

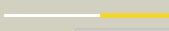


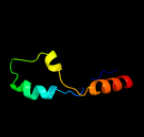









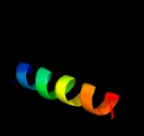

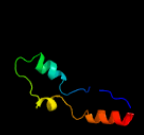



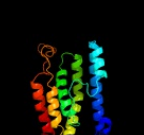


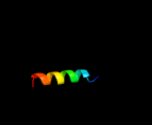



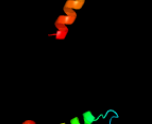
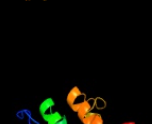



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0473 (-) _563567_564937
Date	Tue Jul 23 14:50:55 BST 2019
Unique Job ID	bb430f09a51be477

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ug3A_	 Alignment		81.5	11	PDB header: translation Chain: A; PDB Molecule: eukaryotic protein synthesis initiation factor PDBTitle: c-terminal portion of human eif4gi
2	c4qmhA_	 Alignment		76.8	14	PDB header: protein binding Chain: A; PDB Molecule: lp04448p; PDBTitle: the xmap215 family drives microtubule polymerization using a2 structurally diverse tog array
3	c3edyA_	 Alignment		61.1	23	PDB header: hydrolase Chain: A; PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure of the precursor form of human tripeptidyl-peptidase2 1
4	c1dvpA_	 Alignment		59.5	9	PDB header: transferase Chain: A; PDB Molecule: hepatocyte growth factor-regulated tyrosine PDBTitle: crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
5	c5jnmA_	 Alignment		54.3	15	PDB header: oxidoreductase Chain: A; PDB Molecule: mannitol-1-phosphate 5-dehydrogenase; PDBTitle: crystal structure of mtdl from staphylococcus aureus at 1.7-angstrom2 resolution
6	d1mhqa_	 Alignment		54.0	12	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
7	d1dvp1	 Alignment		52.8	9	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
8	c6ithA_	 Alignment		50.6	26	PDB header: membrane protein Chain: A; PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
9	d1tlea2	 Alignment		48.1	13	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Subtilase propeptides/inhibitors
10	c3ee6A_	 Alignment		47.7	20	PDB header: hydrolase Chain: A; PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure analysis of tripeptidyl peptidase -i
11	c4mudA_	 Alignment		46.2	9	PDB header: oxidoreductase Chain: A; PDB Molecule: ring oxydation complex/ phenylacetic acid degradation PDBTitle: crystal structure of a ring oxydation complex/ phenylacetic acid2 degradation-like protein (sso1313) from sulfolobus solfataricus p2 at3 2.43 a resolution

12	c3rruA_	Alignment		45.9	9	PDB header: signaling protein Chain: A: PDB Molecule: tom1l1 protein; PDBTitle: x-ray crystal structure of the vhs domain of human tom1-like protein,2 northeast structural genomics consortium target hr3050e
13	c3j3bD_	Alignment		45.0	14	PDB header: ribosome Chain: D: PDB Molecule: 60s ribosomal protein l5; PDBTitle: structure of the human 60s ribosomal proteins
14	c6e8wC_	Alignment		43.1	47	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein gp160; PDBTitle: mper-tm domain of hiv-1 envelope glycoprotein (env)
15	c6dlbB_	Alignment		41.5	37	PDB header: membrane protein Chain: B: PDB Molecule: transmembrane protein gp41; PDBTitle: oligomeric structure of the hiv gp41 mper-tmd in phospholipid bilayers
16	c3zyqA_	Alignment		41.0	11	PDB header: signaling Chain: A: PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.48 a3 resolution
17	c5d8mA_	Alignment		39.0	33	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
18	c2k7rA_	Alignment		38.7	14	PDB header: replication Chain: A: PDB Molecule: primosomal protein dnaI; PDBTitle: n-terminal domain of the bacillus subtilis helicase-loading2 protein dnaI
19	c1x5bA_	Alignment		36.8	9	PDB header: protein binding Chain: A: PDB Molecule: signal transducing adaptor molecule 2; PDBTitle: the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
20	c6humQ_	Alignment		33.1	38	PDB header: proton transport Chain: Q: PDB Molecule: proton-translocating nadh-quinone dehydrogenase subunit q PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
21	d1ujka_	Alignment	not modelled	32.1	15	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
22	c3zf7u_	Alignment	not modelled	32.1	14	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein l21e, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
23	c3h2zA_	Alignment	not modelled	30.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: mannitol-1-phosphate 5-dehydrogenase; PDBTitle: the crystal structure of mannitol-1-phosphate dehydrogenase from2 shigella flexneri
24	c4atgA_	Alignment	not modelled	30.1	11	PDB header: transcription Chain: A: PDB Molecule: taf6; PDBTitle: taf6 c-terminal domain from antonospora locustae
25	d1k3xa1	Alignment	not modelled	29.6	18	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
26	d1rh5b_	Alignment	not modelled	28.7	17	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
27	c2kncA_	Alignment	not modelled	25.7	14	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
28	d1r2za1	Alignment	not modelled	25.4	18	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
29	c5vhvB_	Alignment	not modelled	24.6	11	PDB header: hydrolase/dna Chain: B: PDB Molecule: alkylpurine dna glycosylase alkC; PDBTitle: pseudomonas fluorescens alkylpurine dna glycosylase

						alkc bound to dna2 containing an oxocarbenium-intermediate analog
30	c5t7qA_	Alignment	not modelled	24.3	54	PDB header: signaling protein Chain: A: PDB Molecule: toll/interleukin-1 receptor domain-containing adapter PDBTitle: tirap phosphoinositide-binding motif
31	d1juqa_	Alignment	not modelled	21.5	11	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
32	c5itgA_	Alignment	not modelled	21.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: sorbitol dehydrogenase; PDBTitle: crystal structure of d-sorbitol dehydrogenase in substrate-free form
33	c2mpnB_	Alignment	not modelled	21.2	20	PDB header: membrane protein Chain: B: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
34	c2mpnA_	Alignment	not modelled	20.6	19	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
35	c3j39D_	Alignment	not modelled	20.3	14	PDB header: ribosome Chain: D: PDB Molecule: 60s ribosomal protein l5; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
36	d1xi8a3	Alignment	not modelled	19.9	15	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
37	d1ee8a1	Alignment	not modelled	19.6	21	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
38	c2l8sA_	Alignment	not modelled	18.6	14	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
39	d1xqoa_	Alignment	not modelled	18.5	44	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: AgoG-like
40	d1elka_	Alignment	not modelled	18.1	11	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
41	c2gp4A_	Alignment	not modelled	17.8	12	PDB header: lyase Chain: A: PDB Molecule: 6-phosphogluconate dehydratase; PDBTitle: structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
42	d2gp4a2	Alignment	not modelled	17.2	7	Fold: lVd/EDD N-terminal domain-like Superfamily: lVd/EDD N-terminal domain-like Family: lVd/EDD N-terminal domain-like
43	c2kluA_	Alignment	not modelled	16.9	33	PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
44	d1ug3a1	Alignment	not modelled	16.5	13	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
45	c1t1eA_	Alignment	not modelled	15.8	12	PDB header: hydrolase Chain: A: PDB Molecule: kumamolisin; PDBTitle: high resolution crystal structure of the intact pro-2 kumamolisin, a sedolisin type proteinase (previously3 called kumamolysin or kscp)
46	d1tdza1	Alignment	not modelled	15.8	19	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
47	c6drhC_	Alignment	not modelled	15.5	33	PDB header: toxin Chain: C: PDB Molecule: adp-ribosyl-(dinitrogen reductase) hydrolase; PDBTitle: adp-ribosyltransferase toxin/immunity pair
48	c3zm8A_	Alignment	not modelled	15.5	21	PDB header: hydrolase Chain: A: PDB Molecule: gh26 endo-beta-1,4-mannanase; PDBTitle: crystal structure of podospira anserina gh26-cbm352 beta-(1,4)-mannanase
49	d1jyaa_	Alignment	not modelled	15.3	47	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
50	d1k6za_	Alignment	not modelled	15.2	50	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
51	c5x90B_	Alignment	not modelled	15.2	33	PDB header: protein transport Chain: B: PDB Molecule: icmw; PDBTitle: structure of dotl(656-783)-icms-icmw-lvga derived from legionella2 pneumophila
52	c5ycaA_	Alignment	not modelled	14.5	29	PDB header: membrane protein Chain: A: PDB Molecule: ubiquitin-like protein smt3,bouquet formation protein 4; PDBTitle: crystal structure of inner membrane protein bqt4 in complex with lem2
53	d2crga1	Alignment	not modelled	13.6	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
54	c2gp4B_	Alignment	not modelled	13.3	7	PDB header: lyase Chain: B: PDB Molecule: 6-phosphogluconate dehydratase; PDBTitle: structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
55	c4j8sA_	Alignment	not modelled	13.3	15	PDB header: protein binding Chain: A: PDB Molecule: ccc4-not transcription complex subunit 1; PDBTitle: crystal structure of human cnot1 mif4g domain in complex with a ttp2 peptide

56	c2mn8A_	Alignment	not modelled	13.3	41	PDB header: antimicrobial protein Chain: A: PDB Molecule: maculatin g15; PDBTitle: nmr structure of a peptoid analogue of maculatin g15 containing cis-2 nleu at position 13
57	c2mn9A_	Alignment	not modelled	13.3	41	PDB header: antimicrobial protein Chain: A: PDB Molecule: maculatin g15; PDBTitle: peptoid analogue of maculatin g15 - peptoid trans-nleu at position 13
58	d1rfza_	Alignment	not modelled	12.9	17	Fold: YutG-like Superfamily: YutG-like Family: YutG-like
59	c5j84A_	Alignment	not modelled	12.9	18	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form
60	d1k82a1	Alignment	not modelled	12.7	15	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
61	d1ev7a_	Alignment	not modelled	12.6	33	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease NaeI
62	c3c5yD_	Alignment	not modelled	12.3	14	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
63	c6cokA_	Alignment	not modelled	11.9	11	PDB header: protein binding Chain: A: PDB Molecule: protein stu1; PDBTitle: structure of the 2nd tog domain from yeast clasp protein stu1
64	c4jrbA_	Alignment	not modelled	11.8	12	PDB header: lipid binding protein Chain: A: PDB Molecule: green fluorescent protein; PDBTitle: structure of cockroach allergen bla g 1 tandem repeat as a egfp fusion
65	c3ww0B_	Alignment	not modelled	11.6	9	PDB header: transport protein Chain: B: PDB Molecule: protein hikeshi; PDBTitle: crystal structure of f97a mutant, a new nuclear transport receptor of2 hsp70
66	d1y9ia_	Alignment	not modelled	11.4	15	Fold: YutG-like Superfamily: YutG-like Family: YutG-like
67	c3fk2B_	Alignment	not modelled	11.1	13	PDB header: signaling protein, hydrolase activator Chain: B: PDB Molecule: glucocorticoid receptor dna-binding factor 1; PDBTitle: crystal structure of the rhogap domain of human glucocorticoid2 receptor dna-binding factor 1
68	c5mfaA_	Alignment	not modelled	10.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: myeloperoxidase; PDBTitle: crystal structure of human promyeloperoxidase (prompo)
69	c2gjmA_	Alignment	not modelled	10.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: lactoperoxidase; PDBTitle: crystal structure of buffalo lactoperoxidase at 2.75a resolution
70	d2dt5a1	Alignment	not modelled	10.5	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional repressor Rex, N-terminal domain
71	d2fp1a1	Alignment	not modelled	10.3	20	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Secreted chorismate mutase-like
72	c5yfpG_	Alignment	not modelled	10.1	13	PDB header: exocytosis Chain: G: PDB Molecule: exocyst complex component exo70; PDBTitle: cryo-em structure of the exocyst complex
73	d2vbua1	Alignment	not modelled	10.0	43	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: CTP-dependent riboflavin kinase-like
74	c5oynB_	Alignment	not modelled	9.9	15	PDB header: lyase Chain: B: PDB Molecule: dehydratase, ilvd/edd family; PDBTitle: crystal structure of d-xylonate dehydratase in holo-form
75	c1d2vD_	Alignment	not modelled	9.8	19	PDB header: oxidoreductase Chain: D: PDB Molecule: myeloperoxidase; PDBTitle: crystal structure of bromide-bound human myeloperoxidase isoform c at2 ph 5.5
76	d1h3oa_	Alignment	not modelled	9.8	10	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
77	c1h3oA_	Alignment	not modelled	9.8	10	PDB header: transcription/ebp-associated factors Chain: A: PDB Molecule: transcription initiation factor tfiid 135 kda subunit; PDBTitle: crystal structure of the human taf4-taf12 (tafi1135-tafii20) complex
78	c3l9tA_	Alignment	not modelled	9.7	11	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein smu.31; PDBTitle: the crystal structure of smu.31 from streptococcus mutans ua159
79	c5ze4A_	Alignment	not modelled	9.7	17	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
80	d1qb3a_	Alignment	not modelled	9.1	71	Fold: Cell cycle regulatory proteins Superfamily: Cell cycle regulatory proteins Family: Cell cycle regulatory proteins
81	d1jlja_	Alignment	not modelled	9.1	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like

82	c6ercA_	Alignment	not modelled	9.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxinectin a; PDBTitle: peroxidase a from dictyostelium discoideum (ddpoxa)
83	c3pt5A_	Alignment	not modelled	8.9	25	PDB header: hydrolase Chain: A: PDB Molecule: nans (yjhs), a 9-o-acetyl n-acetylneuraminic acid esterase; PDBTitle: crystal structure of nans
84	c2mg2A_	Alignment	not modelled	8.9	27	PDB header: viral protein Chain: A: PDB Molecule: transmembrane protein gp41; PDBTitle: nmr assignment and structure of a peptide derived from the membrane2 proximal external region of hiv-1 gp41 in the presence of3 hexafluoroisopropanol
85	c2mg3A_	Alignment	not modelled	8.9	27	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein gp41; PDBTitle: nmr assignment and structure of a peptide derived from the membrane2 proximal external region of hiv-1 gp41 in the presence of3 dodecylphosphocholine micelles
86	c2yqkA_	Alignment	not modelled	8.8	25	PDB header: transcription/apoptosis Chain: A: PDB Molecule: arginine-glutamic acid dipeptide repeats protein; PDBTitle: solution structure of the sant domain in arginine-glutamic2 acid dipeptide (re) repeats
87	c2hyjA_	Alignment	not modelled	8.7	10	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: the crystal structure of a tetr-family transcriptional regulator from2 streptomyces coelicolor
88	d2f05a1	Alignment	not modelled	8.6	15	Fold: PAH2 domain Superfamily: PAH2 domain Family: PAH2 domain
89	d1cksa_	Alignment	not modelled	8.5	67	Fold: Cell cycle regulatory proteins Superfamily: Cell cycle regulatory proteins Family: Cell cycle regulatory proteins
90	c5furJ_	Alignment	not modelled	8.5	10	PDB header: transcription Chain: J: PDB Molecule: transcription initiation factor tfiid subunit 6; PDBTitle: structure of human tfiid-ia bound to core promoter dna
91	c6btmD_	Alignment	not modelled	8.4	12	PDB header: membrane protein Chain: D: PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
92	c5da9D_	Alignment	not modelled	8.2	6	PDB header: hydrolase Chain: D: PDB Molecule: putative double-strand break protein; PDBTitle: atp-gamma-s bound rad50 from chaetomium thermophilum in complex with2 the rad50-binding domain of mre11
93	d2ev0a2	Alignment	not modelled	8.1	19	Fold: Iron-dependent repressor protein, dimerization domain Superfamily: Iron-dependent repressor protein, dimerization domain Family: Iron-dependent repressor protein, dimerization domain
94	d1or7a2	Alignment	not modelled	8.1	16	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
95	c3h3pT_	Alignment	not modelled	8.1	57	PDB header: immune system Chain: T: PDB Molecule: 4e10_s0_1tjlc_004_n; PDBTitle: crystal structure of hiv epitope-scaffold 4e10 fv complex
96	d1zmba1	Alignment	not modelled	8.0	30	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Putative acetylxylylan esterase-like
97	c3kg4A_	Alignment	not modelled	8.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from manheimia2 succiniciproducens
98	d2a4ha1	Alignment	not modelled	7.9	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
99	c5bp9A_	Alignment	not modelled	7.8	21	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase protein; PDBTitle: crystal structure of sam-dependent methyltransferase from bacteroides2 fragilis in complex with s-adenosyl-l-homocysteine