



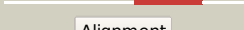




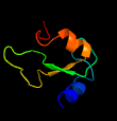






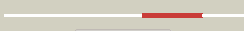
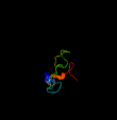

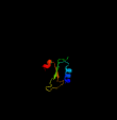


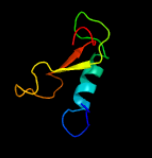

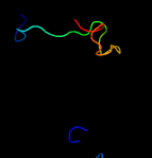

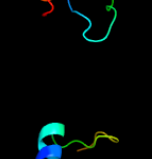

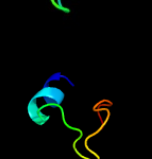

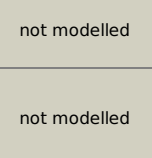


# Phyre2

|               |                                   |
|---------------|-----------------------------------|
| Email         | mdejesus@rockefeller.edu          |
| Description   | RVBD2469c (-)<br>_2772377_2773045 |
| Date          | Wed Aug 7 12:50:09 BST<br>2019    |
| Unique Job ID | 8a6b39f778ce4821                  |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c5vgbA_</a> | <br>Alignment   |    | 99.6       | 27     | <b>PDB header:</b> hydrolase/hydrolase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cas9;<br><b>PDBTitle:</b> crystal structure of nmecas9 hnh domain bound to anti-crispr acric1                       |
| 2  | <a href="#">c2qgpA_</a> | <br>Alignment   |    | 99.6       | 36     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease;<br><b>PDBTitle:</b> x-ray structure of the hnh endonuclease from geobacter2 metallireducens. northeast structural genomics consortium target3 gmr87. |
| 3  | <a href="#">c5mkwA_</a> | <br>Alignment   |    | 99.5       | 28     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna annealing helicase and endonuclease zranb3;<br><b>PDBTitle:</b> crystal structure of the human zranb3 hnh domain   |
| 4  | <a href="#">c5axwA_</a> | <br>Alignment   |    | 99.2       | 28     | <b>PDB header:</b> hydrolase/rna/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cas9;<br><b>PDBTitle:</b> crystal structure of staphylococcus aureus cas9 in complex with sgrna2 and target dna (ttgggt pam)    |
| 5  | <a href="#">c4ogeA_</a> | <br>Alignment |  | 99.1       | 29     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease domain protein;<br><b>PDBTitle:</b> crystal structure of the type ii-c cas9 enzyme from actinomyces2 naeslundii                                       |
| 6  | <a href="#">c6ghcA_</a> | <br>Alignment |  | 99.0       | 40     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 5-methylcytosine-specific restriction enzyme a;<br><b>PDBTitle:</b> modification dependent ecomcra restriction endonuclease  |
| 7  | <a href="#">c5h0mA_</a> | <br>Alignment |  | 99.0       | 27     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease;<br><b>PDBTitle:</b> crystal structure of deep-sea thermophilic bacteriophage gve2 hnh2 endonuclease with zinc ion                                    |
| 8  | <a href="#">c5x1hS_</a> | <br>Alignment |  | 98.7       | 21     | <b>PDB header:</b> protein transport<br><b>Chain:</b> S: <b>PDB Molecule:</b> icmj (dotn);<br><b>PDBTitle:</b> structure of legionella pneumophila dotn  |
| 9  | <a href="#">c4cmqB_</a> | <br>Alignment |  | 98.3       | 29     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> crispr-associated endonuclease cas9/csn1;<br><b>PDBTitle:</b> crystal structure of mn-bound s.pyogenes cas9  |
| 10 | <a href="#">c5zmmD_</a> | <br>Alignment |  | 97.9       | 35     | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein mcra;<br><b>PDBTitle:</b> structure of the type iv phosphorothioation-dependent restriction2 endonuclease scomcra                    |
| 11 | <a href="#">c5g2xC_</a> | <br>Alignment |  | 90.9       | 21     | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> group ii intron-encoded protein ltra;<br><b>PDBTitle:</b> structure a of group ii intron complexed with its reverse2 transcriptase                                   |

|    |                         |           |   |      |    |   |
|----|-------------------------|-----------|---|------|----|---|
| 12 | <a href="#">c6ghsA_</a> | Alignment |     | 88.4 | 23 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tagi restriction endonuclease;<br><b>PDBTitle:</b> modification dependent tagi restriction endonuclease   |
| 13 | <a href="#">c3m7kA_</a> | Alignment |    | 78.9 | 29 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> restriction endonuclease paci;<br><b>PDBTitle:</b> crystal structure of paci-dna enzyme product complex   |
| 14 | <a href="#">d2gykb1</a> | Alignment |    | 65.3 | 29 | <b>Fold:</b> His-Me finger endonucleases<br><b>Superfamily:</b> His-Me finger endonucleases<br><b>Family:</b> HNH-motif   |
| 15 | <a href="#">d1ouoa_</a> | Alignment |    | 51.3 | 22 | <b>Fold:</b> His-Me finger endonucleases<br><b>Superfamily:</b> His-Me finger endonucleases<br><b>Family:</b> Endonuclease I  |
| 16 | <a href="#">c5b2oA_</a> | Alignment |    | 46.3 | 33 | <b>PDB header:</b> hydrolase/rna/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated endonuclease cas9;<br><b>PDBTitle:</b> crystal structure of francisella novicida cas9 in complex with sgrna2 and target dna (tgg pam)   |
| 17 | <a href="#">d1e7la2</a> | Alignment |   | 44.8 | 21 | <b>Fold:</b> His-Me finger endonucleases<br><b>Superfamily:</b> His-Me finger endonucleases<br><b>Family:</b> Recombination endonuclease VII, N-terminal domain   |
| 18 | <a href="#">c1xrzA_</a> | Alignment |  | 33.5 | 42 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger y-chromosomal protein;<br><b>PDBTitle:</b> nmr structure of a zinc finger with cyclohexylalanine2 substituted for the central aromatic residue  |
| 19 | <a href="#">c2qnfB_</a> | Alignment |  | 33.2 | 21 | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> B: <b>PDB Molecule:</b> recombination endonuclease vii;<br><b>PDBTitle:</b> crystal structure of t4 endonuclease vii h43n mutant in2 complex with heteroduplex dna containing base mismatches   |
| 20 | <a href="#">c7znfA_</a> | Alignment |  | 27.5 | 50 | <b>PDB header:</b> zinc finger dna binding domain<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger;<br><b>PDBTitle:</b> alternating zinc fingers in the human male associated2 protein zfy: 2d nmr structure of an even finger and3 implications for "jumping-linker" dna recognition |
| 21 | <a href="#">d7znfa_</a> | Alignment | not modelled  | 27.5 | 50 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2   |
| 22 | <a href="#">c5znfA_</a> | Alignment | not modelled  | 26.0 | 50 | <b>PDB header:</b> zinc finger dna binding domain<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger;<br><b>PDBTitle:</b> alternating zinc fingers in the human male associated2 protein zfy: 2d nmr structure of an even finger and3 implications for "jumping-linker" dna recognition |
| 23 | <a href="#">c1klsA_</a> | Alignment | not modelled  | 25.7 | 50 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger y-chromosomal protein;<br><b>PDBTitle:</b> nmr structure of the zfy-6t[y10l] zinc finger  |
| 24 | <a href="#">c1klrA_</a> | Alignment | not modelled  | 25.2 | 50 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger y-chromosomal protein;<br><b>PDBTitle:</b> nmr structure of the zfy-6t[y10f] zinc finger  |
| 25 | <a href="#">d1klra_</a> | Alignment | not modelled  | 25.2 | 50 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2   |
| 26 | <a href="#">c1pg5B_</a> | Alignment | not modelled  | 24.2 | 33 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aspartate carbamoyltransferase regulatory chain;<br><b>PDBTitle:</b> crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfobus3 acidocaldarius  |
| 27 | <a href="#">c4qkoH_</a> | Alignment | not modelled  | 23.4 | 22 | <b>PDB header:</b> antimicrobial protein<br><b>Chain:</b> H: <b>PDB Molecule:</b> pyocin-s2;<br><b>PDBTitle:</b> the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms   |
|    |                         |           |   |      |    | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aspartate carbamoyltransferase  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 28 | <a href="#">c2h3eB_</a> | Alignment | not modelled | 22.8 | 38 | regulatory chain;<br><b>PDBTitle:</b> structure of wild-type e. coli aspartate transcarbamoylase in the2 presence of n-phosphonacetyl-l-isoadparagine at 2.3a resolution   |
| 29 | <a href="#">c6o6dA_</a> | Alignment | not modelled | 21.1 | 22 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-3;<br><b>PDBTitle:</b> n-terminal domain of translation initiation factor if-3 from2 helicobacter pylori   |
| 30 | <a href="#">c3jyw9_</a> | Alignment | not modelled | 21.1 | 25 | <b>PDB header:</b> ribosome<br><b>Chain:</b> 9: <b>PDB Molecule:</b> 60s ribosomal protein l43;<br><b>PDBTitle:</b> structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution                           |
| 31 | <a href="#">c4uhpA_</a> | Alignment | not modelled | 20.5 | 30 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> large component of pyocin ap41;<br><b>PDBTitle:</b> crystal structure of the pyocin ap41 dnase-immunity complex  |
| 32 | <a href="#">c2be7E_</a> | Alignment | not modelled | 20.0 | 33 | <b>PDB header:</b> transferase<br><b>Chain:</b> E: <b>PDB Molecule:</b> aspartate carbamoyltransferase regulatory chain;<br><b>PDBTitle:</b> crystal structure of the unliganded (t-state) aspartate2 transcarbamoylase of the psychrophilic bacterium moritella profunda        |
| 33 | <a href="#">c5ew5C_</a> | Alignment | not modelled | 19.5 | 30 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> colicin-e9;<br><b>PDBTitle:</b> crystal structure of colicin e9 in complex with its immunity protein2 im9  |
| 34 | <a href="#">c4qiwP_</a> | Alignment | not modelled | 19.1 | 50 | <b>PDB header:</b> transcription<br><b>Chain:</b> P: <b>PDB Molecule:</b> dna-directed rna polymerase subunit p;<br><b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis  |
| 35 | <a href="#">c2ywwA_</a> | Alignment | not modelled | 19.1 | 38 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartate carbamoyltransferase regulatory chain;<br><b>PDBTitle:</b> crystal structure of aspartate carbamoyltransferase2 regulatory chain from methanocaldococcus jannaschii                  |
| 36 | <a href="#">c5vf4A_</a> | Alignment | not modelled | 18.9 | 19 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> thermus aquaticus variable protein (taqvp) from diversity-generating2 retroelements (dgr)  |
| 37 | <a href="#">c3cc4Z_</a> | Alignment | not modelled | 17.8 | 18 | <b>PDB header:</b> ribosome<br><b>Chain:</b> Z: <b>PDB Molecule:</b> 50s ribosomal protein l37ae;<br><b>PDBTitle:</b> co-crystal structure of anisomycin bound to the 50s ribosomal subunit  |
| 38 | <a href="#">c2zkrz_</a> | Alignment | not modelled | 17.5 | 17 | <b>PDB header:</b> ribosomal protein/rna<br><b>Chain:</b> Z: <b>PDB Molecule:</b> e site t-rna;<br><b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 39 | <a href="#">c3j21i_</a> | Alignment | not modelled | 17.3 | 29 | <b>PDB header:</b> ribosome<br><b>Chain:</b> l: <b>PDB Molecule:</b> 50s ribosomal protein l13p;<br><b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)   |
| 40 | <a href="#">c1yshD_</a> | Alignment | not modelled | 17.2 | 21 | <b>PDB header:</b> structural protein/rna<br><b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein l37a;<br><b>PDBTitle:</b> localization and dynamic behavior of ribosomal protein l30e   |
| 41 | <a href="#">c4ndlC_</a> | Alignment | not modelled | 16.8 | 50 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> enh-c2b, computational designed homodimer;<br><b>PDBTitle:</b> computational design and experimental verification of a symmetric2 homodimer  |
| 42 | <a href="#">d1ffkw_</a> | Alignment | not modelled | 16.7 | 25 | <b>Fold:</b> Rubredoxin-like<br><b>Superfamily:</b> Zn-binding ribosomal proteins<br><b>Family:</b> Ribosomal protein L37ae  |
| 43 | <a href="#">d1vqoz1</a> | Alignment | not modelled | 16.7 | 17 | <b>Fold:</b> Rubredoxin-like<br><b>Superfamily:</b> Zn-binding ribosomal proteins<br><b>Family:</b> Ribosomal protein L37ae  |
| 44 | <a href="#">c3pamB_</a> | Alignment | not modelled | 16.6 | 12 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> transmembrane protein;<br><b>PDBTitle:</b> crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1               |
| 45 | <a href="#">d1jj2y_</a> | Alignment | not modelled | 16.6 | 29 | <b>Fold:</b> Rubredoxin-like<br><b>Superfamily:</b> Zn-binding ribosomal proteins<br><b>Family:</b> Ribosomal protein L37ae  |
| 46 | <a href="#">c4a17Y_</a> | Alignment | not modelled | 16.5 | 18 | <b>PDB header:</b> ribosome<br><b>Chain:</b> Y: <b>PDB Molecule:</b> rpl37a;<br><b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.                                    |
| 47 | <a href="#">c3zf7o_</a> | Alignment | not modelled | 15.9 | 18 | <b>PDB header:</b> ribosome<br><b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l13a, putative;<br><b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome  |
| 48 | <a href="#">c3izrm_</a> | Alignment | not modelled | 15.0 | 21 | <b>PDB header:</b> ribosome<br><b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l23 (l14p);<br><b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome                          |
| 49 | <a href="#">c1jrxA_</a> | Alignment | not modelled | 15.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c;<br><b>PDBTitle:</b> crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina  |
| 50 | <a href="#">d1pg5b2</a> | Alignment | not modelled | 14.7 | 38 | <b>Fold:</b> Rubredoxin-like<br><b>Superfamily:</b> Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain<br><b>Family:</b> Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain  |
| 51 | <a href="#">c4h6an_</a> | Alignment | not modelled | 14.7 | 25 | <b>PDB header:</b> ribosome<br><b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l17-a;  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 51 | <a href="#">c4v0ap_</a> | Alignment | not modelled | 14.7 | 29 | <b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1  |
| 52 | <a href="#">d2yt9a1</a> | Alignment | not modelled | 14.5 | 31 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2   |
| 53 | <a href="#">d6rxna_</a> | Alignment | not modelled | 14.3 | 21 | <b>Fold:</b> Rubredoxin-like<br><b>Superfamily:</b> Rubredoxin-like<br><b>Family:</b> Rubredoxin  |
| 54 | <a href="#">c3j39p_</a> | Alignment | not modelled | 13.8 | 17 | <b>PDB header:</b> ribosome<br><b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l17;<br><b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins   |
| 55 | <a href="#">d1tifa_</a> | Alignment | not modelled | 13.6 | 27 | <b>Fold:</b> beta-Grasp (ubiquitin-like)<br><b>Superfamily:</b> Translation initiation factor IF3, N-terminal domain<br><b>Family:</b> Translation initiation factor IF3, N-terminal domain   |
| 56 | <a href="#">c5mq9A_</a> | Alignment | not modelled | 13.5 | 16 | <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)  |
| 57 | <a href="#">c2l8eA_</a> | Alignment | not modelled | 13.4 | 57 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> polyhomeotic-like protein 1;<br><b>PDBTitle:</b> solution nmr structure of fcs domain of human polyhomeotic homolog 12 (hph1)   |
| 58 | <a href="#">d2jb0b1</a> | Alignment | not modelled | 13.3 | 19 | <b>Fold:</b> His-Me finger endonucleases<br><b>Superfamily:</b> His-Me finger endonucleases<br><b>Family:</b> HNH-motif   |
| 59 | <a href="#">d1okba_</a> | Alignment | not modelled | 12.1 | 32 | <b>Fold:</b> Uracil-DNA glycosylase-like<br><b>Superfamily:</b> Uracil-DNA glycosylase-like<br><b>Family:</b> Uracil-DNA glycosylase  |
| 60 | <a href="#">c1rikA_</a> | Alignment | not modelled | 11.9 | 29 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> e6apc1 peptide;<br><b>PDBTitle:</b> e6-binding zinc finger (e6apc1)   |
| 61 | <a href="#">c2m0dA_</a> | Alignment | not modelled | 11.8 | 50 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger and btb domain-containing protein 17;<br><b>PDBTitle:</b> solution structure of miz-1 zinc finger 5   |
| 62 | <a href="#">c5mslA_</a> | Alignment | not modelled | 11.7 | 27 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> anti-sigma-f factor fin;<br><b>PDBTitle:</b> solution structure of the b. subtilis anti-sigma-f factor, fin   |
| 63 | <a href="#">c3cxmA_</a> | Alignment | not modelled | 11.6 | 24 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase;<br><b>PDBTitle:</b> leishmania naiffi uracil-dna glycosylase in complex with 5-bromouracil  |
| 64 | <a href="#">c7ceiB_</a> | Alignment | not modelled | 11.3 | 19 | <b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein (colicin e7 immunity protein);<br><b>PDBTitle:</b> the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein   |
| 65 | <a href="#">d2fzcb2</a> | Alignment | not modelled | 11.3 | 38 | <b>Fold:</b> Rubredoxin-like<br><b>Superfamily:</b> Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain<br><b>Family:</b> Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain   |
| 66 | <a href="#">c5kl1B_</a> | Alignment | not modelled | 10.9 | 24 | <b>PDB header:</b> rna binding protein/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein nanos;<br><b>PDBTitle:</b> crystal structure of the pumilio-nos-hunchback rna complex   |
| 67 | <a href="#">c3lvuB_</a> | Alignment | not modelled | 10.9 | 16 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, periplasmic substrate-binding protein;<br><b>PDBTitle:</b> crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi     |
| 68 | <a href="#">c2jvmA_</a> | Alignment | not modelled | 10.7 | 38 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of rhodobacter sphaeroides protein2 rhos4_26430. northeast structural genomics consortium3 target rhr95 |
| 69 | <a href="#">d1dl6a_</a> | Alignment | not modelled | 10.7 | 16 | <b>Fold:</b> Rubredoxin-like<br><b>Superfamily:</b> Zinc beta-ribbon<br><b>Family:</b> Transcriptional factor domain  |
| 70 | <a href="#">c5lnkb_</a> | Alignment | not modelled | 10.6 | 50 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b><br><b>PDBTitle:</b> entire ovine respiratory complex i   |
| 71 | <a href="#">c1va3A_</a> | Alignment | not modelled | 10.5 | 31 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor sp1;<br><b>PDBTitle:</b> solution structure of transcription factor sp1 dna binding2 domain (zinc finger 3)  |
| 72 | <a href="#">c3alrA_</a> | Alignment | not modelled | 10.3 | 18 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nanos protein;<br><b>PDBTitle:</b> crystal structure of nanos   |
| 73 | <a href="#">c2qa4Z_</a> | Alignment | not modelled | 10.2 | 17 | <b>PDB header:</b> ribosome<br><b>Chain:</b> Z: <b>PDB Molecule:</b> 50s ribosomal protein l37ae;<br><b>PDBTitle:</b> a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit  |
| 74 | <a href="#">c6gcsM_</a> | Alignment | not modelled | 9.9  | 44 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> M: <b>PDB Molecule:</b> numm subunit;<br><b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica  |
| 75 | <a href="#">c2jrrA_</a> | Alignment | not modelled | 9.8  | 50 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of q5lls5 from silicibacter2 pomeroyi. northeast structural genomics consortium target3 sir90           |
| 76 | <a href="#">d3euga_</a> | Alignment | not modelled | 9.6  | 32 | <b>Fold:</b> Uracil-DNA glycosylase-like<br><b>Superfamily:</b> Uracil-DNA glycosylase-like<br><b>Family:</b> Uracil-DNA glycosylase  |
|    |                         |           |              |      |    | <b>PDB header:</b> transferase  |

|    |                         |           |              |     |    |  |
|----|-------------------------|-----------|--------------|-----|----|--|
| 77 | <a href="#">c4uxjB_</a> | Alignment | not modelled | 9.6 | 22 | <b>Chain:</b> B: <b>PDB Molecule:</b> thymidine kinase;<br><b>PDBTitle:</b> leishmania major thymidine kinase in complex with dttp   |
| 78 | <a href="#">c1sp1A_</a> | Alignment | not modelled | 9.6 | 31 | <b>PDB header:</b> zinc finger<br><b>Chain:</b> A: <b>PDB Molecule:</b> sp1f3;<br><b>PDBTitle:</b> nmr structure of a zinc finger domain from transcription2 factor sp1f3, minimized average structure   |
| 79 | <a href="#">d1sp1a_</a> | Alignment | not modelled | 9.6 | 31 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2  |
| 80 | <a href="#">c1areA_</a> | Alignment | not modelled | 9.2 | 18 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> yeast transcription factor adr1;<br><b>PDBTitle:</b> structures of dna-binding mutant zinc finger domains: implications for2 dna binding  |
| 81 | <a href="#">d1laue_</a> | Alignment | not modelled | 9.1 | 36 | <b>Fold:</b> Uracil-DNA glycosylase-like<br><b>Superfamily:</b> Uracil-DNA glycosylase-like<br><b>Family:</b> Uracil-DNA glycosylase   |
| 82 | <a href="#">c3hkzP_</a> | Alignment | not modelled | 8.9 | 50 | <b>PDB header:</b> transferase<br><b>Chain:</b> P: <b>PDB Molecule:</b> dna-directed rna polymerase subunit p;<br><b>PDBTitle:</b> the x-ray crystal structure of rna polymerase from archaea  |
| 83 | <a href="#">c2lvrA_</a> | Alignment | not modelled | 8.9 | 25 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger and btb domain-containing protein 17;<br><b>PDBTitle:</b> solution structure of miz-1 zinc finger 8  |
| 84 | <a href="#">c3t6pA_</a> | Alignment | not modelled | 8.8 | 24 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 2;<br><b>PDBTitle:</b> iap antagonist-induced conformational change in ciap1 promotes e32 ligase activation via dimerization   |
| 85 | <a href="#">c1s1i9_</a> | Alignment | not modelled | 8.7 | 25 | <b>PDB header:</b> ribosome<br><b>Chain:</b> 9: <b>PDB Molecule:</b> 60s ribosomal protein l43;<br><b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h. |
| 86 | <a href="#">c2mpjA_</a> | Alignment | not modelled | 8.4 | 38 | <b>PDB header:</b> nucleotide binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> recq4-helicase-like protein;<br><b>PDBTitle:</b> nmr structure of xenopus recq4 zinc knuckle  |
| 87 | <a href="#">c5lc5R_</a> | Alignment | not modelled | 8.4 | 57 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> R: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 6,<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class2   |
| 88 | <a href="#">c5ldxR_</a> | Alignment | not modelled | 8.3 | 50 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> R: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 6,<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class3.  |
| 89 | <a href="#">c5ldwR_</a> | Alignment | not modelled | 8.3 | 50 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> R: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 6,<br><b>PDBTitle:</b> structure of mammalian respiratory complex i, class1   |
| 90 | <a href="#">d1xf7a_</a> | Alignment | not modelled | 8.1 | 38 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2  |
| 91 | <a href="#">c1xf7A_</a> | Alignment | not modelled | 8.1 | 38 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> wilms' tumor protein;<br><b>PDBTitle:</b> high resolution nmr structure of the wilms' tumor2 suppressor protein (wt1) finger 3   |
| 92 | <a href="#">c1ardA_</a> | Alignment | not modelled | 8.1 | 25 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> yeast transcription factor adr1;<br><b>PDBTitle:</b> structures of dna-binding mutant zinc finger domains: implications for2 dna binding  |
| 93 | <a href="#">c5x3hA_</a> | Alignment | not modelled | 8.0 | 43 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> uracil-dna glycosylase;<br><b>PDBTitle:</b> the y81g mutant of the ung crystal structure from nitratifactor2 salsuginis  |
| 94 | <a href="#">c1rimA_</a> | Alignment | not modelled | 8.0 | 29 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> e6apc2 peptide;<br><b>PDBTitle:</b> e6-binding zinc finger (e6apc2)  |
| 95 | <a href="#">c2qq0B_</a> | Alignment | not modelled | 8.0 | 31 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> thymidine kinase;<br><b>PDBTitle:</b> thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp  |
| 96 | <a href="#">d1nj1a2</a> | Alignment | not modelled | 7.9 | 27 | <b>Fold:</b> IF3-like<br><b>Superfamily:</b> C-terminal domain of ProRS<br><b>Family:</b> C-terminal domain of ProRS   |
| 97 | <a href="#">d2qfaa1</a> | Alignment | not modelled | 7.8 | 30 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat  |
| 98 | <a href="#">d2adra1</a> | Alignment | not modelled | 7.7 | 25 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2  |
| 99 | <a href="#">d2cota1</a> | Alignment | not modelled | 7.7 | 38 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2  |