDB Molecule: trna nuclease cdia; PDBTitle: cdia-ct toxin from burkholderia pseudomallei e479 in complex with 2 cognate cdii immunity protein
80	c2mn4A_	Alignment	not modelled	7.8	36	PDB header: de novo protein Chain: A: PDB Molecule: computational designed protein based on structure template PDBTitle: nmr solution structure of a computational designed protein based on 2 structure template 1cy5
81	c3ztqC_	Alignment	not modelled	7.6	23	PDB header: transferase Chain: C: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: hexagonal crystal form p61 of the aquifex aeolicus nucleoside 2 diphosphate kinase
82	c2qdrA_	Alignment	not modelled	7.5	23	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative dioxygenase (npun_f5605) from nostoc 2 punctiforme pcc 73102 at 2.60 a resolution
83	c2vlvA_	Alignment	not modelled	7.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin h isoform 2.; PDBTitle: crystal structure of barley thioredoxin h isoform 2 in partially 2 radiation-reduced state
84	c2dqdB_	Alignment	not modelled	7.4	23	PDB header: hydrolase, dna binding protein Chain: B: PDB Molecule: deoxyguanosinetriphosphate triphosphohydrolase, putative; PDBTitle: crystal structure of dntp triphosphohydrolase from thermus 2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
85	d2ipqx1	Alignment	not modelled	7.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: STY4665 C-terminal domain-like
86	c2mdtA_	Alignment	not modelled	7.3	15	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilt n-terminus domain protein sso1118 from hyperthermophilic 2 archaeon sulfobolus solfataricus p2
87	d1h2vc2	Alignment	not modelled	7.2	17	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
88	d2dfaa1	Alignment	not modelled	6.7	21	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
89	d1auaa2	Alignment	not modelled	6.7	12	Fold: SpolIaa-like Superfamily: CRAL/TRIO domain Family: CRAL/TRIO domain
90	c6c8vA_	Alignment	not modelled	6.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
91	d1r9wa_	Alignment	not modelled	6.7	23	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Replication initiation protein E1
92	d1s5qb_	Alignment	not modelled	6.7	33	Fold: PAH2 domain Superfamily: PAH2 domain Family: PAH2 domain
93	c3mwdA_	Alignment	not modelled	6.6	13	PDB header: transferase Chain: A: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound
94	d1rq8a_	Alignment	not modelled	6.6	9	Fold: IF3-like Superfamily: YhbY-like Family: YhbY-like
95	c4uqzB_	Alignment	not modelled	6.6	67	PDB header: protein transport Chain: B: PDB Molecule: hsib1; PDBTitle: coevolution of the atpase clpv, the tssb-tssc sheath and 2 the accessory hsie protein distinguishes two type vi3 secretion classes
96	d1bl0a2	Alignment	not modelled	6.6	40	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
97	c3ufxG_	Alignment	not modelled	6.5	23	PDB header: ligase Chain: G: PDB Molecule: succinyl-coa synthetase beta subunit; PDBTitle: thermus aquaticus succinyl-coa synthetase in complex with gdp-mn2+
98	d1xiga_	Alignment	not modelled	6.4	13	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
99	c4dutA_	Alignment	not modelled	6.4	19	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: the structure of nucleoside diphosphate kinase (ndk) from burkholderia 2 thailandensis