

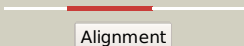
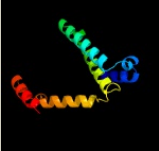
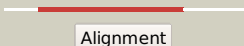






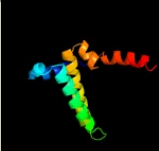
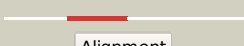
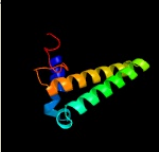








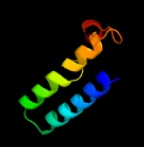

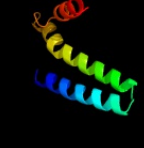
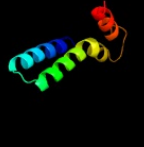
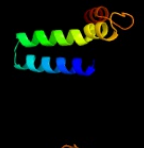
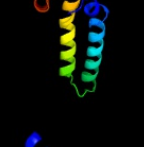





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1021 (-) _1142675_1143652
Date	Wed Jul 31 22:05:09 BST 2019
Unique Job ID	a514e94c666e40b3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3crcB_	 Alignment		100.0	36	PDB header: hydrolase Chain: B: PDB Molecule: protein mazg; PDBTitle: crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response
2	c2yxhB_	 Alignment		100.0	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: mazg-related protein; PDBTitle: crystal structure of mazg-related protein from thermotoga maritima
3	c5n0sA_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: peptide n-methyltransferase; PDBTitle: crystal structure of opha-deltac6 mutant y98a in complex with sam
4	d2a3qa1	 Alignment		99.6	20	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
5	c2q4pA_	 Alignment		99.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein rs21-c6; PDBTitle: ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
6	c3obcB_	 Alignment		99.6	21	PDB header: hydrolase Chain: B: PDB Molecule: pyrophosphatase; PDBTitle: crystal structure of a pyrophosphatase (af1178) from archaeoglobus2 fulgidus at 1.80 a resolution
7	d1vmga_	 Alignment		98.9	21	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
8	d2oiea1	 Alignment		98.3	20	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
9	d2gtad1	 Alignment		98.2	22	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
10	d2gtaa1	 Alignment		97.7	22	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
11	d1yxba1	 Alignment		97.4	29	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)

12	d1y6xa1	Alignment		97.3	35	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)
13	c1yvwd	Alignment		97.1	17	PDB header: hydrolase Chain: D: PDB Molecule: phosphoribosyl-atp pyrophosphatase; PDBTitle: crystal structure of phosphoribosyl-atp2 pyrophosphohydrolase from bacillus cereus. nesgc target3 bcr13.
14	d1yvwa1	Alignment		97.1	17	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)
15	d2a7wa1	Alignment		96.9	24	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)
16	c2a7wF	Alignment		96.9	24	PDB header: hydrolase Chain: F: PDB Molecule: phosphoribosyl-atp pyrophosphatase; PDBTitle: crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7
17	c2q9IA	Alignment		96.7	28	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
18	c2p06A	Alignment		94.5	37	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af_0060; PDBTitle: crystal structure of a predicted coding region af_0060 from2 archaeoglobus fulgidus dsm 4304
19	d2p06a1	Alignment		94.5	37	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: AF0060-like
20	c2yf3F	Alignment		92.8	33	PDB header: hydrolase Chain: F: PDB Molecule: mazg-like nucleoside triphosphate pyrophosphohydrolase; PDBTitle: crystal structure of dr2231, the mazg-like protein from deinococcus2 radiodurans, complex with manganese
21	c3nqwB	Alignment	not modelled	60.5	21	PDB header: hydrolase Chain: B: PDB Molecule: cg11900; PDBTitle: a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
22	c3qk9B	Alignment	not modelled	33.6	23	PDB header: protein transport Chain: B: PDB Molecule: mitochondrial import inner membrane translocase subunit PDBTitle: yeast tim44 c-terminal domain complexed with cymal-3
23	d2fxta1	Alignment	not modelled	33.4	20	Fold: Cystatin-like Superfamily: NTF2-like Family: TIM44-like
24	d2cw9a1	Alignment	not modelled	33.4	14	Fold: Cystatin-like Superfamily: NTF2-like Family: TIM44-like
25	c5h6sB	Alignment	not modelled	33.0	12	PDB header: hydrolase Chain: B: PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase s179a mutant complexed with a2 substrate
26	c5jffD	Alignment	not modelled	29.8	14	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein yhfg; PDBTitle: e. coli ecfct mutant g55r in complex with ecfca
27	c4uqfB	Alignment	not modelled	29.4	8	PDB header: hydrolase Chain: B: PDB Molecule: gtp cyclohydrolase 1; PDBTitle: crystal structure of listeria monocytogenes gtp cyclohydrolase i
28	c3ah5E	Alignment	not modelled	25.0	18	PDB header: transferase Chain: E: PDB Molecule: thymidylate synthase thyx; PDBTitle: crystal structure of flavin dependent thymidylate synthase thyx from2 helicobacter pylori complexed with fad and dump PDB header: electron transport

29	c5b3iB_	Alignment	not modelled	22.0	13	Chain: B; PDB Molecule: cytochrome c prime; PDBTitle: homo-dimeric structure of cytochrome c' from thermophilic2 hydrogenophilus thermoluteolus
30	d2j4ba1	Alignment	not modelled	21.9	25	Fold: Taf5 N-terminal domain-like Superfamily: Taf5 N-terminal domain-like Family: Taf5 N-terminal domain-like
31	d1e85a_	Alignment	not modelled	21.3	23	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
32	c5if9A_	Alignment	not modelled	21.0	8	PDB header: transferase Chain: A; PDB Molecule: nucleoside diphosphate-linked moiety x motif 22; PDBTitle: crystal structure of human nudt22
33	c2rfpA_	Alignment	not modelled	20.7	12	PDB header: hydrolase Chain: A; PDB Molecule: putative ntp pyrophosphohydrolase; PDBTitle: crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
34	c6hn9A_	Alignment	not modelled	20.4	30	PDB header: antimicrobial protein Chain: A; PDB Molecule: nicomicin-1; PDBTitle: nicomicin-1 -- novel antimicrobial peptides from the arctic polychaeta2 nicomache minor provide new molecular insight into biological role of3 the brichos domain
35	d1bpoa1	Alignment	not modelled	19.7	70	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Clathrin heavy-chain linker domain
36	d1cpqa_	Alignment	not modelled	19.2	15	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
37	c5h6tB_	Alignment	not modelled	19.0	12	PDB header: hydrolase Chain: B; PDB Molecule: amidase; PDBTitle: crystal structure of hydrazidase from microbacterium sp. strain hm58-2
38	c2jz8A_	Alignment	not modelled	17.5	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein bh09830; PDBTitle: solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
39	c6feyF_	Alignment	not modelled	17.5	64	PDB header: peptide binding protein Chain: F; PDB Molecule: probable insulin-like peptide 5; PDBTitle: crystal structure of drosophila neural ectodermal development factor2 imp-l2 with drosophila dilp5 insulin
40	c6feyH_	Alignment	not modelled	17.2	64	PDB header: peptide binding protein Chain: H; PDB Molecule: probable insulin-like peptide 5; PDBTitle: crystal structure of drosophila neural ectodermal development factor2 imp-l2 with drosophila dilp5 insulin
41	c3efdK_	Alignment	not modelled	17.2	22	PDB header: immune system Chain: K; PDB Molecule: kcsa; PDBTitle: the crystal structure of the cytoplasmic domain of kcsa
42	c2wfuB_	Alignment	not modelled	16.8	64	PDB header: signaling protein Chain: B; PDB Molecule: probable insulin-like peptide 5 b chain; PDBTitle: crystal structure of dilp5 variant db
43	c6hqaB_	Alignment	not modelled	16.6	26	PDB header: transcription Chain: B; PDB Molecule: subunit (90 kda) of tfiid and saga complexes; PDBTitle: molecular structure of promoter-bound yeast tfiid
44	c2wfvB_	Alignment	not modelled	16.6	64	PDB header: signaling protein Chain: B; PDB Molecule: probable insulin-like peptide 5 b chain; PDBTitle: crystal structure of dilp5 variant c4
45	c1wm9D_	Alignment	not modelled	16.5	5	PDB header: hydrolase Chain: D; PDB Molecule: gtp cyclohydrolase i; PDBTitle: structure of gtp cyclohydrolase i from thermus thermophilus hb8
46	d1wura1	Alignment	not modelled	16.5	5	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
47	c6hqaC_	Alignment	not modelled	16.3	26	PDB header: transcription Chain: C; PDB Molecule: subunit (90 kda) of tfiid and saga complexes; PDBTitle: molecular structure of promoter-bound yeast tfiid
48	c4cimP_	Alignment	not modelled	15.8	31	PDB header: apoptosis Chain: P; PDB Molecule: bcl-2-like protein 2; PDBTitle: complex of a bcl-w bh3 mutant with a bh3 domain
49	c4cimQ_	Alignment	not modelled	15.8	31	PDB header: apoptosis Chain: Q; PDB Molecule: bcl-2-like protein 2; PDBTitle: complex of a bcl-w bh3 mutant with a bh3 domain
50	c5oezA_	Alignment	not modelled	15.8	13	PDB header: hydrolase Chain: A; PDB Molecule: fbp protein; PDBTitle: crystal structure of leishmania major fructose-1,6-bisphosphatase in2 apo form.
51	c6mzcG_	Alignment	not modelled	15.7	28	PDB header: transcription Chain: G; PDB Molecule: transcription initiation factor tfiid subunit 5; PDBTitle: human tfiid bc core
52	c4b6xB_	Alignment	not modelled	15.1	29	PDB header: toxin Chain: B; PDB Molecule: avirulence protein; PDBTitle: crystal structure of in planta processed avrrps4
53	d1ffgb_	Alignment	not modelled	15.0	56	Fold: Ferredoxin-like Superfamily: CheY-binding domain of CheA Family: CheY-binding domain of CheA
54	c1a0oH_	Alignment	not modelled	14.6	56	PDB header: chemotaxis Chain: H; PDB Molecule: chea; PDBTitle: chey-binding domain of chea in complex with chey PDB header: transcription

55	c5olaD_	Alignment	not modelled	14.1	58	Chain: D: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of mitochondrial transcription elongation complex in complex2 with elongation factor tefm
56	c4vj6A_	Alignment	not modelled	13.6	15	PDB header: hydrolase Chain: A: PDB Molecule: aryl acylamidase; PDBTitle: the crystal structure of a bacterial aryl acylamidase belonging to the2 amidase signature (as) enzymes family
57	c5k4bA_	Alignment	not modelled	13.3	22	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit d; PDBTitle: structure of eukaryotic translation initiation factor 3 subunit d2 (eif3d) cap binding domain from nasonia vitripennis, crystal form 1
58	c2la2A_	Alignment	not modelled	13.2	35	PDB header: antimicrobial protein Chain: A: PDB Molecule: cecropin; PDBTitle: solution structure of papilioicin isolated from the swallowtail2 butterfly, papilio xuthus
59	c2ctoA_	Alignment	not modelled	12.7	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: novel protein; PDBTitle: solution structure of the hmg box like domain from human2 hypothetical protein fj14904
60	c6a3kA_	Alignment	not modelled	12.4	20	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: crystal structure of cytochrome c' from shewanella benthica db6705
61	c4b6xA_	Alignment	not modelled	12.3	29	PDB header: toxin Chain: A: PDB Molecule: avirulence protein; PDBTitle: crystal structure of in planta processed avrrps4
62	d1mt5a_	Alignment	not modelled	11.7	14	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
63	c1bpoA_	Alignment	not modelled	11.7	70	PDB header: membrane protein Chain: A: PDB Molecule: protein (clathrin); PDBTitle: clathrin heavy-chain terminal domain and linker
64	d3d1ma1	Alignment	not modelled	11.6	21	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Hedgehog (development protein), N-terminal signaling domain
65	d2ibge1	Alignment	not modelled	11.5	21	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: Hedgehog (development protein), N-terminal signaling domain
66	d1oiza1	Alignment	not modelled	11.5	27	Fold: RuvA C-terminal domain-like Superfamily: CRAL/TRIO N-terminal domain Family: CRAL/TRIO N-terminal domain
67	c2d1IA_	Alignment	not modelled	11.3	18	PDB header: protein binding Chain: A: PDB Molecule: metastasis suppressor protein 1; PDBTitle: structure of f-actin binding domain imd of mim (missing in metastasis)
68	c5lrva_	Alignment	not modelled	11.1	33	PDB header: hydrolase Chain: A: PDB Molecule: otu domain-containing protein 7b; PDBTitle: structure of cezanne/otud7b otu domain bound to lys11-linked2 diubiquitin
69	c3m1nB_	Alignment	not modelled	11.0	21	PDB header: signaling protein Chain: B: PDB Molecule: sonic hedgehog protein; PDBTitle: crystal structure of human sonic hedgehog n-terminal domain
70	c4ulvB_	Alignment	not modelled	10.9	15	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c, class ii; PDBTitle: cytochrome c prime from shewanella frigidimarina
71	c3e4xB_	Alignment	not modelled	10.8	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: apc36150; PDBTitle: crystal structure of putative metal-dependent hydrolases2 apc36150
72	c3muxB_	Alignment	not modelled	10.6	22	PDB header: lyase Chain: B: PDB Molecule: putative 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
73	c5flmK_	Alignment	not modelled	10.6	28	PDB header: transcription Chain: K: PDB Molecule: dna-directed rna polymerase ii subunit rpb11; PDBTitle: structure of transcribing mammalian rna polymerase ii
74	c6c6gA_	Alignment	not modelled	10.2	14	PDB header: hydrolase Chain: A: PDB Molecule: biuret hydrolase; PDBTitle: an unexpected vestigial protein complex reveals the evolutionary2 origins of an s-triazine catabolic enzyme. inhibitor bound complex.
75	c2lfcA_	Alignment	not modelled	10.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase, flavoprotein subunit; PDBTitle: solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
76	d1u5pa2	Alignment	not modelled	10.0	15	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
77	d1ej5a_	Alignment	not modelled	10.0	7	Fold: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain Superfamily: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain Family: Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
78	c3a2qA_	Alignment	not modelled	9.8	10	PDB header: hydrolase Chain: A: PDB Molecule: 6-aminohexanoate-cyclic-dimer hydrolase; PDBTitle: structure of 6-aminohexanoate cyclic dimer hydrolase complexed with2 substrate
79	c3m6yA_	Alignment	not modelled	9.4	17	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.

80	c2pmzL_	Alignment	not modelled	9.4	10	PDB header: translation, transferase Chain: L; PDB Molecule: dna-directed rna polymerase subunit I; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
81	d1bbha_	Alignment	not modelled	9.3	13	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
82	d2j49a1	Alignment	not modelled	9.3	14	Fold: Taf5 N-terminal domain-like Superfamily: Taf5 N-terminal domain-like Family: Taf5 N-terminal domain-like
83	c2ld7B_	Alignment	not modelled	9.3	8	PDB header: transcription Chain: B; PDB Molecule: paired amphipathic helix protein sin3a; PDBTitle: solution structure of the msin3a pah3-sap30 sid complex
84	c4o9lA_	Alignment	not modelled	9.2	22	PDB header: antiviral protein Chain: A; PDB Molecule: mitochondrial antiviral signaling protein (mavs); PDBTitle: crystal structure of horse mavs card domain mutant e26r
85	c2vyaB_	Alignment	not modelled	9.2	13	PDB header: hydrolase Chain: B; PDB Molecule: fatty-acid amide hydrolase 1; PDBTitle: crystal structure of fatty acid amide hydrolase conjugated2 with the drug-like inhibitor pf-750
86	c3kfuE_	Alignment	not modelled	9.1	15	PDB header: ligase/rna Chain: E; PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: crystal structure of the transamidosome
87	c2k42A_	Alignment	not modelled	9.0	10	PDB header: signaling protein Chain: A; PDB Molecule: wiskott-aldrich syndrome protein; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehc effector
88	d2pv7a1	Alignment	not modelled	9.0	8	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
89	d1pswa_	Alignment	not modelled	9.0	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II
90	d2nxpa1	Alignment	not modelled	8.9	31	Fold: Taf5 N-terminal domain-like Superfamily: Taf5 N-terminal domain-like Family: Taf5 N-terminal domain-like
91	d1zyma1	Alignment	not modelled	8.5	11	Fold: SAM domain-like Superfamily: Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain Family: Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain
92	c3o59X_	Alignment	not modelled	8.4	22	PDB header: transferase Chain: X; PDB Molecule: dna polymerase ii large subunit; PDBTitle: dna polymerase d large subunit dp2(1-300) from pyrococcus horikoshii
93	c6mn5A_	Alignment	not modelled	8.3	24	PDB header: transferase/antibiotic Chain: A; PDB Molecule: aminoglycoside n(3)-acetyltransferase, aac(3)-iva; PDBTitle: crystal structure of aminoglycoside acetyltransferase aac(3)-iva,2 h154a mutant, in complex with gentamicin c1a
94	c4dhxC_	Alignment	not modelled	8.3	19	PDB header: transport protein/dna binding protein Chain: C; PDB Molecule: enhancer of yellow 2 transcription factor homolog; PDBTitle: eny2:ganp complex
95	d3bzka2	Alignment	not modelled	8.3	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
96	c4c2mK_	Alignment	not modelled	8.2	17	PDB header: transcription Chain: K; PDB Molecule: dna-directed rna polymerases i and iii subunit rpac2; PDBTitle: structure of rna polymerase i at 2.8 a resolution
97	c6hqgB_	Alignment	not modelled	8.0	15	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome p450; PDBTitle: cytochrome p450-153 from phenylobacterium zucineum
98	c3fnna_	Alignment	not modelled	7.9	24	PDB header: transferase Chain: A; PDB Molecule: thymidylate synthase thyx; PDBTitle: biochemical and structural analysis of an atypical thyx:2 corynebacterium glutamicum nchu 87078 depends on thya for3 thymidine biosynthesis
99	d1omha_	Alignment	not modelled	7.9	16	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: Relaxase domain