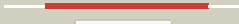
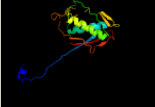


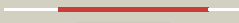







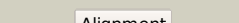
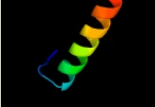



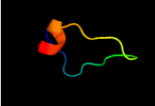






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2630_(-)_2956903_2957442
Date	Wed Aug 7 12:50:27 BST 2019
Unique Job ID	50258ebf4dda48be

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5yzlA_	 Alignment		100.0	16	PDB header: chaperone Chain: A: PDB Molecule: protein archease; PDBTitle: crystal structure of human archease d178a
2	d1jw3a_	 Alignment		100.0	19	Fold: MTH1598-like Superfamily: MTH1598-like Family: MTH1598-like
3	c4n2pC_	 Alignment		100.0	16	PDB header: chaperone Chain: C: PDB Molecule: protein archease; PDBTitle: structure of archease from pyrococcus horikoshii
4	d1j5ua_	 Alignment		100.0	16	Fold: MTH1598-like Superfamily: MTH1598-like Family: MTH1598-like
5	c3gkuB_	 Alignment		88.0	15	PDB header: rna binding protein Chain: B: PDB Molecule: probable rna-binding protein; PDBTitle: crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
6	c2yztA_	 Alignment		71.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha1756; PDBTitle: crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
7	c6g1cV_	 Alignment		43.0	25	PDB header: antitoxin Chain: V: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the n-terminal domain of burkholderia2 pseudomallei antitoxin hicb
8	c5yrzC_	 Alignment		37.7	4	PDB header: antitoxin/hydrolase Chain: C: PDB Molecule: hicb; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
9	c6i7jA_	 Alignment		35.4	36	PDB header: transferase Chain: A: PDB Molecule: pseudomonas aeruginosa earp; PDBTitle: crystal structure of pseudomonas aeruginosa earp
10	d1f2ri_	 Alignment		31.9	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: CAD domain
11	c4p7dA_	 Alignment		31.4	8	PDB header: toxin Chain: A: PDB Molecule: antitoxin hicb3; PDBTitle: antitoxin hicb3 crystal structure

12	c5subuC_	Alignment		28.5	6	PDB header: hydrolase Chain: C; PDB Molecule: putative acetamidase/formamidase; PDBTitle: 2.75 angstrom resolution crystal structure of acetamidase from <i>Yersinia enterocolitica</i> .
13	d2f4la1	Alignment		28.4	12	Fold: CUB-like Superfamily: Acetamidase/Formamidase-like Family: Acetamidase/Formamidase-like
14	d1a9xa5	Alignment		26.9	21	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
15	c2wnmA_	Alignment		26.8	14	PDB header: hydrolase Chain: A; PDB Molecule: gene 2; PDBTitle: solution structure of gp2
16	d1w96c1	Alignment		26.5	19	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
17	c6g1nB_	Alignment		26.1	21	PDB header: antitoxin Chain: B; PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
18	d1k0wa_	Alignment		25.3	19	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
19	d1ulza1	Alignment		24.5	19	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
20	c2lmcA_	Alignment		24.2	14	PDB header: transcription Chain: A; PDB Molecule: bacterial rna polymerase inhibitor; PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex
21	c2ii1A_	Alignment	not modelled	20.9	12	PDB header: hydrolase Chain: A; PDB Molecule: acetamidase; PDBTitle: crystal structure of acetamidase (10172637) from <i>Bacillus halodurans</i> 2 at 1.95 a resolution
22	c2eelA_	Alignment	not modelled	19.2	18	PDB header: apoptosis Chain: A; PDB Molecule: cell death activator cide-a; PDBTitle: solution structure of the cide-n domain of human cell death2 activator cide-a
23	c2ltsA_	Alignment	not modelled	19.1	5	PDB header: rna binding protein Chain: A; PDB Molecule: protein rde-4; PDBTitle: solution structure of rde-4(150-235)
24	d2b7ta1	Alignment	not modelled	18.5	21	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
25	d1w96a1	Alignment	not modelled	17.2	19	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
26	c1lxbB_	Alignment	not modelled	17.1	10	PDB header: hydrolase/hydrolase inhibitor Chain: B; PDB Molecule: chimera of igg binding protein g and dna PDBTitle: nmr structure of dff40 and dff45 n-terminal domain complex
27	d1lxbB_	Alignment	not modelled	17.1	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: CAD domain
28	c4c2mK_	Alignment	not modelled	16.5	23	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
						PDB header: apoptosis

29	c5xpcD	Alignment	not modelled	16.3	11	Chain: D: PDB Molecule: dnaation factor-related protein 4; PDBTitle: crystal structure of drep4 cide domain
30	c3mjiD	Alignment	not modelled	15.7	18	PDB header: hydrolase Chain: D: PDB Molecule: predicted acetamidase/formamidase; PDBTitle: crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
31	d2j9ga1	Alignment	not modelled	15.6	17	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
32	c5x51K	Alignment	not modelled	15.1	15	PDB header: transferase Chain: K: PDB Molecule: rna polymerase ii subunit b12.5; PDBTitle: rna polymerase ii from komagataella pastoris (type-3 crystal)
33	d1d4ba	Alignment	not modelled	14.8	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: CAD domain
34	d1twfk	Alignment	not modelled	14.2	14	Fold: DCoH-like Superfamily: RBP11-like subunits of RNA polymerase Family: RBP11/RpoL
35	c2kl7A	Alignment	not modelled	14.1	23	PDB header: signaling protein, structural protein Chain: A: PDB Molecule: fibulin-4; PDBTitle: solution nmr structure of the egf-like 1 domain of human2 fibulin-4. northeast structural genomics target hr6275
36	c5cffE	Alignment	not modelled	14.0	8	PDB header: transcription/rna binding protein Chain: E: PDB Molecule: staufen; PDBTitle: crystal structure of miranda/staufen dsrbd5 complex
37	d1e4cp	Alignment	not modelled	13.4	22	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
38	c4c24A	Alignment	not modelled	13.4	17	PDB header: lyase Chain: A: PDB Molecule: l-fucose phosphate aldolase; PDBTitle: l-fucose 1-phosphate aldolase
39	c2irpA	Alignment	not modelled	13.2	8	PDB header: lyase Chain: A: PDB Molecule: putative aldolase class 2 protein aq_1979; PDBTitle: crystal structure of the l-fucose-1-phosphate aldolase (aq_1979)2 from aquifex aeolicus vf5
40	d1lqsl	Alignment	not modelled	12.0	45	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
41	c5flmK	Alignment	not modelled	11.7	18	PDB header: transcription Chain: K: PDB Molecule: dna-directed rna polymerase ii subunit rpb11; PDBTitle: structure of transcribing mammalian rna polymerase ii
42	d1pvta	Alignment	not modelled	11.0	6	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
43	d2gdta1	Alignment	not modelled	10.9	9	Fold: SARS Nsp1-like Superfamily: SARS Nsp1-like Family: SARS Nsp1-like
44	c6btdA	Alignment	not modelled	10.7	22	PDB header: lyase Chain: A: PDB Molecule: fucose phosphate aldolase; PDBTitle: crystal structure of deoxyribose-phosphate aldolase from bacillus2 thuringiensis involved in dispatching the ubiquitous radical sam3 enzyme byproduct 5-deoxyribose
45	d1vlka	Alignment	not modelled	10.5	18	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
46	c3ju3A	Alignment	not modelled	10.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; PDBTitle: crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
47	c5gzba	Alignment	not modelled	10.0	20	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional enhancer factor tef-3; PDBTitle: crystal structure of transcription factor tead4 in complex with m-cat2 dna
48	d1lk3a	Alignment	not modelled	9.9	18	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
49	c2opiB	Alignment	not modelled	9.7	11	PDB header: lyase Chain: B: PDB Molecule: l-fucose-1-phosphate aldolase; PDBTitle: crystal structure of l-fucose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
50	d2ilka	Alignment	not modelled	9.2	18	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
51	d1vdha	Alignment	not modelled	9.1	27	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like
52	c2hzda	Alignment	not modelled	9.0	20	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional enhancer factor tef-1; PDBTitle: nmr structure of the dna-binding tea domain and insights2 into tef-1 function
53	c3h0gK	Alignment	not modelled	8.9	12	PDB header: transcription Chain: K: PDB Molecule: dna-directed rna polymerase ii subunit rpb11; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
54	d1gpua3	Alignment	not modelled	8.5	13	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
55	c2z7hA	Alignment	not modelled	8.4	6	PDB header: lyase Chain: A: PDB Molecule: mlr6791 protein;

55	c277aA	Alignment	not modelled	8.4	0	PDBTitle: crystal structure of mesorhizobium loti 3-hydroxy-2-methylpyridine-4,2 5-dicarboxylate decarboxylase
56	c5h3iC	Alignment	not modelled	8.3	6	PDB header: lipid binding protein Chain: C: PDB Molecule: putative acyl-coa-binding protein; PDBTitle: crystal structure of oryza sativa acyl-coa-binding protein 2
57	c5wxkA	Alignment	not modelled	8.1	17	PDB header: transferase Chain: A: PDB Molecule: earp; PDBTitle: earp bound with domain i of ef-p
58	c3ctvA	Alignment	not modelled	8.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of central domain of 3-hydroxyacyl-coa dehydrogenase2 from archaeoglobus fulgidus
59	d1ojra	Alignment	not modelled	8.1	19	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
60	c3m4rA	Alignment	not modelled	8.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the n-terminal class ii aldolase domain of a conserved2 protein from thermoplasma acidophilum
61	c3n6rK	Alignment	not modelled	7.8	26	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
62	c3u9sE	Alignment	not modelled	7.8	22	PDB header: ligase Chain: E: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
63	c3ocrA	Alignment	not modelled	7.8	9	PDB header: lyase Chain: A: PDB Molecule: class ii aldolase/adducin domain protein; PDBTitle: crystal structure of aldolase ii superfamily protein from pseudomonas2 syringae
64	c3ouzA	Alignment	not modelled	7.7	19	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
65	d2r8oa3	Alignment	not modelled	7.5	10	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
66	c4d2kB	Alignment	not modelled	7.5	6	PDB header: apoptosis Chain: B: PDB Molecule: drep2; PDBTitle: crystal structure of drep2 cide domain
67	d1uila	Alignment	not modelled	7.4	12	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
68	c3h7uA	Alignment	not modelled	7.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of the plant stress-response enzyme akr4c9
69	c3u9sl	Alignment	not modelled	7.0	22	PDB header: ligase Chain: I: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
70	d1itza3	Alignment	not modelled	6.6	13	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
71	c3x2dM	Alignment	not modelled	6.6	25	PDB header: viral protein/immune system Chain: M: PDB Molecule: envelope glycoprotein gp1; PDBTitle: crystal structure of marburg virus gp in complex with the human2 survivor antibody mr78
72	c2lrsA	Alignment	not modelled	6.5	13	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease dicer homolog 1; PDBTitle: the second dsrbd domain from a. thaliana dicer-like 1
73	c6d9mA	Alignment	not modelled	6.5	12	PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef
74	c4xxfA	Alignment	not modelled	6.4	11	PDB header: lyase Chain: A: PDB Molecule: fucose-1-phosphate aldolase; PDBTitle: l-fucose 1-phosphate aldolase from glaciozyma antarctica pi12
75	c4m6rA	Alignment	not modelled	6.3	13	PDB header: lyase Chain: A: PDB Molecule: methylthioribulose-1-phosphate dehydratase; PDBTitle: structural and biochemical basis for the inhibition of cell death by2 apip, a methionine salvage enzyme
76	c5ks8B	Alignment	not modelled	6.1	9	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase subunit alpha; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
77	d1r9ja3	Alignment	not modelled	5.9	17	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
78	c6djbB	Alignment	not modelled	5.9	13	PDB header: virus Chain: B: PDB Molecule: major capsid protein; PDBTitle: fako virus
79	c4dkkA	Alignment	not modelled	5.9	15	PDB header: rna binding protein Chain: A: PDB Molecule: double-stranded rna-binding protein staufen homolog 1; PDBTitle: the x-ray crystal structure of the human stau1 ssm-'rbd'5 domain-2 swapped dimer
80	c1ulzA	Alignment	not modelled	5.8	26	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase

81	c2yt4A_	Alignment	not modelled	5.8	10	PDB header: rna binding protein Chain: A: PDB Molecule: protein dgcr8; PDBTitle: crystal structure of human dgcr8 core
82	c2ltrA_	Alignment	not modelled	5.7	6	PDB header: rna binding protein Chain: A: PDB Molecule: protein rde-4; PDBTitle: solution structure of rde-4(32-136)
83	c2gpwC_	Alignment	not modelled	5.7	18	PDB header: ligase Chain: C: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
84	c3vxgA_	Alignment	not modelled	5.7	28	PDB header: oxidoreductase Chain: A: PDB Molecule: conjugated polyketone reductase c2; PDBTitle: crystal structure of conjugated polyketone reductase c2 from candida2 parapsilosis
85	d1t0tv_	Alignment	not modelled	5.6	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like
86	c4dapA_	Alignment	not modelled	5.5	13	PDB header: dna binding protein Chain: A: PDB Molecule: sugar fermentation stimulation protein a; PDBTitle: the structure of escherichia coli sfsa
87	d1hmca_	Alignment	not modelled	5.4	29	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines
88	c1yywB_	Alignment	not modelled	5.4	6	PDB header: hydrolase/rna Chain: B: PDB Molecule: ribonuclease iii; PDBTitle: crystal structure of rnase iii from aquifex aeolicus2 complexed with double stranded rna at 2.8-angstrom3 resolution
89	d1b9wa1	Alignment	not modelled	5.3	25	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: Merozoite surface protein 1 (MSP-1)
90	c3wg6C_	Alignment	not modelled	5.2	31	PDB header: oxidoreductase Chain: C: PDB Molecule: conjugated polyketone reductase c1; PDBTitle: crystal structure of conjugated polyketone reductase c1 from candida2 parapsilosis complexed with nadph
91	c4ikgA_	Alignment	not modelled	5.2	9	PDB header: apoptosis Chain: A: PDB Molecule: cell death activator cide-3; PDBTitle: crystal structure of cell death-inducing dffa-like effector c
92	c1w96B_	Alignment	not modelled	5.2	19	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
93	d1n1ia1	Alignment	not modelled	5.2	21	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: Merozoite surface protein 1 (MSP-1)
94	c5mlkB_	Alignment	not modelled	5.2	13	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: biotin dependent carboxylase acca3 dimer from mycobacterium2 tuberculosis (rv3285)
95	d1ob1c1	Alignment	not modelled	5.1	21	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: Merozoite surface protein 1 (MSP-1)
96	c3mtkA_	Alignment	not modelled	5.1	8	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase/phosphodiesterase; PDBTitle: x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c