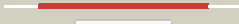



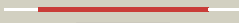
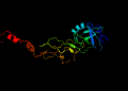



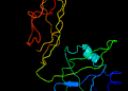









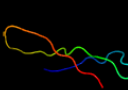

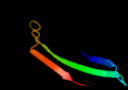
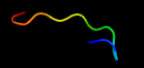
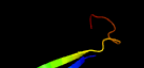
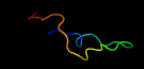
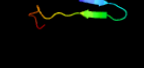
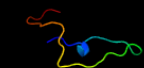

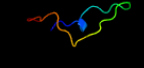
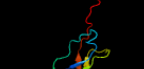



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1015c_(rplY)_1133925_1134572
Date	Wed Jul 31 22:05:08 BST 2019
Unique Job ID	244c8d6a0ef5e59a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60W_	 Alignment		100.0	76	PDB header: ribosome Chain: W; PDB Molecule: 50s ribosomal protein l25; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	d1feua_	 Alignment		100.0	26	Fold: Ribosomal protein L25-like Superfamily: Ribosomal protein L25-like Family: Ribosomal protein L25-like
3	c1njpT_	 Alignment		100.0	30	PDB header: ribosome Chain: T; PDB Molecule: general stress protein ctc; PDBTitle: the crystal structure of the 50s large ribosomal subunit2 from deinococcus radiodurans complexed with a trna3 acceptor stem mimic (asm)
4	d2zjrs1	 Alignment		100.0	30	Fold: Ribosomal protein L25-like Superfamily: Ribosomal protein L25-like Family: Ribosomal protein L25-like
5	c2b9nZ_	 Alignment		100.0	30	PDB header: ribosome Chain: Z; PDB Molecule: 50s ribosomal protein ctc; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf2,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400.
6	c4wfbS_	 Alignment		100.0	25	PDB header: ribosome Chain: S; PDB Molecule: 50s ribosomal protein l25; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with bc-3205
7	c5iznH_	 Alignment		100.0	34	PDB header: ribosomal protein Chain: H; PDB Molecule: 50s ribosomal protein l25; PDBTitle: the crystal structure of 50s ribosomal protein l25 from vibrio2 vulnificus cmcp6
8	d1dfup_	 Alignment		100.0	34	Fold: Ribosomal protein L25-like Superfamily: Ribosomal protein L25-like Family: Ribosomal protein L25-like
9	d1bdfa2	 Alignment		61.2	20	Fold: Insert subdomain of RNA polymerase alpha subunit Superfamily: Insert subdomain of RNA polymerase alpha subunit Family: Insert subdomain of RNA polymerase alpha subunit
10	c2kpsA_	 Alignment		58.1	28	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution structure of domain iv from the ybbr family protein of2 desulfitobacterium hafnience
11	c2lyxA_	 Alignment		45.6	12	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein yqzg; PDBTitle: nmr structure of the protein np_390345.1 from bacilus subtilis

12	d1zaka2	Alignment		43.3	25	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
13	d1htwa_	Alignment		37.7	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: YjeE-like
14	d1ynja2	Alignment		35.6	25	Fold: Insert subdomain of RNA polymerase alpha subunit Superfamily: Insert subdomain of RNA polymerase alpha subunit Family: Insert subdomain of RNA polymerase alpha subunit
15	c6fpeE_	Alignment		31.4	27	PDB header: rna binding protein Chain: E: PDB Molecule: atpase yjee, predicted to have essential role in cell wall PDBTitle: bacterial protein complex
16	c6j9eA_	Alignment		31.2	23	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: cryo-em structure of xanthomonos oryzae transcription elongation2 complex with nusa and the bacteriophage protein p7
17	c5tw1A_	Alignment		29.1	34	PDB header: transcription activator/transferase/dna Chain: A: PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
18	c1bdfC_	Alignment		28.6	18	PDB header: nucleotidyltransferase Chain: C: PDB Molecule: rna polymerase alpha subunit; PDBTitle: structure of escherichia coli rna polymerase alpha subunit2 n-terminal domain
19	c5hqhA_	Alignment		28.5	16	PDB header: unknown function Chain: A: PDB Molecule: lmo2119 protein; PDBTitle: 1.32 angstrom crystal structure of ybbr like domain of lmo2119 protein2 from listeria monocytogenes.
20	c2nvgA_	Alignment		26.0	39	PDB header: oxidoreductase Chain: A: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: soluble domain of rieske iron sulfur protein.
21	c3uc2A_	Alignment	not modelled	24.9	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein with immunoglobulin-like fold; PDBTitle: crystal structure of a duf4426 family protein (pa0388) from2 pseudomonas aeruginosa pao1 at 2.09 a resolution
22	c5j2dA_	Alignment	not modelled	23.9	24	PDB header: transcription/dna/rna Chain: A: PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: crystal structure of t. thermophilus thtb099 class ii transcription2 activation complex: tap-rpo
23	c4ywkA_	Alignment	not modelled	23.6	21	PDB header: cell cycle Chain: A: PDB Molecule: cell division control protein 21; PDBTitle: pyrococcus furiosus mcm n-terminal domain with zinc-binding subdomain2 b deleted
24	c5k5wA_	Alignment	not modelled	22.5	22	PDB header: metal binding protein Chain: A: PDB Molecule: limiting co2-inducible protein lcib; PDBTitle: crystal structure of limiting co2-inducible protein lcib
25	d1bh9b_	Alignment	not modelled	18.5	50	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
26	c3x37B_	Alignment	not modelled	18.1	26	PDB header: replication regulator Chain: B: PDB Molecule: mitochondrial morphogenesis protein sld7; PDBTitle: crystal structure of the n-terminal domain of sid7 in complex with2 sld3
27	c2j8aA_	Alignment	not modelled	18.0	13	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-4 PDBTitle: x-ray structure of the n-terminus rrm domain of set1
28	c1q7lB_	Alignment	not modelled	16.8	24	PDB header: hydrolase Chain: B: PDB Molecule: aminoacylase-1; PDBTitle: zn-binding domain of the t347g mutant of human

						aminoacylase-2 i
29	c1vhoA_	Alignment	not modelled	16.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of a putative peptidase/endoglucanase
30	c2pmzS_	Alignment	not modelled	16.6	16	PDB header: translation, transferase Chain: S: PDB Molecule: dna-directed rna polymerase subunit d; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
31	d1h6kx_	Alignment	not modelled	13.0	7	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
32	c3vzaD_	Alignment	not modelled	12.6	15	PDB header: cell cycle Chain: D: PDB Molecule: spc24 protein; PDBTitle: crystal structure of the chicken spc24-spc25 globular domain in2 complex with cenp-t peptide
33	d2phpa1	Alignment	not modelled	12.3	32	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: Phosphomethylpyrimidine kinase C-terminal domain-like
34	d1riea_	Alignment	not modelled	11.9	6	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
35	c4jspA_	Alignment	not modelled	11.8	27	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase mtor; PDBTitle: structure of mtor-delta-mlst8-atp-gamma-mg complex
36	c4noiA_	Alignment	not modelled	11.1	11	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: 2.17 angstrom crystal structure of dna-directed rna polymerase subunit2 alpha from campylobacter jejuni.
37	c1smyB_	Alignment	not modelled	10.7	23	PDB header: transferase Chain: B: PDB Molecule: dna-directed rna polymerase alpha chain; PDBTitle: structural basis for transcription regulation by alarmone2 ppppp
38	c5mvrA_	Alignment	not modelled	10.7	12	PDB header: transferase Chain: A: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsae; PDBTitle: crystal structure of bacillus subtilus ydib
39	c5yz0A_	Alignment	not modelled	10.5	13	PDB header: cell cycle Chain: A: PDB Molecule: serine/threonine-protein kinase atr; PDBTitle: cryo-em structure of human atr-atr complex
40	c6j69A_	Alignment	not modelled	10.5	33	PDB header: cell cycle Chain: A: PDB Molecule: protein kibra; PDBTitle: structure of kibra and dendrin complex
41	c5jbfB_	Alignment	not modelled	10.4	31	PDB header: transferase Chain: B: PDB Molecule: inactive glucanucrase; PDBTitle: 4,6-alpha-glucanotransferase gtff (d1015n mutant) from lactobacillus2 reuteri 121 complexed with maltopentaose
42	d2hgca1	Alignment	not modelled	10.3	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: YjcQ-like
43	c2hgca_	Alignment	not modelled	10.3	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yjcq protein; PDBTitle: solution nmr structure of the yjcq protein from bacillus2 subtilis. northeast structural genomics target sr346.
44	c1vixA_	Alignment	not modelled	10.3	14	PDB header: hydrolase Chain: A: PDB Molecule: peptidase t; PDBTitle: crystal structure of a putative peptidase t
45	c5htsF_	Alignment	not modelled	10.1	24	PDB header: cell adhesion Chain: F: PDB Molecule: cell surface protein spaa; PDBTitle: crystal structure of shaft pilin spaa from lactobacillus rhamnosus gg2 - d295n mutant
46	c3ls8A_	Alignment	not modelled	10.1	22	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol 3-kinase catalytic subunit PDBTitle: crystal structure of human pik3c3 in complex with 3-[4-(4-2 morpholinyl)thieno[3,2-d]pyrimidin-2-yl]-phenol
47	c2kq1A_	Alignment	not modelled	10.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh0266 protein; PDBTitle: solution structure of protein bh0266 from bacillus2 halodurans. northeast structural genomics consortium target3 bhr97a
48	d1u6ma_	Alignment	not modelled	9.6	17	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
49	c4j2nA_	Alignment	not modelled	9.4	26	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
50	c5h64a_	Alignment	not modelled	9.3	27	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase mtor; PDBTitle: cryo-em structure of mtorc1
51	c4lhfa_	Alignment	not modelled	9.3	37	PDB header: viral protein Chain: A: PDB Molecule: regulatory protein cox; PDBTitle: crystal structure of a dna binding protein from phage p2
52	c4d0mW_	Alignment	not modelled	9.2	33	PDB header: signaling protein Chain: W: PDB Molecule: phosphatidylinositol 4-kinase beta; PDBTitle: phosphatidylinositol 4-kinase iii beta in a complex with rab11a-gtp-2 gamma-s and the rab-binding domain of fip3
53	d1e7ua4	Alignment	not modelled	9.0	22	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Phosphoinositide 3-kinase (PI3K), catalytic domain
54	c3rzaA_	Alignment	not modelled	8.6	23	PDB header: hydrolase Chain: A: PDB Molecule: tripeptidase; PDBTitle: crystal structure of a tripeptidase (sav1512) from staphylococcus2 aureus subsp. aureus mu50 at 2.10 a resolution

55	c4j2nB_	Alignment	not modelled	8.6	26	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
56	c5bxbB_	Alignment	not modelled	8.6	22	PDB header: protein binding Chain: B: PDB Molecule: btb/poz domain-containing protein kctd1; PDBTitle: crystal structure of pentameric kctd1 btb domain form 1
57	c2x6kB_	Alignment	not modelled	8.3	22	PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3 kinase 59f; PDBTitle: the crystal structure of the drosophila class iii pi3-kinase vps34 in2 complex with pi-103
58	c5fvmB_	Alignment	not modelled	8.3	27	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase tor2; PDBTitle: cryo electron microscopy of a complex of tor and lst8
59	d1wi6a1	Alignment	not modelled	8.2	12	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
60	c5of1A_	Alignment	not modelled	7.9	29	PDB header: protein fibril Chain: A: PDB Molecule: spore coat-associated protein n; PDBTitle: the structural versatility of tasa in b. subtilis biofilm formation
61	c2kxyA_	Alignment	not modelled	7.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of sur18c from streptococcus thermophilus.2 northeast structural genomics consortium target sur18c
62	c1r7iB_	Alignment	not modelled	7.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxy-3-methylglutaryl-coenzyme a reductase; PDBTitle: hmg-coa reductase from p. mevalonii, native structure at 2.2 angstroms2 resolution.
63	c6az1S_	Alignment	not modelled	7.6	25	PDB header: ribosome/antibiotic Chain: S: PDB Molecule: ribosomal protein s14; PDBTitle: cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin
64	d1whxa_	Alignment	not modelled	7.5	7	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
65	c2y7uM_	Alignment	not modelled	7.5	16	PDB header: virus Chain: M: PDB Molecule: coat protein; PDBTitle: x-ray structure of the grapevine fanleaf virus
66	d1qo5b_	Alignment	not modelled	7.4	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
67	c6jxaA_	Alignment	not modelled	7.3	20	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase tel1; PDBTitle: tel1 kinase compact monomer
68	c3mmtC_	Alignment	not modelled	7.2	29	PDB header: hydrolase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose bisphosphate aldolase from bartonella2 henselae, bound to fructose bisphosphate
69	c5xonV_	Alignment	not modelled	7.2	13	PDB header: transcription/rna Chain: V: PDB Molecule: transcription elongation factor spt4; PDBTitle: rna polymerase ii elongation complex bound with spt4/5 and tfiis
70	c4qjvC_	Alignment	not modelled	7.0	14	PDB header: transferase Chain: C: PDB Molecule: dna-directed rna polymerase subunit d; PDBTitle: the x-ray crystal structure of rpo3/rpo11 heterodimer of euryarchaeal2 rna polymerase from thermococcus kodakarensis
71	c5is5A_	Alignment	not modelled	7.0	22	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic PDBTitle: discovery and pharmacological characterization of novel quinazoline-2 based pi3k delta-selective inhibitors
72	c2dgyA_	Alignment	not modelled	7.0	14	PDB header: translation Chain: A: PDB Molecule: mgc11102 protein; PDBTitle: solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
73	c4crhA_	Alignment	not modelled	6.9	23	PDB header: protein-binding protein Chain: A: PDB Molecule: sh3kbp1-binding protein 1; PDBTitle: crystal structure of the btb-t1 domain of human shkbp1
74	d1nn7a_	Alignment	not modelled	6.6	17	Fold: POZ domain Superfamily: POZ domain Family: Tetramerization domain of potassium channels
75	d1fdja_	Alignment	not modelled	6.6	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
76	d1rqpa1	Alignment	not modelled	6.6	6	Fold: Bacterial fluorinating enzyme, C-terminal domain Superfamily: Bacterial fluorinating enzyme, C-terminal domain Family: Bacterial fluorinating enzyme, C-terminal domain
77	c2y3aA_	Alignment	not modelled	6.5	22	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic PDBTitle: crystal structure of p110beta in complex with icsh2 of p85beta and the2 drug gdc-0941
78	d1rl6a1	Alignment	not modelled	6.5	23	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
79	c3qauA_	Alignment	not modelled	6.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxy-3-methylglutaryl-coenzyme a reductase; PDBTitle: 3-hydroxy-3-methylglutaryl-coenzyme a reductase from streptococcus2 pneumoniae
80	c5np0A_	Alignment	not modelled	6.4	27	PDB header: signaling protein Chain: A: PDB Molecule: serine-protein kinase atm;

80	c3npvA	Alignment	not modelled	6.4	47	PDBTitle: closed dimer of human atm (ataxia telangiectasia mutated)
81	c3g5bA	Alignment	not modelled	6.3	10	PDB header: apoptosis Chain: A: PDB Molecule: netrin receptor unc5b; PDBTitle: the structure of unc5b cytoplasmic domain
82	c3iydA	Alignment	not modelled	6.3	21	PDB header: transcription/dna Chain: A: PDB Molecule: dna-directed rna polymerase subunit alpha; PDBTitle: three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
83	c2rb7A	Alignment	not modelled	6.3	24	PDB header: hydrolase Chain: A: PDB Molecule: peptidase, m20/m25/m40 family; PDBTitle: crystal structure of co-catalytic metallopeptidase (yp_387682.1) from2 desulfovibrio desulfuricans g20 at 1.60 a resolution
84	d1etha1	Alignment	not modelled	6.3	18	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Colipase-binding domain
85	c5x6oC	Alignment	not modelled	6.2	13	PDB header: transferase/dna binding protein Chain: C: PDB Molecule: serine/threonine-protein kinase mec1; PDBTitle: intact atr/mec1-atrip/ddc2 complex
86	c5zcsB	Alignment	not modelled	6.2	27	PDB header: gene regulation Chain: B: PDB Molecule: serine/threonine-protein kinase mtor; PDBTitle: 4.9 angstrom cryo-em structure of human mtor complex 2
87	c1e8zA	Alignment	not modelled	6.1	22	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol 3-kinase catalytic subunit; PDBTitle: structure determinants of phosphoinositide 3-kinase2 inhibition by wortmannin, ly294002, quercetin, myricetin3 and staurosporine
88	d1smya2	Alignment	not modelled	6.1	17	Fold: Insert subdomain of RNA polymerase alpha subunit Superfamily: Insert subdomain of RNA polymerase alpha subunit Family: Insert subdomain of RNA polymerase alpha subunit
89	c2wxoA	Alignment	not modelled	6.1	22	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic PDBTitle: the crystal structure of the murine class ia pi 3-kinase p110delta in2 complex with as5.
90	c1jgnB	Alignment	not modelled	6.1	40	PDB header: rna binding protein Chain: B: PDB Molecule: polyadenylate-binding protein-interacting PDBTitle: solution structure of the c-terminal pabc domain of human2 poly(a)-binding protein in complex with the peptide from3 paip2
91	c3ifeA	Alignment	not modelled	6.0	17	PDB header: hydrolase Chain: A: PDB Molecule: peptidase t; PDBTitle: 1.55 angstrom resolution crystal structure of peptidase t (pept-1)2 from bacillus anthracis str. 'ames ancestor'.
92	c5dxuA	Alignment	not modelled	6.0	22	PDB header: transferase/inhibitor Chain: A: PDB Molecule: phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic PDBTitle: p110delta/p85alpha with gdc-0326
93	d1xfba1	Alignment	not modelled	5.9	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
94	d1zaia1	Alignment	not modelled	5.8	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
95	d1z2la1	Alignment	not modelled	5.8	7	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
96	c2pc4B	Alignment	not modelled	5.7	16	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
97	c5np1A	Alignment	not modelled	5.7	27	PDB header: transferase Chain: A: PDB Molecule: serine-protein kinase atm; PDBTitle: open protomer of human atm (ataxia telangiectasia mutated)
98	c3ju3A	Alignment	not modelled	5.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; PDBTitle: crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
99	d1a5ca	Alignment	not modelled	5.6	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase