

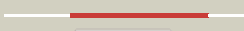












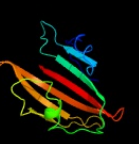



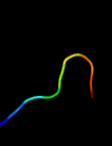

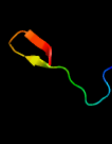


# Phyre2

|               |                                |
|---------------|--------------------------------|
| Email         | mdejesus@rockefeller.edu       |
| Description   | RVBD0583c_(lpqN)_678392_679078 |
| Date          | Fri Jul 26 01:50:14 BST 2019   |
| Unique Job ID | c89360368c2ac0f7               |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c4ol4A_</a> |  Alignment   |    | 100.0      | 17     | <b>PDB header:</b> lipid binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> proline-rich 28 kda antigen;<br><b>PDBTitle:</b> crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis |
| 2  | <a href="#">c3lydA_</a> |  Alignment   |    | 100.0      | 18     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of putative uncharacterized protein from jonesia2 denitrificans       |
| 3  | <a href="#">d1tu1a_</a> |  Alignment   |    | 98.7       | 19     | <b>Fold:</b> Mog1p/PsbP-like<br><b>Superfamily:</b> Mog1p/PsbP-like<br><b>Family:</b> PA0094-like  |
| 4  | <a href="#">c2lnjA_</a> |  Alignment   |   | 97.2       | 13     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sl11418;<br><b>PDBTitle:</b> solution structure of cyanobacterial psbp (cyanop) from synechocystis2 sp. pcc 6803           |
| 5  | <a href="#">c2xb3A_</a> |  Alignment |  | 91.6       | 11     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> A: <b>PDB Molecule:</b> psbp protein;<br><b>PDBTitle:</b> the structure of cyanobacterial psbp  |
| 6  | <a href="#">c5ag8A_</a> |  Alignment |  | 85.9       | 19     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gingipain r2;<br><b>PDBTitle:</b> crystal structure of a mutant (665i6h) of the c-terminal2 domain of rgpb   |
| 7  | <a href="#">d1v2ba_</a> |  Alignment |  | 81.6       | 17     | <b>Fold:</b> Mog1p/PsbP-like<br><b>Superfamily:</b> Mog1p/PsbP-like<br><b>Family:</b> PsbP-like  |
| 8  | <a href="#">c2vu4A_</a> |  Alignment |  | 67.8       | 13     | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxygen-evolving enhancer protein 2;<br><b>PDBTitle:</b> structure of psbp protein from spinacia oleracea at 1.98 a2 resolution                              |
| 9  | <a href="#">c1e0mA_</a> |  Alignment |  | 50.1       | 22     | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> wwprototype;<br><b>PDBTitle:</b> prototype ww domain   |
| 10 | <a href="#">c6j69A_</a> |  Alignment |  | 49.6       | 44     | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein kibra;<br><b>PDBTitle:</b> structure of kibra and dendrin complex   |
| 11 | <a href="#">c1ymzA_</a> |  Alignment |  | 45.5       | 22     | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> cc45;<br><b>PDBTitle:</b> cc45, an artificial ww domain designed using statistical2 coupling analysis   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | <a href="#">c6h9cD_</a> | Alignment |              | 43.6 | 26 | <b>PDB header:</b> virus<br><b>Chain:</b> D; <b>PDB Molecule:</b> vp7;<br><b>PDBTitle:</b> cryo-em structure of archaeal extremophilic internal membrane-2 containing haloarcula californiae icosahedral virus 1 (hcv-1) at 3 3.74 angstroms resolution. |
| 13 | <a href="#">d1c3ga1</a> | Alignment |              | 39.7 | 17 | <b>Fold:</b> HSP40/DnaJ peptide-binding domain<br><b>Superfamily:</b> HSP40/DnaJ peptide-binding domain<br><b>Family:</b> HSP40/DnaJ peptide-binding domain  |
| 14 | <a href="#">c1wr7A_</a> | Alignment |              | 32.7 | 29 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> nedd4-2;<br><b>PDBTitle:</b> solution structure of the third ww domain of nedd4-2   |
| 15 | <a href="#">d2jmfa1</a> | Alignment |              | 28.2 | 43 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain   |
| 16 | <a href="#">c4ba8A_</a> | Alignment |              | 23.9 | 10 | <b>PDB header:</b> immune system<br><b>Chain:</b> A; <b>PDB Molecule:</b> ig mu chain c region secreted form;<br><b>PDBTitle:</b> high resolution nmr structure of the c mu3 domain from igm   |
| 17 | <a href="#">c1wmvA_</a> | Alignment |              | 22.6 | 11 | <b>PDB header:</b> oxidoreductase, apoptosis<br><b>Chain:</b> A; <b>PDB Molecule:</b> ww domain containing oxidoreductase;<br><b>PDBTitle:</b> solution structure of the second ww domain of wwox  |
| 18 | <a href="#">d1dr9a2</a> | Alignment |              | 22.4 | 25 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Immunoglobulin<br><b>Family:</b> C2 set domains  |
| 19 | <a href="#">c2ysbA_</a> | Alignment |              | 21.9 | 28 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A; <b>PDB Molecule:</b> salvador homolog 1 protein;<br><b>PDBTitle:</b> solution structure of the first ww domain from the mouse2 salvador homolog 1 protein (sav1)                                  |
| 20 | <a href="#">d1tk7a2</a> | Alignment |              | 21.8 | 43 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain   |
| 21 | <a href="#">c5ydxA_</a> | Alignment | not modelled | 21.6 | 37 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> ww domain with ppxy motif;<br><b>PDBTitle:</b> nmr structure of yap1-2 ww1 domain with lats1 ppxy motif complex  |
| 22 | <a href="#">d1tk7a1</a> | Alignment | not modelled | 21.6 | 57 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain   |
| 23 | <a href="#">c1yiuA_</a> | Alignment | not modelled | 21.1 | 29 | <b>PDB header:</b> ligase<br><b>Chain:</b> A; <b>PDB Molecule:</b> itchy e3 ubiquitin protein ligase;<br><b>PDBTitle:</b> itch e3 ubiquitin ligase ww3 domain  |
| 24 | <a href="#">c2jmfA_</a> | Alignment | not modelled | 20.9 | 43 | <b>PDB header:</b> ligase/signaling protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase suppressor of deltex;<br><b>PDBTitle:</b> solution structure of the su(dx) ww4- notch py peptide2 complex                               |
| 25 | <a href="#">c2mdwA_</a> | Alignment | not modelled | 20.4 | 33 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> designed protein;<br><b>PDBTitle:</b> nmr structure of a strand-swapped dimer of the ww domain   |
| 26 | <a href="#">c2kxoA_</a> | Alignment | not modelled | 20.2 | 10 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A; <b>PDB Molecule:</b> cell division topological specificity factor;<br><b>PDBTitle:</b> solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae                  |
| 27 | <a href="#">d1k9ra_</a> | Alignment | not modelled | 19.1 | 38 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain   |
| 28 | <a href="#">c5ewoA_</a> | Alignment | not modelled | 19.1 | 17 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> structural protein;<br><b>PDBTitle:</b> crystal structure of the human astrovirus 1 capsid protein spike2 domain at 0.95-a resolution  |
|    |                         |           |              |      |    | <b>PDB header:</b> protein transport   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 29 | <a href="#">c5yfgA_</a> | Alignment | not modelled | 18.8 | 16 | <b>Chain:</b> A: <b>PDB Molecule:</b> ran guanine nucleotide release factor; <b>PDBTitle:</b> solution structure of human mog1  |
| 30 | <a href="#">c3tm6E_</a> | Alignment | not modelled | 18.6 | 17 | <b>PDB header:</b> immune system<br><b>Chain:</b> E: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of the beta-2 microglobulin dimc50 disulphide-linked2 homodimer mutant   |
| 31 | <a href="#">c3tm6C_</a> | Alignment | not modelled | 18.6 | 17 | <b>PDB header:</b> immune system<br><b>Chain:</b> C: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of the beta-2 microglobulin dimc50 disulphide-linked2 homodimer mutant   |
| 32 | <a href="#">c3tm6H_</a> | Alignment | not modelled | 18.6 | 17 | <b>PDB header:</b> immune system<br><b>Chain:</b> H: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of the beta-2 microglobulin dimc50 disulphide-linked2 homodimer mutant   |
| 33 | <a href="#">c3tm6F_</a> | Alignment | not modelled | 18.6 | 17 | <b>PDB header:</b> immune system<br><b>Chain:</b> F: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of the beta-2 microglobulin dimc50 disulphide-linked2 homodimer mutant   |
| 34 | <a href="#">c3tm6G_</a> | Alignment | not modelled | 18.6 | 17 | <b>PDB header:</b> immune system<br><b>Chain:</b> G: <b>PDB Molecule:</b> beta-2-microglobulin; <b>PDBTitle:</b> crystal structure of the beta-2 microglobulin dimc50 disulphide-linked2 homodimer mutant   |
| 35 | <a href="#">c2yshA_</a> | Alignment | not modelled | 18.3 | 29 | <b>PDB header:</b> protein binding<br><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   |
| 36 | <a href="#">c3ov6A_</a> | Alignment | not modelled | 18.2 | 19 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-2-microglobulin, t-cell surface glycoprotein cd1c, t-<br><b>PDBTitle:</b> cd1c in complex with mpm (mannosyl-beta1-phosphomycoketide)  |
| 37 | <a href="#">c2n5xA_</a> | Alignment | not modelled | 17.8 | 39 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> hsp90 co-chaperone cdc37; <b>PDBTitle:</b> c-terminal domain of cdc37 cochaperone   |
| 38 | <a href="#">c2yscA_</a> | Alignment | not modelled | 17.7 | 43 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> amyloid beta a4 precursor protein-binding family<br><b>PDBTitle:</b> solution structure of the ww domain from the human amyloid2 beta a4 precursor protein-binding family b member 3, apbb3                           |
| 39 | <a href="#">c1wr4A_</a> | Alignment | not modelled | 17.5 | 29 | <b>PDB header:</b> ligase<br><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   |
| 40 | <a href="#">c2lawA_</a> | Alignment | not modelled | 17.4 | 29 | <b>PDB header:</b> signaling protein/transcription<br><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  |
| 41 | <a href="#">c3l4hA_</a> | Alignment | not modelled | 16.9 | 17 | <b>PDB header:</b> protein binding<br><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  |
| 42 | <a href="#">c2lb0A_</a> | Alignment | not modelled | 16.6 | 14 | <b>PDB header:</b> signaling protein/transcription<br><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                               |
| 43 | <a href="#">c2lazA_</a> | Alignment | not modelled | 16.6 | 14 | <b>PDB header:</b> signaling protein/transcription<br><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                              |
| 44 | <a href="#">c3s6cA_</a> | Alignment | not modelled | 16.5 | 17 | <b>PDB header:</b> immune system, lipid binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-2-microglobulin, t-cell surface glycoprotein cd1e,<br><b>PDBTitle:</b> structure of human cd1e  |
| 45 | <a href="#">c2ez5W_</a> | Alignment | not modelled | 15.9 | 43 | <b>PDB header:</b> signalling protein, ligase<br><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   |
| 46 | <a href="#">c2kykA_</a> | Alignment | not modelled | 14.5 | 24 | <b>PDB header:</b> ligase<br><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   |
| 47 | <a href="#">c2ysfA_</a> | Alignment | not modelled | 14.0 | 29 | <b>PDB header:</b> protein binding<br><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  |
| 48 | <a href="#">c2ysdA_</a> | Alignment | not modelled | 14.0 | 24 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> membrane-associated guanylate kinase, ww and pdz<br><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 |
| 49 | <a href="#">c4rohA_</a> | Alignment | not modelled | 13.5 | 43 | <b>PDB header:</b> ligase<br><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  |
| 50 | <a href="#">c2l4jA_</a> | Alignment | not modelled | 13.4 | 26 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> yes-associated protein 2 (yap2); <b>PDBTitle:</b> yap ww2   |
| 51 | <a href="#">c4rc1B_</a> | Alignment | not modelled | 13.3 | 8  | <b>PDB header:</b> chaperone<br><b>Chain:</b> B: <b>PDB Molecule:</b> espg3; <b>PDBTitle:</b> structure of espg3 chaperone from the type vii (esx-3) secretion2 system, space group p43212  |
| 52 | <a href="#">c5xmcA_</a> | Alignment | not modelled | 13.2 | 43 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase itchy; <b>PDBTitle:</b> crystal structure of the auto-inhibited nedd4 family e3 ligase itch  |
| 53 | <a href="#">c3iv6C_</a> | Alignment | not modelled | 13.2 | 19 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative zn-dependent alcohol dehydrogenase;   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
|    |                         |           |              |      |    | <b>PDBTitle:</b> crystal structure of putative zn-dependent alcohol dehydrogenases from2 rhodobacter sphaeroides.   |
| 54 | <a href="#">d1f8ab1</a> | Alignment | not modelled | 13.1 | 29 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain  |
| 55 | <a href="#">c2kywA</a>  | Alignment | not modelled | 13.1 | 15 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> adhesion exoprotein;<br><b>PDBTitle:</b> solution nmr structure of a domain of adhesion exoprotein from2 pediococcus pentosaceus, northeast structural genomics consortium3 target ptr41o   |
| 56 | <a href="#">c3bewE</a>  | Alignment | not modelled | 12.9 | 21 | <b>PDB header:</b> immune system<br><b>Chain:</b> E: <b>PDB Molecule:</b> beta-2-microglobulin;<br><b>PDBTitle:</b> 10mer crystal structure of chicken mhc class i haplotype b21  |
| 57 | <a href="#">d1i5hw</a>  | Alignment | not modelled | 12.6 | 19 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain  |
| 58 | <a href="#">c2dvwB</a>  | Alignment | not modelled | 12.5 | 21 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> salvador homolog 1 protein;<br><b>PDBTitle:</b> solution structure of the second ww domain from mouse2 salvador homolog 1 protein (mww45)   |
| 59 | <a href="#">c5ydyA</a>  | Alignment | not modelled | 12.5 | 29 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ww2 domain and ppxy motif complex;<br><b>PDBTitle:</b> nmr structure of yap1-2 ww2 domain with lats1 ppxy motif complex   |
| 60 | <a href="#">c3vwkB</a>  | Alignment | not modelled | 12.1 | 21 | <b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> beta-2-microglobulin;<br><b>PDBTitle:</b> ternary crystal structure of the human nkt tcr-cd1d-4'deoxy-alpha-2 galactosylceramide complex  |
| 61 | <a href="#">d2b0ga1</a> | Alignment | not modelled | 12.0 | 15 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> RNA-binding domain, RBD<br><b>Family:</b> Canonical RBD   |
| 62 | <a href="#">c3tm6A</a>  | Alignment | not modelled | 11.7 | 15 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-2-microglobulin;<br><b>PDBTitle:</b> crystal structure of the beta-2 microglobulin dimc50 disulphide-linked2 homodimer mutant  |
| 63 | <a href="#">c3tm6D</a>  | Alignment | not modelled | 11.7 | 15 | <b>PDB header:</b> immune system<br><b>Chain:</b> D: <b>PDB Molecule:</b> beta-2-microglobulin;<br><b>PDBTitle:</b> crystal structure of the beta-2 microglobulin dimc50 disulphide-linked2 homodimer mutant  |
| 64 | <a href="#">c3tm6B</a>  | Alignment | not modelled | 11.7 | 15 | <b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> beta-2-microglobulin;<br><b>PDBTitle:</b> crystal structure of the beta-2 microglobulin dimc50 disulphide-linked2 homodimer mutant  |
| 65 | <a href="#">d1jroa2</a> | Alignment | not modelled | 11.6 | 16 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> 2Fe-2S ferredoxin-like<br><b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins  |
| 66 | <a href="#">c2djyA</a>  | Alignment | not modelled | 11.6 | 22 | <b>PDB header:</b> ligase/signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> smad ubiquitination regulatory factor 2;<br><b>PDBTitle:</b> solution structure of smurf2 ww3 domain-smad7 py peptide2 complex   |
| 67 | <a href="#">d1w8oa1</a> | Alignment | not modelled | 11.4 | 21 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> E-set domains of sugar-utilizing enzymes  |
| 68 | <a href="#">c2qrsA</a>  | Alignment | not modelled | 11.4 | 21 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> h-2 class i histocompatibility antigen k-b alpha chain,<br><b>PDBTitle:</b> crystal structure of a single chain trimer composed of the mhc i heavy2 chain h-2kb y84a, beta-2microglobulin, and ovalbumin-derived peptide.                     |
| 69 | <a href="#">d1nmva1</a> | Alignment | not modelled | 11.2 | 29 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain  |
| 70 | <a href="#">c2n8tA</a>  | Alignment | not modelled | 11.1 | 18 | <b>PDB header:</b> ligase/peptide<br><b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase nedd4;<br><b>PDBTitle:</b> solution structure of the rnedd4 ww2 domain-cx43ct peptide complex by2 nmr  |
| 71 | <a href="#">c1tk7A</a>  | Alignment | not modelled | 10.9 | 57 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cg4244-pb;<br><b>PDBTitle:</b> nmr structure of ww domains (ww3-4) from suppressor of2 deltex   |
| 72 | <a href="#">d1prtc2</a> | Alignment | not modelled | 10.7 | 23 | <b>Fold:</b> C-type lectin-like<br><b>Superfamily:</b> C-type lectin-like<br><b>Family:</b> Aerolysin/Pertussis toxin (APT) domain  |
| 73 | <a href="#">c2kq0A</a>  | Alignment | not modelled | 10.6 | 33 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase nedd4;<br><b>PDBTitle:</b> human nedd4 3rd ww domain complex with ebola zaire virus matrix2 protein vp40 derived peptide iltappeyme  |
| 74 | <a href="#">c2zajA</a>  | Alignment | not modelled | 10.6 | 22 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> membrane-associated guanylate kinase, ww and pdz<br><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) |
| 75 | <a href="#">c2ysgA</a>  | Alignment | not modelled | 10.0 | 18 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> syntaxin-binding protein 4;<br><b>PDBTitle:</b> solution structure of the ww domain from the human syntaxin-2 binding protein 4   |
| 76 | <a href="#">c3pqyB</a>  | Alignment | not modelled | 9.9  | 15 | <b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> beta-2-microglobulin;<br><b>PDBTitle:</b> crystal structure of 6218 tcr in complex with the h2db-pa224  |
| 77 | <a href="#">c3pqyG</a>  | Alignment | not modelled | 9.9  | 15 | <b>PDB header:</b> immune system<br><b>Chain:</b> G: <b>PDB Molecule:</b> beta-2-microglobulin;<br><b>PDBTitle:</b> crystal structure of 6218 tcr in complex with the h2db-pa224  |
| 78 | <a href="#">c3vvyA</a>  | Alignment | not modelled | 9.7  | 67 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> methyl-cpg-binding domain protein 4;  |

|    |                         |           |              |     |    |   |
|----|-------------------------|-----------|--------------|-----|----|---|
| 78 | <a href="#">c3vxxA_</a> | Alignment | not modelled | 9.7 | 07 | <b>PDBTitle:</b> crystal structure of methyl cpG binding domain of mbd4 in complex with2 the 5mcg/tg sequence   |
| 79 | <a href="#">d2ysca1</a> | Alignment | not modelled | 9.7 | 25 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain  |
| 80 | <a href="#">c5kouB_</a> | Alignment | not modelled | 9.6 | 27 | <b>PDB header:</b> viral protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> capsid polyprotein vp25;<br><b>PDBTitle:</b> crystal structure of the human astrovirus 2 capsid protein spike2 domain at 1.87-a resolution                        |
| 81 | <a href="#">d2ho2a1</a> | Alignment | not modelled | 9.5 | 18 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain  |
| 82 | <a href="#">c2w6iH_</a> | Alignment | not modelled | 9.4 | 26 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> H: <b>PDB Molecule:</b> f1-atpase delta subunit;<br><b>PDBTitle:</b> low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 4b.          |
| 83 | <a href="#">d2itka1</a> | Alignment | not modelled | 9.3 | 33 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain  |
| 84 | <a href="#">d1pina1</a> | Alignment | not modelled | 9.2 | 29 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain  |
| 85 | <a href="#">c2dmvA_</a> | Alignment | not modelled | 9.2 | 18 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> itchy homolog e3 ubiquitin protein ligase;<br><b>PDBTitle:</b> solution structure of the second ww domain of itchy homolog2 e3 ubiquitin protein ligase (itich)          |
| 86 | <a href="#">c3lz8A_</a> | Alignment | not modelled | 9.1 | 16 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative chaperone dnaj;<br><b>PDBTitle:</b> structure of a putative chaperone dnaj from klebsiella pneumoniae2 subsp. pneumoniae mgh 78578 at 2.9 a resolution.      |
| 87 | <a href="#">c2c36B_</a> | Alignment | not modelled | 8.8 | 27 | <b>PDB header:</b> viral protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> glycoprotein d hsv-1;<br><b>PDBTitle:</b> structure of unliganded hsv gd reveals a mechanism for receptor-2 mediated activation of virus entry                    |
| 88 | <a href="#">c3qsgA_</a> | Alignment | not modelled | 8.6 | 23 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> capsid polyprotein;<br><b>PDBTitle:</b> crystal structure of the projection domain of the human astrovirus2 capsid protein  |
| 89 | <a href="#">c3r27A_</a> | Alignment | not modelled | 8.2 | 17 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> heterogeneous nuclear ribonucleoprotein I;<br><b>PDBTitle:</b> crystal structure of the first rrm domain of heterogeneous nuclear2 ribonucleoprotein I (hnrp I) |
| 90 | <a href="#">d1eh9a2</a> | Alignment | not modelled | 8.0 | 18 | <b>Fold:</b> Glycosyl hydrolase domain<br><b>Superfamily:</b> Glycosyl hydrolase domain<br><b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain  |
| 91 | <a href="#">d2f21a1</a> | Alignment | not modelled | 7.9 | 19 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain  |
| 92 | <a href="#">c2xksA_</a> | Alignment | not modelled | 7.8 | 18 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-2-microglobulin;<br><b>PDBTitle:</b> prion-like conversion during amyloid formation at atomic resolution   |
| 93 | <a href="#">c3rgvD_</a> | Alignment | not modelled | 7.8 | 16 | <b>PDB header:</b> immune system<br><b>Chain:</b> D: <b>PDB Molecule:</b> beta-2-microglobulin;<br><b>PDBTitle:</b> a single tcr bound to mhci and mhc ii reveals switchable tcr2 conformers  |
| 94 | <a href="#">d1v97a2</a> | Alignment | not modelled | 7.7 | 32 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> 2Fe-2S ferredoxin-like<br><b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins  |
| 95 | <a href="#">c2xkuA_</a> | Alignment | not modelled | 7.6 | 20 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-2-microglobulin;<br><b>PDBTitle:</b> prion-like conversion during amyloid formation at atomic resolution   |
| 96 | <a href="#">c2kxqA_</a> | Alignment | not modelled | 7.6 | 14 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf2;<br><b>PDBTitle:</b> solution structure of smurf2 ww2 and ww3 bound to smad7 py motif2 containing peptide                    |
| 97 | <a href="#">c3le4A_</a> | Alignment | not modelled | 7.5 | 67 | <b>PDB header:</b> nuclear protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> microprocessor complex subunit dgcr8;<br><b>PDBTitle:</b> crystal structure of the dgcr8 dimerization domain  |
| 98 | <a href="#">d1i8gb_</a> | Alignment | not modelled | 7.5 | 29 | <b>Fold:</b> WW domain-like<br><b>Superfamily:</b> WW domain<br><b>Family:</b> WW domain  |
| 99 | <a href="#">c2x89F_</a> | Alignment | not modelled | 7.4 | 21 | <b>PDB header:</b> immune system<br><b>Chain:</b> F: <b>PDB Molecule:</b> beta-2-microglobulin;<br><b>PDBTitle:</b> structure of the beta2_microglobulin involved in amyloidogenesis  |