


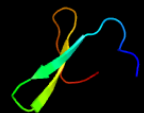

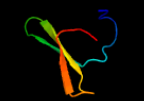



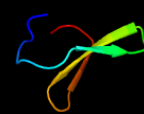



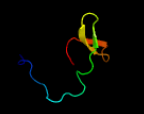

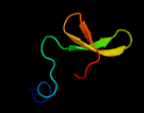



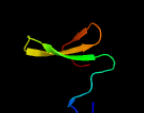

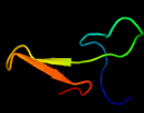

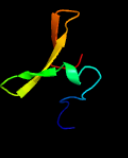
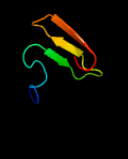


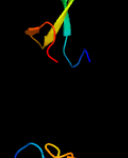
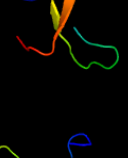

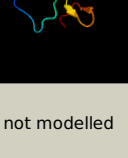


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3437_(-)_3857091_3857567
Date	Fri Aug 9 18:20:11 BST 2019
Unique Job ID	0ee5dbd4b9890d55

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4rohA_</a>	 Alignment		72.3	32	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase itchy homolog; <b>PDBTitle:</b> crystal structure of tandem ww domains of itch in complex with txnip2 peptide
2	<a href="#">d2jmfa1</a>	 Alignment		71.7	33	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
3	<a href="#">c3l4hA_</a>	 Alignment		66.1	26	<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
4	<a href="#">c1yiuA_</a>	 Alignment		64.3	33	<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
5	<a href="#">c2lawA_</a>	 Alignment		60.2	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
6	<a href="#">c2kykA_</a>	 Alignment		59.3	33	<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 Imp2a py motif regulates the2 interaction between aip4ww2domain and py motif
7	<a href="#">c2vysdA_</a>	 Alignment		54.8	21	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> membrane-associated guanylate kinase, ww and pdz <b>PDBTitle:</b> solution structure of the first ww domain from the human2 membrane-associated guanylate kinase, ww and pdz domain-3 containing protein 1. magi-1
8	<a href="#">c2l4jA_</a>	 Alignment		54.0	26	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> yes-associated protein 2 (yap2); <b>PDBTitle:</b> yap ww2
9	<a href="#">c1ymzA_</a>	 Alignment		52.8	31	<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
10	<a href="#">c2ez5W_</a>	 Alignment		52.7	18	<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
11	<a href="#">c2djyA_</a>	 Alignment		51.9	30	<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

12	<a href="#">d1i5hw_</a>	Alignment		50.0	24	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
13	<a href="#">c2ysbA_</a>	Alignment		49.2	26	<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)
14	<a href="#">d1tk7a1</a>	Alignment		48.0	22	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
15	<a href="#">c2jmfA_</a>	Alignment		45.7	33	<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
16	<a href="#">c1wr7A_</a>	Alignment		44.7	27	<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
17	<a href="#">d1tk7a2</a>	Alignment		44.5	33	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
18	<a href="#">c5ydyA_</a>	Alignment		43.7	30	<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
19	<a href="#">c2mdjA_</a>	Alignment		42.9	26	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> histone-lysine n-methyltransferase setd2; <b>PDBTitle:</b> solution structure of ww domain with polyproline stretch (pp2ww) of2 hypb
20	<a href="#">d1f8ab1</a>	Alignment		41.8	25	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
21	<a href="#">c2n8tA_</a>	Alignment	not modelled	41.2	25	<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
22	<a href="#">c1wmvA_</a>	Alignment	not modelled	40.9	27	<b>PDB header:</b> oxidoreductase, apoptosis <b>Chain:</b> A; <b>PDB Molecule:</b> ww domain containing oxidoreductase; <b>PDBTitle:</b> solution structure of the second ww domain of wwox
23	<a href="#">c2dmvA_</a>	Alignment	not modelled	40.2	24	<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)
24	<a href="#">c1wr4A_</a>	Alignment	not modelled	40.0	31	<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
25	<a href="#">c2e3uA_</a>	Alignment	not modelled	39.6	27	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein ph1566; <b>PDBTitle:</b> crystal structure analysis of dim2p from pyrococcus horikoshii ot3
26	<a href="#">c1e0mA_</a>	Alignment	not modelled	39.5	30	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> wwprototype; <b>PDBTitle:</b> prototype ww domain
27	<a href="#">c2ysgA_</a>	Alignment	not modelled	37.7	24	<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
28	<a href="#">c1tuaA_</a>	Alignment	not modelled	37.1	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein ape0754; <b>PDBTitle:</b> 1.5 a crystal structure of a protein of unknown function2 ape0754 from aeropyrum pernix <b>PDB header:</b> protein binding

29	<a href="#">c2dvvB_</a>	Alignment	not modelled	33.8	17	<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)
30	<a href="#">c2ysfA_</a>	Alignment	not modelled	29.2	18	<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
31	<a href="#">d1k9ra_</a>	Alignment	not modelled	29.0	35	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
32	<a href="#">c2kq0A_</a>	Alignment	not modelled	27.5	25	<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 ilptappeyme
33	<a href="#">d1tuaa2</a>	Alignment	not modelled	26.6	25	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
34	<a href="#">c2c36B_</a>	Alignment	not modelled	26.4	22	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycoprotein d hsv-1; <b>PDBTitle:</b> structure of unliganded hsv gd reveals a mechanism for receptor-2 mediated activation of virus entry
35	<a href="#">c1tk7A_</a>	Alignment	not modelled	26.1	27	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cg4244-pb; <b>PDBTitle:</b> nmr structure of ww domains (ww3-4) from suppressor of2 deltex
36	<a href="#">c4b8tA_</a>	Alignment	not modelled	25.4	22	<b>PDB header:</b> transcription/rna <b>Chain:</b> A: <b>PDB Molecule:</b> kh-type splicing regulatory protein; <b>PDBTitle:</b> rna binding protein solution structure of the third kh2 domain of ksrp in complex with the g-rich target sequence.
37	<a href="#">c6g18x_</a>	Alignment	not modelled	24.3	17	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> 40s ribosomal protein s23; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state c
38	<a href="#">c5ydxA_</a>	Alignment	not modelled	24.1	38	<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
39	<a href="#">d1nmva1</a>	Alignment	not modelled	23.5	24	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
40	<a href="#">c2dl0A_</a>	Alignment	not modelled	23.3	32	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sam and sh3 domain-containing protein 1; <b>PDBTitle:</b> solution structure of the sam-domain of the sam and sh32 domain containing protein 1
41	<a href="#">d1dt4a_</a>	Alignment	not modelled	23.0	28	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
42	<a href="#">d2itka1</a>	Alignment	not modelled	21.6	25	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
43	<a href="#">c2yshA_</a>	Alignment	not modelled	20.8	29	<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
44	<a href="#">c2yscA_</a>	Alignment	not modelled	19.9	37	<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
45	<a href="#">d2f21a1</a>	Alignment	not modelled	19.8	29	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
46	<a href="#">c2kxqA_</a>	Alignment	not modelled	19.3	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf2; <b>PDBTitle:</b> solution structure of smurf2 ww2 and ww3 bound to smad7 py motif2 containing peptide
47	<a href="#">c2ysiA_</a>	Alignment	not modelled	16.6	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation regulator 1; <b>PDBTitle:</b> solution structure of the first ww domain from the mouse2 transcription elongation regulator 1, transcription factor3 ca150
48	<a href="#">d1ec6a_</a>	Alignment	not modelled	16.3	31	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
49	<a href="#">d2ho2a1</a>	Alignment	not modelled	15.6	43	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
50	<a href="#">d1pina1</a>	Alignment	not modelled	15.1	28	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
51	<a href="#">c2lb0A_</a>	Alignment	not modelled	15.0	21	<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
52	<a href="#">d2dsya1</a>	Alignment	not modelled	14.7	33	<b>Fold:</b> TTHA1013/TTHA0281-like <b>Superfamily:</b> TTHA1013/TTHA0281-like <b>Family:</b> TTHA0281-like
53	<a href="#">c6emlp_</a>	Alignment	not modelled	14.2	17	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 40s ribosomal protein s0-a; <b>PDBTitle:</b> cryo-em structure of a late pre-40s ribosomal subunit from2 saccharomyces cerevisiae
54	<a href="#">c2zajA_</a>	Alignment	not modelled	13.7	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> membrane-associated guanylate kinase, ww and pdz <b>PDBTitle:</b> 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)
55	<a href="#">dli8gb_</a>	Alignment	not modelled	13.4	29	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
56	<a href="#">d1dtja_</a>	Alignment	not modelled	13.1	26	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
57	<a href="#">c2lazA_</a>	Alignment	not modelled	12.9	21	<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
58	<a href="#">d1x4ma1</a>	Alignment	not modelled	11.8	12	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
59	<a href="#">c5u3kC_</a>	Alignment	not modelled	11.1	22	<b>PDB header:</b> immune system/viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> gp41 mper peptide; <b>PDBTitle:</b> crystal structure of dh511.2 fab in complex with hiv-1 gp41 mper 662-2 683 peptide
60	<a href="#">d2ysca1</a>	Alignment	not modelled	10.8	41	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
61	<a href="#">c5u3kP_</a>	Alignment	not modelled	10.6	22	<b>PDB header:</b> immune system/viral protein <b>Chain:</b> P: <b>PDB Molecule:</b> gp41 mper peptide; <b>PDBTitle:</b> crystal structure of dh511.2 fab in complex with hiv-1 gp41 mper 662-2 683 peptide
62	<a href="#">c1loiA_</a>	Alignment	not modelled	10.4	100	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic 3',5'-amp specific phosphodiesterase rd1; <b>PDBTitle:</b> n-terminal splice region of rat c-amp phosphodiesterase,2 nmr, 7 structures
63	<a href="#">c2w0cS_</a>	Alignment	not modelled	10.3	29	<b>PDB header:</b> virus <b>Chain:</b> S: <b>PDB Molecule:</b> protein p3; <b>PDBTitle:</b> x-ray structure of the entire lipid-containing bacteriophage pm2
64	<a href="#">c6htnE_</a>	Alignment	not modelled	10.3	23	<b>PDB header:</b> sugar binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> fucose-binding lectin; <b>PDBTitle:</b> structure of a fucose lectin from kordia zhangzhouensis in complex2 with methyl-fucoside
65	<a href="#">d1xmeb2</a>	Alignment	not modelled	10.2	35	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
66	<a href="#">c2hh2A_</a>	Alignment	not modelled	9.7	25	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> kh-type splicing regulatory protein; <b>PDBTitle:</b> solution structure of the fourth kh domain of ksrp
67	<a href="#">c1javA_</a>	Alignment	not modelled	9.2	22	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane glycoprotein (gp41); <b>PDBTitle:</b> average nmr solution structure of the trp-rich peptide of2 hiv gp41 bound to dpc micelles
68	<a href="#">c2g57A_</a>	Alignment	not modelled	8.9	67	<b>PDB header:</b> oncoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> beta-catenin; <b>PDBTitle:</b> structure of the phosphorylation motif of the oncogenic2 protein beta-catenin recognized by a selective monoclonal3 antibody
69	<a href="#">c1jauA_</a>	Alignment	not modelled	8.8	22	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane glycoprotein (gp41); <b>PDBTitle:</b> nmr solution structure of the trp-rich peptide of hiv gp412 bound to dpc micelles
70	<a href="#">d3bmva3</a>	Alignment	not modelled	8.7	56	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
71	<a href="#">d1smpi_</a>	Alignment	not modelled	7.9	39	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> beta-Barrel protease inhibitors <b>Family:</b> Metalloprotease inhibitor
72	<a href="#">c6mttP_</a>	Alignment	not modelled	7.8	22	<b>PDB header:</b> immune system <b>Chain:</b> P: <b>PDB Molecule:</b> rv217 founder virus gp41 peptide; <b>PDBTitle:</b> crystal structure of vrc46.01 fab in complex with gp41 peptide
73	<a href="#">c2dgrA_</a>	Alignment	not modelled	7.6	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ring finger and kh domain-containing protein 1; <b>PDBTitle:</b> solution structure of the second kh domain in ring finger2 and kh domain containing protein 1
74	<a href="#">d1lgha_</a>	Alignment	not modelled	7.4	43	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
75	<a href="#">c2pv6A_</a>	Alignment	not modelled	7.3	22	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> hiv-1 gp41 membrane proximal ectodomain region peptide in2 dpc micelle
76	<a href="#">c6acvA_</a>	Alignment	not modelled	7.1	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-cpg-binding domain-containing protein 11; <b>PDBTitle:</b> the solution nmr structure of mbd domain
77	<a href="#">c4ce41_</a>	Alignment	not modelled	6.9	50	<b>PDB header:</b> ribosome <b>Chain:</b> 1: <b>PDB Molecule:</b> mrpl28; <b>PDBTitle:</b> 39s large subunit of the porcine mitochondrial ribosome
78	<a href="#">c5wvmA_</a>	Alignment	not modelled	6.7	35	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,two-component system <b>PDBTitle:</b> crystal structure of baes cocrystallized with 2 mm indole
79	<a href="#">c4pqkA_</a>	Alignment	not modelled	6.7	55	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose abc transporter periplasmic protein, truncated <b>PDBTitle:</b> c-terminal domain of dna binding protein
						<b>PDB header:</b> transport protein

80	<a href="#">c4v3aC_</a>	Alignment	not modelled	6.5	70	<b>Chain:</b> C; <b>PDB Molecule:</b> pleurotolysin b; <b>PDBTitle:</b> membrane bound pleurotolysin prepore (tmh1 lock) trapped with2 engineered disulphide cross-link
81	<a href="#">c3j20W_</a>	Alignment	not modelled	6.4	38	<b>PDB header:</b> ribosome <b>Chain:</b> W; <b>PDB Molecule:</b> 30s ribosomal protein s27e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
82	<a href="#">d1j4wa2</a>	Alignment	not modelled	6.4	22	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
83	<a href="#">c2me1A_</a>	Alignment	not modelled	6.4	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> gp41; <b>PDBTitle:</b> hiv-1 gp41 clade b double alanine mutant membrane proximal external2 region peptide in dpc micelle
84	<a href="#">c4o14A_</a>	Alignment	not modelled	6.0	13	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> proline-rich 28 kda antigen; <b>PDBTitle:</b> crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis
85	<a href="#">c3cglF_</a>	Alignment	not modelled	5.9	56	<b>PDB header:</b> fluorescent protein <b>Chain:</b> F; <b>PDB Molecule:</b> gfp-like fluorescent chromoprotein dsfp483; <b>PDBTitle:</b> crystal structure and raman studies of dsfp483, a cyan fluorescent2 protein from discosoma striata
86	<a href="#">c2mnsA_</a>	Alignment	not modelled	5.8	36	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> membrane fusion protein p15; <b>PDBTitle:</b> solution nmr structure of the reovirus p15 fusion-associated small2 transmembrane (fast) protein fusion-inducing lipid packing sensor3 (flips) motif in dodecyl phosphocholine (dpc) micelles
87	<a href="#">d2ctla1</a>	Alignment	not modelled	5.7	29	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
88	<a href="#">d1wvna1</a>	Alignment	not modelled	5.7	18	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
89	<a href="#">c4p1nA_</a>	Alignment	not modelled	5.6	36	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> atg1 tmit; <b>PDBTitle:</b> crystal structure of atg1-atg13 complex
90	<a href="#">c2jniA_</a>	Alignment	not modelled	5.6	83	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> arenicin-2; <b>PDBTitle:</b> spatial structure of antimicrobial peptide arenicin-2 in2 aqueous solution
91	<a href="#">c2l8xB_</a>	Alignment	not modelled	5.6	83	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B; <b>PDB Molecule:</b> arenicin-2; <b>PDBTitle:</b> spatial structure of antimicrobial peptide arenicin-2 dimer in dpc2 micelles
92	<a href="#">c2jsbA_</a>	Alignment	not modelled	5.6	83	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> arenicin-1; <b>PDBTitle:</b> solution structure of arenicin-1
93	<a href="#">c2y5pB_</a>	Alignment	not modelled	5.5	22	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> internalin b; <b>PDBTitle:</b> b-repeat of listeria monocytogenes inlb (internalin b)
94	<a href="#">c3uiyA_</a>	Alignment	not modelled	5.4	50	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> chimera protein of sefd and sefa; <b>PDBTitle:</b> crystal structure of sefd_dscA in h2o
95	<a href="#">c2l8xA_</a>	Alignment	not modelled	5.4	83	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> arenicin-2; <b>PDBTitle:</b> spatial structure of antimicrobial peptide arenicin-2 dimer in dpc2 micelles
96	<a href="#">c2jzxA_</a>	Alignment	not modelled	5.3	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> poly(rc)-binding protein 2; <b>PDBTitle:</b> pcbp2 kh1-kh2 domains
97	<a href="#">c3v xvA_</a>	Alignment	not modelled	5.1	67	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> methyl-cpg-binding domain protein 4; <b>PDBTitle:</b> crystal structure of methyl cpg binding domain of mbd4 in complex with2 the 5mcg/tg sequence