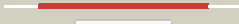


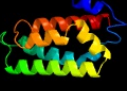
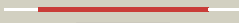
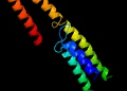






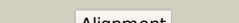



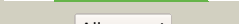







# Phyre2

|               |                               |
|---------------|-------------------------------|
| Email         | mdejesus@rockefeller.edu      |
| Description   | RVBD2822c_(-)_3128983_3129357 |
| Date          | Wed Aug 7 12:50:48 BST 2019   |
| Unique Job ID | 79f3ca5db745e7ff              |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">c6ifuB_</a> |  Alignment   |    | 100.0      | 48     | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> type iii-a crispr-associated protein csm2;<br><b>PDBTitle:</b> cryo-em structure of type iii-a csm-ctr2-dsdna complex                                   |
| 2  | <a href="#">c6ae1B_</a> |  Alignment   |    | 100.0      | 30     | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> crispr-associated protein, tm1810 family;<br><b>PDBTitle:</b> crystal structure of csm2 of the type iii-a crispr-cas effector2 complex                  |
| 3  | <a href="#">c5an6A_</a> |  Alignment   |    | 100.0      | 24     | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> crispr-associated protein, csm2 family;<br><b>PDBTitle:</b> crystal structure of thermotoga maritima csm2   |
| 4  | <a href="#">c6musB_</a> |  Alignment   |    | 100.0      | 16     | <b>PDB header:</b> rna binding protein/rna<br><b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein csm2;<br><b>PDBTitle:</b> cryo-em structure of larger csm-crrna-target rna ternary complex in2 type iii-a crispr-cas system |
| 5  | <a href="#">d3cr5x1</a> |  Alignment |  | 79.1       | 11     | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> S100 proteins  |
| 6  | <a href="#">c2rgiA_</a> |  Alignment |  | 78.8       | 13     | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> protein s100-a2;<br><b>PDBTitle:</b> crystal structure of ca2+-free s100a2 at 1.6 a resolution  |
| 7  | <a href="#">d1qlka_</a> |  Alignment |  | 75.4       | 16     | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> S100 proteins  |
| 8  | <a href="#">c3jq3A_</a> |  Alignment |  | 66.1       | 19     | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> lombricine kinase;<br><b>PDBTitle:</b> crystal structure of lombricine kinase, complexed with substrate adp   |
| 9  | <a href="#">c2kaxA_</a> |  Alignment |  | 59.9       | 14     | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> protein s100-a5;<br><b>PDBTitle:</b> solution structure and dynamics of s100a5 in the apo and2 ca2+ -bound states                                     |
| 10 | <a href="#">c5ady6_</a> |  Alignment |  | 51.8       | 25     | <b>PDB header:</b> ribosome<br><b>Chain:</b> 6; <b>PDB Molecule:</b> gtpase hflx;<br><b>PDBTitle:</b> cryo-em structures of the 50s ribosome subunit bound with hflx  |
| 11 | <a href="#">d1zfsa1</a> |  Alignment |  | 45.1       | 16     | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> S100 proteins  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 12 | <a href="#">d1qlsa_</a> | Alignment |              | 40.2 | 12 | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> S100 proteins  |
| 13 | <a href="#">d1ksoa_</a> | Alignment |              | 38.6 | 11 | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> S100 proteins  |
| 14 | <a href="#">d1q3ma_</a> | Alignment |              | 35.6 | 38 | <b>Fold:</b> GLA-domain<br><b>Superfamily:</b> GLA-domain<br><b>Family:</b> GLA-domain  |
| 15 | <a href="#">c1qk1H_</a> | Alignment |              | 31.9 | 11 | <b>PDB header:</b> transferase (creatine kinase)<br><b>Chain:</b> H: <b>PDB Molecule:</b> creatine kinase, ubiquitous mitochondrial;<br><b>PDBTitle:</b> crystal structure of human ubiquitous mitochondrial creatine kinase  |
| 16 | <a href="#">c5hydA_</a> | Alignment |              | 29.7 | 20 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein s100-z;<br><b>PDBTitle:</b> crystal structure of calcium-free human s100z   |
| 17 | <a href="#">c1rl9A_</a> | Alignment |              | 29.0 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arginine kinase;<br><b>PDBTitle:</b> crystal structure of creatine- <i>adp</i> arginine kinase ternary2 complex   |
| 18 | <a href="#">d1dc1a_</a> | Alignment |              | 26.4 | 13 | <b>Fold:</b> Restriction endonuclease-like<br><b>Superfamily:</b> Restriction endonuclease-like<br><b>Family:</b> Restriction endonuclease BsoBI  |
| 19 | <a href="#">d1q8ha_</a> | Alignment |              | 24.2 | 29 | <b>Fold:</b> GLA-domain<br><b>Superfamily:</b> GLA-domain<br><b>Family:</b> GLA-domain  |
| 20 | <a href="#">c1q8hA_</a> | Alignment |              | 24.2 | 29 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> osteocalcin;<br><b>PDBTitle:</b> crystal structure of porcine osteocalcin   |
| 21 | <a href="#">d3c1va1</a> | Alignment | not modelled | 23.9 | 13 | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> S100 proteins  |
| 22 | <a href="#">c3zpnD_</a> | Alignment | not modelled | 23.6 | 36 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> D: <b>PDB Molecule:</b> photosystem ii reaction center psb28 protein;<br><b>PDBTitle:</b> structure of psb28   |
| 23 | <a href="#">c3pf6C_</a> | Alignment | not modelled | 21.7 | 27 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein pp-luz7_gp033;<br><b>PDBTitle:</b> the structure of uncharacterized protein pp-luz7_gp033 from2 pseudomonas phage luz7.  |
| 24 | <a href="#">c2l0vB_</a> | Alignment | not modelled | 21.5 | 11 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein s100-a16;<br><b>PDBTitle:</b> solution structure of calcium(ii) bound s100a16   |
| 25 | <a href="#">c2kvoA_</a> | Alignment | not modelled | 20.9 | 43 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> A: <b>PDB Molecule:</b> photosystem ii reaction center psb28 protein;<br><b>PDBTitle:</b> solution nmr structure of photosystem ii reaction center psb28 protein2 from synechocystis sp.(strain pcc 6803), northeast structural3 genomics consortium target sgr171 |
| 26 | <a href="#">c3ju6A_</a> | Alignment | not modelled | 19.0 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arginine kinase;<br><b>PDBTitle:</b> crystal structure of dimeric arginine kinase in complex with2 amppnp and arginine  |
| 27 | <a href="#">d1a4pa_</a> | Alignment | not modelled | 19.0 | 18 | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> S100 proteins  |
| 28 | <a href="#">d1m15a1</a> | Alignment | not modelled | 18.0 | 9  | <b>Fold:</b> Guanido kinase N-terminal domain<br><b>Superfamily:</b> Guanido kinase N-terminal domain<br><b>Family:</b> Guanido kinase N-terminal domain  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 29 | <a href="#">d1gs0a1</a> | Alignment | not modelled | 16.6 | 9  | <b>Fold:</b> Domain of poly(ADP-ribose) polymerase<br><b>Superfamily:</b> Domain of poly(ADP-ribose) polymerase<br><b>Family:</b> Domain of poly(ADP-ribose) polymerase   |
| 30 | <a href="#">c4wo8A_</a> | Alignment | not modelled | 15.7 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> taurocyamine kinase;<br><b>PDBTitle:</b> the substrate-free duplicated taurocyamine kinase from schistosoma2 mansoni  |
| 31 | <a href="#">c1wn4A_</a> | Alignment | not modelled | 15.6 | 63 | <b>PDB header:</b> plant protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> vontr protein;<br><b>PDBTitle:</b> nmr structure of vontr   |
| 32 | <a href="#">c1vzmB_</a> | Alignment | not modelled | 15.1 | 40 | <b>PDB header:</b> calcium-binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> osteocalcin;<br><b>PDBTitle:</b> osteocalcin from fish argyrosomus regius   |
| 33 | <a href="#">c3bpjD_</a> | Alignment | not modelled | 14.6 | 17 | <b>PDB header:</b> translation<br><b>Chain:</b> D: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit j;<br><b>PDBTitle:</b> crystal structure of human translation initiation factor 3, subunit 12 alpha  |
| 34 | <a href="#">c2dlrA_</a> | Alignment | not modelled | 14.6 | 21 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> regulator of g-protein signaling 10;<br><b>PDBTitle:</b> solution structure of the rgs domain of human regulator of 2 g-protein signaling 10  |
| 35 | <a href="#">c1i0eD_</a> | Alignment | not modelled | 14.0 | 11 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> creatine kinase,m chain;<br><b>PDBTitle:</b> crystal structure of creatine kinase from human muscle   |
| 36 | <a href="#">c4rf9A_</a> | Alignment | not modelled | 13.9 | 10 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arginine kinase;<br><b>PDBTitle:</b> crystal structure of double-domain arginine kinase from anthopleura2 japonicas in complex with l-arginine and atpgs  |
| 37 | <a href="#">c1gs0B_</a> | Alignment | not modelled | 13.7 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> poly (adp-ribose) polymerase-2;<br><b>PDBTitle:</b> crystal structure of the catalytic fragment of murine poly2 (adp-ribose) polymerase-2   |
| 38 | <a href="#">d1j55a_</a> | Alignment | not modelled | 13.6 | 27 | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> S100 proteins  |
| 39 | <a href="#">c4drwC_</a> | Alignment | not modelled | 13.6 | 18 | <b>PDB header:</b> exocytosis/protein binding<br><b>Chain:</b> C: <b>PDB Molecule:</b> protein s100-a10/annexin a2 chimeric protein;<br><b>PDBTitle:</b> crystal structure of the ternary complex between s100a10, an annexin2 a2 n-terminal peptide and an ahnak peptide |
| 40 | <a href="#">c2y5fF_</a> | Alignment | not modelled | 13.5 | 16 | <b>PDB header:</b> metal-binding protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> s100 calcium binding protein z;<br><b>PDBTitle:</b> s100z from zebrafish in complex with calcium  |
| 41 | <a href="#">d1fs1b1</a> | Alignment | not modelled | 12.9 | 14 | <b>Fold:</b> Skp1 dimerisation domain-like<br><b>Superfamily:</b> Skp1 dimerisation domain-like<br><b>Family:</b> Skp1 dimerisation domain-like   |
| 42 | <a href="#">d1ztda1</a> | Alignment | not modelled | 12.7 | 56 | <b>Fold:</b> RNase III domain-like<br><b>Superfamily:</b> RNase III domain-like<br><b>Family:</b> PF0609-like   |
| 43 | <a href="#">d1nexa1</a> | Alignment | not modelled | 12.1 | 7  | <b>Fold:</b> Skp1 dimerisation domain-like<br><b>Superfamily:</b> Skp1 dimerisation domain-like<br><b>Family:</b> Skp1 dimerisation domain-like   |
| 44 | <a href="#">c3l2eB_</a> | Alignment | not modelled | 12.0 | 0  | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> glycocyanine kinase beta chain;<br><b>PDBTitle:</b> glycocyanine kinase, alpha-beta heterodimer from marine worm2 namalycastis sp.  |
| 45 | <a href="#">d1t6sa2</a> | Alignment | not modelled | 11.1 | 33 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> ScpB/YpuH-like   |
| 46 | <a href="#">c2x0lB_</a> | Alignment | not modelled | 11.1 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> rest corepressor 1;<br><b>PDBTitle:</b> crystal structure of a neuro-specific splicing variant of 2 human histone lysine demethylase Lsd1.  |
| 47 | <a href="#">c2iw5B_</a> | Alignment | not modelled | 11.1 | 17 | <b>PDB header:</b> oxidoreductase/transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> rest corepressor 1;<br><b>PDBTitle:</b> structural basis for corest-dependent demethylation of nucleosomes by 2 the human Lsd1 histone demethylase                     |
| 48 | <a href="#">c2v1dB_</a> | Alignment | not modelled | 11.1 | 17 | <b>PDB header:</b> oxidoreductase/repressor<br><b>Chain:</b> B: <b>PDB Molecule:</b> rest corepressor 1;<br><b>PDBTitle:</b> structural basis of Lsd1-corest selectivity in histone h32 recognition   |
| 49 | <a href="#">c2xajB_</a> | Alignment | not modelled | 11.1 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> rest corepressor 1;<br><b>PDBTitle:</b> crystal structure of Lsd1-corest in complex with (-)-trans-2 2-phenylcyclopropyl-1-amine  |
| 50 | <a href="#">d2oc5a1</a> | Alignment | not modelled | 11.0 | 20 | <b>Fold:</b> Ferritin-like<br><b>Superfamily:</b> Ferritin-like<br><b>Family:</b> PMT1231-like  |
| 51 | <a href="#">d1k8ua_</a> | Alignment | not modelled | 11.0 | 24 | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> S100 proteins  |
| 52 | <a href="#">d1u6ra1</a> | Alignment | not modelled | 10.8 | 5  | <b>Fold:</b> Guanido kinase N-terminal domain<br><b>Superfamily:</b> Guanido kinase N-terminal domain<br><b>Family:</b> Guanido kinase N-terminal domain  |
| 53 | <a href="#">d1fs2b1</a> | Alignment | not modelled | 10.8 | 13 | <b>Fold:</b> Skp1 dimerisation domain-like<br><b>Superfamily:</b> Skp1 dimerisation domain-like<br><b>Family:</b> Skp1 dimerisation domain-like   |
| 54 | <a href="#">d1efya1</a> | Alignment | not modelled | 10.8 | 12 | <b>Fold:</b> Domain of poly(ADP-ribose) polymerase<br><b>Superfamily:</b> Domain of poly(ADP-ribose) polymerase<br><b>Family:</b> Domain of poly(ADP-ribose) polymerase   |
|    |                         |           |              |      |    | <b>Fold:</b> Skp1 dimerisation domain-like  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 55 | <a href="#">d2ovra1</a> | Alignment | not modelled | 10.7 | 13 | <b>Superfamily:</b> Skp1 dimerisation domain-like<br><b>Family:</b> Skp1 dimerisation domain-like   |
| 56 | <a href="#">d2rd6a1</a> | Alignment | not modelled | 10.7 | 14 | <b>Fold:</b> Domain of poly(ADP-ribose) polymerase<br><b>Superfamily:</b> Domain of poly(ADP-ribose) polymerase<br><b>Family:</b> Domain of poly(ADP-ribose) polymerase   |
| 57 | <a href="#">d2dt5a1</a> | Alignment | not modelled | 10.5 | 36 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Transcriptional repressor Rex, N-terminal domain   |
| 58 | <a href="#">c1q68A_</a> | Alignment | not modelled | 10.5 | 44 | <b>PDB header:</b> membrane protein/transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> t-cell surface glycoprotein cd4;<br><b>PDBTitle:</b> solution structure of t-cell surface glycoprotein cd4 and2 proto-oncogene tyrosine-protein kinase lck fragments |
| 59 | <a href="#">d1vrpa1</a> | Alignment | not modelled | 10.2 | 5  | <b>Fold:</b> Guanido kinase N-terminal domain<br><b>Superfamily:</b> Guanido kinase N-terminal domain<br><b>Family:</b> Guanido kinase N-terminal domain  |
| 60 | <a href="#">d1crka1</a> | Alignment | not modelled | 10.0 | 5  | <b>Fold:</b> Guanido kinase N-terminal domain<br><b>Superfamily:</b> Guanido kinase N-terminal domain<br><b>Family:</b> Guanido kinase N-terminal domain  |
| 61 | <a href="#">c2a8vA_</a> | Alignment | not modelled | 9.7  | 22 | <b>PDB header:</b> protein/rna<br><b>Chain:</b> A; <b>PDB Molecule:</b> rna binding domain of rho transcription<br><b>PDBTitle:</b> rho transcription termination factor/rna complex  |
| 62 | <a href="#">c4ggfT_</a> | Alignment | not modelled | 9.5  | 14 | <b>PDB header:</b> antimicrobial protein<br><b>Chain:</b> T; <b>PDB Molecule:</b> protein s100-a9;<br><b>PDBTitle:</b> crystal structure of mn2+ bound calprotectin   |
| 63 | <a href="#">d1i0ea1</a> | Alignment | not modelled | 9.4  | 5  | <b>Fold:</b> Guanido kinase N-terminal domain<br><b>Superfamily:</b> Guanido kinase N-terminal domain<br><b>Family:</b> Guanido kinase N-terminal domain  |
| 64 | <a href="#">d2qpva1</a> | Alignment | not modelled | 9.4  | 23 | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Bet v1-like<br><b>Family:</b> Atu1531-like   |
| 65 | <a href="#">c2paxA_</a> | Alignment | not modelled | 9.0  | 10 | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> poly(adp-ribose) polymerase;<br><b>PDBTitle:</b> the catalytic fragment of poly(adp-ribose) polymerase2 complexed with 4-amino-1,8-naphthalimide                                      |
| 66 | <a href="#">d1qh4a1</a> | Alignment | not modelled | 9.0  | 5  | <b>Fold:</b> Guanido kinase N-terminal domain<br><b>Superfamily:</b> Guanido kinase N-terminal domain<br><b>Family:</b> Guanido kinase N-terminal domain  |
| 67 | <a href="#">d1g0wa1</a> | Alignment | not modelled | 8.4  | 5  | <b>Fold:</b> Guanido kinase N-terminal domain<br><b>Superfamily:</b> Guanido kinase N-terminal domain<br><b>Family:</b> Guanido kinase N-terminal domain  |
| 68 | <a href="#">c4dqyF_</a> | Alignment | not modelled | 8.3  | 13 | <b>PDB header:</b> transferase/dna<br><b>Chain:</b> F; <b>PDB Molecule:</b> poly [adp-ribose] polymerase 1;<br><b>PDBTitle:</b> structure of human parp-1 bound to a dna double strand break  |
| 69 | <a href="#">c2lpyA_</a> | Alignment | not modelled | 8.1  | 13 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> matrix protein p10;<br><b>PDBTitle:</b> solution structure of the m-pmv myristoylated matrix protein  |
| 70 | <a href="#">d1a62a2</a> | Alignment | not modelled | 8.1  | 22 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Cold shock DNA-binding domain-like  |
| 71 | <a href="#">d1a03a_</a> | Alignment | not modelled | 8.1  | 16 | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> S100 proteins  |
| 72 | <a href="#">d1tw9a1</a> | Alignment | not modelled | 8.0  | 8  | <b>Fold:</b> GST C-terminal domain-like<br><b>Superfamily:</b> GST C-terminal domain-like<br><b>Family:</b> Glutathione S-transferase (GST), C-terminal domain  |
| 73 | <a href="#">c3zpv0_</a> | Alignment | not modelled | 8.0  | 25 | <b>PDB header:</b> transcription<br><b>Chain:</b> 0; <b>PDB Molecule:</b> protein bc19 homolog;<br><b>PDB Fragment:</b> phd domain, residues 747-804; <b>PDBTitle:</b> crystal structure of drosophila pygo phd finger in complex2 with legless hd1 domain    |
| 74 | <a href="#">c2ptmA_</a> | Alignment | not modelled | 7.8  | 3  | <b>PDB header:</b> transport protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> hyperpolarization-activated (ih) channel;<br><b>PDBTitle:</b> structure and rearrangements in the carboxy-terminal region of spih2 channels                                     |
| 75 | <a href="#">d1psra_</a> | Alignment | not modelled | 7.5  | 9  | <b>Fold:</b> EF Hand-like<br><b>Superfamily:</b> EF-hand<br><b>Family:</b> S100 proteins  |
| 76 | <a href="#">c2khnA_</a> | Alignment | not modelled | 7.3  | 18 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> intersectin-1;<br><b>PDBTitle:</b> nmr solution structure of the eh 1 domain from human2 intersectin-1 protein. northeast structural genomics3 consortium target hr3646e.       |
| 77 | <a href="#">d1qk1a1</a> | Alignment | not modelled | 7.1  | 5  | <b>Fold:</b> Guanido kinase N-terminal domain<br><b>Superfamily:</b> Guanido kinase N-terminal domain<br><b>Family:</b> Guanido kinase N-terminal domain  |
| 78 | <a href="#">c1r6rA_</a> | Alignment | not modelled | 6.9  | 29 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> genome polyprotein;<br><b>PDBTitle:</b> solution structure of dengue virus capsid protein reveals a2 new fold   |
| 79 | <a href="#">d1r6ra_</a> | Alignment | not modelled | 6.9  | 29 | <b>Fold:</b> Flavivirus capsid protein C<br><b>Superfamily:</b> Flavivirus capsid protein C<br><b>Family:</b> Flavivirus capsid protein C   |
| 80 | <a href="#">c5a48B_</a> | Alignment | not modelled | 6.7  | 18 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B; <b>PDB Molecule:</b> maternal effect protein oskar;<br><b>PDBTitle:</b> crystal structure of the lotus domain (aa 139-240) of drosophila2 oskar in p65   |
| 81 | <a href="#">c2gslE_</a> | Alignment | not modelled | 6.6  | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> E; <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> x-ray crystal structure of protein fn1578 from  |

|    |                         |           |              |     |    |  |
|----|-------------------------|-----------|--------------|-----|----|--|
|    |                         |           |              |     |    | fusobacterium2 nucleatum. northeast structural genomics consortium target nr1.   |
| 82 | <a href="#">c4i98C_</a> | Alignment | not modelled | 6.6 | 50 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> C: <b>PDB Molecule:</b> segregation and condensation protein b;<br><b>PDBTitle:</b> crystal structure of the complex between scpa(residues 1-160)-2 scpb(residues 1-183)  |
| 83 | <a href="#">c5yrgE_</a> | Alignment | not modelled | 6.4 | 17 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> dna repair protein rad5,dna repair protein rev1;<br><b>PDBTitle:</b> crystal structure of rad5 and rev1  |
| 84 | <a href="#">d1z9ha1</a> | Alignment | not modelled | 6.2 | 12 | <b>Fold:</b> GST C-terminal domain-like<br><b>Superfamily:</b> GST C-terminal domain-like<br><b>Family:</b> Glutathione S-transferase (GST), C-terminal domain   |
| 85 | <a href="#">d1sfkb_</a> | Alignment | not modelled | 6.2 | 31 | <b>Fold:</b> Flavivirus capsid protein C<br><b>Superfamily:</b> Flavivirus capsid protein C<br><b>Family:</b> Flavivirus capsid protein C  |
| 86 | <a href="#">c2kluA_</a> | Alignment | not modelled | 6.1 | 44 | <b>PDB header:</b> immune system, membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd4;<br><b>PDBTitle:</b> nmr structure of the transmembrane and cytoplasmic domains2 of human cd4  |
| 87 | <a href="#">c5lxjA_</a> | Alignment | not modelled | 6.0 | 27 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphoprotein;<br><b>PDBTitle:</b> solution nmr structure of the x domain of peste des petits ruminants2 phosphoprotein   |
| 88 | <a href="#">c1t6sB_</a> | Alignment | not modelled | 5.9 | 33 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical protein;<br><b>PDBTitle:</b> crystal structure of a conserved hypothetical protein from chlorobium2 tepidum                                   |
| 89 | <a href="#">c3u0kA_</a> | Alignment | not modelled | 5.7 | 13 | <b>PDB header:</b> fluorescent protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> rcamp;<br><b>PDBTitle:</b> crystal structure of the genetically encoded calcium indicator rcamp  |
| 90 | <a href="#">c3w6jC_</a> | Alignment | not modelled | 5.7 | 50 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> C: <b>PDB Molecule:</b> scpb;<br><b>PDBTitle:</b> crystal structure of scpab core complex   |
| 91 | <a href="#">c4e8iA_</a> | Alignment | not modelled | 5.6 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lincosamide resistance protein;<br><b>PDBTitle:</b> crystal structure of lincosamide antibiotic adenylyltransferase lina,2 apo   |
| 92 | <a href="#">d2f76x1</a> | Alignment | not modelled | 5.6 | 13 | <b>Fold:</b> Retroviral matrix proteins<br><b>Superfamily:</b> Retroviral matrix proteins<br><b>Family:</b> Mason-Pfizer monkey virus matrix protein   |
| 93 | <a href="#">c3bn8A_</a> | Alignment | not modelled | 5.4 | 7  | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative sterol carrier protein 2;<br><b>PDBTitle:</b> crystal structure of a putative sterol carrier protein type 2 (af1534)2 from archaeoglobus fulgidus dsm 4304 at 2.11 a resolution |
| 94 | <a href="#">d1mrza2</a> | Alignment | not modelled | 5.4 | 20 | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like<br><b>Superfamily:</b> Nucleotidylyl transferase<br><b>Family:</b> Adenylyltransferase  |
| 95 | <a href="#">d1sfka_</a> | Alignment | not modelled | 5.4 | 27 | <b>Fold:</b> Flavivirus capsid protein C<br><b>Superfamily:</b> Flavivirus capsid protein C<br><b>Family:</b> Flavivirus capsid protein C  |
| 96 | <a href="#">c1rh5C_</a> | Alignment | not modelled | 5.4 | 30 | <b>PDB header:</b> protein transport<br><b>Chain:</b> C: <b>PDB Molecule:</b> secbeta;<br><b>PDBTitle:</b> the structure of a protein conducting channel   |
| 97 | <a href="#">d1rh5c_</a> | Alignment | not modelled | 5.4 | 30 | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> Sec-beta subunit<br><b>Family:</b> Sec-beta subunit   |
| 98 | <a href="#">c4pcwD_</a> | Alignment | not modelled | 5.4 | 17 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> filaggrin;<br><b>PDBTitle:</b> crystal structure of the n-terminal domain of human profilaggrin at2 2.2 a resolution   |
| 99 | <a href="#">c5ow2A_</a> | Alignment | not modelled | 5.2 | 27 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein;<br><b>PDBTitle:</b> japanese encephalitis virus capsid protein   |