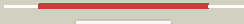

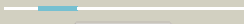









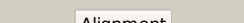







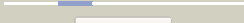

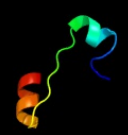
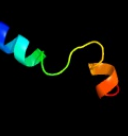

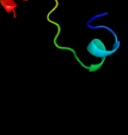
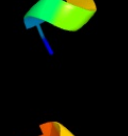
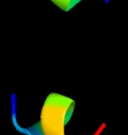
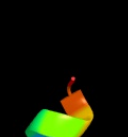

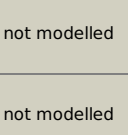


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1873 (-)_2123181_2123618
Date	Fri Aug 2 13:30:48 BST 2019
Unique Job ID	45756619547c307b

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2jeka1	 Alignment		100.0	100	Fold: Rv1873-like Superfamily: Rv1873-like Family: Rv1873-like
2	c6jo52_	 Alignment		36.2	59	PDB header: photosynthesis Chain: 2: PDB Molecule: chlorophyll a-b binding protein, chloroplastic; PDBTitle: structure of the green algal photosystem i supercomplex with light-2 harvesting complex i
3	c5cwuC_	 Alignment		27.0	19	PDB header: transport protein Chain: C: PDB Molecule: nucleoporin nup188; PDBTitle: crystal structure of chaetomium thermophilum nup188 tail domain
4	c4trbA_	 Alignment		26.6	20	PDB header: transferase Chain: A: PDB Molecule: purine phosphoribosyltransferase (gpt-1); PDBTitle: sulfolobus solfataricus adenine phosphoribosyltransferase
5	c2mg3A_	 Alignment		26.2	29	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 of 3 dodecylphosphocholine micelles
6	c2mg2A_	 Alignment		25.1	29	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 of 3 hexafluoroisopropanol
7	c5aonB_	 Alignment		24.6	20	PDB header: signaling protein Chain: B: PDB Molecule: peroxin 14; PDBTitle: crystal structure of the conserved n-terminal domain of 2 pex14 from trypanosoma brucei
8	c3ff5B_	 Alignment		22.8	20	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the 2 peroxisomal matrix-protein-import receptor, pex14p
9	c5u3kC_	 Alignment		22.6	29	PDB header: immune system/viral protein Chain: C: PDB Molecule: gp41 mper peptide; PDBTitle: crystal structure of dh511.2 fab in complex with hiv-1 gp41 mper 662-2 683 peptide
10	c5u3lC_	 Alignment		22.4	29	PDB header: immune system/viral protein Chain: C: PDB Molecule: gp41 mper peptide; PDBTitle: crystal structure of dh511.2 fab in complex with hiv-1 gp41 mper 670-2 683 peptide
11	c5u3lP_	 Alignment		22.4	29	PDB header: immune system/viral protein Chain: P: PDB Molecule: gp41 mper peptide; PDBTitle: crystal structure of dh511.2 fab in complex with hiv-1 gp41 mper 670-2 683 peptide

12	c3bsuF_	Alignment		22.3	24	PDB header: hydrolase/rna/dna Chain: F; PDB Molecule: ribonuclease h1; PDBTitle: hybrid-binding domain of human rnase h1 in complex with 12-2 mer rna/dna
13	d1b25a1	Alignment		22.1	35	Fold: Aldehyde ferredoxin oxidoreductase, C-terminal domains Superfamily: Aldehyde ferredoxin oxidoreductase, C-terminal domains Family: Aldehyde ferredoxin oxidoreductase, C-terminal domains
14	c5l87A_	Alignment		20.8	20	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 trypanosomiases.
15	d1qhka_	Alignment		20.3	29	Fold: MbtH/L9 domain-like Superfamily: L9 N-domain-like Family: N-terminal domain of RNase HI
16	c4g6fF_	Alignment		19.8	29	PDB header: immune system Chain: F; PDB Molecule: gp41 mper peptide; PDBTitle: crystal structure of 10e8 fab in complex with an hiv-1 gp41 peptide
17	c5ghwP_	Alignment		19.6	29	PDB header: immune system Chain: P; PDB Molecule: endogenous retrovirus group k member 8 env polyprotein; PDBTitle: crystal structure of broad neutralizing antibody 10e8 with long2 epitope bound
18	c4g6fP_	Alignment		19.3	29	PDB header: immune system Chain: P; PDB Molecule: gp41 mper peptide; PDBTitle: crystal structure of 10e8 fab in complex with an hiv-1 gp41 peptide
19	c5u3kP_	Alignment		19.2	29	PDB header: immune system/viral protein Chain: P; PDB Molecule: gp41 mper peptide; PDBTitle: crystal structure of dh511.2 fab in complex with hiv-1 gp41 mper 662-2 683 peptide
20	c5u3nA_	Alignment		19.2	29	PDB header: immune system/viral protein Chain: A; PDB Molecule: gp41 mper peptide; PDBTitle: crystal structure of dh511.12p fab in complex with hiv-1 gp41 mper2 peptide
21	c2me2A_	Alignment	not modelled	19.1	29	PDB header: membrane protein Chain: A; PDB Molecule: envelope glycoprotein gp160; PDBTitle: hiv-1 gp41 clade c membrane proximal external region peptide in dpc2 micelle
22	c5u3mA_	Alignment	not modelled	19.0	29	PDB header: immune system/viral protein Chain: A; PDB Molecule: gp41 mper peptide; PDBTitle: crystal structure of dh511.11p fab in complex with hiv-1 gp41 mper2 peptide
23	c4p4oA_	Alignment	not modelled	19.0	23	PDB header: transferase/dna Chain: A; PDB Molecule: dna polymerase beta; PDBTitle: crystal structure of leishmania infantum polymerase beta: ternary gap2 complex
24	c2me1A_	Alignment	not modelled	18.7	29	PDB header: membrane protein Chain: A; PDB Molecule: gp41; PDBTitle: hiv-1 gp41 clade b double alanine mutant membrane proximal external2 region peptide in dpc micelle
25	c3g9rF_	Alignment	not modelled	18.7	29	PDB header: viral protein Chain: F; PDB Molecule: fusion complex of hiv-1 envelope glycoprotein and PDBTitle: structure of the hiv-1 gp41 membrane-proximal ectodomain region in a2 putative prefusion conformation
26	c1jauA_	Alignment	not modelled	18.4	29	PDB header: viral protein Chain: A; PDB Molecule: transmembrane glycoprotein (gp41); PDBTitle: nmr solution structure of the trp-rich peptide of hiv gp412 bound to dpc micelles
27	c1javA_	Alignment	not modelled	18.3	29	PDB header: viral protein Chain: A; PDB Molecule: transmembrane glycoprotein (gp41); PDBTitle: average nmr solution structure of the trp-rich peptide of2 hiv gp41 bound to dpc micelles
28	d1chka_	Alignment	not modelled	18.3	16	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Chitosanase

29	c2pv6A	Alignment	not modelled	18.2	29	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: hiv-1 gp41 membrane proximal ectodomain region peptide in2 dpc micelle
30	c2me3A	Alignment	not modelled	17.8	29	PDB header: membrane protein Chain: A: PDB Molecule: envelope glycoprotein gp160; PDBTitle: hiv-1 gp41 clade c membrane proximal external region peptide in dpc2 micelle
31	c6mttP	Alignment	not modelled	17.7	29	PDB header: immune system Chain: P: PDB Molecule: rv217 founder virus gp41 peptide; PDBTitle: crystal structure of vrc46.01 fab in complex with gp41 peptide
32	c2nctA	Alignment	not modelled	17.7	29	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 hexafluoroisopropanol
33	c3anyB	Alignment	not modelled	17.7	23	PDB header: lyase Chain: B: PDB Molecule: ethanolamine ammonia-lyase light chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
34	c2me4A	Alignment	not modelled	17.7	29	PDB header: membrane protein Chain: A: PDB Molecule: envelope glycoprotein gp160; PDBTitle: hiv-1 gp41 clade c membrane proximal external region peptide in dpc2 micelle
35	c2w85A	Alignment	not modelled	16.9	20	PDB header: protein transport Chain: A: PDB Molecule: peroxisomal membrane anchor protein pex14; PDBTitle: structure of pex14 in complex with pex19
36	c3absD	Alignment	not modelled	16.9	23	PDB header: lyase Chain: D: PDB Molecule: ethanolamine ammonia-lyase light chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
37	c3bkhA	Alignment	not modelled	16.0	14	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
38	c1ujwB	Alignment	not modelled	15.2	29	PDB header: transport protein/hydrolase Chain: B: PDB Molecule: colicin e3; PDBTitle: structure of the complex between btub and colicin e3 receptor binding2 domain
39	d1mhyd	Alignment	not modelled	14.9	17	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
40	c6abfC	Alignment	not modelled	14.9	23	PDB header: viral protein/rna Chain: C: PDB Molecule: polymerase pb2; PDBTitle: structure of influenza d virus polymerase bound to vrna promoter in2 mode b conformation (class b1)
41	c2z0rA	Alignment	not modelled	14.6	55	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha0547; PDBTitle: crystal structure of hypothetical protein ttha0547
42	c6gr8B	Alignment	not modelled	13.9	19	PDB header: transferase Chain: B: PDB Molecule: inner centromere protein; PDBTitle: human aurkc incenp complex bound to brd-7880
43	c2kqpA	Alignment	not modelled	13.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of agrobacterium tumefaciens protein atu1219:2 northeast structural genomics consortium target att14
44	c2z2uA	Alignment	not modelled	11.7	17	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
45	d1fs1b1	Alignment	not modelled	11.7	36	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
46	d1aora1	Alignment	not modelled	11.6	22	Fold: Aldehyde ferredoxin oxidoreductase, C-terminal domains Superfamily: Aldehyde ferredoxin oxidoreductase, C-terminal domains Family: Aldehyde ferredoxin oxidoreductase, C-terminal domains
47	c1b4nD	Alignment	not modelled	11.3	35	PDB header: oxidoreductase Chain: D: PDB Molecule: formaldehyde ferredoxin oxidoreductase; PDBTitle: formaldehyde ferredoxin oxidoreductase from pyrococcus furiosus,2 complexed with glutarate
48	d2lisa	Alignment	not modelled	11.0	23	Fold: Fertilization protein Superfamily: Fertilization protein Family: Fertilization protein
49	d2bgxa1	Alignment	not modelled	10.8	20	Fold: PGBD-like Superfamily: PGBD-like Family: Peptidoglycan binding domain, PGBD
50	c3n5bB	Alignment	not modelled	10.1	38	PDB header: transcription regulator Chain: B: PDB Molecule: asr0485 protein; PDBTitle: the complex of pii and pipx from anabaena
51	c2lp7C	Alignment	not modelled	10.0	29	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein; PDBTitle: structure of gp41-m-mat, a membrane associated mper trimer from hiv-12 gp41.
52	d2o4ta1	Alignment	not modelled	10.0	23	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
53	c2xg8D	Alignment	not modelled	9.9	50	PDB header: transcription Chain: D: PDB Molecule: pipx; PDBTitle: structural basis of gene regulation by protein pii: the2 crystal complex of pii and pipx from synechococcus3 elongatus pcc 7942
54	c5c2uA	Alignment	not modelled	9.9	20	PDB header: transport protein Chain: A: PDB Molecule: nup54;

54	c3c2uA	Alignment	not modelled	9.9	20	PDBTitle: ferredoxin-like domain of nucleoporin nup54 bound to a nanobody PDB header: lyase Chain: B: PDB Molecule: beta-subunit 2-hydroxyacyl-coa dehydratase; PDBTitle: (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
55	c3o3nB	Alignment	not modelled	9.7	18	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
56	d1nexa1	Alignment	not modelled	9.3	36	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
57	d1fs2b1	Alignment	not modelled	9.3	36	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
58	d3lyna	Alignment	not modelled	9.2	23	Fold: Fertilization protein Superfamily: Fertilization protein Family: Fertilization protein
59	c6e8wC	Alignment	not modelled	9.2	29	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein gp160; PDBTitle: mper-tm domain of hiv-1 envelope glycoprotein (env)
60	d2ovra1	Alignment	not modelled	9.2	36	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
61	d1nkda	Alignment	not modelled	8.9	23	Fold: ROP-like Superfamily: ROP protein Family: ROP protein
62	d1utra	Alignment	not modelled	8.9	24	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
63	d1idra	Alignment	not modelled	8.8	5	Fold: Globin-like Superfamily: Globin-like Family: Truncated hemoglobin
64	c1nomA	Alignment	not modelled	8.6	30	PDB header: nucleotidyltransferase Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mnc12 (5 millimolar)
65	c4wrtC	Alignment	not modelled	8.2	18	PDB header: transferase/rna Chain: C: PDB Molecule: pb2; PDBTitle: crystal structure of influenza b polymerase with bound vrna promoter2 (form flub2)
66	c3jcuR	Alignment	not modelled	8.0	43	PDB header: membrane protein Chain: R: PDB Molecule: chlorophyll a-b binding protein 29 kd (cp29); PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
67	c6igz2	Alignment	not modelled	7.8	40	PDB header: plant protein Chain: 2: PDB Molecule: lhca-c; PDBTitle: structure of psi-lhci
68	d1rwta	Alignment	not modelled	7.7	29	Fold: Chlorophyll a-b binding protein Superfamily: Chlorophyll a-b binding protein Family: Chlorophyll a-b binding protein
69	c5y1zB	Alignment	not modelled	7.6	12	PDB header: transcription Chain: B: PDB Molecule: drebrin; PDBTitle: crystal structure of zmynd8 phd-bromo-pwpp tandem in complex with2 drebrin adf-h domain
70	c2yx0A	Alignment	not modelled	7.5	28	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
71	c1lt1G	Alignment	not modelled	7.3	26	PDB header: de novo protein Chain: G: PDB Molecule: l13g-df1; PDBTitle: sliding helix induced change of coordination geometry in a2 model di-mn(ii) protein
72	c2ct6A	Alignment	not modelled	7.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sh3 domain-binding glutamic acid-rich-like PDBTitle: solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2
73	c1kdhA	Alignment	not modelled	7.2	23	PDB header: transferase/dna Chain: A: PDB Molecule: terminal deoxynucleotidyltransferase short PDBTitle: binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
74	c2ekkA	Alignment	not modelled	7.2	50	PDB header: protein binding Chain: A: PDB Molecule: uba domain from e3 ubiquitin-protein ligase PDBTitle: solution structure of ruh-074, a human uba domain
75	d1qx8a	Alignment	not modelled	7.2	23	Fold: ROP-like Superfamily: ROP protein Family: ROP protein
76	d1l0nk	Alignment	not modelled	7.2	36	Fold: Single transmembrane helix Superfamily: Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
77	d1v54i	Alignment	not modelled	7.1	83	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIc Family: Mitochondrial cytochrome c oxidase subunit VIc
78	c5fmzF	Alignment	not modelled	7.1	19	PDB header: transcription Chain: F: PDB Molecule: polymerase basic protein 2; PDBTitle: crystal structure of influenza b polymerase with bound 5' vrna
79	c4wsaC	Alignment	not modelled	7.1	19	PDB header: transferase/rna Chain: C: PDB Molecule: pb2; PDBTitle: crystal structure of influenza b polymerase bound to the vrna promoter2 (flub1 form) Fold: SAM domain-like

80	d1jmsa3	Alignment	not modelled	7.0	23	Superfamily: PsbU/PolX domain-like Family: DNA polymerase beta-like, second domain
81	d1utga	Alignment	not modelled	7.0	12	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
82	c6ijj7	Alignment	not modelled	6.9	36	PDB header: membrane protein Chain: 7: PDB Molecule: lhca7; PDBTitle: photosystem i of chlamydomonas reinhardtii
83	c6abeC	Alignment	not modelled	6.9	23	PDB header: viral protein/rna Chain: C: PDB Molecule: polymerase pb2; PDBTitle: structure of influenza d virus polymerase bound to vrna promoter in2 mode b conformation (class b2)
84	c8iczA	Alignment	not modelled	6.8	29	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase beta (e.c.2.7.7.7)); PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of of datp3 (1 millimolar), mncl2 (5 millimolar), and lithium sulfate4 (75 millimolar)
85	c3e21A	Alignment	not modelled	6.7	36	PDB header: apoptosis Chain: A: PDB Molecule: fas-associated factor 1; PDBTitle: crystal structure of faf-1 uba domain
86	d2fxta1	Alignment	not modelled	6.6	14	Fold: Cystatin-like Superfamily: NTF2-like Family: TIM44-like
87	c6igz5	Alignment	not modelled	6.5	26	PDB header: plant protein Chain: 5: PDB Molecule: lhca-a; PDBTitle: structure of psi-lhci
88	c5oold	Alignment	not modelled	6.5	13	PDB header: ribosome Chain: D: PDB Molecule: 39s ribosomal protein l2, mitochondrial; PDBTitle: structure of a native assembly intermediate of the human mitochondrial2 ribosome with unfolded interfacial rna
89	c2wdtA	Alignment	not modelled	6.4	13	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase l3; PDBTitle: crystal structure of plasmodium falciparum uchl3 in complex2 with the suicide inhibitor ubvme
90	c4xgqD	Alignment	not modelled	6.4	29	PDB header: toxin/antitoxin Chain: D: PDB Molecule: antitoxin vapb30; PDBTitle: crystal structure of addiction module from mycobacterial species
91	c3auoB	Alignment	not modelled	6.4	29	PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase beta family (x family); PDBTitle: dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
92	c3h01A	Alignment	not modelled	6.2	29	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein gp160; PDBTitle: structure of the c-terminal domain of a putative hiv-1 gp41 fusion2 intermediate
93	d1ccda	Alignment	not modelled	6.2	24	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
94	c4xgqB	Alignment	not modelled	6.2	29	PDB header: toxin/antitoxin Chain: B: PDB Molecule: antitoxin vapb30; PDBTitle: crystal structure of addiction module from mycobacterial species
95	d1ufza	Alignment	not modelled	6.1	31	Fold: RuvA C-terminal domain-like Superfamily: HBS1-like domain Family: HBS1-like domain
96	c3l9kX	Alignment	not modelled	6.1	26	PDB header: motor protein Chain: X: PDB Molecule: dynein intermediate chain, cytosolic; PDBTitle: insights into dynein assembly from a dynein intermediate chain-light2 chain roadblock structure
97	c3l9kZ	Alignment	not modelled	6.1	26	PDB header: motor protein Chain: Z: PDB Molecule: dynein intermediate chain, cytosolic; PDBTitle: insights into dynein assembly from a dynein intermediate chain-light2 chain roadblock structure
98	c3x38B	Alignment	not modelled	6.1	15	PDB header: replication regulator Chain: B: PDB Molecule: mitochondrial morphogenesis protein sld7; PDBTitle: crystal structure of the c-terminal domain of sid7
99	d1h72c1	Alignment	not modelled	6.1	18	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain