
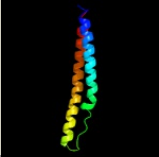





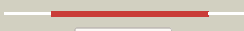








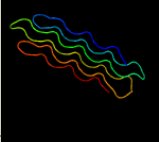


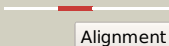





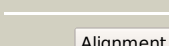











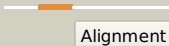

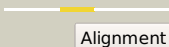
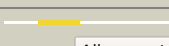


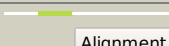



# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3590c\_(PE\_PGRS58)\_4031583\_4033337  
 Date Fri Aug 9 18:20:27 BST 2019  
 Unique Job ID c70b38dd0ca853ab

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c5xfsA_</a> | <br>Alignment   |    | 100.0      | 49     | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein pe8;<br><b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis  |
| 2  | <a href="#">d2g38a1</a> | <br>Alignment   |    | 100.0      | 36     | <b>Fold:</b> Ferritin-like<br><b>Superfamily:</b> PE/PPE dimer-like<br><b>Family:</b> PE   |
| 3  | <a href="#">c2g38A_</a> | <br>Alignment   |    | 100.0      | 36     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein;<br><b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis  |
| 4  | <a href="#">c1ygvA_</a> | <br>Alignment   |   | 99.8       | 27     | <b>PDB header:</b> structural protein/contractile protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> collagen i alpha 1;<br><b>PDBTitle:</b> the structure of collagen type i. single type i collagen2 molecule: rigid refinement  |
| 5  | <a href="#">c1y0fB_</a> | <br>Alignment |   | 99.8       | 26     | <b>PDB header:</b> structural protein/contractile protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> collagen i alpha 2;<br><b>PDBTitle:</b> the structure of collagen type i. single type i collagen2 molecule  |
| 6  | <a href="#">c3hqvB_</a> | <br>Alignment |   | 99.7       | 32     | <b>PDB header:</b> structural protein, contractile protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-2(i) chain;<br><b>PDBTitle:</b> low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement |
| 7  | <a href="#">c3bogB_</a> | <br>Alignment |  | 97.2       | 51     | <b>PDB header:</b> antifreeze protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein;<br><b>PDBTitle:</b> snow flea antifreeze protein quasi-racemate  |
| 8  | <a href="#">c3bogA_</a> | <br>Alignment |  | 97.2       | 51     | <b>PDB header:</b> antifreeze protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein;<br><b>PDBTitle:</b> snow flea antifreeze protein quasi-racemate  |
| 9  | <a href="#">c2pneA_</a> | <br>Alignment |  | 97.2       | 48     | <b>PDB header:</b> antifreeze protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein;<br><b>PDBTitle:</b> crystal structure of the snow flea antifreeze protein  |
| 10 | <a href="#">c3boiB_</a> | <br>Alignment |  | 97.2       | 48     | <b>PDB header:</b> antifreeze protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein;<br><b>PDBTitle:</b> snow flea antifreeze protein racemate  |
| 11 | <a href="#">c3boiA_</a> | <br>Alignment |  | 97.2       | 48     | <b>PDB header:</b> antifreeze protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein;<br><b>PDBTitle:</b> snow flea antifreeze protein racemate  |

|    |                         |   |   |      |    |  |
|----|-------------------------|---|---|------|----|--|
| 12 | <a href="#">c5ctdB_</a> |  Alignment   |    | 93.9 | 35 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-2(i) chain,collagen alpha-2(ix) chain;<br><b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen               |
| 13 | <a href="#">c5ctdA_</a> |  Alignment   |    | 93.8 | 33 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(i) chain,collagen alpha-1(ix) chain;<br><b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen               |
| 14 | <a href="#">c5ctiC_</a> |  Alignment   |    | 93.7 | 33 | <b>PDB header:</b> structural protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> collagen alpha-1(i) chain,collagen alpha-3(ix) chain;<br><b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form) |
| 15 | <a href="#">c1nayC_</a> |  Alignment   |    | 93.5 | 25 | <b>PDB header:</b> structural protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide;<br><b>PDBTitle:</b> gpp-foldon:x-ray structure   |
| 16 | <a href="#">d1wa8a1</a> |  Alignment   |    | 91.8 | 9  | <b>Fold:</b> Ferritin-like<br><b>Superfamily:</b> EsxAB dimer-like<br><b>Family:</b> ESAT-6 like   |
| 17 | <a href="#">c3gvmA_</a> |  Alignment   |    | 91.7 | 15 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sag1039;<br><b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae   |
| 18 | <a href="#">c4iogD_</a> |  Alignment |  | 89.7 | 12 | <b>PDB header:</b> unknown function<br><b>Chain:</b> D: <b>PDB Molecule:</b> secreted protein esxb;<br><b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne  |
| 19 | <a href="#">c4wj2A_</a> |  Alignment |  | 88.9 | 15 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48;<br><b>PDBTitle:</b> mycobacterial protein  |
| 20 | <a href="#">c4lwsA_</a> |  Alignment |  | 88.1 | 20 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata  |
| 21 | <a href="#">c3zbhC_</a> |  Alignment | not modelled  | 83.8 | 15 | <b>PDB header:</b> unknown function<br><b>Chain:</b> C: <b>PDB Molecule:</b> esxa;<br><b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i   |
| 22 | <a href="#">c2vs0B_</a> |  Alignment | not modelled  | 80.6 | 9  | <b>PDB header:</b> cell invasion<br><b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa;<br><b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa   |
| 23 | <a href="#">c2klwA_</a> |  Alignment | not modelled  | 77.4 | 37 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> (pkg)10;<br><b>PDBTitle:</b> solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions   |
| 24 | <a href="#">c6nb3B_</a> |  Alignment | not modelled  | 74.3 | 24 | <b>PDB header:</b> virus<br><b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein;<br><b>PDBTitle:</b> mers-cov complex with human neutralizing Ica60 antibody fab fragment2 (state 1)  |
| 25 | <a href="#">c2kg7A_</a> |  Alignment | not modelled  | 72.2 | 47 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein esxg (pe family protein);<br><b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288   |
| 26 | <a href="#">c2kg7B_</a> |  Alignment | not modelled  | 69.2 | 17 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> esat-6-like protein esxh;<br><b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288   |
| 27 | <a href="#">d1wa8b1</a> |  Alignment | not modelled  | 64.4 | 15 | <b>Fold:</b> Ferritin-like<br><b>Superfamily:</b> EsxAB dimer-like<br><b>Family:</b> ESAT-6 like   |
| 28 | <a href="#">c6g7oA_</a> |  Alignment | not modelled  | 61.9 | 20 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> alkaline ceramidase 3,soluble cytochrome b562;<br><b>PDBTitle:</b> crystal structure of human alkaline ceramidase 3 (acer3)   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
|    |                         |           |              |      |    | at 2.72 angstrom resolution  |
| 29 | <a href="#">c5x5bB_</a> | Alignment | not modelled | 58.8 | 22 | <b>PDB header:</b> viral protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein;<br><b>PDBTitle:</b> prefusion structure of sars-cov spike glycoprotein, conformation 2   |
| 30 | <a href="#">d1n7ka_</a> | Alignment | not modelled | 58.5 | 18 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase  |
| 31 | <a href="#">c3u8pB_</a> | Alignment | not modelled | 57.5 | 19 | <b>PDB header:</b> fluorescent protein, electron transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome b562 integral fusion with enhanced green<br><b>PDBTitle:</b> cytochrome b562 integral fusion with egfp  |
| 32 | <a href="#">c2cuoF_</a> | Alignment | not modelled | 52.7 | 37 | <b>PDB header:</b> structural protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9;<br><b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9  |
| 33 | <a href="#">c2cuoC_</a> | Alignment | not modelled | 52.7 | 37 | <b>PDB header:</b> structural protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9;<br><b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9  |
| 34 | <a href="#">c2w0cR_</a> | Alignment | not modelled | 52.3 | 25 | <b>PDB header:</b> virus<br><b>Chain:</b> R: <b>PDB Molecule:</b> protein p3;<br><b>PDBTitle:</b> x-ray structure of the entire lipid-containing bacteriophage pm2   |
| 35 | <a href="#">c2z2sD_</a> | Alignment | not modelled | 49.1 | 22 | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> anti-sigma factor chrr, transcriptional activator chrr;<br><b>PDBTitle:</b> crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr                   |
| 36 | <a href="#">c3onjA_</a> | Alignment | not modelled | 48.2 | 17 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> t-snare vti1;<br><b>PDBTitle:</b> crystal structure of yeast vti1p_habc domain   |
| 37 | <a href="#">c1k6fA_</a> | Alignment | not modelled | 46.1 | 31 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> collagen triple helix;<br><b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3  |
| 38 | <a href="#">c1k6fE_</a> | Alignment | not modelled | 46.1 | 31 | <b>PDB header:</b> structural protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> collagen triple helix;<br><b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3  |
| 39 | <a href="#">c1k6fD_</a> | Alignment | not modelled | 46.1 | 31 | <b>PDB header:</b> structural protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> collagen triple helix;<br><b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3  |
| 40 | <a href="#">c1k6fF_</a> | Alignment | not modelled | 46.1 | 31 | <b>PDB header:</b> structural protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> collagen triple helix;<br><b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3  |
| 41 | <a href="#">c1k6fB_</a> | Alignment | not modelled | 46.1 | 31 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> collagen triple helix;<br><b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3  |
| 42 | <a href="#">c1k6fC_</a> | Alignment | not modelled | 46.1 | 31 | <b>PDB header:</b> structural protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> collagen triple helix;<br><b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3  |
| 43 | <a href="#">c6cs2A_</a> | Alignment | not modelled | 45.9 | 22 | <b>PDB header:</b> viral protein/hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein,fibrinin;<br><b>PDBTitle:</b> sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles                               |
| 44 | <a href="#">c5x5fC_</a> | Alignment | not modelled | 45.5 | 24 | <b>PDB header:</b> viral protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> s protein;<br><b>PDBTitle:</b> prefusion structure of mers-cov spike glycoprotein, conformation 2  |
| 45 | <a href="#">c2ebal_</a> | Alignment | not modelled | 44.9 | 8  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> I: <b>PDB Molecule:</b> putative glutaryl-coa dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the putative glutaryl-coa dehydrogenase from2 thermus thermophilus                                    |
| 46 | <a href="#">c3ah9D_</a> | Alignment | not modelled | 41.8 | 39 | <b>PDB header:</b> structural protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide;<br><b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution  |
| 47 | <a href="#">c3ah9F_</a> | Alignment | not modelled | 38.8 | 36 | <b>PDB header:</b> structural protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide;<br><b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution  |
| 48 | <a href="#">c5szsC_</a> | Alignment | not modelled | 37.6 | 24 | <b>PDB header:</b> viral protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein;<br><b>PDBTitle:</b> glycan shield and epitope masking of a coronavirus spike protein2 observed by cryo-electron microscopy                                       |
| 49 | <a href="#">d1lghb_</a> | Alignment | not modelled | 36.8 | 29 | <b>Fold:</b> Light-harvesting complex subunits<br><b>Superfamily:</b> Light-harvesting complex subunits<br><b>Family:</b> Light-harvesting complex subunits  |
| 50 | <a href="#">c3ah9A_</a> | Alignment | not modelled | 36.8 | 38 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide;<br><b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution  |
| 51 | <a href="#">c4rglA_</a> | Alignment | not modelled | 36.4 | 22 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> filamentation induced by camp protein fic;<br><b>PDBTitle:</b> crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution |
| 52 | <a href="#">c2cuoE_</a> | Alignment | not modelled | 35.4 | 35 | <b>PDB header:</b> structural protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9;<br><b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9  |
| 53 | <a href="#">c2cuoD_</a> | Alignment | not modelled | 35.4 | 35 | <b>PDB header:</b> structural protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9;<br><b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9  |
| 54 | <a href="#">c2cuoA_</a> | Alignment | not modelled | 35.4 | 35 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9;<br><b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 55 | <a href="#">c2cuoB_</a> | Alignment | not modelled | 35.4 | 35 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9;<br><b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9  |
| 56 | <a href="#">c5mgzA_</a> | Alignment | not modelled | 34.9 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 8-demethylnovobioc acid c(8)-methyltransferase;<br><b>PDBTitle:</b> streptomyces spheroides novo (8-demethylnovobioc acid2 methyltransferase) with sah   |
| 57 | <a href="#">c4z9cB_</a> | Alignment | not modelled | 34.8 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> subtilase cytotoxin subunit b-like protein;<br><b>PDBTitle:</b> ecpltab oxidized   |
| 58 | <a href="#">c3h6pB_</a> | Alignment | not modelled | 34.8 | 40 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> esat-6 like protein exxs;<br><b>PDBTitle:</b> crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis   |
| 59 | <a href="#">c3ah9C_</a> | Alignment | not modelled | 34.1 | 36 | <b>PDB header:</b> structural protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide;<br><b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution  |
| 60 | <a href="#">c3ah9B_</a> | Alignment | not modelled | 34.1 | 36 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide;<br><b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution  |
| 61 | <a href="#">c3ah9E_</a> | Alignment | not modelled | 34.1 | 36 | <b>PDB header:</b> structural protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide;<br><b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution  |
| 62 | <a href="#">c5i08A_</a> | Alignment | not modelled | 34.0 | 25 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein, envelope glycoprotein chimera;<br><b>PDBTitle:</b> prefusion structure of a human coronavirus spike protein  |
| 63 | <a href="#">c4kjsB_</a> | Alignment | not modelled | 33.9 | 21 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> cation exchanger yfke;<br><b>PDBTitle:</b> structure of native yfke  |
| 64 | <a href="#">d1bpoa1</a> | Alignment | not modelled | 33.6 | 27 | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> ARM repeat<br><b>Family:</b> Clathrin heavy-chain linker domain   |
| 65 | <a href="#">d1umya_</a> | Alignment | not modelled | 32.8 | 16 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Homocysteine S-methyltransferase<br><b>Family:</b> Homocysteine S-methyltransferase  |
| 66 | <a href="#">d1lt7a_</a> | Alignment | not modelled | 32.8 | 15 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Homocysteine S-methyltransferase<br><b>Family:</b> Homocysteine S-methyltransferase  |
| 67 | <a href="#">c3w5mA_</a> | Alignment | not modelled | 32.2 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative rhamnosidase;<br><b>PDBTitle:</b> crystal structure of streptomyces avermitilis alpha-l-rhamnosidase  |
| 68 | <a href="#">c3o7kA_</a> | Alignment | not modelled | 31.3 | 22 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ohcu decarboxylase;<br><b>PDBTitle:</b> crystal structure of 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazole2 decarboxylase from klebsiella pneumoniae   |
| 69 | <a href="#">c5fsgA_</a> | Alignment | not modelled | 30.9 | 16 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein, hantavirus<br><b>PDBTitle:</b> structure of the hantavirus nucleoprotein provides insights2 into the mechanism of rna encapsidation and a template for3 drug design |
| 70 | <a href="#">c5g4yA_</a> | Alignment | not modelled | 30.9 | 27 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein;<br><b>PDBTitle:</b> structural basis for carboxylic acid recognition by a cache2 chemosensory domain.  |
| 71 | <a href="#">c3a0mF_</a> | Alignment | not modelled | 30.7 | 36 | <b>PDB header:</b> structural protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide;<br><b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal  |
| 72 | <a href="#">d2pv7a1</a> | Alignment | not modelled | 29.4 | 14 | <b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like<br><b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like<br><b>Family:</b> TyrA dimerization domain-like  |
| 73 | <a href="#">c4jkvA_</a> | Alignment | not modelled | 29.2 | 20 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562, smoothed homolog;<br><b>PDBTitle:</b> structure of the human smoothed 7tm receptor in complex with an2 antitumor agent   |
| 74 | <a href="#">c5n7kD_</a> | Alignment | not modelled | 29.0 | 34 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> D: <b>PDB Molecule:</b> marvel domain-containing protein 2;<br><b>PDBTitle:</b> crystal structure of the coiled-coil domain of human tricellulin   |
| 75 | <a href="#">c2vsgB_</a> | Alignment | not modelled | 26.5 | 12 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> variant surface glycoprotein iltat 1.24;<br><b>PDBTitle:</b> a structural motif in the variant surface glycoproteins of trypanosoma2 brucei   |
| 76 | <a href="#">c1wrgA_</a> | Alignment | not modelled | 25.7 | 29 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> light-harvesting protein b-880, beta chain;<br><b>PDBTitle:</b> light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum   |
| 77 | <a href="#">c2v8sV_</a> | Alignment | not modelled | 25.6 | 22 | <b>PDB header:</b> protein transport<br><b>Chain:</b> V: <b>PDB Molecule:</b> vesicle transport through interaction with<br><b>PDBTitle:</b> vti1b habc domain - epsinr enth domain complex  |
| 78 | <a href="#">d256ba_</a> | Alignment | not modelled | 24.9 | 19 | <b>Fold:</b> Four-helical up-and-down bundle<br><b>Superfamily:</b> Cytochromes<br><b>Family:</b> Cytochrome b562  |
| 79 | <a href="#">c5v8wG_</a> | Alignment | not modelled | 24.9 | 33 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> G: <b>PDB Molecule:</b> integrator complex subunit 9;<br><b>PDBTitle:</b> crystal structure of human integrator ints9-ints11 ctd complex   |
| 80 | <a href="#">c5xlrC_</a> | Alignment | not modelled | 24.8 | 21 | <b>PDB header:</b> viral protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein;  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
|    |                         |           |              |      |    | <b>PDBTitle:</b> structure of sars-cov spike glycoprotein  |
| 81 | <a href="#">c2z8jA_</a> | Alignment | not modelled | 24.1 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase;<br><b>PDBTitle:</b> crystal structure of escherichia coli gamma-glutamyltranspeptidase in2 complex with azaserine prepared in the dark |
| 82 | <a href="#">c3ks8D_</a> | Alignment | not modelled | 23.1 | 24 | <b>PDB header:</b> viral protein/rna<br><b>Chain:</b> D: <b>PDB Molecule:</b> polymerase cofactor vp35;<br><b>PDBTitle:</b> crystal structure of reston ebolavirus vp35 rna binding domain in2 complex with 18bp dsrna                       |
| 83 | <a href="#">c3kthD_</a> | Alignment | not modelled | 21.9 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent clp protease proteolytic subunit;<br><b>PDBTitle:</b> structure of clpp from bacillus subtilis in orthorhombic crystal form                              |
| 84 | <a href="#">d2nlza1</a> | Alignment | not modelled | 21.5 | 22 | <b>Fold:</b> Ntn hydrolase-like<br><b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases)<br><b>Family:</b> Gamma-glutamyltranspeptidase-like   |
| 85 | <a href="#">c4krrA_</a> | Alignment | not modelled | 21.4 | 12 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> wnt inhibitor of dorsal protein;<br><b>PDBTitle:</b> crystal structure of drosophila wntd n-terminal domain-linker2 (residues 31-240)                          |
| 86 | <a href="#">c1bpoA_</a> | Alignment | not modelled | 21.0 | 26 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (clathrin);<br><b>PDBTitle:</b> clathrin heavy-chain terminal domain and linker   |
| 87 | <a href="#">c6b7nC_</a> | Alignment | not modelled | 20.9 | 18 | <b>PDB header:</b> viral protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> spike protein;<br><b>PDBTitle:</b> cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state                          |
| 88 | <a href="#">c2e0wA_</a> | Alignment | not modelled | 20.6 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase;<br><b>PDBTitle:</b> t391a precursor mutant protein of gamma-glutamyltranspeptidase from2 escherichia coli                              |
| 89 | <a href="#">c2a1tC_</a> | Alignment | not modelled | 20.2 | 14 | <b>PDB header:</b> oxidoreductase/electron transport<br><b>Chain:</b> C: <b>PDB Molecule:</b> acyl-coa dehydrogenase, medium-chain specific,<br><b>PDBTitle:</b> structure of the human mcad:etf e165betaa complex                           |
| 90 | <a href="#">c6mvtA_</a> | Alignment | not modelled | 20.1 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase;<br><b>PDBTitle:</b> structure of a bacterial aldh16 complexed with nadh   |
| 91 | <a href="#">c6et5u_</a> | Alignment | not modelled | 20.0 | 36 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> U: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain;<br><b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis                                     |
| 92 | <a href="#">c4gdxA_</a> | Alignment | not modelled | 20.0 | 28 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyltranspeptidase 1 heavy chain;<br><b>PDBTitle:</b> crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex                           |
| 93 | <a href="#">c6nzkB_</a> | Alignment | not modelled | 19.9 | 19 | <b>PDB header:</b> viral protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> spike surface glycoprotein;<br><b>PDBTitle:</b> structural basis for human coronavirus attachment to sialic acid2 receptors  |
| 94 | <a href="#">c3jclC_</a> | Alignment | not modelled | 19.8 | 22 | <b>PDB header:</b> viral protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein;<br><b>PDBTitle:</b> cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer   |
| 95 | <a href="#">c2ml3A_</a> | Alignment | not modelled | 19.8 | 18 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 6;<br><b>PDBTitle:</b> solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase            |
| 96 | <a href="#">c4x2eA_</a> | Alignment | not modelled | 19.3 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fic family protein putative filamentation induced by camp<br><b>PDBTitle:</b> clostridium difficile wild type fic protein  |
| 97 | <a href="#">c5jw9B_</a> | Alignment | not modelled | 18.9 | 31 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase ii elongation factor ell2;<br><b>PDBTitle:</b> the crystal structure of ell2 ocludin domain and aff4 peptide                                      |
| 98 | <a href="#">c3g9kD_</a> | Alignment | not modelled | 18.3 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> capsule biosynthesis protein capd;<br><b>PDBTitle:</b> crystal structure of bacillus anthracis transpeptidase enzyme capd  |
| 99 | <a href="#">c2jifA_</a> | Alignment | not modelled | 18.3 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> short/branched chain specific acyl-coa dehydrogenase;<br><b>PDBTitle:</b> structure of human short-branched chain acyl-coa dehydrogenase2 (acadsb)                |