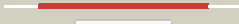


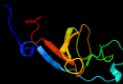
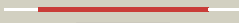
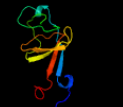

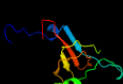





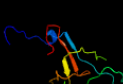



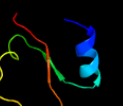

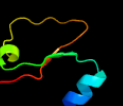

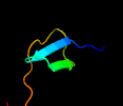
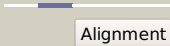

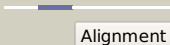
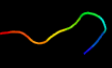
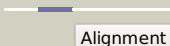


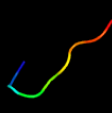


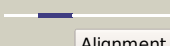

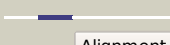

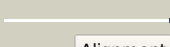

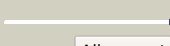
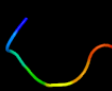


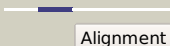


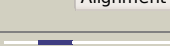
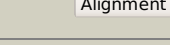
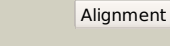


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2755c_(hsdS.1)_3068199_3068474
Date	Wed Aug 7 12:50:41 BST 2019
Unique Job ID	5c957992857272c2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1ydx2</a>	 Alignment		99.6	16	<b>Fold:</b> DNA methylase specificity domain <b>Superfamily:</b> DNA methylase specificity domain <b>Family:</b> Type I restriction modification DNA specificity domain
2	<a href="#">c1ydxA</a>	 Alignment		99.4	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction enzyme specificity protein mg438; <b>PDBTitle:</b> crystal structure of type-i restriction-modification system s subunit2 from m. genitalium
3	<a href="#">d1ydx1</a>	 Alignment		99.1	10	<b>Fold:</b> DNA methylase specificity domain <b>Superfamily:</b> DNA methylase specificity domain <b>Family:</b> Type I restriction modification DNA specificity domain
4	<a href="#">c1yf2A</a>	 Alignment		98.8	13	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction-modification enzyme, s subunit; <b>PDBTitle:</b> three-dimensional structure of dna sequence specificity (s) subunit of2 a type i restriction-modification enzyme and its functional3 implications
5	<a href="#">c3okgB</a>	 Alignment		98.8	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> restriction endonuclease s subunits; <b>PDBTitle:</b> crystal structure of hdsd subunit from thermoanaerobacter2 tengcongensis
6	<a href="#">d1yf2a2</a>	 Alignment		98.7	10	<b>Fold:</b> DNA methylase specificity domain <b>Superfamily:</b> DNA methylase specificity domain <b>Family:</b> Type I restriction modification DNA specificity domain
7	<a href="#">c2y7cA</a>	 Alignment		98.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type-1 restriction enzyme ecoki specificity protein; <b>PDBTitle:</b> atomic model of the ocr-bound methylase complex from the type i2 restriction-modification enzyme ecoki (m2s1). based on fitting into3 em map 1534.
8	<a href="#">d1yf2a1</a>	 Alignment		98.1	16	<b>Fold:</b> DNA methylase specificity domain <b>Superfamily:</b> DNA methylase specificity domain <b>Family:</b> Type I restriction modification DNA specificity domain
9	<a href="#">c3bmaC</a>	 Alignment		20.5	16	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> d-alanyl-lipoteichoic acid synthetase; <b>PDBTitle:</b> crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6
10	<a href="#">c6pfxB</a>	 Alignment		20.3	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> d-alanyl transferase dltD; <b>PDBTitle:</b> d-alanyl transferase dltD from enterococcus faecium
11	<a href="#">c5uc0B</a>	 Alignment		17.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein cog5400; <b>PDBTitle:</b> crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus

12	<a href="#">c2yshA_</a>			10.6	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> growth-arrest-specific protein 7; <b>PDBTitle:</b> solution structure of the ww domain from the human growth-2 arrest-specific protein 7, gas-7
13	<a href="#">d2f21a1</a>			10.1	22	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
14	<a href="#">c2lb0A_</a>			10.1	11	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf1; <b>PDBTitle:</b> structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
15	<a href="#">c2lazA_</a>			10.1	11	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf1; <b>PDBTitle:</b> structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
16	<a href="#">c1e0mA_</a>			9.8	22	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> wwprototype; <b>PDBTitle:</b> prototype ww domain
17	<a href="#">d1k9ra_</a>			9.5	22	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
18	<a href="#">d2jmfA1</a>			9.4	22	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
19	<a href="#">c2lrfA_</a>			9.1	25	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> anti-lipopolysaccharide factor; <b>PDBTitle:</b> nmr structure of the scylla serrata anti lipopolysaccharide factor-242 (ssalf-24) peptide
20	<a href="#">c2mdIA_</a>			9.1	25	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> anti-lipopolysaccharide factor; <b>PDBTitle:</b> structure and nmr assignments of scylla serrata anti2 lipopolysaccharide factor-24 (ssalf-24)
21	<a href="#">c2jmfA_</a>		not modelled	8.9	22	<b>PDB header:</b> ligase/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase suppressor of deltex; <b>PDBTitle:</b> solution structure of the su(dx) ww4- notch py peptide2 complex
22	<a href="#">c1ymzA_</a>		not modelled	8.7	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cc45; <b>PDBTitle:</b> cc45, an artificial ww domain designed using statistical2 coupling analysis
23	<a href="#">c2kq0A_</a>		not modelled	8.6	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase nedd4; <b>PDBTitle:</b> human nedd4 3rd ww domain complex with ebola zaire virus matrix2 protein vp40 derived peptide ilptappeynea
24	<a href="#">c2ysgA_</a>		not modelled	8.5	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> syntaxin-binding protein 4; <b>PDBTitle:</b> solution structure of the ww domain from the human syntaxin-2 binding protein 4
25	<a href="#">c1wr4A_</a>		not modelled	8.4	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-protein ligase nedd4-2; <b>PDBTitle:</b> solution structure of the second ww domain of nedd4-2
26	<a href="#">d1pina1</a>		not modelled	8.4	25	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
27	<a href="#">c2dmvA_</a>		not modelled	8.3	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> itchy homolog e3 ubiquitin protein ligase; <b>PDBTitle:</b> solution structure of the second ww domain of itchy homolog2 e3 ubiquitin protein ligase (itch)
28	<a href="#">c2djyA_</a>		not modelled	7.9	22	<b>PDB header:</b> ligase/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> smad ubiquitination regulatory factor 2; <b>PDBTitle:</b> solution structure of smurf2 ww3 domain-smad7 py peptide2 complex

29	<a href="#">c2yscA_</a>	Alignment	not modelled	7.8	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> amyloid beta a4 precursor protein-binding family <b>PDBTitle:</b> solution structure of the ww domain from the human amyloid2 beta a4 precursor protein-binding family b member 3, apbb3
30	<a href="#">c2lawA_</a>	Alignment	not modelled	7.8	33	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> yorkie homolog; <b>PDBTitle:</b> structure of the second ww domain from human yap in complex with a2 human smad1 derived peptide
31	<a href="#">c6o93A_</a>	Alignment	not modelled	7.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanyl transferase dltD; <b>PDBTitle:</b> d-alanyl transferase dltD from enterococcus faecalis
32	<a href="#">c1yiuA_</a>	Alignment	not modelled	7.6	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> itchy e3 ubiquitin protein ligase; <b>PDBTitle:</b> itch e3 ubiquitin ligase ww3 domain
33	<a href="#">d2itka1</a>	Alignment	not modelled	7.5	25	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
34	<a href="#">c2ysfA_</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase itchy homolog; <b>PDBTitle:</b> solution structure of the fourth ww domain from the human2 e3 ubiquitin-protein ligase itchy homolog, itch
35	<a href="#">c2ysbA_</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> salvador homolog 1 protein; <b>PDBTitle:</b> solution structure of the first ww domain from the mouse2 salvador homolog 1 protein (sav1)
36	<a href="#">c6roiA_</a>	Alignment	not modelled	7.0	23	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> probable phospholipid-transporting atpase drs2; <b>PDBTitle:</b> cryo-em structure of the partially activated drs2p-cdc50p
37	<a href="#">c5ydyA_</a>	Alignment	not modelled	6.9	38	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ww2 domain and ppxy motif complex; <b>PDBTitle:</b> nmr structure of yap1-2 ww2 domain with lats1 ppxy motif complex
38	<a href="#">c2ez5W_</a>	Alignment	not modelled	6.9	11	<b>PDB header:</b> signalling protein,ligase <b>Chain:</b> W: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase nedd4; <b>PDBTitle:</b> solution structure of the dnedd4 ww3* domain- comm lpsy2 peptide complex
39	<a href="#">d1i8gb_</a>	Alignment	not modelled	6.8	25	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
40	<a href="#">d1tk7a1</a>	Alignment	not modelled	6.7	33	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
41	<a href="#">c2n8tA_</a>	Alignment	not modelled	6.6	22	<b>PDB header:</b> ligase/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase nedd4; <b>PDBTitle:</b> solution structure of the rnedd4 ww2 domain-cx43ct peptide complex by2 nmr
42	<a href="#">c3l4hA_</a>	Alignment	not modelled	6.5	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase hecw1; <b>PDBTitle:</b> helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
43	<a href="#">d1tk7a2</a>	Alignment	not modelled	6.3	22	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
44	<a href="#">c2l4jA_</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> yes-associated protein 2 (yap2); <b>PDBTitle:</b> yap ww2
45	<a href="#">c2kykA_</a>	Alignment	not modelled	6.1	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase itchy homolog; <b>PDBTitle:</b> the sandwich region between two lmp2a py motif regulates the2 interaction between aip4ww2domain and py motif
46	<a href="#">c1wr7A_</a>	Alignment	not modelled	5.9	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> nedd4-2; <b>PDBTitle:</b> solution structure of the third ww domain of nedd4-2
47	<a href="#">d1f8ab1</a>	Alignment	not modelled	5.6	22	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
48	<a href="#">c2dvwB_</a>	Alignment	not modelled	5.6	22	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> salvador homolog 1 protein; <b>PDBTitle:</b> solution structure of the second ww domain from mouse2 salvador homolog 1 protein (mww45)
49	<a href="#">d1nmva1</a>	Alignment	not modelled	5.2	25	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
50	<a href="#">c2m6oA_</a>	Alignment	not modelled	5.1	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the actinobacterial transcription factor rbpa binds to the principal2 sigma subunit of rna polymerase
51	<a href="#">c5ydxA_</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ww domain with ppxy motif; <b>PDBTitle:</b> nmr structure of yap1-2 ww1 domain with lats1 ppxy motif complex