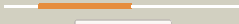

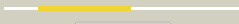









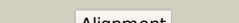










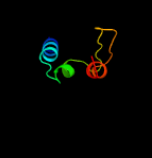
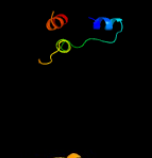

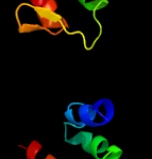
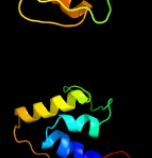
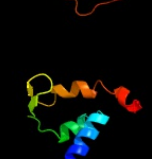
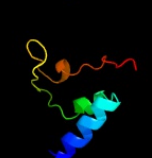
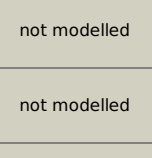


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3172c_(-)_3540879_3541361
Date	Thu Aug 8 16:20:36 BST 2019
Unique Job ID	7e2be7e79a054bec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g0kA_	 Alignment		88.1	13	PDB header: ca-binding protein Chain: A: PDB Molecule: putative membrane protein; PDBTitle: crystal structure of a protein of unknown function with a cystatin-2 like fold (saro_2880) from novosphingobium aromaticivorans dsm at3 1.30 a resolution
2	c3hk4B_	 Alignment		75.3	11	PDB header: lyase Chain: B: PDB Molecule: mlr7391 protein; PDBTitle: crystal structure of a putative snoal-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution
3	c3robC_	 Alignment		71.3	7	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776
4	d2f99a1	 Alignment		69.8	13	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
5	d2gexa1	 Alignment		66.8	10	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
6	c5x7IA_	 Alignment		66.1	11	PDB header: isomerase Chain: A: PDB Molecule: tsrd; PDBTitle: structure of tsrd from streptomyces laurentii
7	c3f9sB_	 Alignment		64.7	15	PDB header: lyase Chain: B: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (lferr_0659) from2 acidithiobacillus ferrooxidans atcc at 1.76 a resolution
8	c4lqqA_	 Alignment		64.4	19	PDB header: lyase Chain: A: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of a putative polyketide cyclase (cv_0247) from2 chromobacterium violaceum atcc 12472 at 2.72 a resolution
9	c3fsdA_	 Alignment		64.4	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntf2-like protein of unknown function in nutrient uptake; PDBTitle: crystal structure of ntf2-like protein of unknown function in nutrient2 uptake (yp_427473.1) from rhodospirillum rubrum atcc 11170 at 1.70 a3 resolution
10	d2geya1	 Alignment		64.3	22	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
11	d2r4ia1	 Alignment		59.1	8	Fold: Cystatin-like Superfamily: NTF2-like Family: CHU142-like

12	c6of9G_	Alignment		56.2	18	PDB header: unknown function Chain: G: PDB Molecule: camkii hub; PDBTitle: structure of the chlamydomonas reinhardtii camkii hub homology domain
13	c3bb9D_	Alignment		56.1	10	PDB header: unknown function Chain: D: PDB Molecule: putative orphan protein; PDBTitle: crystal structure of a putative ketosteroid isomerase (sfri_1973) from shewanella frigidimarina ncimb 400 at 1.80 a resolution
14	d1mi1a1	Alignment		53.0	22	Fold: BEACH domain Superfamily: BEACH domain Family: BEACH domain
15	c5ig5E_	Alignment		51.9	10	PDB header: transferase Chain: E: PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2
16	c3kspA_	Alignment		39.7	15	PDB header: unknown function Chain: A: PDB Molecule: calcium/calmodulin-dependent kinase ii association domain; PDBTitle: crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution
17	c3kkqA_	Alignment		39.0	15	PDB header: lyase Chain: A: PDB Molecule: putative snoal-like polyketide cyclase; PDBTitle: crystal structure of putative snoal-like polyketide cyclase2 (yp_509242.1) from jannaschia sp. ccs1 at 1.40 a resolution
18	c3k0zB_	Alignment		38.0	11	PDB header: lyase Chain: B: PDB Molecule: putative polyketide cyclase; PDBTitle: crystal structure of putative polyketide cyclase (np_977253.1) from bacillus cereus atcc 10987 at 1.91 a resolution
19	d1hkxa_	Alignment		38.0	14	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
20	c3f7sA_	Alignment		37.2	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution
21	d1t77a1	Alignment	not modelled	35.8	19	Fold: BEACH domain Superfamily: BEACH domain Family: BEACH domain
22	c5ig4A_	Alignment	not modelled	35.7	8	PDB header: transferase Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of n. vectensis camkii-a hub
23	d3ebta1	Alignment	not modelled	35.6	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Snoal-like polyketide cyclase
24	d3cu3a1	Alignment	not modelled	32.4	9	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
25	c4z9cB_	Alignment	not modelled	32.3	30	PDB header: transferase Chain: B: PDB Molecule: subtilase cytotoxin subunit b-like protein; PDBTitle: ecpltab oxidized
26	c1mi1A_	Alignment	not modelled	31.5	22	PDB header: signaling protein Chain: A: PDB Molecule: neurobeachin; PDBTitle: crystal structure of the ph-beach domain of human2 neurobeachin
27	d2ux0a1	Alignment	not modelled	29.5	9	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
28	c4ovmE_	Alignment	not modelled	29.3	19	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus
						Fold: Periplasmic binding protein-like II

29	d1vr5a1	Alignment	not modelled	25.0	11	Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
30	c3hx8A	Alignment	not modelled	23.5	10	PDB header: isomerase Chain: A: PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (np_103587.1) from2 mesorhizobium loti at 1.45 a resolution
31	d3b7ca1	Alignment	not modelled	22.9	11	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
32	d1sjwa	Alignment	not modelled	21.3	18	Fold: Cystatin-like Superfamily: NTF2-like Family: SnoAL-like polyketide cyclase
33	c4k6iC	Alignment	not modelled	21.1	28	PDB header: toxin Chain: C: PDB Molecule: putative pertussis-like toxin subunit; PDBTitle: structure of typhoid toxin
34	c4i4kB	Alignment	not modelled	19.7	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein sgcj; PDBTitle: streptomyces globosporus c-1027 9-membered enediyne conserved protein2 sgce6
35	c4fprC	Alignment	not modelled	19.1	15	PDB header: protein binding Chain: C: PDB Molecule: avirulence effector avrlm4-7; PDBTitle: structure of a fungal protein
36	c5z62N	Alignment	not modelled	18.3	27	PDB header: electron transport Chain: N: PDB Molecule: cytochrome c oxidase subunit ndufa4; PDBTitle: structure of human cytochrome c oxidase
37	c3t0yB	Alignment	not modelled	18.2	31	PDB header: transcription regulator/protein binding Chain: B: PDB Molecule: nepr; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
38	c5whvF	Alignment	not modelled	17.1	31	PDB header: toxin Chain: F: PDB Molecule: artb protein; PDBTitle: crystal structure of artb
39	d3bb9a1	Alignment	not modelled	16.2	13	Fold: Cystatin-like Superfamily: NTF2-like Family: SO0125-like
40	c3t0yD	Alignment	not modelled	16.2	31	PDB header: transcription regulator/protein binding Chain: D: PDB Molecule: nepr; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
41	c2kesA	Alignment	not modelled	16.2	40	PDB header: protein binding Chain: A: PDB Molecule: synphilin-1; PDBTitle: solution structure of the coiled-coil domain of synphilin-1
42	c4hr1A	Alignment	not modelled	15.1	24	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of pav1-137, a protein from the virus pav1 that infects2 pyrococcus abyssi.
43	c1tuhA	Alignment	not modelled	15.1	6	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein egc068; PDBTitle: structure of bal32a from a soil-derived mobile gene cassette
44	d1tuha	Alignment	not modelled	15.1	6	Fold: Cystatin-like Superfamily: NTF2-like Family: Hypothetical protein egc068 from a soil-derived mobile gene cassette
45	c3h3hA	Alignment	not modelled	13.9	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized snoal-like protein; PDBTitle: crystal structure of a snoal-like protein of unknown function2 (bth_ji0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
46	d1m0da	Alignment	not modelled	13.5	53	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Endonuclease I (Holliday junction resolvase)
47	c4jzIA	Alignment	not modelled	12.5	33	PDB header: apoptosis, transport protein Chain: A: PDB Molecule: b-cell receptor-associated protein 31; PDBTitle: crystal structure of bap31 vded at alkaline ph
48	c3msoA	Alignment	not modelled	12.4	6	PDB header: isomerase Chain: A: PDB Molecule: steroid delta-isomerase; PDBTitle: crystal structure of a steroid delta-isomerase (np_250810.1) from2 pseudomonas aeruginosa at 2.57 a resolution
49	c3gzrA	Alignment	not modelled	12.4	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein with a ntf2-like fold; PDBTitle: crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution
50	c4w7yB	Alignment	not modelled	11.9	28	PDB header: transport protein Chain: B: PDB Molecule: b-cell receptor-associated protein 29; PDBTitle: dimeric bap29 vded with disulfide bonds in crystal contacts
51	c5aiiP	Alignment	not modelled	11.7	20	PDB header: hydrolase Chain: P: PDB Molecule: limonene-1,2-epoxide hydrolase; PDBTitle: discovery and characterization of thermophilic limonene-1,2-epoxide2 hydrolases from hot spring metagenomic libraries.3 ch55-sample-peg complex
52	c4pfwA	Alignment	not modelled	11.3	14	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: crystal structure of mannohexaose bound oligopeptide abc transporter,2 periplasmic oligopeptide-binding protein (tm1226) from thermotoga3 maritima at 2.2 a resolution
53	c1algA	Alignment	not modelled	11.1	75	PDB header: oxidoreductase Chain: A: PDB Molecule: p11; PDBTitle: solution structure of an hgr inhibitor, nmr, 10 structures
54	c4efzB	Alignment	not modelled	11.0	26	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of a hypothetical metallo-beta-lactamase

						from2 burkholderia pseudomallei
55	c3k6qB_	Alignment	not modelled	10.8	21	PDB header: ligand binding protein Chain: B: PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
56	d3bofa2	Alignment	not modelled	10.4	29	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
57	c6d34B_	Alignment	not modelled	10.1	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: terc; PDBTitle: apo crystal structure of terc, a terfestatin biosynthesis enzyme
58	c3dwqD_	Alignment	not modelled	10.0	21	PDB header: toxin Chain: D: PDB Molecule: subtilase cytotoxin, subunit b; PDBTitle: crystal structure of the a-subunit of the ab5 toxin from e.2 coli with neu5gc-2,3gal-1,3glcnac
59	c4f3nA_	Alignment	not modelled	9.9	38	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized acr, cog1565 superfamily; PDBTitle: high resolution native crystal structure of an uncharacterized acr,2 cog1565 superfamily protein from burkholderia thailandensis, solved3 by iodide ion sad
60	c1lw7A_	Alignment	not modelled	9.9	24	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulator nadr; PDBTitle: nadr protein from haemophilus influenzae
61	c3g8zA_	Alignment	not modelled	9.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function with cystatin-like fold; PDBTitle: crystal structure of protein of unknown function with cystatin-like2 fold (np_639274.1) from xanthomonas campestris at 1.90 a resolution
62	c5aigA_	Alignment	not modelled	9.8	10	PDB header: hydrolase Chain: A: PDB Molecule: limonene-1,2-epoxide hydrolase; PDBTitle: discovery and characterization of thermophilic limonene-1,2-epoxide2 hydrolases from hot spring metagenomic libraries. tomsk-sample-3 valpromide complex
63	d1wjna_	Alignment	not modelled	9.5	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
64	d1ss6a_	Alignment	not modelled	9.0	35	Fold: NSFL1 (p97 ATPase) cofactor p47, SEP domain Superfamily: NSFL1 (p97 ATPase) cofactor p47, SEP domain Family: NSFL1 (p97 ATPase) cofactor p47, SEP domain
65	c3fgyB_	Alignment	not modelled	8.9	12	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized ntf2-like protein; PDBTitle: crystal structure of a ntf2-like protein (bx_e_b1094) from burkholderia2 xenovorans lb400 at 1.59 a resolution
66	c4uwqK_	Alignment	not modelled	8.8	71	PDB header: hydrolase Chain: K: PDB Molecule: soxy protein; PDBTitle: crystal structure of the disulfide-linked complex of the2 thiosulfuryolase soxb with the carrier-protein soxyz from3 thermus thermophilus
67	c3iwcD_	Alignment	not modelled	8.7	11	PDB header: lyase Chain: D: PDB Molecule: s-adenosylmethionine decarboxylase; PDBTitle: t. maritima adometdc complex with s-adenosylmethionine methyl ester
68	c3gwrA_	Alignment	not modelled	8.5	13	PDB header: protein binding Chain: A: PDB Molecule: putative calcium/calmodulin-dependent protein kinase type PDBTitle: crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution
69	c3bl4B_	Alignment	not modelled	8.1	22	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function (arth_0117) from2 arthrobacter sp. fb24 at 2.20 a resolution
70	c1jdhB_	Alignment	not modelled	8.1	35	PDB header: transcription Chain: B: PDB Molecule: htcf-4; PDBTitle: crystal structure of beta-catenin and htcf-4
71	d1pdaa2	Alignment	not modelled	7.9	32	Fold: dsRBD-like Superfamily: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain Family: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
72	c2o7jA_	Alignment	not modelled	7.9	11	PDB header: sugar binding protein Chain: A: PDB Molecule: oligopeptide abc transporter, periplasmic PDBTitle: the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
73	d1rh8a_	Alignment	not modelled	7.8	17	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
74	c2b3rA_	Alignment	not modelled	7.5	31	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol-4-phosphate 3-kinase c2 domain- PDBTitle: crystal structure of the c2 domain of class ii phosphatidylinositide2 3-kinase c2
75	c4ytoA_	Alignment	not modelled	7.4	20	PDB header: cell cycle Chain: A: PDB Molecule: synaptonemal complex protein 1; PDBTitle: structure of coiled-coil domain of sycp1
76	d1u5ua_	Alignment	not modelled	7.4	9	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Allene oxide synthase
77	d1lt7a_	Alignment	not modelled	7.2	29	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
78	c1e1bC_	Alignment	not modelled	7.1	18	PDB header: hydrolase Chain: C: PDB Molecule: botulinum neurotoxin type a light chain;

78	c1e1nc_	Alignment	not modelled	7.1	10	PDBTitle: crystal structure of recombinant botulinum neurotoxin type a light2 chain, self-inhibiting zn endopeptidase.
79	d1f83a_	Alignment	not modelled	7.0	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Clostridium neurotoxins, catalytic domain
80	d1tp6a_	Alignment	not modelled	6.9	15	Fold: Cystatin-like Superfamily: NTF2-like Family: PA1314-like
81	d2gxfa1	Alignment	not modelled	6.8	10	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
82	c4boeA_	Alignment	not modelled	6.8	70	PDB header: cholesterol binding protein Chain: A: PDB Molecule: japanin; PDBTitle: japanin from rhipicephalus appendiculatus bound to cholesterol:2 tetragonal crystal form
83	c6a56A_	Alignment	not modelled	6.7	18	PDB header: sugar binding protein Chain: A: PDB Molecule: ajlec; PDBTitle: ajlec from the sea anemone anthopleura japonica
84	d2vzsa2	Alignment	not modelled	6.7	41	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
85	c6bmcA_	Alignment	not modelled	6.6	38	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: the structure of a dimeric type ii dah7ps associated with pyocyanin2 biosynthesis in pseudomonas aeruginosa
86	d1nwwa_	Alignment	not modelled	6.6	15	Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like
87	d1wglA_	Alignment	not modelled	6.6	25	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain
88	c3ry3B_	Alignment	not modelled	6.6	3	PDB header: transport protein Chain: B: PDB Molecule: putative solute-binding protein; PDBTitle: putative solute-binding protein from yersinia pestis.
89	c4gl8B_	Alignment	not modelled	6.5	3	PDB header: protein transport Chain: B: PDB Molecule: oligopeptide abc transporter oppaiv; PDBTitle: x-ray crystal structure of a periplasmic oligopeptide-binding2 protein/oligopeptide abc transporter(oppaiv) from borrelia3 burgdorferi
90	c3k3qB_	Alignment	not modelled	6.5	18	PDB header: immune system Chain: B: PDB Molecule: botulinum neurotoxin type a; PDBTitle: crystal structure of a llama antibody complexed with the c. botulinum2 neurotoxin serotype a catalytic domain
91	d1byna_	Alignment	not modelled	6.4	14	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: Synaptotagmin-like (S variant)
92	d1b0nb_	Alignment	not modelled	6.4	33	Fold: Dimerisation interlock Superfamily: SinR repressor dimerisation domain-like Family: SinR repressor dimerisation domain-like
93	c1b0nB_	Alignment	not modelled	6.4	33	PDB header: transcription regulator Chain: B: PDB Molecule: protein (sini protein); PDBTitle: sinr protein/sini protein complex
94	c3ehcA_	Alignment	not modelled	6.4	15	PDB header: unknown function Chain: A: PDB Molecule: snoal-like polyketide cyclase; PDBTitle: crystal structure of a snoal-like polyketide cyclase (atu3018) from2 agrobacterium tumefaciens str. c58 at 2.12 a resolution
95	c5ibzD_	Alignment	not modelled	6.3	30	PDB header: lyase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a novel cyclase (pfam04199).
96	c3ke7A_	Alignment	not modelled	6.2	5	PDB header: isomerase Chain: A: PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distazonis atcc 8503 at 1.45 a resolution
97	d1flia_	Alignment	not modelled	6.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ets domain
98	c3h5jA_	Alignment	not modelled	6.0	67	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
99	c1ztyA_	Alignment	not modelled	6.0	14	PDB header: sugar binding protein, signaling protein Chain: A: PDB Molecule: chitin oligosaccharide binding protein; PDBTitle: crystal structure of the chitin oligasaccharide binding2 protein