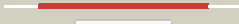



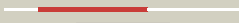


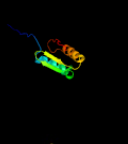



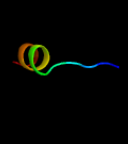
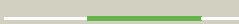
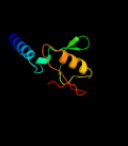





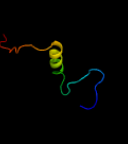




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0566c (-) _657551_658042
Date	Fri Jul 26 01:50:12 BST 2019
Unique Job ID	eb297e9356e4b7b8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1in0B_	 Alignment		100.0	43	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yajq protein; PDBTitle: yajq protein (hi1034)
2	c5b7wB_	 Alignment		100.0	40	PDB header: unknown function Chain: B: PDB Molecule: upf0234 protein xc_3703; PDBTitle: crystal structure of the yajq-family protein xc_3703 from xanthomonas2 campestris pv.campestris
3	d1in0a1	 Alignment		100.0	29	Fold: Ferredoxin-like Superfamily: YajQ-like Family: YajQ-like
4	d1in0a2	 Alignment		100.0	59	Fold: Ferredoxin-like Superfamily: YajQ-like Family: YajQ-like
5	d1wiha_	 Alignment		69.0	23	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
6	c2lvaA_	 Alignment		58.5	57	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 28; PDBTitle: nmr solution structure of the n-terminal domain of human usp28,2 northeast structural genomics consortium target ht8470a
7	d1wqga1	 Alignment		55.1	21	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
8	c2muxA_	 Alignment		54.2	50	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 25; PDBTitle: sumo2 non-covalently interacts with usp25 and downregulates its2 activity
9	d1vqoe2	 Alignment		49.6	16	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
10	c3aqaD_	 Alignment		49.3	17	PDB header: membrane protein Chain: D: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: structure and function of a membrane component secdf that enhances2 protein export
11	c2kyzA_	 Alignment		46.3	26	PDB header: metal binding protein Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima

12	c4gfqA_	Alignment		44.1	16	PDB header: translation Chain: A; PDB Molecule: ribosome-recycling factor; PDBTitle: 2.65 angstrom resolution crystal structure of ribosome recycling2 factor (frr) from bacillus anthracis
13	d1ek8a_	Alignment		44.0	16	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
14	d1is1a_	Alignment		42.5	23	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
15	d1eh1a_	Alignment		39.8	16	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
16	c4alzA_	Alignment		33.1	15	PDB header: membrane protein Chain: A; PDB Molecule: yop proteins translocation protein d; PDBTitle: the yersinia t3ss basal body component yscd reveals a different2 structural periplasmic domain organization to known homologue prgh
17	c5lq6A_	Alignment		29.5	26	PDB header: immunosuppressant Chain: A; PDB Molecule: virulence protein vsde; PDBTitle: salmonella effector spvd - r161 variant
18	c4djgA_	Alignment		26.8	32	PDB header: protein binding Chain: A; PDB Molecule: plectin-related protein; PDBTitle: crystal structure of the coiled-coil 1 domain of actin-binding protein2 scab1
19	c3ci9B_	Alignment		24.1	10	PDB header: transcription Chain: B; PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
20	d1yq2a1	Alignment		21.0	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
21	c4mo0A_	Alignment	not modelled	19.4	15	PDB header: translation Chain: A; PDB Molecule: protein translation factor sui1 homolog; PDBTitle: crystal structure of aif1 from methanocaldococcus jannaschii
22	d1j2jb_	Alignment	not modelled	19.3	29	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
23	c4cvoA_	Alignment	not modelled	19.2	46	PDB header: hydrolase Chain: A; PDB Molecule: dna excision repair protein ercc-6; PDBTitle: crystal structure of the n-terminal coiled-coil domain of human dna2 excision repair protein ercc-6
24	d1vpka2	Alignment	not modelled	18.7	17	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase III, beta subunit
25	d2if1a_	Alignment	not modelled	18.5	17	Fold: eIF1-like Superfamily: eIF1-like Family: eIF1-like
26	d1jz8a2	Alignment	not modelled	18.5	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
27	c2jpiA_	Alignment	not modelled	18.1	20	PDB header: structural genomics Chain: A; PDB Molecule: hypothetical protein; PDBTitle: chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
28	c5wceB_	Alignment	not modelled	18.0	15	PDB header: transferase Chain: B; PDB Molecule: dna polymerase iii subunit beta; PDBTitle: caulobacter crescentus pol iii beta
						Fold: beta-Grasp (ubiquitin-like)

29	d1wxma1	Alignment	not modelled	18.0	15	Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
30	d1nh2a1	Alignment	not modelled	17.9	13	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
31	d1pvgA2	Alignment	not modelled	17.7	17	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
32	c3fryB_	Alignment	not modelled	16.8	20	PDB header: hydrolase Chain: B: PDB Molecule: probable copper-exporting p-type atpase a; PDBTitle: crystal structure of the copa c-terminal metal binding domain
33	d1hywa_	Alignment	not modelled	16.4	29	Fold: gpW/XkdW-like Superfamily: Head-to-tail joining protein W, gpW Family: Head-to-tail joining protein W, gpW
34	d1e32a1	Alignment	not modelled	16.3	50	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
35	c1x7fa_	Alignment	not modelled	16.3	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: outer surface protein; PDBTitle: crystal structure of an uncharacterized b. cereus protein
36	c3ijmA_	Alignment	not modelled	15.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized restriction endonuclease-like fold PDBTitle: the structure of a restriction endonuclease-like fold superfamily2 protein from spiroplasma linguale.
37	c1bo1A_	Alignment	not modelled	15.6	17	PDB header: transferase Chain: A: PDB Molecule: protein (phosphatidylinositol phosphate kinase PDBTitle: phosphatidylinositol phosphate kinase type ii beta
38	d1bo1a_	Alignment	not modelled	15.6	17	Fold: SAICAR synthase-like Superfamily: SAICAR synthase-like Family: Phosphatidylinositol phosphate kinase IIbeta, PIPK IIbeta
39	d1x7fa2	Alignment	not modelled	15.1	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain
40	d1ge9a_	Alignment	not modelled	14.6	24	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
41	d1dd5a_	Alignment	not modelled	14.5	17	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
42	c5nocA_	Alignment	not modelled	14.5	18	PDB header: dna binding protein Chain: A: PDB Molecule: stage 0 sporulation protein j; PDBTitle: solution nmr structure of the c-terminal domain of parb (spo0j)
43	c4tz7A_	Alignment	not modelled	14.1	25	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol-4-phosphate 5-kinase, type i, alpha; PDBTitle: crystal structure of type i phosphatidylinositol 4-phosphate 5-kinase2 alpha from zebrafish
44	c1vpkA_	Alignment	not modelled	13.2	14	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii, beta subunit; PDBTitle: crystal structure of dna polymerase iii, beta subunit (tm0262) from2 thermotoga maritima at 2.00 a resolution
45	c2gk9D_	Alignment	not modelled	13.0	27	PDB header: transferase Chain: D: PDB Molecule: phosphatidylinositol-4-phosphate 5-kinase, type ii, gamma; PDBTitle: human phosphatidylinositol-4-phosphate 5-kinase, type ii, gamma
46	c4rkiA_	Alignment	not modelled	12.8	10	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit beta; PDBTitle: crystal structure of sliding beta clamp from helicobacter pylori
47	c5zcyA_	Alignment	not modelled	12.7	15	PDB header: translation Chain: A: PDB Molecule: protein translation factor sui1 homolog; PDBTitle: crystal structure of archaeal translation initiation factor 1 at 1.52 angstroms resolution
48	c5uz5C_	Alignment	not modelled	12.6	24	PDB header: nuclear protein/rna Chain: C: PDB Molecule: u1 small nuclear ribonucleoprotein a,tap tag; PDBTitle: s. cerevisiae u1 snrnp
49	d1qnaa1	Alignment	not modelled	12.5	13	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
50	c2ftcF_	Alignment	not modelled	12.4	24	PDB header: ribosome Chain: F: PDB Molecule: 39s ribosomal protein I12, mitochondrial; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
51	d1cdwa1	Alignment	not modelled	11.3	13	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
52	c3fb1A_	Alignment	not modelled	11.2	50	PDB header: structural protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of orf132 of the archaeal virus acidianus2 filamentous virus 1 (afv1)
53	d1cc8a_	Alignment	not modelled	10.9	13	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
54	c5dtcA_	Alignment	not modelled	10.9	18	PDB header: protein binding Chain: A: PDB Molecule: ribosome biogenesis protein ytm1; PDBTitle: ubl structure

55	c4y2iA_	Alignment	not modelled	10.0	22	PDB header: metal transport Chain: A: PDB Molecule: putative metal-binding transport protein; PDBTitle: gold ion bound to golb
56	d1ok7a2	Alignment	not modelled	9.9	9	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase III, beta subunit
57	c6gsiK_	Alignment	not modelled	9.8	38	PDB header: virus Chain: K: PDB Molecule: vp2; PDBTitle: feline calicivirus strain f9 bound to a soluble ectodomain fragment of f2 feline junctional adhesion molecule a - leading to assembly of a3 portal structure at a unique three-fold axis.
58	d1jcb4	Alignment	not modelled	9.3	19	Fold: Ferredoxin-like Superfamily: Anticodon-binding domain of PheRS Family: Anticodon-binding domain of PheRS
59	c6gy4B_	Alignment	not modelled	9.3	21	PDB header: rna binding protein Chain: B: PDB Molecule: protein bicaudal c homolog 1; PDBTitle: crystal structure of the n-terminal kh domain of human bicc1
60	c5mu4A_	Alignment	not modelled	9.2	30	PDB header: viral protein Chain: A: PDB Molecule: tail tubular protein a; PDBTitle: tail tubular protein a of klebsiella pneumoniae bacteriophage kp32
61	c1giyl_	Alignment	not modelled	9.1	40	PDB header: ribosome Chain: J: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of the ribosome at 5.5 a resolution. this2 file, 1giy, contains the 50s ribosome subunit. the 30s3 ribosome subunit, three trna, and mrna molecules are in the4 file 1gix
62	c3lnuA_	Alignment	not modelled	9.0	21	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase iv subunit b; PDBTitle: crystal structure of pare subunit
63	c3nzqB_	Alignment	not modelled	8.9	15	PDB header: lyase Chain: B: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
64	c6gsil_	Alignment	not modelled	8.8	38	PDB header: virus Chain: I: PDB Molecule: vp2; PDBTitle: feline calicivirus strain f9 bound to a soluble ectodomain fragment of f2 feline junctional adhesion molecule a - leading to assembly of a3 portal structure at a unique three-fold axis.
65	c6ivsA_	Alignment	not modelled	8.7	32	PDB header: transcription Chain: A: PDB Molecule: anti-sigma-i factor rsg1; PDBTitle: solution structure of the n-terminal domain of the anti-sigma factor2 rsg1 from clostridium thermocellum
66	d1dd3a2	Alignment	not modelled	8.5	40	Fold: ClpS-like Superfamily: ClpS-like Family: Ribosomal protein L7/12, C-terminal domain
67	c2g0cA_	Alignment	not modelled	8.4	15	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dbpa; PDBTitle: structure of the rna binding domain (residues 404-479) of the bacillus2 subtilis yxin protein
68	c4b6ai_	Alignment	not modelled	8.4	19	PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein l10; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
69	c2gva3_	Alignment	not modelled	8.2	36	PDB header: ribosome Chain: 3: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: structure of the 50s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056
70	c4f6cA_	Alignment	not modelled	8.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: ausa reductase domain protein; PDBTitle: crystal structure of aureusimine biosynthetic cluster reductase domain
71	c2xznF_	Alignment	not modelled	7.9	18	PDB header: ribosome Chain: F: PDB Molecule: eif1; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
72	d1ctfa_	Alignment	not modelled	7.9	38	Fold: ClpS-like Superfamily: ClpS-like Family: Ribosomal protein L7/12, C-terminal domain
73	c2yx5A_	Alignment	not modelled	7.8	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0062 protein mj1593; PDBTitle: crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
74	c1vw4c_	Alignment	not modelled	7.8	14	PDB header: ribosome Chain: C: PDB Molecule: PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
75	c3j3bi_	Alignment	not modelled	7.7	40	PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein l10-like; PDBTitle: structure of the human 60s ribosomal proteins
76	c6p0qA_	Alignment	not modelled	7.5	26	PDB header: rna binding protein Chain: A: PDB Molecule: ribosome biogenesis protein wdr12; PDBTitle: crystal structure of ubiquitin-like domain of human wdr12
77	d2cc6a1	Alignment	not modelled	7.4	25	Fold: Dodecin subunit-like Superfamily: Dodecin-like Family: Dodecin-like
78	c3n2oA_	Alignment	not modelled	7.2	13	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
79	d1vjea_	Alianment	not modelled	7.2	26	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase

						Family: Autoinducer-2 production protein LuxS
80	c3m0zD_	Alignment	not modelled	7.1	29	PDB header: lyase Chain: D: PDB Molecule: putative aldolase; PDBTitle: crystal structure of putative aldolase from klebsiella pneumoniae.
81	c3ke2A_	Alignment	not modelled	7.1	27	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yp_928783.1; PDBTitle: crystal structure of a duf2131 family protein (sama_2911) from shewanella amazonensis sb2b at 2.50 a resolution
82	c3k1tA_	Alignment	not modelled	7.1	6	PDB header: ligase Chain: A: PDB Molecule: glutamate--cysteine ligase gsha; PDBTitle: crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
83	c1zuyB_	Alignment	not modelled	7.0	20	PDB header: contractile protein Chain: B: PDB Molecule: myosin-5 isoform; PDBTitle: high-resolution structure of yeast myo5 sh3 domain
84	c4a19Q_	Alignment	not modelled	7.0	20	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l36; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
85	c1d1rA_	Alignment	not modelled	6.9	15	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 11.4 kd protein ycih in pyrfo-smb PDBTitle: nmr solution structure of the product of the e. coli ycih2 gene.
86	d1d1ra_	Alignment	not modelled	6.9	15	Fold: eIF1-like Superfamily: eIF1-like Family: eIF1-like
87	c1mv4B_	Alignment	not modelled	6.8	44	PDB header: de novo protein Chain: B: PDB Molecule: tropomyosin 1 alpha chain; PDBTitle: tm9a251-284: a peptide model of the c-terminus of a rat2 striated alpha tropomyosin
88	c4jwhB_	Alignment	not modelled	6.7	17	PDB header: transferase Chain: B: PDB Molecule: trna (guanine(9)-n1)-methyltransferase; PDBTitle: crystal structure of sptm10(full length)-sah complex
89	c3okqA_	Alignment	not modelled	6.6	58	PDB header: protein binding Chain: A: PDB Molecule: bud site selection protein 6; PDBTitle: crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
90	c5mlpA_	Alignment	not modelled	6.5	24	PDB header: ligase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of cdps from rickettsiella grylli
91	c4a54A_	Alignment	not modelled	6.4	24	PDB header: rna binding protein/hydrolase Chain: A: PDB Molecule: edc3; PDBTitle: structural basis of the dcp1:dcp2 mrna decapping complex activation2 by edc3 and scd6
92	d1rfza_	Alignment	not modelled	6.4	10	Fold: YutG-like Superfamily: YutG-like Family: YutG-like
93	c2zjq5_	Alignment	not modelled	6.4	32	PDB header: ribosome Chain: 5: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: interaction of l7 with l11 induced by micrococcin binding to the2 deinococcus radiodurans 50s subunit
94	d2zjq51	Alignment	not modelled	6.4	32	Fold: ClpS-like Superfamily: ClpS-like Family: Ribosomal protein L7/12, C-terminal domain
95	c3izck_	Alignment	not modelled	6.3	19	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein rpl16 (l13p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
96	c4tr6A_	Alignment	not modelled	6.2	14	PDB header: dna binding protein Chain: A: PDB Molecule: dna polymerase iii subunit beta; PDBTitle: crystal structure of dna polymerase sliding clamp from bacillus2 subtilis
97	c4phxE_	Alignment	not modelled	6.0	50	PDB header: cell adhesion Chain: E: PDB Molecule: protein aggb; PDBTitle: crystal structure of aggb, the minor subunit of aggregative adherence2 fimbriae type i from the escherichia coli o4h104
98	c3j39i_	Alignment	not modelled	6.0	38	PDB header: ribosome Chain: l: PDB Molecule: 60s ribosomal protein l10; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
99	c5w7gV_	Alignment	not modelled	6.0	57	PDB header: virus Chain: V: PDB Molecule: orf132; PDBTitle: an envelope of a filamentous hyperthermophilic virus carries lipids in2 a horseshoe conformation