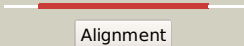

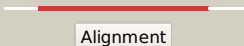

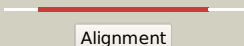







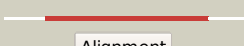




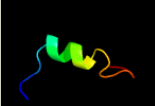

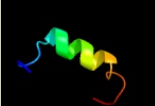


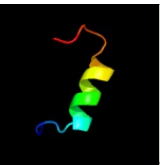
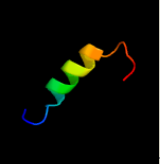

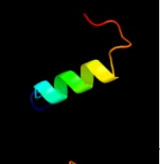

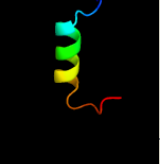
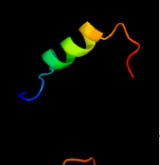
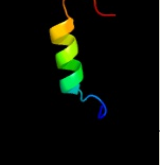
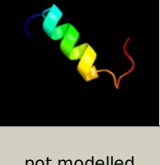


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1159A_phhB_1286289_1286573
Date	Wed Jul 31 22:05:24 BST 2019
Unique Job ID	fcacb5c8a5f7ce80

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ebbA_	 Alignment		100.0	32	PDB header: lyase Chain: A: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
2	c3jstA_	 Alignment		100.0	36	PDB header: lyase Chain: A: PDB Molecule: putative pterin-4-alpha-carbinolamine dehydratase; PDBTitle: crystal structure of transcriptional coactivator/pterin dehydratase2 from brucella melitensis
3	d1ru0a_	 Alignment		100.0	29	Fold: DCoH-like Superfamily: PCD-like Family: PCD-like
4	d1dcpa_	 Alignment		100.0	30	Fold: DCoH-like Superfamily: PCD-like Family: PCD-like
5	c2v6uB_	 Alignment		100.0	28	PDB header: lyase Chain: B: PDB Molecule: pterin-4a-carbinolamine dehydratase; PDBTitle: high resolution crystal structure of pterin-4a-2 carbinolamine dehydratase from toxoplasma gondii
6	d1usma_	 Alignment		99.9	37	Fold: DCoH-like Superfamily: PCD-like Family: PCD-like
7	c4lowA_	 Alignment		99.9	24	PDB header: unknown function Chain: A: PDB Molecule: acraf; PDBTitle: structure and identification of a pterin dehydratase-like protein as a2 rubisco assembly factor in the alpha-carboxysome
8	c1z9bA_	 Alignment		61.2	36	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: solution structure of the c1-subdomain of bacillus2 stearothermophilus translation initiation factor if2
9	c5mz2I_	 Alignment		59.4	24	PDB header: photosynthesis Chain: I: PDB Molecule: rubisco small subunit; PDBTitle: rubisco from thalassiosira antarctica
10	d1bwvs_	 Alignment		59.3	24	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
11	d1a8ya3	 Alignment		58.0	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Caisequestrin

12	d1svdm1	Alignment		55.0	18	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
13	d1bxni	Alignment		52.9	43	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
14	c5nv3P	Alignment		51.1	41	PDB header: lyase Chain: P: PDB Molecule: ribulose biphosphate carboxylase small chain 1; PDBTitle: structure of rubisco from rhodobacter sphaeroides in complex with cabp
15	d1rbli	Alignment		49.6	23	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
16	c2ybvN	Alignment		48.6	18	PDB header: lyase Chain: N: PDB Molecule: ribulose biphosphate carboxylase small subunit; PDBTitle: structure of rubisco from thermosynechococcus elongatus
17	d1gk8i	Alignment		48.2	41	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
18	d1ir1s	Alignment		46.7	32	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
19	d1uzhc1	Alignment		43.6	41	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
20	d2v6ai1	Alignment		42.3	41	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
21	d1wdds	Alignment	not modelled	42.1	27	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
22	d8rucj	Alignment	not modelled	41.7	32	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
23	d1uzdc1	Alignment	not modelled	37.4	41	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
24	d1ej7s	Alignment	not modelled	36.7	36	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
25	c1qysA	Alignment	not modelled	24.3	19	PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
26	c3ns6B	Alignment	not modelled	22.5	3	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: crystal structure of hte rna recognition motif of yeast eif3b residues2 76-170
27	c2jvfA	Alignment	not modelled	22.5	12	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein
28	c3j4jA	Alignment	not modelled	20.9	27	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: model of full-length t. thermophilus translation initiation factor 22 refined against its cryo-em density from a 30s initiation complex map

29	c4n3gA_	Alignment	not modelled	20.5	9	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 5b-like protein, PDBTitle: crystal structure of eukaryotic translation initiation factor eif5b2 (870-1116) from chaetomium thermophilum, domains iii and iv
30	d1g7sa3	Alignment	not modelled	19.0	19	Fold: Initiation factor IF2/eIF5b, domain 3 Superfamily: Initiation factor IF2/eIF5b, domain 3 Family: Initiation factor IF2/eIF5b, domain 3
31	d1w4ta1	Alignment	not modelled	18.9	50	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
32	c2kieA_	Alignment	not modelled	15.7	15	PDB header: hydrolase Chain: A; PDB Molecule: inositol polyphosphate 5-phosphatase ocr1-1; PDBTitle: a ph domain within ocr1 bridges clathrin mediated membrane2 trafficking to phosphoinositide metabolis
33	d1mv8a1	Alignment	not modelled	13.8	13	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
34	c4yk1A_	Alignment	not modelled	13.4	20	PDB header: protein binding Chain: A; PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the bid domain of bep6 from bartonella rochalimae
35	d1prt2	Alignment	not modelled	12.9	20	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Aerolysin/Pertussis toxin (APT) domain
36	c2yfwC_	Alignment	not modelled	12.3	33	PDB header: cell cycle Chain: C; PDB Molecule: histone h3-like centromeric protein cse4; PDBTitle: heterotetramer structure of kluyveromyces lactis cse4,h4
37	d1dlja1	Alignment	not modelled	12.2	13	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
38	c3s6eB_	Alignment	not modelled	12.1	22	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
39	c4gicB_	Alignment	not modelled	12.0	12	PDB header: oxidoreductase Chain: B; PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
40	c2hueB_	Alignment	not modelled	11.6	42	PDB header: dna binding protein Chain: B; PDB Molecule: histone h3; PDBTitle: structure of the h3-h4 chaperone asf1 bound to histones h3 and h4
41	c5zojE_	Alignment	not modelled	10.8	19	PDB header: dna binding protein Chain: E; PDB Molecule: inner nuclear membrane protein man1; PDBTitle: crystal structure of human smad2-man1 complex
42	c4ky3A_	Alignment	not modelled	10.6	18	PDB header: de novo protein Chain: A; PDB Molecule: designed protein or327; PDBTitle: three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesh) target or327
43	c2ahqA_	Alignment	not modelled	10.6	14	PDB header: transcription Chain: A; PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
44	d2j0sd1	Alignment	not modelled	10.3	28	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
45	d1sqwa2	Alignment	not modelled	9.6	25	Fold: Cystatin-like Superfamily: Pre-PUA domain Family: Nip7p homolog, N-terminal domain
46	c4d10H_	Alignment	not modelled	9.6	25	PDB header: signaling protein Chain: H; PDB Molecule: cop9 signalosome complex subunit 8; PDBTitle: crystal structure of the cop9 signalosome
47	c6f0fB_	Alignment	not modelled	9.5	31	PDB header: chaperone Chain: B; PDB Molecule: ip2_s; PDBTitle: crystal structure asf1-ip2_s
48	c3wbkB_	Alignment	not modelled	9.4	13	PDB header: biosynthetic protein Chain: B; PDB Molecule: eukaryotic translation initiation factor 5b; PDBTitle: crystal structure analysis of eukaryotic translation initiation factor2 5b and 1a complex
49	c2mztA_	Alignment	not modelled	9.3	22	PDB header: rna binding protein Chain: A; PDB Molecule: protein hrb1; PDBTitle: nmr structure of the rrm3 domain of hrb1
50	d1prtb2	Alignment	not modelled	8.9	20	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Aerolysin/Pertussis toxin (APT) domain
51	c2jd3B_	Alignment	not modelled	8.7	26	PDB header: dna binding protein Chain: B; PDB Molecule: stbb protein; PDBTitle: parr from plasmid pb171
52	c2fhoA_	Alignment	not modelled	8.6	35	PDB header: rna binding protein Chain: A; PDB Molecule: spliceosomal protein sf3b155; PDBTitle: nmr solution structure of the human spliceosomal protein2 complex p14-sf3b155
53	d1rk8a_	Alignment	not modelled	8.5	31	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD

54	d1tzyc_	Alignment	not modelled	8.1	42	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
55	c3izyP_	Alignment	not modelled	8.1	33	PDB header: rna, ribosomal protein Chain: P: PDB Molecule: translation initiation factor if-2, mitochondrial; PDBTitle: mammalian mitochondrial translation initiation factor 2
56	c5mmjv_	Alignment	not modelled	8.1	31	PDB header: ribosome Chain: V: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
57	c2qt7B_	Alignment	not modelled	8.0	18	PDB header: hydrolase Chain: B: PDB Molecule: receptor-type tyrosine-protein phosphatase-like n; PDBTitle: crystallographic structure of the mature ectodomain of the human2 receptor-type protein-tyrosine phosphatase ia-2 at 1.30 angstroms
58	c5l87A_	Alignment	not modelled	7.7	21	PDB header: membrane protein Chain: A: PDB Molecule: peroxin 14; PDBTitle: targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis.
59	c4kp1A_	Alignment	not modelled	7.7	13	PDB header: isomerase Chain: A: PDB Molecule: isopropylmalate/citramalate isomerase large subunit; PDBTitle: crystal structure of ipm isomerase large subunit from methanococcus2 jannaschii (mj0499)
60	d1eqzg_	Alignment	not modelled	7.5	42	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
61	d1o0pa_	Alignment	not modelled	7.5	19	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
62	c3nquA_	Alignment	not modelled	7.5	25	PDB header: dna binding protein Chain: A: PDB Molecule: histone h3-like centromeric protein a; PDBTitle: crystal structure of partially trypsinized (cenp-a/h4)2 heterotetramer
63	c5aonB_	Alignment	not modelled	7.4	25	PDB header: signaling protein Chain: B: PDB Molecule: peroxin 14; PDBTitle: crystal structure of the conserved n-terminal domain of2 pex14 from trypanosoma brucei
64	c4kp2A_	Alignment	not modelled	7.3	13	PDB header: lyase Chain: A: PDB Molecule: homoaconitase large subunit; PDBTitle: crystal structure of homoaconitase large subunit from methanococcus2 jannaschii (mj1003)
65	d1id3a_	Alignment	not modelled	7.2	25	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
66	c2e44A_	Alignment	not modelled	7.2	31	PDB header: rna binding protein Chain: A: PDB Molecule: insulin-like growth factor 2 mrna binding PDBTitle: solution structure of rna binding domain in insulin-like2 growth factor 2 mrna binding protein 3
67	c3km3B_	Alignment	not modelled	7.1	20	PDB header: hydrolase Chain: B: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: crystal structure of eoexcytidine triphosphate deaminase from2 anaplasma phagocytophilum at 2.1a resolution
68	c2o8kA_	Alignment	not modelled	7.1	14	PDB header: transcription/dna Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
69	c3nqjA_	Alignment	not modelled	7.0	25	PDB header: dna binding protein Chain: A: PDB Molecule: histone h3-like centromeric protein a; PDBTitle: crystal structure of (cenp-a/h4)2 heterotetramer
70	c2dnqA_	Alignment	not modelled	6.7	12	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein 4b; PDBTitle: solution structure of rna binding domain 1 in rna-binding2 protein 30
71	d1vpka3	Alignment	not modelled	6.7	14	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase III, beta subunit
72	d1p3ie_	Alignment	not modelled	6.6	42	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
73	c2f9jP_	Alignment	not modelled	6.5	38	PDB header: rna binding protein Chain: P: PDB Molecule: splicing factor 3b subunit 1; PDBTitle: 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
74	d1rz4a1	Alignment	not modelled	6.5	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Eukaryotic translation initiation factor 3 subunit 12, eIF3k, C-terminal domain
75	c3btpB_	Alignment	not modelled	6.4	38	PDB header: dna binding protein, chaperone Chain: B: PDB Molecule: protein vire1; PDBTitle: crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
76	c4uqtA_	Alignment	not modelled	6.4	24	PDB header: translation Chain: A: PDB Molecule: u2 snrnp component ist3; PDBTitle: rrm-peptide structure in res complex
77	d2dita1	Alignment	not modelled	6.4	19	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
78	d1whza_	Alignment	not modelled	6.3	25	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: YcfA-like
79	c4v1ao_	Alignment	not modelled	6.3	38	PDB header: ribosome Chain: O: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian

						mitoribosome, part 22 of 2
80	c4kjzD	Alignment	not modelled	6.2	46	PDB header: translation Chain: D; PDB Molecule: translation initiation factor if-2; PDBTitle: crystal structure of thermus thermophilus if2, apo and gdp-bound forms2 (2-474)
81	c6e0cA	Alignment	not modelled	6.1	25	PDB header: nuclear protein Chain: A; PDB Molecule: histone h3-like centromeric protein a; PDBTitle: cryo-em structure of the cenp-a nucleosome (w601) in complex with a2 single chain antibody fragment
82	d1fjeb2	Alignment	not modelled	6.1	12	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
83	d1kx5a	Alignment	not modelled	6.0	42	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
84	c2mt3A	Alignment	not modelled	6.0	21	PDB header: transcription Chain: A; PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: structure of -24 dna binding domain of sigma 54 from e.coli
85	c5vbdA	Alignment	not modelled	6.0	14	PDB header: signaling protein Chain: A; PDB Molecule: usp9x; PDBTitle: crystal structure of a putative ubl domain of usp9x
86	c6an0A	Alignment	not modelled	5.9	24	PDB header: oxidoreductase Chain: A; PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
87	c4a8xB	Alignment	not modelled	5.9	33	PDB header: transcription Chain: B; PDB Molecule: hook-like, isoform a; PDBTitle: structure of the core asap complex
88	c2jyaA	Alignment	not modelled	5.7	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein atu1810; PDBTitle: nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
89	c2osrA	Alignment	not modelled	5.7	27	PDB header: rna binding protein Chain: A; PDB Molecule: nucleolar protein 3; PDBTitle: nmr structure of rrm-2 of yeast npl3 protein
90	c5vldC	Alignment	not modelled	5.6	17	PDB header: oxidoreductase Chain: C; PDB Molecule: histidinol dehydrogenase, chloroplastic; PDBTitle: crystal structure of medicago truncatula l-histidinol dehydrogenase in2 complex with l-histidine and nad+
91	c2w85A	Alignment	not modelled	5.5	50	PDB header: protein transport Chain: A; PDB Molecule: peroxisomal membrane anchor protein pex14; PDBTitle: structure of pex14 in complex with pex19
92	c6b4jC	Alignment	not modelled	5.4	25	PDB header: transport protein Chain: C; PDB Molecule: nucleoporin like 2; PDBTitle: crystal structure of human gle1 ctd-nup42 gbm-ddx19b(amppnp) complex
93	c2o3dA	Alignment	not modelled	5.4	11	PDB header: rna binding protein Chain: A; PDB Molecule: splicing factor, arginine/serine-rich 1; PDBTitle: structure of human sf2/asf rna recognition motif 2 (rrm2)
94	c4bptC	Alignment	not modelled	5.3	38	PDB header: oxidoreductase Chain: C; PDB Molecule: phenylalanine-4-hydroxylase (pah) (phe-4-monoxygenase); PDBTitle: structural and thermodynamic insight into phenylalanine2 hydroxylase from the human pathogen legionella pneumophila
95	d1oiaa	Alignment	not modelled	5.3	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
96	c3tcyA	Alignment	not modelled	5.3	19	PDB header: oxidoreductase Chain: A; PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: crystallographic structure of phenylalanine hydroxylase from2 chromobacterium violaceum (cpah) bound to phenylalanine in a site3 distal to the active site
97	c2jvoA	Alignment	not modelled	5.3	19	PDB header: rna binding protein Chain: A; PDB Molecule: nucleolar protein 3; PDBTitle: segmental isotope labeling of npl3
98	c6b4fD	Alignment	not modelled	5.3	25	PDB header: transport protein Chain: D; PDB Molecule: nucleoporin like 2; PDBTitle: crystal structure of human gle1 ctd-nup42 gbm complex
99	d1ivta	Alignment	not modelled	5.2	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain