



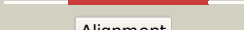

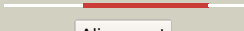
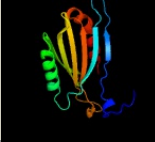








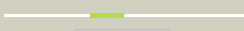
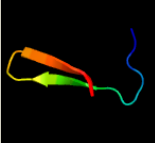



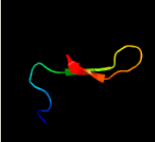






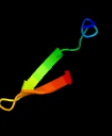
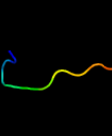
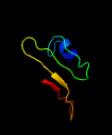


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1016c_(lpqT)_1134789_1135469
Date	Wed Jul 31 22:05:08 BST 2019
Unique Job ID	2df0aef3c2eb99c1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6e5fA_	 Alignment		100.0	20	PDB header: lipid binding protein Chain: A: PDB Molecule: lipid binding protein lpqn; PDBTitle: crystal structure of lpqn involved in cell envelope biogenesis of2 mycobacterium tuberculosis
2	c4ol4A_	 Alignment		100.0	34	PDB header: lipid binding protein Chain: A: PDB Molecule: proline-rich 28 kda antigen; PDBTitle: crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis
3	c3lydA_	 Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative uncharacterized protein from jonesia2 denitrificans
4	d1tu1a_	 Alignment		98.5	13	Fold: Mog1p/PsbP-like Superfamily: Mog1p/PsbP-like Family: PA0094-like
5	c2lnjA_	 Alignment		97.1	12	PDB header: photosynthesis Chain: A: PDB Molecule: putative uncharacterized protein sll1418; PDBTitle: solution structure of cyanobacterial psbp (cyanop) from synechocystis2 sp. pcc 6803
6	c2xb3A_	 Alignment		96.0	10	PDB header: photosynthesis Chain: A: PDB Molecule: psbp protein; PDBTitle: the structure of cyanobacterial psbp
7	d1v2ba_	 Alignment		89.8	16	Fold: Mog1p/PsbP-like Superfamily: Mog1p/PsbP-like Family: PsbP-like
8	c2vu4A_	 Alignment		80.1	17	PDB header: photosynthesis Chain: A: PDB Molecule: oxygen-evolving enhancer protein 2; PDBTitle: structure of psbp protein from spinacia oleracea at 1.98 a2 resolution
9	c1ymzA_	 Alignment		61.4	25	PDB header: unknown function Chain: A: PDB Molecule: cc45; PDBTitle: cc45, an artificial ww domain designed using statistical2 coupling analysis
10	c6j69A_	 Alignment		59.1	25	PDB header: cell cycle Chain: A: PDB Molecule: protein kibra; PDBTitle: structure of kibra and dendrin complex
11	c1e0mA_	 Alignment		56.8	33	PDB header: de novo protein Chain: A: PDB Molecule: wwprototype; PDBTitle: prototype ww domain

12	d2jmfA1	Alignment		41.6	38	Fold: WW domain-like Superfamily: WW domain Family: WW domain
13	c1yiuA	Alignment		38.9	46	PDB header: ligase Chain: A: PDB Molecule: itchy e3 ubiquitin protein ligase; PDBTitle: itch e3 ubiquitin ligase ww3 domain
14	c3n6zA	Alignment		33.0	23	PDB header: hydrolase Chain: A: PDB Molecule: putative immunoglobulin a1 protease; PDBTitle: crystal structure of a putative immunoglobulin a1 protease2 (bacova_03286) from bacteroides ovatus at 1.30 a resolution
15	c2kywA	Alignment		32.4	15	PDB header: cell adhesion Chain: A: PDB Molecule: adhesion exoprotein; PDBTitle: solution nmr structure of a domain of adhesion exoprotein from2 pediococcus pentosaceus, northeast structural genomics consortium3 target ptr410
16	c1wr7A	Alignment		31.9	27	PDB header: ligase Chain: A: PDB Molecule: nedd4-2; PDBTitle: solution structure of the third ww domain of nedd4-2
17	c2ysbA	Alignment		30.6	25	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)
18	c3l4hA	Alignment		30.3	14	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
19	c2lawA	Alignment		30.0	31	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
20	d1q5fa	Alignment		29.5	9	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
21	c5ydxA	Alignment	not modelled	25.6	17	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
22	d1k9ra	Alignment	not modelled	25.5	31	Fold: WW domain-like Superfamily: WW domain Family: WW domain
23	c1wmvA	Alignment	not modelled	25.4	21	PDB header: oxidoreductase, apoptosis Chain: A: PDB Molecule: ww domain containing oxidoreductase; PDBTitle: solution structure of the second ww domain of wwox
24	c1wr4A	Alignment	not modelled	25.2	31	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-protein ligase nedd4-2; PDBTitle: solution structure of the second ww domain of nedd4-2
25	c2djiA	Alignment	not modelled	22.7	26	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
26	d1tk7a1	Alignment	not modelled	22.7	29	Fold: WW domain-like Superfamily: WW domain Family: WW domain
27	c2l4jA	Alignment	not modelled	21.8	30	PDB header: transcription Chain: A: PDB Molecule: yes-associated protein 2 (yap2); PDBTitle: yap ww2
28	c2ysdA	Alignment	not modelled	20.6	21	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

29	d1tk7a2	Alignment	not modelled	20.4	38	Fold: WW domain-like Superfamily: WW domain Family: WW domain
30	c2dmvA	Alignment	not modelled	20.1	31	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)
31	c2jmfA	Alignment	not modelled	20.1	26	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
32	c4xz7A	Alignment	not modelled	19.7	19	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a tgase
33	c2kykA	Alignment	not modelled	19.1	26	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
34	d4croa	Alignment	not modelled	18.7	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
35	d2f21a1	Alignment	not modelled	18.6	31	Fold: WW domain-like Superfamily: WW domain Family: WW domain
36	c2dwvB	Alignment	not modelled	18.6	17	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)
37	c2pijB	Alignment	not modelled	18.3	54	PDB header: transcription Chain: B: PDB Molecule: prophage pfl 6 cro; PDBTitle: structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
38	c2yshA	Alignment	not modelled	17.5	26	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
39	d1a4ia1	Alignment	not modelled	17.3	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
40	c6j1xB	Alignment	not modelled	16.6	26	PDB header: ligase Chain: B: PDB Molecule: nedd4-like e3 ubiquitin-protein ligase wwp1; PDBTitle: wwp1 close conformation
41	c3ud2C	Alignment	not modelled	16.5	36	PDB header: protein binding Chain: C: PDB Molecule: ankyrin-1; PDBTitle: crystal structure of selenomethionine zu5a-zu5b protein domains of2 human erythrocyte ankyrin
42	c2n8tA	Alignment	not modelled	15.4	21	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
43	c5ydyA	Alignment	not modelled	15.3	24	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
44	d1i5hw	Alignment	not modelled	15.3	24	Fold: WW domain-like Superfamily: WW domain Family: WW domain
45	c2vdaB	Alignment	not modelled	15.0	55	PDB header: protein transport Chain: B: PDB Molecule: maltoporin; PDBTitle: solution structure of the seca-signal peptide complex
46	d1u2ca1	Alignment	not modelled	14.9	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cadherin-like Family: Dystroglycan, N-terminal domain
47	c2mdwA	Alignment	not modelled	14.5	67	PDB header: de novo protein Chain: A: PDB Molecule: designed protein; PDBTitle: nmr structure of a strand-swapped dimer of the ww domain
48	d1tlea2	Alignment	not modelled	14.1	12	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Subtilase propeptides/inhibitors
49	c4rohA	Alignment	not modelled	14.1	46	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
50	d1d1la	Alignment	not modelled	14.1	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
51	c1ai4B	Alignment	not modelled	13.7	15	PDB header: antibiotic resistance Chain: B: PDB Molecule: penicillin amidohydrolase; PDBTitle: penicillin acylase complexed with 3,4-dihydroxyphenylacetic acid
52	c2ysgA	Alignment	not modelled	13.6	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
53	c2ysfA	Alignment	not modelled	13.1	21	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
54	d1w8oa1	Alignment	not modelled	12.8	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes PDB header: hydrolase

55	c4hrsB	Alignment	not modelled	12.7	12	Chain: B: PDB Molecule: glutaryl-7-aminocephalosporanic acid acylase beta chain; PDBTitle: crystal structure of a class iii engineered cephalosporin acylase
56	c2yscA	Alignment	not modelled	12.7	57	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
57	c2ez5W	Alignment	not modelled	12.7	21	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
58	c1tleA	Alignment	not modelled	12.1	13	PDB header: hydrolase Chain: A: PDB Molecule: kumamolisin; PDBTitle: high resolution crystal structure of the intact pro-2 kumamolisin, a sedolisin type proteinase (previously3 called kumamolysin or kscp)
59	c6p0qA	Alignment	not modelled	12.0	38	PDB header: rna binding protein Chain: A: PDB Molecule: ribosome biogenesis protein wdr12; PDBTitle: crystal structure of ubiquitin-like domain of human wdr12
60	c2lb0A	Alignment	not modelled	12.0	15	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
61	c2kq0A	Alignment	not modelled	11.9	38	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
62	c3edyA	Alignment	not modelled	11.8	17	PDB header: hydrolase Chain: A: PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure of the precursor form of human tripeptidyl-peptidase2 1
63	c2zajA	Alignment	not modelled	10.9	31	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)
64	d1b0aa1	Alignment	not modelled	10.9	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
65	d1f8ab1	Alignment	not modelled	10.7	31	Fold: WW domain-like Superfamily: WW domain Family: WW domain
66	d1nmva1	Alignment	not modelled	10.5	31	Fold: WW domain-like Superfamily: WW domain Family: WW domain
67	d2ho2a1	Alignment	not modelled	10.4	27	Fold: WW domain-like Superfamily: WW domain Family: WW domain
68	c2lazA	Alignment	not modelled	10.3	15	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
69	d2itka1	Alignment	not modelled	9.9	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
70	c3ee6A	Alignment	not modelled	9.9	17	PDB header: hydrolase Chain: A: PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure analysis of tripeptidyl peptidase -i
71	c3k3wB	Alignment	not modelled	9.7	12	PDB header: hydrolase Chain: B: PDB Molecule: penicillin g acylase; PDBTitle: thermostable penicillin g acylase from alcaligenes faecalis in2 orthorhombic form
72	d1m9sa4	Alignment	not modelled	9.3	9	Fold: SH3-like barrel Superfamily: Prokaryotic SH3-related domain Family: GW domain
73	c5dtcA	Alignment	not modelled	9.2	31	PDB header: protein binding Chain: A: PDB Molecule: ribosome biogenesis protein ytm1; PDBTitle: ubl structure
74	c1cp9B	Alignment	not modelled	9.1	10	PDB header: hydrolase Chain: B: PDB Molecule: penicillin g amidase; PDBTitle: crystal structure of penicillin g acylase from the bro1 mutant strain2 of providencia rettgeri
75	c4fxwB	Alignment	not modelled	9.0	50	PDB header: protein binding Chain: B: PDB Molecule: splicing factor 1; PDBTitle: structure of phosphorylated sf1 complex with u2af65-uhm domain
76	c4yfaC	Alignment	not modelled	8.6	27	PDB header: hydrolase Chain: C: PDB Molecule: protein related to penicillin acylase; PDBTitle: structure of n-acylhomoserine lactone acylase macq in complex with2 decanoic acid
77	c1tk7A	Alignment	not modelled	8.6	31	PDB header: signaling protein Chain: A: PDB Molecule: cg4244-pb; PDBTitle: nmr structure of ww domains (ww3-4) from suppressor of2 deltex
78	c3nh8A	Alignment	not modelled	8.0	13	PDB header: hydrolase Chain: A: PDB Molecule: aspartoacylase-2; PDBTitle: crystal structure of murine aminoacylase 3 in complex with n-acetyl-s-2 1,2-dichlorovinyl-l-cysteine
79	d1nlta1	Alignment	not modelled	7.8	9	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain

80	d1jroa2	Alignment	not modelled	7.8	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
81	d1pina1	Alignment	not modelled	7.7	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
82	c2kxoA	Alignment	not modelled	7.7	19	PDB header: cell cycle Chain: A: PDB Molecule: cell division topological specificity factor; PDBTitle: solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
83	d2gu2a1	Alignment	not modelled	7.6	15	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like
84	d3orca	Alignment	not modelled	7.5	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
85	c4a5oB	Alignment	not modelled	7.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
86	d1c3ga1	Alignment	not modelled	7.3	33	Fold: HSP40/Dnaj peptide-binding domain Superfamily: HSP40/Dnaj peptide-binding domain Family: HSP40/Dnaj peptide-binding domain
87	c5xmcA	Alignment	not modelled	7.3	36	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy; PDBTitle: crystal structure of the auto-inhibited nedd4 family e3 ligase itch
88	d1a9xa2	Alignment	not modelled	7.1	13	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
89	c1yn9B	Alignment	not modelled	7.1	14	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
90	c1s1hO	Alignment	not modelled	7.0	24	PDB header: ribosome Chain: O: PDB Molecule: 40s ribosomal protein s13; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
91	c1a4iB	Alignment	not modelled	6.9	25	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
92	c4uzmA	Alignment	not modelled	6.7	28	PDB header: structural protein Chain: A: PDB Molecule: putative membrane protein igaa homolog; PDBTitle: shotgun proteolysis: a practical application
93	c6apeA	Alignment	not modelled	6.6	27	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional protein fold from helicobacter2 pylori
94	c2mdjA	Alignment	not modelled	6.6	24	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setd2; PDBTitle: solution structure of ww domain with polyproline stretch (pp2ww) of2 hypb
95	c2kxqA	Alignment	not modelled	6.5	14	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
96	c2muyA	Alignment	not modelled	6.5	25	PDB header: nucleotide binding protein Chain: A: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: the solution structure of the ftsh periplasmic n-domain
97	c4v1a1	Alignment	not modelled	6.4	33	PDB header: ribosome Chain: L: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
98	c4b4uB	Alignment	not modelled	6.4	8	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of acinetobacter baumannii n5,2 n10-methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)3 complexed with nadp cofactor
99	c5ag8A	Alignment	not modelled	6.3	22	PDB header: hydrolase Chain: A: PDB Molecule: gingipain r2; PDBTitle: crystal structure of a mutant (665i6h) of the c-terminal2 domain of rgpb