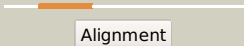

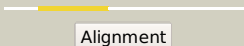

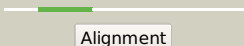

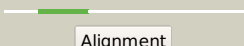

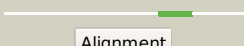

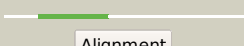

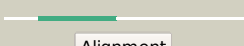


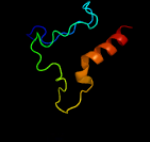

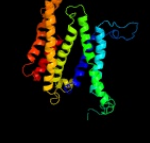

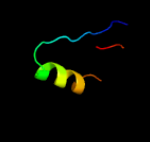




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0064 (-)_68617_71556
Date	Tue Jul 23 14:50:09 BST 2019
Unique Job ID	d0064d33143d8098

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5gasN_	 Alignment		85.1	11	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
2	c5z1fA_	 Alignment		72.2	15	PDB header: metal transport Chain: A: PDB Molecule: csc1-like protein erd4; PDBTitle: structure of atosca3.1 channel
3	c5ir6B_	 Alignment		59.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: bd-type quinol oxidase subunit ii; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
4	d2bs2c1	 Alignment		51.3	14	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Fumarate reductase respiratory complex cytochrome b subunit, FrdC
5	c2jysA_	 Alignment		51.2	19	PDB header: hydrolase Chain: A: PDB Molecule: protease/reverse transcriptase; PDBTitle: solution structure of simian foamy virus (mac) protease
6	c6oceB_	 Alignment		50.1	14	PDB header: transport protein Chain: B: PDB Molecule: stress-gated cation channel 1.2; PDBTitle: structure of the rice hyperosmolality-gated ion channel osca1.2
7	c4witB_	 Alignment		49.5	11	PDB header: lipid transport Chain: B: PDB Molecule: predicted protein; PDBTitle: tmem16 lipid scramblase in crystal form 2
8	c4g59D_	 Alignment		45.1	20	PDB header: immune system Chain: D: PDB Molecule: m152 protein; PDBTitle: crystal structure of the murine cytomegalovirus mhc-i homolog m1522 with ligand rae-1 gamma
9	c6f0kC_	 Alignment		42.5	14	PDB header: membrane protein Chain: C: PDB Molecule: polysulphide reductase nrfd; PDBTitle: alternative complex iii
10	d1njra_	 Alignment		42.4	15	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
11	c4zwiA_	 Alignment		41.8	12	PDB header: signaling protein Chain: A: PDB Molecule: chimera protein of human rhodopsin, mouse s-arrestin, and PDBTitle: crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser

12	c1xl6B_	Alignment		40.9	13	PDB header: metal transport Chain: B: PDB Molecule: inward rectifier potassium channel; PDBTitle: intermediate gating structure 2 of the inwardly rectifying k+ channel2 kirbac3.1
13	c5woyA_	Alignment		40.7	20	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: nmr solution structure of enzyme i (neit) protein using two 4d-spectra
14	c3wvfA_	Alignment		37.8	16	PDB header: chaperone Chain: A: PDB Molecule: membrane protein insertase yidc; PDBTitle: crystal structure of yidc from escherichia coli
15	c1ezaA_	Alignment		36.3	24	PDB header: phosphotransferase Chain: A: PDB Molecule: enzyme i; PDBTitle: amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
16	c4zwcC_	Alignment		35.5	12	PDB header: signaling protein Chain: C: PDB Molecule: chimera protein of human rhodopsin, mouse s-arrestin, and PDBTitle: crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser
17	c5x89A_	Alignment		34.1	25	PDB header: hydrolase Chain: A: PDB Molecule: enda-like protein,trna-splicing endonuclease; PDBTitle: the x-ray crystal structure of subunit fusion rna splicing2 endonuclease from methanopyrus kandleri
18	c6fleA_	Alignment		33.8	23	PDB header: immune system Chain: A: PDB Molecule: interferon gamma; PDBTitle: crystal structure of olive flounder [paralichthys olivaceus]2 interferon gamma at 2.3 angstrom resolution
19	c3edyA_	Alignment		32.6	27	PDB header: hydrolase Chain: A: PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure of the precursor form of human tripeptidyl-peptidase2 1
20	c4exrA_	Alignment		32.4	24	PDB header: unknown function Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of a putative lipoprotein (cd1622) from clostridium2 difficile 630 at 1.85 a resolution
21	d3eeqa2	Alignment	not modelled	31.9	15	Fold: CbiG N-terminal domain-like Superfamily: CbiG N-terminal domain-like Family: CbiG N-terminal domain-like
22	c2vvdA_	Alignment	not modelled	30.3	16	PDB header: viral protein Chain: A: PDB Molecule: spike protein p1; PDBTitle: crystal structure of the receptor binding domain of the2 spike protein p1 from bacteriophage pm2
23	c6mhdV_	Alignment	not modelled	29.9	14	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily v PDBTitle: structure of human trpv3 in the presence of 2-apb in c4 symmetry
24	c3rj2X_	Alignment	not modelled	29.7	41	PDB header: protein binding Chain: X: PDB Molecule: putative uncharacterized protein; PDBTitle: structural and functional characterization of a novel histone h32 binding protein orf158l from the singapore grouper iridovirus (sgiv)
25	c5tloB_	Alignment	not modelled	29.7	30	PDB header: transferase Chain: B: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase ptsp; PDBTitle: solution-state nmr and saxes structural ensemble of npr (1-85) in2 complex with ein-ntr (170-424)
26	c5my7A_	Alignment	not modelled	29.4	16	PDB header: cell adhesion Chain: A: PDB Molecule: adhesin; PDBTitle: adhesin complex protein from neisseria meningitidis
27	c4k4kA_	Alignment	not modelled	29.1	17	PDB header: cell adhesion Chain: A: PDB Molecule: putative cell adhesion protein; PDBTitle: crystal structure of a putative cell adhesion protein (bacuni_00621)2 from bacteroides uniformis atcc 8492 at 1.67 a resolution
						PDB header: structural genomics, unknown function

28	c3eeqB_	Alignment	not modelled	28.4	16	Chain: B: PDB Molecule: putative cobalamin biosynthesis protein g homolog; PDBTitle: crystal structure of a putative cobalamin biosynthesis protein g2 homolog from <i>sulfolobus solfataricus</i>
29	d1losya_	Alignment	not modelled	28.2	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fungal immunomodulatory protein, FIP Family: Fungal immunomodulatory protein, FIP
30	c5cajB_	Alignment	not modelled	27.0	17	PDB header: unknown function Chain: B: PDB Molecule: upf0246 protein yaaa; PDBTitle: crystal structure of e. coli yaaa, a member of the duf328/upf02462 family
31	d1ouoa_	Alignment	not modelled	25.4	21	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: Endonuclease I
32	c6btmC_	Alignment	not modelled	25.3	10	PDB header: membrane protein Chain: C: PDB Molecule: alternative complex iii subunit c; PDBTitle: structure of alternative complex iii from <i>flavobacterium johnsoniae</i> 2 (wild type)
33	c1y08A_	Alignment	not modelled	25.1	26	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein spy0861; PDBTitle: structure of the streptococcal endopeptidase ides, a novel2 cysteine proteinase with strict specificity for igg
34	d1y08a_	Alignment	not modelled	25.1	26	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: IgG-specific endopeptidase IdeS (Sib38)
35	c2llhA_	Alignment	not modelled	25.0	12	PDB header: dna binding protein, chaperone Chain: A: PDB Molecule: nucleophosmin; PDBTitle: nmr structure of npm1_c70
36	c4zv4C_	Alignment	not modelled	24.7	29	PDB header: translation Chain: C: PDB Molecule: tse6; PDBTitle: structure of tse6 in complex with ef-tu
37	c1no1C_	Alignment	not modelled	24.5	22	PDB header: replication Chain: C: PDB Molecule: replisome organizer; PDBTitle: structure of truncated variant of b.subtilis spp1 phage g39p helicase2 loader/inhibitor protein
38	d1no1a_	Alignment	not modelled	24.5	22	Fold: Replisome organizer (g39p helicase loader/inhibitor protein) Superfamily: Replisome organizer (g39p helicase loader/inhibitor protein) Family: Replisome organizer (g39p helicase loader/inhibitor protein)
39	c4ce4l_	Alignment	not modelled	24.1	21	PDB header: ribosome Chain: L: PDB Molecule: PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
40	c4drvA_	Alignment	not modelled	24.0	18	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein vp4; PDBTitle: cell attachment protein vp8* of a human rotavirus specifically2 interacts with a-type histo-blood group antigen
41	d1zya2	Alignment	not modelled	23.7	19	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
42	c5boiA_	Alignment	not modelled	23.3	33	PDB header: unknown function Chain: A: PDB Molecule: germination protein ypeb; PDBTitle: bacillus megaterium ypeb c-terminal domain
43	c2qksA_	Alignment	not modelled	23.2	13	PDB header: metal transport Chain: A: PDB Molecule: kir3.1-prokaryotic kir channel chimera; PDBTitle: crystal structure of a kir3.1-prokaryotic kir channel chimera
44	c5nl2A_	Alignment	not modelled	22.6	14	PDB header: membrane protein Chain: A: PDB Molecule: anoctamin-1; PDBTitle: cryo-em structure of the mtmem16a ion channel at 6.6 a resolution.
45	d1kf6c_	Alignment	not modelled	22.3	15	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
46	c3riaC_	Alignment	not modelled	21.9	11	PDB header: transport protein/immune system Chain: C: PDB Molecule: avermectin-sensitive glutamate-gated chloride channel gluc1 PDBTitle: c. elegans glutamate-gated chloride channel (gluc1) in complex with2 fab, ivermectin and iodide.
47	d1sr3a_	Alignment	not modelled	21.7	10	Fold: OB-fold Superfamily: Heme chaperone CcmE Family: Heme chaperone CcmE
48	c2wnmA_	Alignment	not modelled	21.6	50	PDB header: hydrolase Chain: A: PDB Molecule: gene 2; PDBTitle: solution structure of gp2
49	c2lmcA_	Alignment	not modelled	21.6	50	PDB header: transcription Chain: A: PDB Molecule: bacterial rna polymerase inhibitor; PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex
50	c3f3hA_	Alignment	not modelled	21.6	20	PDB header: antitumor protein Chain: A: PDB Molecule: immunomodulatory protein ling zhi-8; PDBTitle: crystal structure and anti-tumor activity of lz-8 from the fungus2 ganoderma lucidium
51	c3ajvA_	Alignment	not modelled	21.2	20	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: splicing endonuclease from <i>aeropyrum pernix</i>
52	c6nrb3_	Alignment	not modelled	21.1	16	PDB header: chaperone Chain: 3: PDB Molecule: prefoldin subunit 3; PDBTitle: htric-hpfd class2
53	d1vmja_	Alignment	not modelled	21.1	26	Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like

54	c6nrB5_	Alignment	not modelled	20.5	21	PDB header: chaperone Chain: 5: PDB Molecule: prefoldin subunit 5; PDBTitle: htric-hpfd class2
55	c1qk1H_	Alignment	not modelled	20.5	27	PDB header: transferase (creatine kinase) Chain: H: PDB Molecule: creatine kinase, ubiquitous mitochondrial; PDBTitle: crystal structure of human ubiquitous mitochondrial creatine kinase
56	c2vveB_	Alignment	not modelled	20.3	16	PDB header: viral protein Chain: B: PDB Molecule: spike protein p1; PDBTitle: crystal structure of the stem and receptor binding domain2 of the spike protein p1 from bacteriophage pm2
57	c2yvxD_	Alignment	not modelled	19.9	26	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
58	c3nqyA_	Alignment	not modelled	19.7	31	PDB header: hydrolase Chain: A: PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of the autoprocessed complex of vibriolysin mcp-022 with a single point mutation e346a
59	d1x3zb1	Alignment	not modelled	19.4	19	Fold: XPC-binding domain Superfamily: XPC-binding domain Family: XPC-binding domain
60	c5lw8A_	Alignment	not modelled	19.3	22	PDB header: metal transport Chain: A: PDB Molecule: protein tonb; PDBTitle: nmr solution structure of helicobacter pylori tonb-ctd (residues 194-2 285)
61	d3duea1	Alignment	not modelled	19.1	15	Fold: BLIP-like Superfamily: BT0923-like Family: BT0923-like
62	c4o9uB_	Alignment	not modelled	19.0	20	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
63	c5x5sA_	Alignment	not modelled	18.5	18	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: ligand induced structure of amyp-sbd
64	c3omsA_	Alignment	not modelled	18.4	15	PDB header: transferase Chain: A: PDB Molecule: phnb protein; PDBTitle: putative 3-demethylubiquinone-9 3-methyltransferase, phnb protein,2 from bacillus cereus.
65	c2w0cL_	Alignment	not modelled	18.4	16	PDB header: virus Chain: L: PDB Molecule: protein 2; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
66	c1tujA_	Alignment	not modelled	18.3	70	PDB header: transport protein Chain: A: PDB Molecule: odorant binding protein asp2; PDBTitle: solution structure of the honey bee general odorant binding2 protein asp2 in complex with trimethylsilyl-d4 propionate
67	c3m1gC_	Alignment	not modelled	18.3	21	PDB header: transferase Chain: C: PDB Molecule: putative glutathione s-transferase; PDBTitle: the structure of a putative glutathione s-transferase from2 corynebacterium glutamicum
68	c5wc3S_	Alignment	not modelled	18.0	23	PDB header: protein transport Chain: S: PDB Molecule: spoiiaag, stage iii sporulation engulfment assemblyprotein; PDBTitle: spoiiaag
69	c6o7ua_	Alignment	not modelled	17.9	12	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
70	c3rkoM_	Alignment	not modelled	17.7	12	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-quinone oxidoreductase subunit m; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
71	c5vrhA_	Alignment	not modelled	17.6	16	PDB header: transferase Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: apolipoprotein n-acyltransferase c387s active site mutant
72	d3elga1	Alignment	not modelled	17.6	24	Fold: BLIP-like Superfamily: BT0923-like Family: BT0923-like
73	c5yd1B_	Alignment	not modelled	17.6	15	PDB header: metal transport Chain: B: PDB Molecule: protein osca1; PDBTitle: structure of atosca1.1 channel
74	d1ru3a_	Alignment	not modelled	17.1	29	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Acetyl-CoA synthase
75	c1mwuA_	Alignment	not modelled	17.1	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: penicillin-binding protein 2a; PDBTitle: structure of methicillin acyl-penicillin binding protein 2a from2 methicillin resistant staphylococcus aureus strain 27r at 2.60 a3 resolution.
76	c5ws4A_	Alignment	not modelled	17.1	15	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
77	c3eudE_	Alignment	not modelled	17.1	17	PDB header: nuclear protein Chain: E: PDB Molecule: protein shq1; PDBTitle: structure of the cs domain of the essential h/aca rnp assembly protein2 shq1p
78	d2bdra1	Alignment	not modelled	17.0	19	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Ureidoglycolate hydrolase AIIA
79	c1b43A_	Alignment	not modelled	16.9	14	PDB header: transferase Chain: A: PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
						PDB header: de novo protein

80	c5j0hA_	Alignment	not modelled	16.9	41	Chain: A: PDB Molecule: design construct 2l6hc3_13; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
81	d2fhzb1	Alignment	not modelled	16.8	19	Fold: Colicin D/E5 nuclease domain Superfamily: Colicin D/E5 nuclease domain Family: Colicin E5 nuclease domain
82	c6e1oA_	Alignment	not modelled	16.6	12	PDB header: lipid transport Chain: A: PDB Molecule: plasma membrane channel protein (aqy1), putative; PDBTitle: aftmem16 reconstituted in nanodiscs in the presence of ca2+ and2 ceramide 24:0
83	c2lx0A_	Alignment	not modelled	16.6	53	PDB header: membrane protein Chain: A: PDB Molecule: membrane fusion protein p14; PDBTitle: arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
84	c4ev6E_	Alignment	not modelled	16.5	12	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
85	d1qk1a1	Alignment	not modelled	16.5	34	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
86	c4dsdA_	Alignment	not modelled	16.2	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of a putative periplasmic protein (bacova_05534)2 from bacteroides ovatus atcc 8483 at 1.75 a resolution
87	c3ez0D_	Alignment	not modelled	16.0	27	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein with ferritin-like fold; PDBTitle: crystal structure of protein of unknown function with ferritin-like2 fold (yp_832262.1) from arthrobacter sp. fb24 at 2.33 a resolution
88	c1sazA_	Alignment	not modelled	16.0	23	PDB header: transferase Chain: A: PDB Molecule: probable butyrate kinase 2; PDBTitle: membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
89	c4v1a1_	Alignment	not modelled	15.9	23	PDB header: ribosome Chain: L: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
90	c4gx2B_	Alignment	not modelled	15.8	25	PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: gsuk channel bound to nad
91	c6eznF_	Alignment	not modelled	15.5	19	PDB header: membrane protein Chain: F: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
92	d1k38a_	Alignment	not modelled	15.5	24	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
93	c3ee6A_	Alignment	not modelled	15.5	23	PDB header: hydrolase Chain: A: PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure analysis of tripeptidyl peptidase -i
94	c1j6qA_	Alignment	not modelled	15.3	13	PDB header: chaperone Chain: A: PDB Molecule: cytochrome c maturation protein e; PDBTitle: solution structure and characterization of the heme2 chaperone ccme
95	d1j6qa_	Alignment	not modelled	15.3	13	Fold: OB-fold Superfamily: Heme chaperone CcmE Family: Heme chaperone CcmE
96	c1hymB_	Alignment	not modelled	15.2	46	PDB header: hydrolase (serine proteinase) Chain: B: PDB Molecule: hydrolyzed cucurbita maxima trypsin inhibitor v; PDBTitle: hydrolyzed trypsin inhibitor (cmti-v, minimized average nmr structure)
97	c5mrwG_	Alignment	not modelled	15.1	30	PDB header: hydrolase Chain: G: PDB Molecule: potassium-transporting atpase kdpc subunit; PDBTitle: structure of the kdpcfabc complex
98	c2k8gA_	Alignment	not modelled	15.0	17	PDB header: structural protein Chain: A: PDB Molecule: protein shq1; PDBTitle: nmr structure of shq1p n-terminal domain
99	c5n9yB_	Alignment	not modelled	14.9	4	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb