

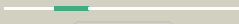




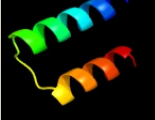





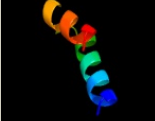



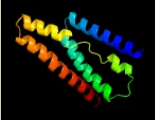






# Phyre2

|               |                              |
|---------------|------------------------------|
| Email         | mdejesus@rockefeller.edu     |
| Description   | RVBD3737_(-)_4187877_4189466 |
| Date          | Fri Aug 9 18:20:43 BST 2019  |
| Unique Job ID | d00815b4a8a14bcc             |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">d2pp4a1</a> |  Alignment   |    | 79.7       | 18     | <b>Fold:</b> TAFH domain-like<br><b>Superfamily:</b> TAFH domain-like<br><b>Family:</b> TAFH domain-like  |
| 2  | <a href="#">c2y0sj_</a> |  Alignment   |    | 48.2       | 16     | <b>PDB header:</b> transferase<br><b>Chain:</b> J; <b>PDB Molecule:</b> rna polymerase subunit 13;<br><b>PDBTitle:</b> crystal structure of sulfolobus shibatae rna polymerase in p21 space2 group  |
| 3  | <a href="#">c2y0sQ_</a> |  Alignment   |    | 48.2       | 16     | <b>PDB header:</b> transferase<br><b>Chain:</b> Q; <b>PDB Molecule:</b> rna polymerase subunit 13;<br><b>PDBTitle:</b> crystal structure of sulfolobus shibatae rna polymerase in p21 space2 group  |
| 4  | <a href="#">c4b1pl_</a> |  Alignment   |   | 47.6       | 18     | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> J; <b>PDB Molecule:</b> rna polymerase subunit 13;<br><b>PDBTitle:</b> archaeal rnap-dna binary complex at 4.32ang  |
| 5  | <a href="#">c4aybQ_</a> |  Alignment |  | 46.4       | 18     | <b>PDB header:</b> transferase<br><b>Chain:</b> Q; <b>PDB Molecule:</b> dna-directed rna polymerase;<br><b>PDBTitle:</b> rnap at 3.2ang   |
| 6  | <a href="#">c5xj6A_</a> |  Alignment |  | 43.8       | 18     | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> glycerol-3-phosphate acyltransferase;<br><b>PDBTitle:</b> crystal structure of plsy (ygih), an integral membrane glycerol 3-2 phosphate acyltransferase - the glycerol 3-phosphate form |
| 7  | <a href="#">d1vp7a_</a> |  Alignment |  | 41.6       | 31     | <b>Fold:</b> Spectrin repeat-like<br><b>Superfamily:</b> XseB-like<br><b>Family:</b> XseB-like  |
| 8  | <a href="#">c5x3xm_</a> |  Alignment |  | 41.2       | 15     | <b>PDB header:</b> transport protein<br><b>Chain:</b> M; <b>PDB Molecule:</b> cobalt transport protein cbim;<br><b>PDBTitle:</b> 2.8a resolution structure of a cobalt energy-coupling factor2 transporter-cbimqo   |
| 9  | <a href="#">c5a40C_</a> |  Alignment |  | 40.6       | 17     | <b>PDB header:</b> transport protein<br><b>Chain:</b> C; <b>PDB Molecule:</b> putative fluoride ion transporter crcb;<br><b>PDBTitle:</b> crystal structure of a dual topology fluoride ion channel.  |
| 10 | <a href="#">c3hkzY_</a> |  Alignment |  | 38.0       | 11     | <b>PDB header:</b> transferase<br><b>Chain:</b> Y; <b>PDB Molecule:</b> dna-directed rna polymerase subunit 13;<br><b>PDBTitle:</b> the x-ray crystal structure of rna polymerase from archaea  |
| 11 | <a href="#">d1vp7b_</a> |  Alignment |  | 34.7       | 31     | <b>Fold:</b> Spectrin repeat-like<br><b>Superfamily:</b> XseB-like<br><b>Family:</b> XseB-like  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | <a href="#">c3hkzZ_</a> | Alignment |              | 33.6 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> Z; <b>PDB Molecule:</b> dna-directed rna polymerase subunit 13;<br><b>PDBTitle:</b> the x-ray crystal structure of rna polymerase from archaea   |
| 13 | <a href="#">c4m5bA_</a> | Alignment |              | 32.4 | 18 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> cobalamin biosynthesis protein cbim;<br><b>PDBTitle:</b> crystal structure of an truncated transition metal transporter   |
| 14 | <a href="#">c4m5cA_</a> | Alignment |              | 32.4 | 18 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> cobalamin biosynthesis protein cbim;<br><b>PDBTitle:</b> crystal structure of an truncated transition metal transporter   |
| 15 | <a href="#">c4b1oQ_</a> | Alignment |              | 32.2 | 18 | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> Q; <b>PDB Molecule:</b> rna polymerase subunit 13;<br><b>PDBTitle:</b> archaeal rnap-dna binary complex at 4.32ang   |
| 16 | <a href="#">c2jvdA_</a> | Alignment |              | 30.1 | 14 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> upf0291 protein yznc;<br><b>PDBTitle:</b> solution nmr structure of the folded n-terminal fragment of2 upf0291 protein yznc from bacillus subtilis. northeast3 structural genomics target sr384-1-46 |
| 17 | <a href="#">c3bhpA_</a> | Alignment |              | 27.3 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> upf0291 protein yznc;<br><b>PDBTitle:</b> crystal structure of upf0291 protein yznc from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384              |
| 18 | <a href="#">c5n9qA_</a> | Alignment |              | 27.0 | 3  | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> inactive poly [adp-ribose] polymerase rcd1;<br><b>PDBTitle:</b> structure of a. thaliana rcd1(468-567)   |
| 19 | <a href="#">d2hepa1</a> | Alignment |              | 26.0 | 15 | <b>Fold:</b> Long alpha-hairpin<br><b>Superfamily:</b> Yznc-like<br><b>Family:</b> Yznc-like   |
| 20 | <a href="#">c2hepA_</a> | Alignment |              | 26.0 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A; <b>PDB Molecule:</b> upf0291 protein yznc;<br><b>PDBTitle:</b> solution nmr structure of the upf0291 protein yznc from2 bacillus subtilis. northeast structural genomics target3 sr384.                                   |
| 21 | <a href="#">c2wb1Q_</a> | Alignment | not modelled | 23.1 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> Q; <b>PDB Molecule:</b> dna-directed rna polymerase rpo13 subunit;<br><b>PDBTitle:</b> the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase   |
| 22 | <a href="#">d2p6va1</a> | Alignment | not modelled | 22.6 | 15 | <b>Fold:</b> TAFH domain-like<br><b>Superfamily:</b> TAFH domain-like<br><b>Family:</b> TAFH domain-like   |
| 23 | <a href="#">c2wb1J_</a> | Alignment | not modelled | 22.3 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> J; <b>PDB Molecule:</b> dna-directed rna polymerase rpo13 subunit;<br><b>PDBTitle:</b> the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase   |
| 24 | <a href="#">c4ezdB_</a> | Alignment | not modelled | 22.1 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> urea transporter 1;<br><b>PDBTitle:</b> crystal structure of the ut-b urea transporter from bos taurus bound2 to selenourea  |
| 25 | <a href="#">c2waqQ_</a> | Alignment | not modelled | 21.8 | 14 | <b>PDB header:</b> transcription<br><b>Chain:</b> Q; <b>PDB Molecule:</b> dna-directed rna polymerase rpo13 subunit;<br><b>PDBTitle:</b> the complete structure of the archaeal 13-subunit dna-directed rna2 polymerase  |
| 26 | <a href="#">c5ecjA_</a> | Alignment | not modelled | 20.3 | 18 | <b>PDB header:</b> gene regulation/transcription<br><b>Chain:</b> A; <b>PDB Molecule:</b> pr domain zinc finger protein 14,protein cbfa2t2;<br><b>PDBTitle:</b> crystal structure of monobody mb(s4) bound to prdm14 in complex with2 mtgr1  |
| 27 | <a href="#">c4ejyA_</a> | Alignment | not modelled | 17.4 | 8  | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A; <b>PDB Molecule:</b> 3-methyladenine dna glycosylase;<br><b>PDBTitle:</b> structure of mboggl in complex with high affinity dna ligand<br><b>PDB header:</b> dna-binding protein  |

|    |                          |           |              |      |    |  |
|----|--------------------------|-----------|--------------|------|----|--|
| 28 | <a href="#">c1sfeA_</a>  | Alignment | not modelled | 17.2 | 24 | <b>Chain:</b> A: <b>PDB Molecule:</b> ada o6-methylguanine-dna methyltransferase;<br><b>PDBTitle:</b> ada o6-methylguanine-dna methyltransferase from escherichia coli   |
| 29 | <a href="#">c6d0nA_</a>  | Alignment | not modelled | 16.3 | 21 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> clc-type fluoride/proton antiporter;<br><b>PDBTitle:</b> crystal structure of a clc-type fluoride/proton antiporter, v319g2 mutant   |
| 30 | <a href="#">c5gasN_</a>  | Alignment | not modelled | 15.8 | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> N: <b>PDB Molecule:</b> archaeal/vacuolar-type h+-atpase subunit i;<br><b>PDBTitle:</b> thermus thermophilus v/a-atpase, conformation 2  |
| 31 | <a href="#">d1vd6a1</a>  | Alignment | not modelled | 14.5 | 15 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> PLC-like phosphodiesterases<br><b>Family:</b> Glycerophosphoryl diester phosphodiesterase  |
| 32 | <a href="#">c2ql8A_</a>  | Alignment | not modelled | 14.2 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative redox protein;<br><b>PDBTitle:</b> crystal structure of a putative redox protein (Isei_0423) from2 lactobacillus casei atcc 334 at 1.50 a resolution   |
| 33 | <a href="#">c4bhcA_</a>  | Alignment | not modelled | 13.8 | 36 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methylated-dna--protein-cysteine methyltransferase;<br><b>PDBTitle:</b> crystal structure of the m. tuberculosis o6-methylguanine2 methyltransferase r371 variant  |
| 34 | <a href="#">d1ml8a_</a>  | Alignment | not modelled | 12.9 | 13 | <b>Fold:</b> OsmC-like<br><b>Superfamily:</b> OsmC-like<br><b>Family:</b> YhfA-like  |
| 35 | <a href="#">d1sfea1</a>  | Alignment | not modelled | 12.3 | 23 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain<br><b>Family:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain   |
| 36 | <a href="#">d2jf2a1</a>  | Alignment | not modelled | 12.3 | 14 | <b>Fold:</b> Single-stranded left-handed beta-helix<br><b>Superfamily:</b> Trimeric LpxA-like enzymes<br><b>Family:</b> UDP N-acetylglucosamine acyltransferase  |
| 37 | <a href="#">c5mmjm_</a>  | Alignment | not modelled | 12.2 | 33 | <b>PDB header:</b> ribosome<br><b>Chain:</b> M: <b>PDB Molecule:</b><br><b>PDBTitle:</b> structure of the small subunit of the chloroplast ribosome  |
| 38 | <a href="#">c3zeyM_</a>  | Alignment | not modelled | 12.1 | 38 | <b>PDB header:</b> ribosome<br><b>Chain:</b> M: <b>PDB Molecule:</b> 40s ribosomal protein s18, putative;<br><b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome   |
| 39 | <a href="#">c1t39A_</a>  | Alignment | not modelled | 12.0 | 36 | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> methylated-dna--protein-cysteine<br><b>PDBTitle:</b> human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna   |
| 40 | <a href="#">d1o1za_</a>  | Alignment | not modelled | 12.0 | 14 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> PLC-like phosphodiesterases<br><b>Family:</b> Glycerophosphoryl diester phosphodiesterase  |
| 41 | <a href="#">c3cjeA_</a>  | Alignment | not modelled | 12.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> osmc-like protein;<br><b>PDBTitle:</b> crystal structure of an osmc-like hydroperoxide resistance protein2 (jann_2040) from jannaschia sp. ccs1 at 1.70 a resolution  |
| 42 | <a href="#">c6o58C_</a>  | Alignment | not modelled | 11.8 | 21 | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> calcium uniporter protein, mitochondrial;<br><b>PDBTitle:</b> human mcu-emre complex, dimer of channel   |
| 43 | <a href="#">c2xznM_</a>  | Alignment | not modelled | 11.8 | 42 | <b>PDB header:</b> ribosome<br><b>Chain:</b> M: <b>PDB Molecule:</b> rps18e;<br><b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2   |
| 44 | <a href="#">c3bbnM_</a>  | Alignment | not modelled | 11.4 | 38 | <b>PDB header:</b> ribosome<br><b>Chain:</b> M: <b>PDB Molecule:</b> ribosomal protein s13;<br><b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.  |
| 45 | <a href="#">c1v1cA_</a>  | Alignment | not modelled | 11.2 | 39 | <b>PDB header:</b> sh3-domain<br><b>Chain:</b> A: <b>PDB Molecule:</b> obscurin;<br><b>PDBTitle:</b> solution structure of the sh3 domain of obscurin  |
| 46 | <a href="#">c1powA_</a>  | Alignment | not modelled | 11.2 | 5  | <b>PDB header:</b> oxidoreductase(oxygen as acceptor)<br><b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate oxidase;<br><b>PDBTitle:</b> the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum   |
| 47 | <a href="#">d1luspa_</a> | Alignment | not modelled | 11.2 | 17 | <b>Fold:</b> OsmC-like<br><b>Superfamily:</b> OsmC-like<br><b>Family:</b> Ohr/OsmC resistance proteins   |
| 48 | <a href="#">c2bjoA_</a>  | Alignment | not modelled | 11.0 | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> organic hydroperoxide resistance protein ohrb;<br><b>PDBTitle:</b> crystal structure of the organic hydroperoxide resistance2 protein ohrb of bacillus subtilis   |
| 49 | <a href="#">c2kimA_</a>  | Alignment | not modelled | 10.6 | 32 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> o6-methylguanine-dna methyltransferase;<br><b>PDBTitle:</b> 1.7-mm microcryoprobe solution nmr structure of an o6-methylguanine2 dna methyltransferase family protein from vibrio parahaemolyticus.3 northeast structural genomics consortium target vpr247. |
| 50 | <a href="#">d2pn2a1</a>  | Alignment | not modelled | 10.4 | 7  | <b>Fold:</b> OsmC-like<br><b>Superfamily:</b> OsmC-like<br><b>Family:</b> Ohr/OsmC resistance proteins   |
| 51 | <a href="#">c6mjnC_</a>  | Alignment | not modelled | 10.2 | 7  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> organic hydroperoxide resistance protein;<br><b>PDBTitle:</b> crystal structure of an organic hydroperoxide resistance protein osmc,2 predicted redox protein, regulator of sulfide bond formation from3 legionella pneumophila                           |
| 52 | <a href="#">c4mh4B_</a>  | Alignment | not modelled | 10.1 | 10 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> osmc-like protein;<br><b>PDBTitle:</b> crystal structure of osmc-like protein from burkholderia  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
|    |                         |           |              |      |    | cenocepacia2 j2315  |
| 53 | <a href="#">c4nozA_</a> | Alignment | not modelled | 10.1 | 13 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> organic hydroperoxide resistance protein;<br><b>PDBTitle:</b> crystal structure of an organic hydroperoxide resistance protein from2 burkholderia cenocepacia   |
| 54 | <a href="#">c3ipdB_</a> | Alignment | not modelled | 10.0 | 13 | <b>PDB header:</b> exocytosis<br><b>Chain:</b> B: <b>PDB Molecule:</b> syntaxin-1a;<br><b>PDBTitle:</b> helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21   |
| 55 | <a href="#">c5jxxC_</a> | Alignment | not modelled | 9.8  | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o-<br><b>PDBTitle:</b> crystal structure of udp-n-acetylglucosamine o-acyltransferase (lpxa)2 from moraxella catarrhalis rh4.                           |
| 56 | <a href="#">c3iz6M_</a> | Alignment | not modelled | 9.8  | 42 | <b>PDB header:</b> ribosome<br><b>Chain:</b> M: <b>PDB Molecule:</b> 40s ribosomal protein s18 (s13p);<br><b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome                             |
| 57 | <a href="#">c3eerA_</a> | Alignment | not modelled | 9.6  | 0  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> organic hydroperoxide resistance protein, putative;<br><b>PDBTitle:</b> high resolution structure of putative organic hydroperoxide resistance2 protein from vibrio cholerae o1 biovar eltor str. n16961 |
| 58 | <a href="#">c3j20O_</a> | Alignment | not modelled | 9.6  | 38 | <b>PDB header:</b> ribosome<br><b>Chain:</b> O: <b>PDB Molecule:</b> 30s ribosomal protein s13p;<br><b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)       |
| 59 | <a href="#">c2qdqA_</a> | Alignment | not modelled | 9.5  | 6  | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> tal1n-1;<br><b>PDBTitle:</b> crystal structure of the talin dimerisation domain  |
| 60 | <a href="#">d1n2fa_</a> | Alignment | not modelled | 9.4  | 7  | <b>Fold:</b> OsmC-like<br><b>Superfamily:</b> OsmC-like<br><b>Family:</b> Ohr/OsmC resistance proteins  |
| 61 | <a href="#">c4b6at_</a> | Alignment | not modelled | 9.0  | 15 | <b>PDB header:</b> ribosome<br><b>Chain:</b> T: <b>PDB Molecule:</b> 60s ribosomal protein l21-a;<br><b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1   |
| 62 | <a href="#">d1lqla_</a> | Alignment | not modelled | 8.8  | 10 | <b>Fold:</b> OsmC-like<br><b>Superfamily:</b> OsmC-like<br><b>Family:</b> Ohr/OsmC resistance proteins  |
| 63 | <a href="#">c1lqlE_</a> | Alignment | not modelled | 8.8  | 10 | <b>PDB header:</b> unknown function<br><b>Chain:</b> E: <b>PDB Molecule:</b> osmotic inducible protein c like family;<br><b>PDBTitle:</b> crystal structure of osmC like protein from mycoplasma2 pneumoniae  |
| 64 | <a href="#">c3p5nA_</a> | Alignment | not modelled | 8.6  | 9  | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin uptake protein;<br><b>PDBTitle:</b> structure and mechanism of the s component of a bacterial ecf2 transporter   |
| 65 | <a href="#">c4xk2A_</a> | Alignment | not modelled | 8.5  | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aldo/keto reductase;<br><b>PDBTitle:</b> crystal structure of aldo-keto reductase from polaromonas sp. js666   |
| 66 | <a href="#">c4uw8F_</a> | Alignment | not modelled | 8.4  | 26 | <b>PDB header:</b> viral protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> l-shaped tail fiber protein;<br><b>PDBTitle:</b> structure of the carboxy-terminal domain of the bacteriophage t5 l-2 shaped tail fiber with its intra-molecular chaperone domain                         |
| 67 | <a href="#">c4lh9A_</a> | Alignment | not modelled | 8.2  | 31 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> heterocyst differentiation control protein;<br><b>PDBTitle:</b> crystal structure of the refolded hood domain (asp256-gly295) of hetr   |
| 68 | <a href="#">c5mkbF_</a> | Alignment | not modelled | 7.9  | 13 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> male1;<br><b>PDBTitle:</b> maltodextrin binding protein male1 from l. casei b123 without ligand   |
| 69 | <a href="#">c2zqkm_</a> | Alignment | not modelled | 7.8  | 42 | <b>PDB header:</b> ribosomal protein/rna<br><b>Chain:</b> M: <b>PDB Molecule:</b><br><b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map                  |
| 70 | <a href="#">c1cq0A_</a> | Alignment | not modelled | 7.6  | 26 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (new hypothalamic neuropeptide/orexin-b28);<br><b>PDBTitle:</b> solution structure of a human hypocretin-2/orexin-b 'solution structure2 of a human hypocretin-2/orexin-b '                     |
| 71 | <a href="#">d1qd1a2</a> | Alignment | not modelled | 7.4  | 19 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> Formiminotransferase domain of formiminotransferase-cyclodeaminase.<br><b>Family:</b> Formiminotransferase domain of formiminotransferase-cyclodeaminase.   |
| 72 | <a href="#">c2egtA_</a> | Alignment | not modelled | 7.2  | 14 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein aq_1549;<br><b>PDBTitle:</b> crystal structure of hypothetical protein (aq1549) from aquifex2 aeolicus   |
| 73 | <a href="#">c3vxbA_</a> | Alignment | not modelled | 7.1  | 15 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar-binding lipoprotein;<br><b>PDBTitle:</b> crystal structure of bxl from streptomyces thermoviolaceus opc-520  |
| 74 | <a href="#">d2ez9a1</a> | Alignment | not modelled | 6.9  | 5  | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain   |
| 75 | <a href="#">d1q8la_</a> | Alignment | not modelled | 6.8  | 8  | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> HMA, heavy metal-associated domain<br><b>Family:</b> HMA, heavy metal-associated domain   |
| 76 | <a href="#">c5o5jM_</a> | Alignment | not modelled | 6.8  | 39 | <b>PDB header:</b> ribosome<br><b>Chain:</b> M: <b>PDB Molecule:</b> 30s ribosomal protein s13;<br><b>PDBTitle:</b> structure of the 30s small ribosomal subunit from   |

|    |                         |           |              |     |    |   |
|----|-------------------------|-----------|--------------|-----|----|---|
|    |                         |           |              |     |    | mycobacterium2 smegmatis  |
| 77 | <a href="#">c2i6kA</a>  | Alignment | not modelled | 6.8 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> isopentenyl-diphosphate delta-isomerase 1;<br><b>PDBTitle:</b> crystal structure of human type i ipp isomerase complexed with a2 substrate analog   |
| 78 | <a href="#">c3c6cA</a>  | Alignment | not modelled | 6.7 | 10 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-keto-5-aminohexanoate cleavage enzyme;<br><b>PDBTitle:</b> crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution                             |
| 79 | <a href="#">c3no5C</a>  | Alignment | not modelled | 6.7 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution                             |
| 80 | <a href="#">c2otdC</a>  | Alignment | not modelled | 6.6 | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> glycerophosphodiester phosphodiesterase;<br><b>PDBTitle:</b> the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a  |
| 81 | <a href="#">c6dt0D</a>  | Alignment | not modelled | 6.6 | 18 | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> mitochondrial calcium uniporter;<br><b>PDBTitle:</b> cryo-em structure of a mitochondrial calcium uniporter   |
| 82 | <a href="#">d2gy9m1</a> | Alignment | not modelled | 6.6 | 43 | <b>Fold:</b> S13-like H2TH domain<br><b>Superfamily:</b> S13-like H2TH domain<br><b>Family:</b> Ribosomal protein S13   |
| 83 | <a href="#">c6nplA</a>  | Alignment | not modelled | 6.6 | 10 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 12 (sodium/potassium/chloride<br><b>PDBTitle:</b> cryo-em structure of nkcc1   |
| 84 | <a href="#">d1zaia1</a> | Alignment | not modelled | 6.5 | 22 | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Aldolase<br><b>Family:</b> Class I aldolase   |
| 85 | <a href="#">c4ox3A</a>  | Alignment | not modelled | 6.5 | 9  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxypeptidase yodj;<br><b>PDBTitle:</b> structure of the ldcb ld-carboxypeptidase reveals the molecular basis2 of peptidoglycan recognition   |
| 86 | <a href="#">c3e02A</a>  | Alignment | not modelled | 6.4 | 10 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein duf849;<br><b>PDBTitle:</b> crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution  |
| 87 | <a href="#">d1viaa</a>  | Alignment | not modelled | 6.4 | 13 | <b>Fold:</b> OsmC-like<br><b>Superfamily:</b> OsmC-like<br><b>Family:</b> YhfA-like   |
| 88 | <a href="#">c4qi6A</a>  | Alignment | not modelled | 6.4 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cellobiose dehydrogenase;<br><b>PDBTitle:</b> cellobiose dehydrogenase from myriococcus thermophilum, mtdh   |
| 89 | <a href="#">c6d80A</a>  | Alignment | not modelled | 6.4 | 15 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial calcium uniporter;<br><b>PDBTitle:</b> cryo-em structure of the mitochondrial calcium uniporter from n.2 fischeri bound to saposin  |
| 90 | <a href="#">c2y7eA</a>  | Alignment | not modelled | 6.3 | 23 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-keto-5-aminohexanoate cleavage enzyme;<br><b>PDBTitle:</b> crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)                                      |
| 91 | <a href="#">c5zmyF</a>  | Alignment | not modelled | 6.1 | 3  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> F: <b>PDB Molecule:</b> cis-epoxysuccinate hydrolase;<br><b>PDBTitle:</b> crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids   |
| 92 | <a href="#">d2onfa1</a> | Alignment | not modelled | 6.1 | 13 | <b>Fold:</b> OsmC-like<br><b>Superfamily:</b> OsmC-like<br><b>Family:</b> Ohr/OsmC resistance proteins  |
| 93 | <a href="#">c1x4pA</a>  | Alignment | not modelled | 6.1 | 25 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative splicing factor, arginine/serine-rich<br><b>PDBTitle:</b> solution structure of surp domain in sfrs14 protei   |
| 94 | <a href="#">d1fuia1</a> | Alignment | not modelled | 6.1 | 24 | <b>Fold:</b> Reductase/isomerase/elongation factor common domain<br><b>Superfamily:</b> Fucl/AraA C-terminal domain-like<br><b>Family:</b> L-fucose isomerase, C-terminal domain  |
| 95 | <a href="#">c3lotC</a>  | Alignment | not modelled | 6.1 | 13 | <b>PDB header:</b> structure genomics, unknown function<br><b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution  |
| 96 | <a href="#">c5x5yF</a>  | Alignment | not modelled | 6.0 | 12 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> a membrane protein complex  |
| 97 | <a href="#">c5xyiS</a>  | Alignment | not modelled | 5.9 | 43 | <b>PDB header:</b> ribosome<br><b>Chain:</b> S: <b>PDB Molecule:</b> ribosomal protein s13p/s18e, putative;<br><b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome   |
| 98 | <a href="#">c3i10A</a>  | Alignment | not modelled | 5.7 | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative glycerophosphoryl diester phosphodiesterase;<br><b>PDBTitle:</b> crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (np_812074.1) from bacteroides thetaiotaomicron3 vpi-5482 at 1.35 a resolution |
| 99 | <a href="#">c2j6yB</a>  | Alignment | not modelled | 5.7 | 4  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphoserine phosphatase rsbu;<br><b>PDBTitle:</b> structural and functional characterisation of partner switching2 regulating the environmental stress response in bacillus subtilis  |