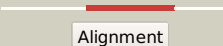
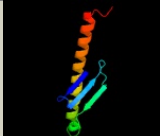


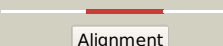

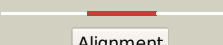

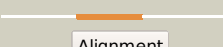

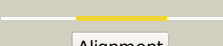



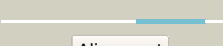






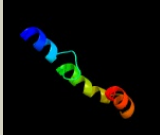


# Phyre2

|                  |                                   |
|------------------|-----------------------------------|
| Email            | mdejesus@rockefeller.edu          |
| Description      | RVBD3614c (-<br>)_4054321_4054875 |
| Date             | Fri Aug 9 18:20:30 BST<br>2019    |
| Unique Job<br>ID | 1bb420e28d9a018b                  |

Detailed template  
information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|--|---|------------|--------|---|
| 1  | <a href="#">d1puga_</a> | <br>Alignment   |    | 97.5       | 13     | <b>Fold:</b> YbaB-like<br><b>Superfamily:</b> YbaB-like<br><b>Family:</b> YbaB-like   |
| 2  | <a href="#">d1j8ba_</a> | <br>Alignment   |    | 96.7       | 11     | <b>Fold:</b> YbaB-like<br><b>Superfamily:</b> YbaB-like<br><b>Family:</b> YbaB-like   |
| 3  | <a href="#">c1ybxA_</a> | <br>Alignment   |    | 96.4       | 20     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein;<br><b>PDBTitle:</b> conserved hypothetical protein cth-383 from clostridium thermocellum  |
| 4  | <a href="#">d1pugb_</a> | <br>Alignment   |   | 93.2       | 14     | <b>Fold:</b> YbaB-like<br><b>Superfamily:</b> YbaB-like<br><b>Family:</b> YbaB-like   |
| 5  | <a href="#">c5yrxA_</a> | <br>Alignment |  | 86.5       | 13     | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nucleoid-associated protein rv3716c;<br><b>PDBTitle:</b> crystal structure of a hypothetical protein rv3716c from mycobacterium2 tuberculosis   |
| 6  | <a href="#">c3f42A_</a> | <br>Alignment |  | 72.2       | 10     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein hp0035;<br><b>PDBTitle:</b> crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori   |
| 7  | <a href="#">c6bbqA_</a> | <br>Alignment |  | 48.5       | 26     | <b>PDB header:</b> lipid binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytohesin-3,adp-ribosylation factor 6;<br><b>PDBTitle:</b> model for extended volume of truncated monomeric cytohesin-3 (grp1;2 amino acids 63-399) e161a arf6 q67l fusion protein  |
| 8  | <a href="#">c4oivA_</a> | <br>Alignment |  | 39.0       | 19     | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein transport protein sec7;<br><b>PDBTitle:</b> crystal structure of sec7p catalytic domain   |
| 9  | <a href="#">c3l8nA_</a> | <br>Alignment |  | 36.0       | 30     | <b>PDB header:</b> nucleotide-binding protein, metal-bindin<br><b>Chain:</b> A: <b>PDB Molecule:</b> brefeldin a-inhibited guanine nucleotide-exchange<br><b>PDBTitle:</b> crystal structure of a domain of brefeldin a-inhibited2 guanine nucleotide-exchange protein 2 (brefeldina-inhibited3 gep 2) from homo sapiens (human). northeast structural4 genomics consortium target id hr5562a |
| 10 | <a href="#">d2ivda2</a> | <br>Alignment |  | 35.9       | 19     | <b>Fold:</b> FAD-linked reductases, C-terminal domain<br><b>Superfamily:</b> FAD-linked reductases, C-terminal domain<br><b>Family:</b> L-aminoacid/polyamine oxidase   |
| 11 | <a href="#">d1aepa_</a> | <br>Alignment |  | 33.2       | 32     | <b>Fold:</b> Apolipoporphin-III<br><b>Superfamily:</b> Apolipoporphin-III<br><b>Family:</b> Apolipoporphin-III  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | <a href="#">d1re0b_</a> | Alignment |              | 33.0 | 23 | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> Sec7 domain<br><b>Family:</b> Sec7 domain   |
| 13 | <a href="#">d1seza2</a> | Alignment |              | 31.2 | 18 | <b>Fold:</b> FAD-linked reductases, C-terminal domain<br><b>Superfamily:</b> FAD-linked reductases, C-terminal domain<br><b>Family:</b> L-aminoacid/polyamine oxidase  |
| 14 | <a href="#">d1pbva_</a> | Alignment |              | 30.5 | 22 | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> Sec7 domain<br><b>Family:</b> Sec7 domain   |
| 15 | <a href="#">c4e6za_</a> | Alignment |              | 26.5 | 15 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> apicoplast tic22, putative;<br><b>PDBTitle:</b> tic22 from plasmodium falciparum   |
| 16 | <a href="#">c3rhiB_</a> | Alignment |              | 26.5 | 10 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein hu;<br><b>PDBTitle:</b> dna-binding protein hu from bacillus anthracis   |
| 17 | <a href="#">d1xsza1</a> | Alignment |              | 25.1 | 20 | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> Sec7 domain<br><b>Family:</b> Sec7 domain   |
| 18 | <a href="#">d2r09a1</a> | Alignment |              | 25.0 | 24 | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> Sec7 domain<br><b>Family:</b> Sec7 domain   |
| 19 | <a href="#">d1ku1a_</a> | Alignment |              | 23.8 | 11 | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> Sec7 domain<br><b>Family:</b> Sec7 domain   |
| 20 | <a href="#">c4c0aA_</a> | Alignment |              | 23.5 | 15 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> iq motif and sec7 domain-containing protein 1;<br><b>PDBTitle:</b> arf1(delta1-17)in complex with brag2 sec7-ph domain   |
| 21 | <a href="#">c3dinB_</a> | Alignment | not modelled | 22.5 | 30 | <b>PDB header:</b> membrane protein, protein transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein translocase subunit seca;<br><b>PDBTitle:</b> crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase |
| 22 | <a href="#">d1bc9a_</a> | Alignment | not modelled | 22.0 | 24 | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> Sec7 domain<br><b>Family:</b> Sec7 domain   |
| 23 | <a href="#">c3juxA_</a> | Alignment | not modelled | 22.0 | 30 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein translocase subunit seca;<br><b>PDBTitle:</b> structure of the translocation atpase seca from thermotoga2 maritima   |
| 24 | <a href="#">c1ls4A_</a> | Alignment | not modelled | 22.0 | 30 | <b>PDB header:</b> lipid transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein-iii;<br><b>PDBTitle:</b> nmr structure of apolipoprotein-iii from locusta migratoria  |
| 25 | <a href="#">c1xsza_</a> | Alignment | not modelled | 21.9 | 20 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> guanine nucleotide exchange protein;<br><b>PDBTitle:</b> the structure of ralp   |
| 26 | <a href="#">d1sf9a_</a> | Alignment | not modelled | 20.4 | 30 | <b>Fold:</b> SH3-like barrel<br><b>Superfamily:</b> Hypothetical protein YfhH<br><b>Family:</b> Hypothetical protein YfhH  |
| 27 | <a href="#">d1hn0a3</a> | Alignment | not modelled | 20.1 | 13 | <b>Fold:</b> Hyaluronate lyase-like, C-terminal domain<br><b>Superfamily:</b> Hyaluronate lyase-like, C-terminal domain<br><b>Family:</b> Hyaluronate lyase-like, C-terminal domain  |
| 28 | <a href="#">c4u3qA_</a> | Alignment | not modelled | 18.9 | 38 | <b>PDB header:</b> lipid binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 17 kda lipoprotein;<br><b>PDBTitle:</b> crystal structure of recombinant tp0435 from treponema pallidum  |
| 29 | <a href="#">c2r09a</a>  | Alignment | not modelled | 18.7 | 24 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytohesin-3;   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | <a href="#">c2lv9A_</a> | Alignment | not modelled | 18.7 | 24 | <b>PDBTitle:</b> crystal structure of autoinhibited form of grp1 arf gtpase exchange2 factor<br><b>PDB header:</b> isomerase   |
| 30 | <a href="#">c3no0B_</a> | Alignment | not modelled | 18.7 | 33 | <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit a;<br><b>PDBTitle:</b> aquifex aeolicus type iia topoisomerase c-terminal domain  |
| 31 | <a href="#">c1mpgB_</a> | Alignment | not modelled | 18.4 | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyladenine dna glycosylase ii;<br><b>PDBTitle:</b> 3-methyladenine dna glycosylase ii from escherichia coli   |
| 32 | <a href="#">c3bs6B_</a> | Alignment | not modelled | 17.6 | 18 | <b>PDB header:</b> membrane protein, protein transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> inner membrane protein oxaa;<br><b>PDBTitle:</b> 1.8 angstrom crystal structure of the periplasmic domain of2 the membrane insertase yidc                                  |
| 33 | <a href="#">d1r8se_</a> | Alignment | not modelled | 17.4 | 22 | <b>Fold:</b> alpha-alpha superhelix<br><b>Superfamily:</b> Sec7 domain<br><b>Family:</b> Sec7 domain   |
| 34 | <a href="#">c3blcB_</a> | Alignment | not modelled | 17.3 | 18 | <b>PDB header:</b> chaperone,protein transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> inner membrane protein oxaa;<br><b>PDBTitle:</b> crystal structure of the periplasmic domain of the escherichia coli2 yidc   |
| 35 | <a href="#">d2a9da1</a> | Alignment | not modelled | 16.8 | 33 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Molybdenum-containing oxidoreductases-like dimerisation domain   |
| 36 | <a href="#">c4ph8B_</a> | Alignment | not modelled | 14.3 | 39 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> B: <b>PDB Molecule:</b> aggregative adherence fimbrial subunit agga;<br><b>PDBTitle:</b> crystal structure of agga, the major subunit of aggregative adherence2 fimbriae type i (aaf/i) from the escherichia coli o4h104 |
| 37 | <a href="#">c3dl8B_</a> | Alignment | not modelled | 14.2 | 26 | <b>PDB header:</b> protein transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein translocase subunit seca;<br><b>PDBTitle:</b> structure of the complex of aquifex aeolicus secyeg and bacillus2 subtilis seca  |
| 38 | <a href="#">d1ogpa1</a> | Alignment | not modelled | 13.7 | 38 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Molybdenum-containing oxidoreductases-like dimerisation domain   |
| 39 | <a href="#">d1ofcx1</a> | Alignment | not modelled | 13.3 | 33 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> Myb/SANT domain  |
| 40 | <a href="#">c5n76C_</a> | Alignment | not modelled | 13.3 | 32 | <b>PDB header:</b> nickel-binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> coot;<br><b>PDBTitle:</b> crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum  |
| 41 | <a href="#">c6n2lA_</a> | Alignment | not modelled | 13.1 | 7  | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> histone family protein dna-binding protein;<br><b>PDBTitle:</b> crystal structure of a histone family protein dna-binding protein from2 burkholderia ambifaria                             |
| 42 | <a href="#">c1tf2A_</a> | Alignment | not modelled | 12.5 | 26 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> preprotein translocase seca subunit;<br><b>PDBTitle:</b> crystal structure of seca:adp in an open conformation from2 bacillus subtilis   |
| 43 | <a href="#">c5hqhA_</a> | Alignment | not modelled | 12.3 | 19 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> lmo2119 protein;<br><b>PDBTitle:</b> 1.32 angstrom crystal structure of ybbr like domain of lmo2119 protein2 from listeria monocytogenes.   |
| 44 | <a href="#">c5fmfV_</a> | Alignment | not modelled | 11.9 | 3  | <b>PDB header:</b> transcription<br><b>Chain:</b> V: <b>PDB Molecule:</b> transcription initiation factor iif subunit beta, tfg2;<br><b>PDBTitle:</b> the p-lobe of rna polymerase ii pre-initiation complex   |
| 45 | <a href="#">c2mvnA_</a> | Alignment | not modelled | 11.8 | 53 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1-delta;<br><b>PDBTitle:</b> solution structure of eef1bdelta car domain in tctp-bound state   |
| 46 | <a href="#">c2mvmA_</a> | Alignment | not modelled | 11.8 | 53 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1-delta;<br><b>PDBTitle:</b> solution structure of eef1bdelta car domain   |
| 47 | <a href="#">c2vdaA_</a> | Alignment | not modelled | 11.6 | 33 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> translocase subunit seca;<br><b>PDBTitle:</b> solution structure of the seca-signal peptide complex  |
| 48 | <a href="#">d1huua_</a> | Alignment | not modelled | 11.1 | 17 | <b>Fold:</b> IHF-like DNA-binding proteins<br><b>Superfamily:</b> IHF-like DNA-binding proteins<br><b>Family:</b> Prokaryotic DNA-bending protein  |
| 49 | <a href="#">c1junB_</a> | Alignment | not modelled | 11.1 | 26 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> B: <b>PDB Molecule:</b> c-jun homodimer;<br><b>PDBTitle:</b> nmr study of c-jun homodimer   |
| 50 | <a href="#">c3bovA_</a> | Alignment | not modelled | 11.0 | 35 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death 1 ligand 2;<br><b>PDBTitle:</b> crystal structure of the receptor binding domain of mouse pd-l2  |
| 51 | <a href="#">d1b33n_</a> | Alignment | not modelled | 10.8 | 46 | <b>Fold:</b> Allophycocyanin linker chain (domain)<br><b>Superfamily:</b> Allophycocyanin linker chain (domain)<br><b>Family:</b> Allophycocyanin linker chain (domain)  |
| 52 | <a href="#">c2auhB_</a> | Alignment | not modelled | 10.3 | 27 | <b>PDB header:</b> transferase/signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> growth factor receptor-bound protein 14;<br><b>PDBTitle:</b> crystal structure of the grb14 bps region in complex with2 the insulin receptor tyrosine kinase                     |
| 53 | <a href="#">d3bzka3</a> | Alignment | not modelled | 10.3 | 14 | <b>Fold:</b> Tex N-terminal region-like<br><b>Superfamily:</b> Tex N-terminal region-like<br><b>Family:</b> Tex N-terminal region-like   |
| 54 | <a href="#">c5mq9A_</a> | Alignment | not modelled | 10.3 | 15 | <b>PDB header:</b> translation<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yacp;<br><b>PDBTitle:</b> crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)   |
|    |                         |           |              |      |    | <b>PDB header:</b> transport protein   |

|    |                          |           |              |      |    |  |
|----|--------------------------|-----------|--------------|------|----|--|
| 55 | <a href="#">c2ipcB_</a>  | Alignment | not modelled | 10.2 | 46 | <b>Chain:</b> B: <b>PDB Molecule:</b> preprotein translocase seca subunit;<br><b>PDBTitle:</b> crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer  |
| 56 | <a href="#">d2ifta1</a>  | Alignment | not modelled | 9.9  | 19 | <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases<br><b>Family:</b> YhhF-like  |
| 57 | <a href="#">d1cz5a2</a>  | Alignment | not modelled | 9.6  | 21 | <b>Fold:</b> Cdc48 domain 2-like<br><b>Superfamily:</b> Cdc48 domain 2-like<br><b>Family:</b> Cdc48 domain 2-like  |
| 58 | <a href="#">d1owfa_</a>  | Alignment | not modelled | 9.5  | 7  | <b>Fold:</b> IHF-like DNA-binding proteins<br><b>Superfamily:</b> IHF-like DNA-binding proteins<br><b>Family:</b> Prokaryotic DNA-binding protein  |
| 59 | <a href="#">c4bpyA_</a>  | Alignment | not modelled | 9.4  | 12 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> sco protein;<br><b>PDBTitle:</b> crystal structure of the c90a mutant of the sco copper chaperone2 protein from streptomyces lividans  |
| 60 | <a href="#">c1nl3B_</a>  | Alignment | not modelled | 9.3  | 27 | <b>PDB header:</b> protein transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> preprotein translocase seca 1 subunit;<br><b>PDBTitle:</b> crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form   |
| 61 | <a href="#">d1py9a_</a>  | Alignment | not modelled | 9.2  | 21 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Immunoglobulin<br><b>Family:</b> V set domains (antibody variable domain-like)   |
| 62 | <a href="#">c5ekaA_</a>  | Alignment | not modelled | 9.0  | 7  | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein hu;<br><b>PDBTitle:</b> hu dna-binding protein from thermus thermophilus   |
| 63 | <a href="#">c3c4iA_</a>  | Alignment | not modelled | 8.3  | 15 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein hu homolog;<br><b>PDBTitle:</b> crystal structure analysis of n terminal region containing the2 dimerization domain and dna binding domain of hu protein(histone like3 protein-dna binding) from mycobacterium tuberculosis [h37rv]                |
| 64 | <a href="#">c1ygaA_</a>  | Alignment | not modelled | 8.3  | 3  | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 37.9 kda protein in bio3-hxt17<br><b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae yn9a protein,2 new york structural genomics consortium   |
| 65 | <a href="#">c4ev1A_</a>  | Alignment | not modelled | 8.2  | 21 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> anabena tic22;<br><b>PDBTitle:</b> anabaena tic22 (protein transport)  |
| 66 | <a href="#">d1nsza_</a>  | Alignment | not modelled | 8.2  | 27 | <b>Fold:</b> Supersandwich<br><b>Superfamily:</b> Galactose mutarotase-like<br><b>Family:</b> Aldose 1-epimerase (mutarotase)  |
| 67 | <a href="#">c2yxyA_</a>  | Alignment | not modelled | 8.0  | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical conserved protein, gk0453;<br><b>PDBTitle:</b> crystal structure of hypothetical conserved protein, gk0453  |
| 68 | <a href="#">d1exea_</a>  | Alignment | not modelled | 7.9  | 15 | <b>Fold:</b> IHF-like DNA-binding proteins<br><b>Superfamily:</b> IHF-like DNA-binding proteins<br><b>Family:</b> Prokaryotic DNA-binding protein  |
| 69 | <a href="#">c5bncB_</a>  | Alignment | not modelled | 7.8  | 25 | <b>PDB header:</b> heme binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> heme binding protein msmeG_6519;<br><b>PDBTitle:</b> structure of heme binding protein msmeG_6519 from mycobacterium2 smegmatis   |
| 70 | <a href="#">d1h0ha1</a>  | Alignment | not modelled | 7.8  | 8  | <b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain  |
| 71 | <a href="#">d1ndba2</a>  | Alignment | not modelled | 7.8  | 18 | <b>Fold:</b> CoA-dependent acyltransferases<br><b>Superfamily:</b> CoA-dependent acyltransferases<br><b>Family:</b> Choline/Carnitine O-acyltransferase  |
| 72 | <a href="#">c3ogiC_</a>  | Alignment | not modelled | 7.6  | 33 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative esat-6-like protein 6;<br><b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esxp2 complex (rv2346c-rv2347c)  |
| 73 | <a href="#">c1s5rA_</a>  | Alignment | not modelled | 7.5  | 36 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> high mobility group box transcription factor 1;<br><b>PDBTitle:</b> solution structure of hbp1 sid-msin3a pah2 complex   |
| 74 | <a href="#">c4gZR_A_</a> | Alignment | not modelled | 7.5  | 33 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> esat-6-like protein 6;<br><b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esxp2 (rv2346c-rv2347c) complex in space group c2221  |
| 75 | <a href="#">c4uaqA_</a>  | Alignment | not modelled | 7.5  | 33 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein translocase subunit seca 2;<br><b>PDBTitle:</b> crystal structure of the accessory translocation atpase, seca2, from2 mycobacterium tuberculosis   |
| 76 | <a href="#">d1jmta_</a>  | Alignment | not modelled | 7.5  | 38 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> RNA-binding domain, RBD<br><b>Family:</b> Splicing factor U2AF subunits  |
| 77 | <a href="#">d1jmx1</a>   | Alignment | not modelled | 7.4  | 18 | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2  |
| 78 | <a href="#">c2lf6A_</a>  | Alignment | not modelled | 7.4  | 24 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> effector protein hopab1;<br><b>PDBTitle:</b> solution nmr structure of hopabpph1448_220_320 from pseudomonas2 syringae pv. phaseolicola str. 1448a, midwest center for structural3 genomics target apc40132.4 and northeast structural genomics4 consortium target pst3a |
| 79 | <a href="#">c3v8vB_</a>  | Alignment | not modelled | 7.3  | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase I;<br><b>PDBTitle:</b> crystal structure of bifunctional methyltransferase ycbY (rlmIk) from2 escherichia coli, sam binding  |
| 80 | <a href="#">c4niuB_</a>  | Alignment | not modelled | 7.1  | 22 | <b>PDB header:</b> dna binding protein/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein hu;  |

|    |                         |           |              |     |    |   |
|----|-------------------------|-----------|--------------|-----|----|---|
| 80 | <a href="#">c4qj0B</a>  | Alignment | not modelled | 7.1 | 42 | <b>PDBTitle:</b> crystal structure of dna-bound nucleoid associated protein, sav1473<br><b>PDB header:</b> structural genomics, unknown function  |
| 81 | <a href="#">c3na2C</a>  | Alignment | not modelled | 7.0 | 38 | <b>Chain:</b> C; <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of protein of unknown function from mine drainage2 metagenome leptospirillum rubarum   |
| 82 | <a href="#">c6raoH</a>  | Alignment | not modelled | 7.0 | 38 | <b>PDB header:</b> virus like particle<br><b>Chain:</b> H; <b>PDB Molecule:</b> afp9;<br><b>PDBTitle:</b> cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised   |
| 83 | <a href="#">d1b8za</a>  | Alignment | not modelled | 6.6 | 8  | <b>Fold:</b> IHF-like DNA-binding proteins<br><b>Superfamily:</b> IHF-like DNA-binding proteins<br><b>Family:</b> Prokaryotic DNA-bending protein   |
| 84 | <a href="#">c4il7A</a>  | Alignment | not modelled | 6.4 | 21 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a223 c-terminal domain, a structural protein from2 sulfolobus turreted icosahedral virus (stiv)                              |
| 85 | <a href="#">d1ntca</a>  | Alignment | not modelled | 6.4 | 50 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> FIS-like  |
| 86 | <a href="#">d1pkoa</a>  | Alignment | not modelled | 6.2 | 21 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Immunoglobulin<br><b>Family:</b> V set domains (antibody variable domain-like)  |
| 87 | <a href="#">d1kqfa1</a> | Alignment | not modelled | 6.1 | 12 | <b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain   |
| 88 | <a href="#">c4rs7R</a>  | Alignment | not modelled | 6.1 | 18 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> R; <b>PDB Molecule:</b> parb-c;<br><b>PDBTitle:</b> structure of pnob8 parb-c   |
| 89 | <a href="#">c3b1sB</a>  | Alignment | not modelled | 6.1 | 24 | <b>PDB header:</b> protein transport<br><b>Chain:</b> B; <b>PDB Molecule:</b> flagellar biosynthetic protein flhb;<br><b>PDBTitle:</b> crystal structure of the cytoplasmic domain of flhb from aquifex2 aeolicus   |
| 90 | <a href="#">d1we6a</a>  | Alignment | not modelled | 6.0 | 26 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> Ubiquitin-like<br><b>Family:</b> Ubiquitin-related  |
| 91 | <a href="#">c5lvtC</a>  | Alignment | not modelled | 6.0 | 15 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> C; <b>PDB Molecule:</b> dna-binding protein hu;<br><b>PDBTitle:</b> structure of hu protein from lactococcus lactis   |
| 92 | <a href="#">c3bvsA</a>  | Alignment | not modelled | 5.9 | 8  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A; <b>PDB Molecule:</b> alkylpurine dna glycosylase alkd;<br><b>PDBTitle:</b> crystal structure of bacillus cereus alkylpurine dna glycosylase alkd   |
| 93 | <a href="#">c2vt1B</a>  | Alignment | not modelled | 5.9 | 14 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> surface presentation of antigens protein spa5;<br><b>PDBTitle:</b> crystal structure of the cytoplasmic domain of spa40, the specificity2 switch for the shigella flexneri type iii secretion system |
| 94 | <a href="#">c3k2kA</a>  | Alignment | not modelled | 5.7 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A; <b>PDB Molecule:</b> putative carboxypeptidase;<br><b>PDBTitle:</b> crystal structure of putative carboxypeptidase (yp_103406.1) from2 burkholderia mallei atcc 23344 at 2.49 a resolution                                       |
| 95 | <a href="#">c4b24A</a>  | Alignment | not modelled | 5.6 | 17 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A; <b>PDB Molecule:</b> probable dna-3-methyladenine glycosylase 2;<br><b>PDBTitle:</b> unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2   |
| 96 | <a href="#">c2n51A</a>  | Alignment | not modelled | 5.6 | 53 | <b>PDB header:</b> translation<br><b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor 1-delta;<br><b>PDBTitle:</b> nmr structure of the c-terminal region of human eukaryotic elongation2 factor 1b   |
| 97 | <a href="#">d1pbya1</a> | Alignment | not modelled | 5.4 | 21 | <b>Fold:</b> Cytochrome c<br><b>Superfamily:</b> Cytochrome c<br><b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2   |
| 98 | <a href="#">c2n51A</a>  | Alignment | not modelled | 5.3 | 46 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A; <b>PDB Molecule:</b> ribonuclease zc3h12a;<br><b>PDBTitle:</b> regnase-1 c-terminal domain   |
| 99 | <a href="#">c2f1mA</a>  | Alignment | not modelled | 5.3 | 17 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> acriflavine resistance protein a;<br><b>PDBTitle:</b> conformational flexibility in the multidrug efflux system protein acra  |