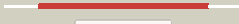
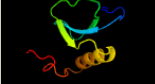


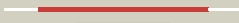
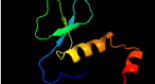



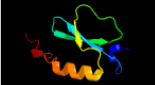














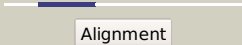
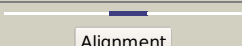
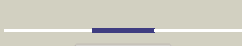
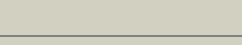
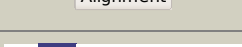

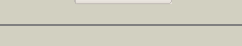
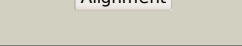

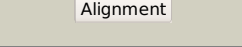
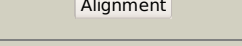
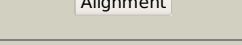
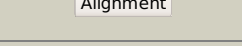
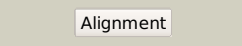
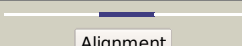
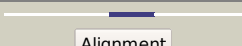
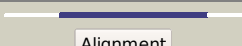

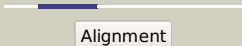




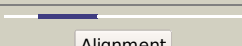

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2377c_(mbtH)_2656225_2656440
Date	Mon Aug 5 13:25:53 BST 2019
Unique Job ID	3650ba0221caa959

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2khrA_	 Alignment		100.0	99	PDB header: biosynthetic protein Chain: A: PDB Molecule: protein mbth; PDBTitle: solution structure of rv2377c, a mbth-like protein from mycobacterium2 tuberculosis
2	d2gpfa1	 Alignment		100.0	46	Fold: MbtH/L9 domain-like Superfamily: MbtH-like Family: MbtH-like
3	c2lpdA_	 Alignment		100.0	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of a mbth-like protein from burkholderia2 pseudomallei, the etiological agent responsible for melioidosis,3 seattle structural genomics center for infectious disease target4 bupsa.13472.b
4	c5wmmB_	 Alignment		100.0	69	PDB header: biosynthetic protein Chain: B: PDB Molecule: mbth homologue; PDBTitle: crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
5	c5ja1B_	 Alignment		100.0	42	PDB header: ligase Chain: B: PDB Molecule: enterobactin biosynthesis protein ybdz; PDBTitle: entf, a terminal nonribosomal peptide synthetase module bound to the2 mbth-like protein ybdz
6	c5u89B_	 Alignment		100.0	52	PDB header: hydrolase/inhibitor Chain: B: PDB Molecule: mbth domain protein; PDBTitle: crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
7	d2pstx1	 Alignment		100.0	46	Fold: MbtH/L9 domain-like Superfamily: MbtH-like Family: MbtH-like
8	c4gr5B_	 Alignment		97.1	49	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of sign1deltaasub in complex with ampcpp
9	c6n8eA_	 Alignment		90.8	56	PDB header: hydrolase Chain: A: PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
10	c5xswA_	 Alignment		41.7	33	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of an archaean chitinase in the substrate-complex2 form (p63)
11	d2b6ca1	 Alignment		25.9	16	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: BC3264-like

12	d1iqqa_	Alignment		13.6	17	Fold: Ribonuclease Rh-like Superfamily: Ribonuclease Rh-like Family: Ribonuclease Rh-like
13	c5jvvA_	Alignment		12.5	17	PDB header: transferase Chain: A; PDB Molecule: beta-1,3-glucosyltransferase; PDBTitle: crystal structure and characterization an elongating gh family 162 beta-1,3-glucosyltransferase
14	c5ydxA_	Alignment		12.2	26	PDB header: signaling protein Chain: A; PDB Molecule: ww domain with ppxy motif; PDBTitle: nmr structure of yap1-2 ww1 domain with lats1 ppxy motif complex
15	d1f8ab1	Alignment		12.1	22	Fold: WW domain-like Superfamily: WW domain Family: WW domain
16	d1j0ha2	Alignment		11.7	26	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
17	c6j69A_	Alignment		11.2	18	PDB header: cell cycle Chain: A; PDB Molecule: protein kibra; PDBTitle: structure of kibra and dendrin complex
18	c3cf5G_	Alignment		10.7	31	PDB header: ribosome/antibiotic Chain: G; PDB Molecule: 50s ribosomal protein l13; PDBTitle: thiopeptide antibiotic thiostrepton bound to the large ribosomal2 subunit of deinococcus radiodurans
19	d2zjrg1	Alignment		10.7	31	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
20	d1nmva1	Alignment		10.6	22	Fold: WW domain-like Superfamily: WW domain Family: WW domain
21	c4wfaG_	Alignment	not modelled	10.3	23	PDB header: ribosome Chain: G; PDB Molecule: 50s ribosomal protein l13; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with linezolid
22	c3j3wj_	Alignment	not modelled	10.3	31	PDB header: ribosome Chain: J; PDB Molecule: 50s ribosomal protein l13; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
23	c5o60K_	Alignment	not modelled	10.3	31	PDB header: ribosome Chain: K; PDB Molecule: 50s ribosomal protein l13; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
24	d2glia5	Alignment	not modelled	10.1	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
25	c1vw4H_	Alignment	not modelled	10.0	31	PDB header: ribosome Chain: H; PDB Molecule: 54s ribosomal protein l23, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
26	d1k9ra_	Alignment	not modelled	9.9	26	Fold: WW domain-like Superfamily: WW domain Family: WW domain
27	c1ymzA_	Alignment	not modelled	9.8	19	PDB header: unknown function Chain: A; PDB Molecule: cc45; PDBTitle: cc45, an artificial ww domain designed using statistical2 coupling analysis
28	c4e5xH_	Alignment	not modelled	9.7	57	PDB header: immune system/transcription Chain: H; PDB Molecule: early e3 18.5 kda glycoprotein; PDBTitle: crystal structure of a complex between the human adenovirus type 2 e3-2 19k protein and mhc class i molecule hla-2/tax

29	c4l1bB_		Alignment	not modelled	9.5	26	PDB header: signaling protein/transferase/inhibitor Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: crystal structure of p110alpha complexed with nish2 of p85alpha
30	d2ho2a1		Alignment	not modelled	9.5	46	Fold: WW domain-like Superfamily: WW domain Family: WW domain
31	c2zajA_		Alignment	not modelled	9.4	20	PDB header: protein binding Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz PDBTitle: solution structure of the short-isoform of the second ww2 domain from the human membrane-associated guanylate kinase,3 ww and pdz domain-containing protein 1 (magi-1)
32	d2ilxa1		Alignment	not modelled	9.3	28	Fold: LigT-like Superfamily: LigT-like Family: 2',3'-cyclic nucleotide 3'-phosphodiesterase, catalytic domain
33	c4v19N_		Alignment	not modelled	9.2	31	PDB header: ribosome Chain: N: PDB Molecule: mitoribosomal protein ul13m, mrp13; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
34	d1pina1		Alignment	not modelled	9.2	29	Fold: WW domain-like Superfamily: WW domain Family: WW domain
35	c2yclA_		Alignment	not modelled	9.1	18	PDB header: transferase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoid/iron-sulfur PDBTitle: complete structure of the corrinoid,iron-sulfur protein including2 the n-terminal domain with a 4fe-4s cluster
36	c2mdjA_		Alignment	not modelled	9.1	15	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setd2; PDBTitle: solution structure of ww domain with polyproline stretch (pp2ww) of2 hypb
37	c2ftcH_		Alignment	not modelled	9.0	31	PDB header: ribosome Chain: H: PDB Molecule: 39s ribosomal protein l13, mitochondrial; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
38	d2ysca1		Alignment	not modelled	8.7	50	Fold: WW domain-like Superfamily: WW domain Family: WW domain
39	c3mc2C_		Alignment	not modelled	8.7	22	PDB header: lyase inhibitor Chain: C: PDB Molecule: inhibitor of carbonic anhydrase; PDBTitle: crystal structure of the murine inhibitor of carbonic anhydrase
40	c3nicA_		Alignment	not modelled	8.5	33	PDB header: hydrolase/dna Chain: A: PDB Molecule: eco29kir; PDBTitle: dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
41	c3d5bN_		Alignment	not modelled	8.5	38	PDB header: ribosome Chain: N: PDB Molecule: 50s ribosomal protein l13; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
42	c2ysbA_		Alignment	not modelled	8.4	28	PDB header: protein binding Chain: A: PDB Molecule: salvador homolog 1 protein; PDBTitle: solution structure of the first ww domain from the mouse2 salvador homolog 1 protein (sav1)
43	c2kykA_		Alignment	not modelled	7.9	27	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: the sandwich region between two lmp2a py motif regulates the2 interaction between aip4ww2domain and py motif
44	c1tk7A_		Alignment	not modelled	7.9	24	PDB header: signaling protein Chain: A: PDB Molecule: cg4244-pb; PDBTitle: nmr structure of ww domains (ww3-4) from suppressor of2 deltex
45	d2j01n1		Alignment	not modelled	7.8	38	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
46	d1g0wa2		Alignment	not modelled	7.8	35	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
47	c5mlcL_		Alignment	not modelled	7.6	46	PDB header: ribosome Chain: L: PDB Molecule: 50s ribosomal protein l13, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
48	c2lawA_		Alignment	not modelled	7.5	20	PDB header: signaling protein/transcription Chain: A: PDB Molecule: yorkie homolog; PDBTitle: structure of the second ww domain from human yap in complex with a2 human smad1 derived peptide
49	d2itka1		Alignment	not modelled	7.5	31	Fold: WW domain-like Superfamily: WW domain Family: WW domain
50	c2lb0A_		Alignment	not modelled	7.5	13	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
51	d1u6ra2		Alignment	not modelled	7.4	40	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
52	c3bboL_		Alignment	not modelled	7.3	46	PDB header: ribosome Chain: L: PDB Molecule: ribosomal protein l13; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
53	c3pfyA_		Alignment	not modelled	7.2	35	PDB header: hydrolase Chain: A: PDB Molecule: otu domain-containing protein 5;

						PDBTitle: the catalytic domain of human otud5
54	c1e0mA	Alignment	not modelled	7.2	19	PDB header: de novo protein Chain: A: PDB Molecule: wwprototype; PDBTitle: prototype ww domain
55	c3l4hA	Alignment	not modelled	7.2	17	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase hecw1; PDBTitle: helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
56	d2f21a1	Alignment	not modelled	7.0	29	Fold: WW domain-like Superfamily: WW domain Family: WW domain
57	c4o7kA	Alignment	not modelled	7.0	21	PDB header: antitumor protein Chain: A: PDB Molecule: protein osa; PDBTitle: crystal structure of oncogenic suppression activity protein - a2 plasmid fertility inhibition factor
58	d1m15a2	Alignment	not modelled	6.9	40	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
59	c2ysgA	Alignment	not modelled	6.9	16	PDB header: protein binding Chain: A: PDB Molecule: syntaxin-binding protein 4; PDBTitle: solution structure of the ww domain from the human syntaxin-2 binding protein 4
60	d2jmfA1	Alignment	not modelled	6.8	27	Fold: WW domain-like Superfamily: WW domain Family: WW domain
61	c2lazA	Alignment	not modelled	6.8	13	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
62	d1iama2	Alignment	not modelled	6.7	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: ! set domains
63	c1wr4A	Alignment	not modelled	6.7	25	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-protein ligase nedd4-2; PDBTitle: solution structure of the second ww domain of nedd4-2
64	c2ai4A	Alignment	not modelled	6.7	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein so1698; PDBTitle: structure of protein of unknown function so1698 from shewanella2 oneidensis
65	d1i8gb	Alignment	not modelled	6.6	29	Fold: WW domain-like Superfamily: WW domain Family: WW domain
66	c2n8tA	Alignment	not modelled	6.5	25	PDB header: ligase/peptide Chain: A: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: solution structure of the rnedd4 ww2 domain-cx43ct peptide complex by2 nmr
67	c2djyA	Alignment	not modelled	6.5	27	PDB header: ligase/signaling protein Chain: A: PDB Molecule: smad ubiquitination regulatory factor 2; PDBTitle: solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
68	c3bvsA	Alignment	not modelled	6.4	31	PDB header: hydrolase Chain: A: PDB Molecule: alkylpurine dna glycosylase alkD; PDBTitle: crystal structure of bacillus cereus alkylpurine dna glycosylase alkD
69	d1dota2	Alignment	not modelled	6.4	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
70	c1ce2A	Alignment	not modelled	6.3	19	PDB header: metal transport Chain: A: PDB Molecule: protein (lactoferrin); PDBTitle: structure of diferric buffalo lactoferrin at 2.5a resolution
71	d1b1xa2	Alignment	not modelled	6.3	25	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
72	c5iroD	Alignment	not modelled	6.3	33	PDB header: immune system/transcription Chain: D: PDB Molecule: e3 19 kda protein; PDBTitle: crystal structure of a complex between the human adenovirus type 4 e3-2 19k protein and mhc class molecule hla-a2/tax
73	c2dx0B	Alignment	not modelled	6.2	21	PDB header: hydrolase Chain: B: PDB Molecule: phospholipase c, gamma 2; PDBTitle: crystal structure of the n-terminal sh2 domain of mouse2 phospholipase c-gamma 2
74	d1qh4a2	Alignment	not modelled	6.2	35	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
75	c1qk1H	Alignment	not modelled	6.1	25	PDB header: transferase (creatine kinase) Chain: H: PDB Molecule: creatine kinase, ubiquitous mitochondrial; PDBTitle: crystal structure of human ubiquitous mitochondrial creatine kinase
76	c2l4jA	Alignment	not modelled	6.0	21	PDB header: transcription Chain: A: PDB Molecule: yes-associated protein 2 (yap2); PDBTitle: yap ww2
77	c2vncB	Alignment	not modelled	6.0	25	PDB header: hydrolase Chain: B: PDB Molecule: glycogen operon protein glgX; PDBTitle: crystal structure of glycogen debranching enzyme trex from2 sulfobolus solfataricus
78	c1yiuA	Alignment	not modelled	6.0	27	PDB header: ligase Chain: A: PDB Molecule: itchy e3 ubiquitin protein ligase; PDBTitle: itch e3 ubiquitin ligase ww3 domain
79	c1lfgA	Alignment	not modelled	6.0	25	PDB header: transferrin Chain: A: PDB Molecule: lactoferrin; PDBTitle: structure of diferric human lactoferrin

80	c2e45a1	Alignment	not modelled	5.9	67	Fold: WW domain-like Superfamily: WW domain Family: WW domain
81	d1dota1	Alignment	not modelled	5.9	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
82	c3t0aA	Alignment	not modelled	5.9	18	PDB header: hydrolase Chain: A; PDB Molecule: ribonuclease t2; PDBTitle: crystal structure analysis of human rnase t2
83	d1qk1a2	Alignment	not modelled	5.9	25	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
84	d2fkia1	Alignment	not modelled	5.8	22	Fold: Secretion chaperone-like Superfamily: Yjbr-like Family: Yjbr-like
85	c2yscA	Alignment	not modelled	5.8	38	PDB header: protein binding Chain: A; PDB Molecule: amyloid beta a4 precursor protein-binding family PDBTitle: solution structure of the ww domain from the human amyloid2 beta a4 precursor protein-binding family b member 3, apbb3
86	c2kxqA	Alignment	not modelled	5.7	16	PDB header: protein binding Chain: A; PDB Molecule: e3 ubiquitin-protein ligase smurf2; PDBTitle: solution structure of smurf2 ww2 and ww3 bound to smad7 py motif2 containing peptide
87	c4nn7A	Alignment	not modelled	5.7	38	PDB header: cytokine/cytokine receptor Chain: A; PDB Molecule: thymic stromal lymphopietin; PDBTitle: cytokine receptor complex - crystal form 2
88	c4rohA	Alignment	not modelled	5.7	27	PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: crystal structure of tandem ww domains of itch in complex with txnip2 peptide
89	c1ryxA	Alignment	not modelled	5.6	19	PDB header: metal transport Chain: A; PDB Molecule: ovotransferrin; PDBTitle: crystal structure of hen serum transferrin in apo- form
90	c6acvA	Alignment	not modelled	5.6	14	PDB header: dna binding protein Chain: A; PDB Molecule: methyl-cpg-binding domain-containing protein 11; PDBTitle: the solution nmr structure of mbd domain
91	d1vrpa2	Alignment	not modelled	5.5	30	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
92	c5ydyA	Alignment	not modelled	5.4	20	PDB header: signaling protein Chain: A; PDB Molecule: ww2 domain and ppxy motif complex; PDBTitle: nmr structure of yap1-2 ww2 domain with lats1 ppxy motif complex
93	d1crka2	Alignment	not modelled	5.4	25	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
94	c3j9eD	Alignment	not modelled	5.2	17	PDB header: viral protein Chain: D; PDB Molecule: vp5; PDBTitle: atomic structure of a non-enveloped virus reveals ph sensors for a2 coordinated process of cell entry
95	c2kq0A	Alignment	not modelled	5.2	43	PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: human nedd4 3rd ww domain complex with ebola zaire virus matrix2 protein vp40 derived peptide ilptappeynea
96	c2ysfA	Alignment	not modelled	5.1	20	PDB header: protein binding Chain: A; PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: solution structure of the fourth ww domain from the human2 e3 ubiquitin-protein ligase itchy homolog, itch
97	c2yshA	Alignment	not modelled	5.1	21	PDB header: protein binding Chain: A; PDB Molecule: growth-arrest-specific protein 7; PDBTitle: solution structure of the ww domain from the human growth-2 arrest-specific protein 7, gas-7
98	d2c5ra1	Alignment	not modelled	5.1	31	Fold: Phage replication organizer domain Superfamily: Phage replication organizer domain Family: Phage replication organizer domain
99	c2hauA	Alignment	not modelled	5.0	25	PDB header: metal transport Chain: A; PDB Molecule: serotransferrin; PDBTitle: apo-human serum transferrin (non-glycosylated)