




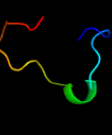


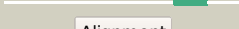
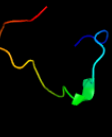
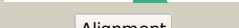

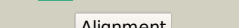

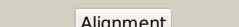

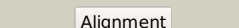

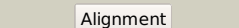








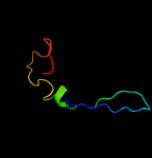


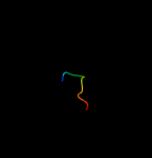


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2114 (-)_2373842_2374465
Date	Mon Aug 5 13:25:23 BST 2019
Unique Job ID	61f801dbbb0447ff

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3m3iC_	 Alignment		67.2	16	PDB header: unknown function Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: hypothetical protein from leishmania major
2	d1yuda1	 Alignment		46.6	20	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: YML079-like
3	d1ejxb_	 Alignment		45.9	38	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
4	d1vm9a_	 Alignment		43.4	18	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
5	c4z42B_	 Alignment		40.9	23	PDB header: hydrolase Chain: B: PDB Molecule: urease subunit beta; PDBTitle: crystal structure of urease from yersinia enterocolitica
6	c3lzzB_	 Alignment		40.6	26	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structures of cupin superfamily bbduf985 from branchiostoma2 belcheri tsingtauense in apo and gdp-bound forms
7	d2axoa1	 Alignment		40.5	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Atu2684-like
8	d1q1oa_	 Alignment		37.9	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
9	d1e9ya1	 Alignment		37.8	27	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
10	d4ubpb_	 Alignment		37.7	31	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
11	c3l4ha_	 Alignment		36.8	47	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

12	c1e9zA_	Alignment		36.2	27	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit alpha; PDBTitle: crystal structure of helicobacter pylori urease
13	c1zofB_	Alignment		35.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxide-reductase; PDBTitle: crystal structure of alkyl hydroperoxide-reductase (ahpc)2 from helicobacter pylori
14	c2axoA_	Alignment		34.8	20	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein atu2684; PDBTitle: x-ray crystal structure of protein agr_c_4864 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr35.
15	c2mdwA_	Alignment		34.5	44	PDB header: de novo protein Chain: A: PDB Molecule: designed protein; PDBTitle: nmr structure of a strand-swapped dimer of the ww domain
16	c5h3kA_	Alignment		34.0	30	PDB header: unknown function Chain: A: PDB Molecule: slr0280 protein; PDBTitle: crystal structure of a hypothetical protein from synechocystis
17	c1zswA_	Alignment		32.6	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: glyoxalase family protein; PDBTitle: crystal structure of bacillus cereus metallo protein from glyoxalase2 family
18	c1ymzA_	Alignment		31.1	45	PDB header: unknown function Chain: A: PDB Molecule: cc45; PDBTitle: cc45, an artificial ww domain designed using statistical2 coupling analysis
19	c2v2gC_	Alignment		30.3	21	PDB header: oxidoreductase Chain: C: PDB Molecule: peroxiredoxin 6; PDBTitle: crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
20	d2e45a1	Alignment		30.2	50	Fold: WW domain-like Superfamily: WW domain Family: WW domain
21	c2ysbA_	Alignment	not modelled	29.8	57	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)
22	c3qgaD_	Alignment	not modelled	28.6	23	PDB header: hydrolase Chain: D: PDB Molecule: fusion of urease beta and gamma subunits; PDBTitle: 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
23	c1e0mA_	Alignment	not modelled	26.6	33	PDB header: de novo protein Chain: A: PDB Molecule: wwprototype; PDBTitle: prototype ww domain
24	c2lb0A_	Alignment	not modelled	26.0	40	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
25	c2lazA_	Alignment	not modelled	26.0	40	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
26	c2ysfA_	Alignment	not modelled	25.5	40	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
27	d2ysca1	Alignment	not modelled	25.5	67	Fold: WW domain-like Superfamily: WW domain Family: WW domain
28	c3qsjA_	Alignment	not modelled	25.3	18	PDB header: hydrolase Chain: A: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from alicyclobacillus2

						acidocaldarius
29	c4huza_	Alignment	not modelled	25.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,6-dichloro-p-hydroquinone 1,2-dioxygenase; PDBTitle: 2,6-dichloro-p-hydroquinone 1,2-dioxygenase
30	d1ig4a_	Alignment	not modelled	24.4	27	Fold: DNA-binding domain Superfamily: DNA-binding domain Family: Methyl-CpG-binding domain, MBD
31	d2ho2a1	Alignment	not modelled	24.2	71	Fold: WW domain-like Superfamily: WW domain Family: WW domain
32	c3e0rC_	Alignment	not modelled	24.0	14	PDB header: hydrolase Chain: C: PDB Molecule: c3-degrading proteinase (cppa protein); PDBTitle: crystal structure of cppa protein from streptococcus pneumoniae tigr4
33	c2ky8A_	Alignment	not modelled	23.7	36	PDB header: transcription/dna Chain: A: PDB Molecule: methyl-cpg-binding domain protein 2; PDBTitle: solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
34	d1xe7a_	Alignment	not modelled	23.6	28	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YML079-like
35	d1pina1	Alignment	not modelled	23.5	57	Fold: WW domain-like Superfamily: WW domain Family: WW domain
36	c2jmfA_	Alignment	not modelled	23.4	44	PDB header: ligase/signaling protein Chain: A: PDB Molecule: e3 ubiquitin-protein ligase suppressor of deltex; PDBTitle: solution structure of the su(dx) ww4- notch py peptide2 complex
37	c2yshA_	Alignment	not modelled	23.3	40	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
38	c2ez5W_	Alignment	not modelled	23.3	44	PDB header: signalling protein,ligase Chain: W: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: solution structure of the dnedd4 ww3* domain- comm lpsy2 peptide complex
39	d1qk9a_	Alignment	not modelled	23.2	36	Fold: DNA-binding domain Superfamily: DNA-binding domain Family: Methyl-CpG-binding domain, MBD
40	c2ysdA_	Alignment	not modelled	23.2	33	PDB header: protein binding Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz PDBTitle: solution structure of the first ww domain from the human2 membrane-associated guanylate kinase, ww and pdz domain-3 containing protein 1. magi-1
41	c1wr4A_	Alignment	not modelled	23.1	44	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-protein ligase nedd4-2; PDBTitle: solution structure of the second ww domain of nedd4-2
42	c2dwwB_	Alignment	not modelled	22.6	46	PDB header: protein binding Chain: B: PDB Molecule: salvador homolog 1 protein; PDBTitle: solution structure of the second ww domain from mouse2 salvador homolog 1 protein (mww45)
43	d1eh9a2	Alignment	not modelled	22.6	24	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
44	c1yiuA_	Alignment	not modelled	22.5	56	PDB header: ligase Chain: A: PDB Molecule: itchy e3 ubiquitin protein ligase; PDBTitle: itch e3 ubiquitin ligase ww3 domain
45	d1tk7a2	Alignment	not modelled	22.5	44	Fold: WW domain-like Superfamily: WW domain Family: WW domain
46	c3itwA_	Alignment	not modelled	22.2	25	PDB header: peptide binding protein Chain: A: PDB Molecule: protein tox; PDBTitle: crystal structure of tox from micromonospora sp. ml1
47	d1i8gb_	Alignment	not modelled	22.2	57	Fold: WW domain-like Superfamily: WW domain Family: WW domain
48	c4lqbA_	Alignment	not modelled	21.9	28	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein kfla3161
49	c5ydyA_	Alignment	not modelled	21.6	44	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
50	c2djyA_	Alignment	not modelled	21.5	44	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
51	c2kq0A_	Alignment	not modelled	21.4	44	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 iltappeyme
52	d2jmf1	Alignment	not modelled	21.3	44	Fold: WW domain-like Superfamily: WW domain Family: WW domain
53	d1k9ra_	Alignment	not modelled	21.1	56	Fold: WW domain-like Superfamily: WW domain Family: WW domain
54	c3gknA_	Alignment	not modelled	21.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: bacterioferritin comigratory protein; PDBTitle: insights into the alkyl peroxide reduction activity of

						xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
55	c2kykA	Alignment	not modelled	20.7	44	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: the sandwich region between two Imp2a py motif regulates the2 interaction between aip4ww2domain and py motif
56	c2ysgA	Alignment	not modelled	20.5	40	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
57	c6j69A	Alignment	not modelled	20.4	45	PDB header: cell cycle Chain: A: PDB Molecule: protein kibra; PDBTitle: structure of kibra and dendrin complex
58	d1tk7a1	Alignment	not modelled	19.8	44	Fold: WW domain-like Superfamily: WW domain Family: WW domain
59	d2itka1	Alignment	not modelled	19.7	44	Fold: WW domain-like Superfamily: WW domain Family: WW domain
60	c3oajA	Alignment	not modelled	19.7	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative ring-cleaving dioxygenase mhqo; PDBTitle: crystal structure of putative dioxygenase from bacillus subtilis2 subsp. subtilis str. 168
61	c3vzvA	Alignment	not modelled	19.7	27	PDB header: hydrolase/dna Chain: A: PDB Molecule: methyl-cpg-binding domain protein 4; PDBTitle: crystal structure of methyl cpg binding domain of mbd4 in complex with2 the 5mcg/tg sequence
62	d1ub1a	Alignment	not modelled	19.7	36	Fold: DNA-binding domain Superfamily: DNA-binding domain Family: Methyl-CpG-binding domain, MBD
63	d1i5hw	Alignment	not modelled	19.3	56	Fold: WW domain-like Superfamily: WW domain Family: WW domain
64	d2cuqa1	Alignment	not modelled	19.2	29	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
65	c1wr7A	Alignment	not modelled	19.0	44	PDB header: ligase Chain: A: PDB Molecule: nedd4-2; PDBTitle: solution structure of the third ww domain of nedd4-2
66	d1avaa1	Alignment	not modelled	18.8	60	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
67	d3ovwa	Alignment	not modelled	18.8	21	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
68	c2dmvA	Alignment	not modelled	18.7	44	PDB header: ligase Chain: A: PDB Molecule: itchy homolog e3 ubiquitin protein ligase; PDBTitle: solution structure of the second ww domain of itchy homolog2 e3 ubiquitin protein ligase (itch)
69	d1nmva1	Alignment	not modelled	18.4	40	Fold: WW domain-like Superfamily: WW domain Family: WW domain
70	c2yscA	Alignment	not modelled	18.2	44	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
71	c2lawA	Alignment	not modelled	18.1	44	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
72	d1tu1a	Alignment	not modelled	18.0	25	Fold: Mog1p/PsbP-like Superfamily: Mog1p/PsbP-like Family: PA0094-like
73	c2qkdA	Alignment	not modelled	17.9	19	PDB header: signaling protein, cell cycle Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
74	c2v43A	Alignment	not modelled	17.9	18	PDB header: regulator Chain: A: PDB Molecule: sigma-e factor regulatory protein rseb; PDBTitle: crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
75	c3m6wA	Alignment	not modelled	17.8	21	PDB header: transferase Chain: A: PDB Molecule: rrna methylase; PDBTitle: multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
76	d1f8ab1	Alignment	not modelled	17.4	44	Fold: WW domain-like Superfamily: WW domain Family: WW domain
77	c2vcba	Alignment	not modelled	17.4	45	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylglucosaminidase; PDBTitle: family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac
78	c5uz9A	Alignment	not modelled	17.2	33	PDB header: immune system/rna Chain: A: PDB Molecule: crispr-associated protein csy1; PDBTitle: cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crrna-guided crispr surveillance complex
79	d2f21a1	Alignment	not modelled	17.2	44	Fold: WW domain-like Superfamily: WW domain Family: WW domain
80	c5fma1	Alignment	not modelled	16.9	13	PDB header: hydrolase Chain: L: PDB Molecule: proteasome subunit beta type;

80	c3mrgL	Alignment	not modelled	16.9	13	PDBTitle: structure and function based design of plasmodium-selective proteasome2 inhibitors PDB header: hydrolase
81	c4xwhA	Alignment	not modelled	16.7	22	Chain: A: PDB Molecule: alpha-n-acetylglucosaminidase; PDBTitle: crystal structure of the human n-acetyl-alpha-glucosaminidase
82	c2n8tA	Alignment	not modelled	16.4	36	PDB header: ligase/peptide Chain: A: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: solution structure of the nedd4 ww2 domain-cx43ct peptide complex by2 nmr
83	c4mymA	Alignment	not modelled	16.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: crystal structure of a glyoxalase/ bleomycin resistance protein/2 dioxygenase from nocardioides
84	c5vf3Z	Alignment	not modelled	16.2	44	PDB header: virus Chain: Z: PDB Molecule: highly immunogenic outer capsid protein; PDBTitle: bacteriophage t4 isometric capsid
85	c6f8sD	Alignment	not modelled	16.1	18	PDB header: toxin Chain: D: PDB Molecule: putative killer protein; PDBTitle: toxin-antitoxin complex grata
86	c5ydxA	Alignment	not modelled	15.9	56	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
87	c1wmvA	Alignment	not modelled	15.8	56	PDB header: oxidoreductase, apoptosis Chain: A: PDB Molecule: ww domain containing oxidoreductase; PDBTitle: solution structure of the second ww domain of wwox
88	d1b1xa1	Alignment	not modelled	15.8	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
89	d1ygsa	Alignment	not modelled	15.5	21	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
90	c5xyiN	Alignment	not modelled	15.5	20	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s13, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
91	c6feuj	Alignment	not modelled	15.5	26	PDB header: oxidoreductase Chain: J: PDB Molecule: peroxiredoxin; PDBTitle: nmr structure of prxq2, a 1-cys peroxiredoxin of the thermo-acidophilic archaeon2 sulfobolus islandicus
92	c2l4jA	Alignment	not modelled	15.4	44	PDB header: transcription Chain: A: PDB Molecule: yes-associated protein 2 (yap2); PDBTitle: yap ww2
93	d2bdea1	Alignment	not modelled	15.3	10	Fold: HAD-like Superfamily: HAD-like Family: 5' nucleotidase-like
94	c3s8jB	Alignment	not modelled	15.2	33	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: latex serine proteinase inhibitor; PDBTitle: crystal structure of a papaya latex serine protease inhibitor (ppi) at2 2.6a resolution
95	c3j20Q	Alignment	not modelled	15.2	27	PDB header: ribosome Chain: Q: PDB Molecule: 30s ribosomal protein s15p/s13e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
96	d1ce2a1	Alignment	not modelled	15.2	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
97	c5xmcA	Alignment	not modelled	15.0	27	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy; PDBTitle: crystal structure of the auto-inhibited nedd4 family e3 ligase itch
98	d1dd1a	Alignment	not modelled	14.7	26	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
99	d1eg1a	Alignment	not modelled	14.2	33	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core