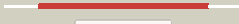

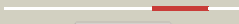


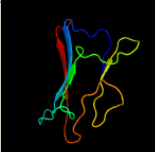











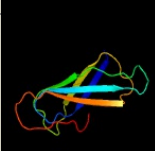

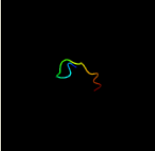
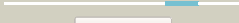
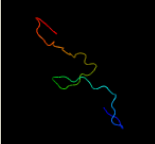


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3531c (-)_3967996_3969123
Date	Fri Aug 9 18:20:21 BST 2019
Unique Job ID	8be996c891aefc3b

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ansD	 Alignment		100.0	27	PDB header: unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 burkholderia cenocepacia
2	c3u07A	 Alignment		98.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vpa0106; PDBTitle: crystal structure of the vpa0106 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr106.
3	d2p3ya1	 Alignment		97.6	16	Fold: VPA0735-like Superfamily: VPA0735-like Family: VPA0735-like
4	c2p3yA	 Alignment		97.6	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein vpa0735; PDBTitle: crystal structure of vpa0735 from vibrio parahaemolyticus. northeast2 structural genomics target vpr109
5	c4tq2A	 Alignment		70.9	10	PDB header: lyase Chain: A: PDB Molecule: putative phycoerythrin lyase; PDBTitle: structure of s-type phycobiliprotein lyase cpes from guillardia theta
6	c3bdrA	 Alignment		52.1	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ycf58 protein; PDBTitle: crystal structure of fatty acid-binding protein-like ycf58 from2 thermosyneccoccus elongatus. northeast structural genomics consortium3 target ter13.
7	c3h3iA	 Alignment		49.4	30	PDB header: lipid binding protein Chain: A: PDB Molecule: putative lipid binding protein; PDBTitle: crystal structure of a putative lipid binding protein (bt_2261) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
8	c1n10A	 Alignment		44.1	14	PDB header: allergen Chain: A: PDB Molecule: pollen allergen phl p 1; PDBTitle: crystal structure of phl p 1, a major timothy grass pollen allergen
9	d1rp1a1	 Alignment		38.7	14	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Colipase-binding domain
10	d2proc1	 Alignment		31.8	29	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
11	c3j38V	 Alignment		30.3	14	PDB header: ribosome Chain: V: PDB Molecule: 40s ribosomal protein s21; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins

12	c3iswA_	Alignment		28.7	13	PDB header: structural protein Chain: A: PDB Molecule: filamin-a; PDBTitle: crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cftr
13	c4dy5A_	Alignment		26.8	14	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: gifsy-1 prophage protein; PDBTitle: crystal structure of salmonella typhimurium plig, a periplasmic2 lysozyme inhibitor of g-type lysozyme
14	c5xtdo_	Alignment		26.5	21	PDB header: oxidoreductase/electron transport Chain: O: PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 2, PDBTitle: cryo-em structure of human respiratory complex i
15	c4pbdA_	Alignment		24.7	19	PDB header: protein binding Chain: A: PDB Molecule: protein shq1 homolog; PDBTitle: crystal structure of the n-terminal cs domain of human shq1
16	d1ddwa_	Alignment		23.7	7	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
17	c2glwA_	Alignment		22.7	19	PDB header: transcription Chain: A: PDB Molecule: 92aa long hypothetical protein; PDBTitle: the solution structure of phs018 from pyrococcus horikoshii
18	d2nysa1	Alignment		22.3	17	Fold: SspB-like Superfamily: SspB-like Family: AGR C 3712p-like
19	c2nysA_	Alignment		22.3	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: agr_c_3712p; PDBTitle: x-ray crystal structure of protein agr_c_3712 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr88.
20	c2qasA_	Alignment		21.4	13	PDB header: hydrolase activator Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of caulobacter crescentus sspb ortholog
21	d2q1ma1	Alignment	not modelled	19.9	23	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
22	c5jsdB_	Alignment	not modelled	19.6	12	PDB header: viral protein Chain: B: PDB Molecule: phiab6 tailspike; PDBTitle: crystal structure of phiab6 tailspike in complex with five-repeated2 oligosaccharides of acinetobacter baumannii surface polysaccharide
23	d1r0ah1	Alignment	not modelled	19.2	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
24	d1xu1a_	Alignment	not modelled	19.1	31	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
25	c4nreA_	Alignment	not modelled	19.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: arachidonate 15-lipoxygenase b; PDBTitle: the structure of human 15-lipoxygenase-2 with a substrate mimic
26	c5npxS_	Alignment	not modelled	18.9	18	PDB header: virus Chain: S: PDB Molecule: polyprotein; PDBTitle: atomic structure of the broad bean stain virus (bbsv) by cryo-em
27	d1mvfa_	Alignment	not modelled	18.9	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
28	d2fhzb1	Alignment	not modelled	18.8	19	Fold: Colicin D/E5 nuclease domain Superfamily: Colicin D/E5 nuclease domain Family: Colicin E5 nuclease domain

29	c3o8yA_	Alignment	not modelled	18.6	30	PDB header: oxidoreductase Chain: A: PDB Molecule: arachidonate 5-lipoxygenase; PDBTitle: stable-5-lipoxygenase
30	c4k3eI_	Alignment	not modelled	18.3	20	PDB header: immune system Chain: I: PDB Molecule: bovine antibody with ultralong cdr h3, heavy chain; PDBTitle: crystal structure of bovine antibody blv5b8 with ultralong cdr h3
31	c2ds4A_	Alignment	not modelled	18.0	21	PDB header: protein binding Chain: A: PDB Molecule: tripartite motif protein 45; PDBTitle: solution structure of the filamin domain from human2 tripartite motif protein 45
32	c5yvU_	Alignment	not modelled	17.9	42	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: crystal structures of unlinked full length ns3 from dengue virus2 provide insights into dynamics of protease domain
33	c5nwmA_	Alignment	not modelled	17.4	24	PDB header: signaling protein Chain: A: PDB Molecule: nuclear receptor coactivator 1; PDBTitle: insight into the molecular recognition mechanism of the coactivator2 ncoa1 by stat6
34	c4g4fA_	Alignment	not modelled	17.1	25	PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor ligand superfamily member 18; PDBTitle: crystal structure of gitrl from bushbaby
35	c1rj8B_	Alignment	not modelled	16.8	21	PDB header: hormone/growth factor Chain: B: PDB Molecule: ectodysplasin-a isoform eda-a2; PDBTitle: the crystal structure of tnf family member eda-a2
36	d1rj8a_	Alignment	not modelled	16.8	21	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
37	d1dg6a_	Alignment	not modelled	16.6	24	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
38	c1dg6A_	Alignment	not modelled	16.6	24	PDB header: apoptosis Chain: A: PDB Molecule: apo2l/tnf-related apoptis inducing ligand (trail); PDBTitle: crystal structure of apo2l/trail
39	d1qfha1	Alignment	not modelled	16.5	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
40	c4chmB_	Alignment	not modelled	16.4	31	PDB header: cell cycle Chain: B: PDB Molecule: imc sub-compartment protein isp1; PDBTitle: structure of inner membrane complex (imc) sub-compartment protein 12 (isp1) from toxoplasma gondii
41	c2hczX_	Alignment	not modelled	15.8	9	PDB header: allergen Chain: X: PDB Molecule: beta-expansin 1a; PDBTitle: crystal structure of expb1 (zea m 1), a beta-expansin and group-12 pollen allergen from maize
42	d2bp3a1	Alignment	not modelled	15.5	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
43	d1unaa_	Alignment	not modelled	15.3	18	Fold: RNA bacteriophage capsid protein Superfamily: RNA bacteriophage capsid protein Family: RNA bacteriophage capsid protein
44	c5gkka_	Alignment	not modelled	15.1	13	PDB header: hydrolase Chain: A: PDB Molecule: putative homing endonuclease; PDBTitle: crystal structure of a homing endonuclease, I-tnai
45	d1pgl11	Alignment	not modelled	15.0	16	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
46	d1af5a_	Alignment	not modelled	14.9	27	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
47	c1osgC_	Alignment	not modelled	14.7	31	PDB header: immune system Chain: C: PDB Molecule: tumor necrosis factor ligand superfamily member PDBTitle: complex between baff and a br3 derived peptide presented in2 a beta-hairpin scaffold
48	d1kxga_	Alignment	not modelled	14.7	31	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
49	c2h1xB_	Alignment	not modelled	14.6	14	PDB header: hydrolase Chain: B: PDB Molecule: 5-hydroxyisourate hydrolase (formerly known as PDBTitle: crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
50	d1s55a1	Alignment	not modelled	14.2	38	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
51	d2q8oa1	Alignment	not modelled	14.1	23	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
52	c2bsdC_	Alignment	not modelled	14.0	19	PDB header: receptor Chain: C: PDB Molecule: receptor binding protein; PDBTitle: structure of lactococcal bacteriophage p2 receptor binding protein
53	c3zeyR_	Alignment	not modelled	14.0	21	PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein s21, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
54	c2ee6A_	Alignment	not modelled	13.9	14	PDB header: structural protein Chain: A: PDB Molecule: filamin-b; PDBTitle: solution structure of the 21th filamin domain from human2 filamin-b

55	c1pyuD_	Alignment	not modelled	13.5	30	PDB header: lyase Chain: D: PDB Molecule: aspartate 1-decarboxylase alfa chain; PDBTitle: processed aspartate decarboxylase mutant with ser25 mutated to cys
56	c3eudE_	Alignment	not modelled	13.4	21	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
57	c2npbA_	Alignment	not modelled	13.3	27	PDB header: oxidoreductase Chain: A: PDB Molecule: selenoprotein w; PDBTitle: nmr solution structure of mouse selw
58	c3i2dA_	Alignment	not modelled	13.2	29	PDB header: ligase Chain: A: PDB Molecule: e3 sumo-protein ligase siz1; PDBTitle: crystal structure of s. cerevisiae sumo e3 ligase siz1
59	c5f4zB_	Alignment	not modelled	13.2	16	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
60	d1pxva_	Alignment	not modelled	13.1	17	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Papain-like
61	c4chjA_	Alignment	not modelled	12.9	38	PDB header: cell cycle Chain: A: PDB Molecule: imc sub-compartment protein isp3; PDBTitle: structure of inner membrane complex (imc) sub-compartment2 protein 3 (isp3) from toxoplasma gondii
62	d1t9ia_	Alignment	not modelled	12.9	20	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
63	d1m5xa_	Alignment	not modelled	12.9	33	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
64	c5a72B_	Alignment	not modelled	12.8	20	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna endonuclease i-cvui; PDBTitle: crystal structure of the homing endonuclease i-cvui in complex2 with its target (sro1.3) in the presence of 2 mm ca
65	c3oq0D_	Alignment	not modelled	12.7	25	PDB header: cell cycle Chain: D: PDB Molecule: dbf4; PDBTitle: crystal structure of motif n of saccharomyces cerevisiae dbf4
66	c3b8eB_	Alignment	not modelled	12.5	22	PDB header: hydrolase/transport protein Chain: B: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
67	c3rghA_	Alignment	not modelled	12.4	23	PDB header: cell adhesion Chain: A: PDB Molecule: filamin-a; PDBTitle: structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
68	c4ht1T_	Alignment	not modelled	12.4	30	PDB header: immune system Chain: T: PDB Molecule: tumor necrosis factor ligand superfamily member 12; PDBTitle: human tweak in complex with the fab fragment of a neutralizing2 antibody
69	c4i19A_	Alignment	not modelled	12.3	19	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
70	c4o7jB_	Alignment	not modelled	12.2	31	PDB header: antibiotic resistance Chain: B: PDB Molecule: carg; PDBTitle: crystal structure of carg
71	c4m4xA_	Alignment	not modelled	12.2	22	PDB header: transcription Chain: A: PDB Molecule: aryl hydrocarbon receptor; PDBTitle: structure and dimerization properties of the aryl hydrocarbon receptor2 (ahr) pas-a domain
72	c1vc3B_	Alignment	not modelled	12.0	40	PDB header: lyase Chain: B: PDB Molecule: l-aspartate-alpha-decarboxylase heavy chain; PDBTitle: crystal structure of l-aspartate-alpha-decarboxylase
73	d2zgwa1	Alignment	not modelled	12.0	43	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: Biotin repressor (BirA)
74	d1bu8a1	Alignment	not modelled	11.9	14	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Colipase-binding domain
75	c4msvA_	Alignment	not modelled	11.9	21	PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor ligand superfamily member 6; PDBTitle: crystal structure of fasl and dcr3 complex
76	d1mowa1	Alignment	not modelled	11.7	27	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
77	d1rbli_	Alignment	not modelled	11.7	13	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
78	c2brqB_	Alignment	not modelled	11.6	11	PDB header: structural protein Chain: B: PDB Molecule: filamin a; PDBTitle: crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide
79	c5d55A_	Alignment	not modelled	11.6	19	PDB header: cell adhesion Chain: A: PDB Molecule: hdab,hdaa (adhesin), hus-associated diffuse adherence; PDBTitle: crystal structure of the e. coli hda pilus minor tip subunit, hdab
80	d1tnra_	Alignment	not modelled	11.5	21	Fold: TNF-like Superfamily: TNF-like Family: TNF-like

81	d1kdga2	Alignment	not modelled	11.5	18	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GMC oxidoreductases
82	d1aoya	Alignment	not modelled	11.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
83	c3u1iA	Alignment	not modelled	11.4	36	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine protease subunit ns2b; PDBTitle: dengue virus protease covalently bound to a peptide
84	d1npia	Alignment	not modelled	10.8	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Long-chain scorpion toxins
85	c3e54A	Alignment	not modelled	10.7	33	PDB header: hydrolase/dna Chain: A: PDB Molecule: rrna intron-encoded endonuclease; PDBTitle: archaeal intron-encoded homing endonuclease i-vdi141i complexed with2 dna
86	d2f1da2	Alignment	not modelled	10.7	36	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
87	c5xyiV	Alignment	not modelled	10.4	15	PDB header: ribosome Chain: V: PDB Molecule: 40s ribosomal protein s21; PDBTitle: small subunit of trichomonas vaginalis ribosome
88	c6d7yA	Alignment	not modelled	10.3	8	PDB header: toxin Chain: A: PDB Molecule: hemagglutinin; PDBTitle: 1.75 angstrom resolution crystal structure of the toxic c-terminal tip2 of cdia from pseudomonas aeruginosa in complex with immune protein
89	c4wmaA	Alignment	not modelled	10.2	33	PDB header: transferase/protein binding Chain: A: PDB Molecule: xyloside xylosyltransferase 1; PDBTitle: crystal structure of mouse xyloside xylosyltransferase 1 complexed2 with manganese,acceptor ligand and udp-glucose
90	c3d00A	Alignment	not modelled	10.2	21	PDB header: metal binding protein Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit e; PDBTitle: crystal structure of a tungsten formylmethanofuran dehydrogenase2 subunit e (fmd-e)-like protein (syn_00638) from syntrophus3 aciditrophicus at 1.90 a resolution
91	d1mexh1	Alignment	not modelled	10.2	5	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
92	c5j57B	Alignment	not modelled	10.0	14	PDB header: hydrolase/immune system Chain: B: PDB Molecule: vhh single chain antibody v5e1; PDBTitle: v5e1-rta complex
93	c2obkE	Alignment	not modelled	10.0	19	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: selt/selw/selh selenoprotein domain; PDBTitle: x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
94	d2pf5a1	Alignment	not modelled	9.9	16	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Link domain
95	c1skoA	Alignment	not modelled	9.9	40	PDB header: signaling protein Chain: A: PDB Molecule: mitogen-activated protein kinase kinase 1 PDBTitle: mp1-p14 complex
96	c2lw3A	Alignment	not modelled	9.6	38	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein mmps4; PDBTitle: solution structure of the soluble domain of mmps4 from mycobacterium2 tuberculosis
97	c2p0mB	Alignment	not modelled	9.5	12	PDB header: oxidoreductase Chain: B: PDB Molecule: arachidonate 15-lipoxygenase; PDBTitle: revised structure of rabbit reticulocyte 15s-lipoxygenase
98	c2rngA	Alignment	not modelled	9.4	24	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor iie subunit PDBTitle: solution structure of the c-terminal acidic domain of tfiie2 alpha
99	d1v05a	Alignment	not modelled	9.4	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)