

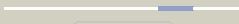


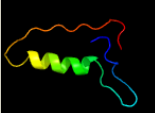





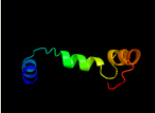
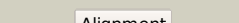




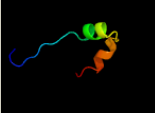

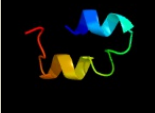
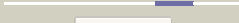



# Phyre2

|               |                                  |
|---------------|----------------------------------|
| Email         | mdejesus@rockefeller.edu         |
| Description   | RVBD2628 (-)<br>_2955068_2955430 |
| Date          | Wed Aug 7 12:50:27 BST<br>2019   |
| Unique Job ID | d2d55dbe4f61ec9e                 |

Detailed template information

| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">d1b24a2</a> |  Alignment   |    | 26.8       | 35     | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease  |
| 2  | <a href="#">c4csoD_</a> |  Alignment   |    | 24.6       | 50     | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> orfy protein, transcription factor;<br><b>PDBTitle:</b> the structure of orfy from thermoproteus tenax  |
| 3  | <a href="#">c6dqxA_</a> |  Alignment   |    | 23.7       | 18     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ribonucleoside-diphosphate reductase, alpha chain;<br><b>PDBTitle:</b> actinobacillus ureae class id ribonucleotide reductase alpha subunit  |
| 4  | <a href="#">c1v4qA_</a> |  Alignment   |    | 22.1       | 88     | <b>PDB header:</b> toxin<br><b>Chain:</b> A: <b>PDB Molecule:</b> omega-conotoxin mviic;<br><b>PDBTitle:</b> three-dimensional solution structure of the analogue2 peptide of omega-conotoxin mviic   |
| 5  | <a href="#">c3m1uB_</a> |  Alignment |  | 19.3       | 23     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative gamma-d-glutamyl-l-diamino acid endopeptidase;<br><b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dву_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution |
| 6  | <a href="#">c6n39A_</a> |  Alignment |  | 18.3       | 22     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dephospho-coa kinase;<br><b>PDBTitle:</b> crystal structure of an dephospho-coa kinase coae from mycobacterium2 paratuberculosis  |
| 7  | <a href="#">c3hilB_</a> |  Alignment |  | 17.8       | 27     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1;<br><b>PDBTitle:</b> sam domain of human ephrin type-a receptor 1 (epha1)  |
| 8  | <a href="#">c2qkqA_</a> |  Alignment |  | 14.6       | 19     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-b receptor 4;<br><b>PDBTitle:</b> structure of the sam domain of human ephrin type-b receptor2 4  |
| 9  | <a href="#">c4ye7A_</a> |  Alignment |  | 13.1       | 45     | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> orf22 similar to xcgv orf19;<br><b>PDBTitle:</b> n-terminal domain of orf22, a cydia pomonella granulovirus envelope2 protein   |
| 10 | <a href="#">c1v85A_</a> |  Alignment |  | 13.0       | 31     | <b>PDB header:</b> apoptosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> similar to ring finger protein 36;<br><b>PDBTitle:</b> sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator  |
| 11 | <a href="#">c3h8mB_</a> |  Alignment |  | 13.0       | 20     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 7;<br><b>PDBTitle:</b> sam domain of human ephrin type-a receptor 7 (epha7)  |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | <a href="#">c6fxfA_</a> | Alignment |              | 12.7 | 19 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sam and sh3 domain-containing protein 3;<br><b>PDBTitle:</b> crystal structure of the sam domain of murine sly1  |
| 13 | <a href="#">c5zrzA_</a> | Alignment |              | 12.5 | 15 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 5;<br><b>PDBTitle:</b> crystal structure of epha5/samd5 complex   |
| 14 | <a href="#">c3npfB_</a> | Alignment |              | 11.8 | 30 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative dipeptidyl-peptidase vi;<br><b>PDBTitle:</b> crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution |
| 15 | <a href="#">c1b0xA_</a> | Alignment |              | 11.7 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (epha4 receptor tyrosine kinase);<br><b>PDBTitle:</b> the crystal structure of an eph receptor sam domain reveals2 a mechanism for modular dimerization.         |
| 16 | <a href="#">d1b0xa_</a> | Alignment |              | 11.7 | 19 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> SAM/Pointed domain<br><b>Family:</b> SAM (sterile alpha motif) domain  |
| 17 | <a href="#">c3g7dA_</a> | Alignment |              | 10.8 | 62 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> phpd;<br><b>PDBTitle:</b> native phpd with cadmium atoms  |
| 18 | <a href="#">d1wiga2</a> | Alignment |              | 10.8 | 50 | <b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain)<br><b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain)<br><b>Family:</b> LIM domain   |
| 19 | <a href="#">d1sgga_</a> | Alignment |              | 10.8 | 32 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> SAM/Pointed domain<br><b>Family:</b> SAM (sterile alpha motif) domain  |
| 20 | <a href="#">c5f3xB_</a> | Alignment |              | 10.5 | 9  | <b>PDB header:</b> structural protein/protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> ankyrin repeat and sam domain-containing protein 4b;<br><b>PDBTitle:</b> crystal structure of harmonin npdz1 in complex with anks4b sam-pbm       |
| 21 | <a href="#">c4ddiB_</a> | Alignment | not modelled | 10.4 | 21 | <b>PDB header:</b> hydrolase/ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-conjugating enzyme e2 d2, ubiquitin thioesterase<br><b>PDBTitle:</b> crystal structure of human otub1/ubch5b~ub/ub  |
| 22 | <a href="#">d1coka_</a> | Alignment | not modelled | 10.4 | 30 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> SAM/Pointed domain<br><b>Family:</b> SAM (sterile alpha motif) domain  |
| 23 | <a href="#">c5zrzB_</a> | Alignment | not modelled | 9.7  | 27 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2,<br><b>PDBTitle:</b> crystal structure of epha2/ship2 complex   |
| 24 | <a href="#">c3rc8A_</a> | Alignment | not modelled | 9.3  | 56 | <b>PDB header:</b> hydrolase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase supv3l1, mitochondrial;<br><b>PDBTitle:</b> human mitochondrial helicase suv3 in complex with short rna fragment                            |
| 25 | <a href="#">c4llyA_</a> | Alignment | not modelled | 8.9  | 42 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-processing atp-dependent rna helicase prp5;<br><b>PDBTitle:</b> crystal structure of rna splicing effector prp5 in complex with adp                               |
| 26 | <a href="#">c2uwjG_</a> | Alignment | not modelled | 8.8  | 37 | <b>PDB header:</b> chaperone<br><b>Chain:</b> G: <b>PDB Molecule:</b> type iii export protein pscg;<br><b>PDBTitle:</b> structure of the heterotrimeric complex which regulates type iii2 secretion needle formation                             |
| 27 | <a href="#">c2dkzA_</a> | Alignment | not modelled | 8.8  | 20 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein loc64762;<br><b>PDBTitle:</b> solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762                                  |
| 28 | <a href="#">c2laqA_</a> | Alignment | not modelled | 8.6  | 83 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> accessory gland-specific peptide 70a;<br><b>PDBTitle:</b> solution structure of the sex peptide from drosophila  |

|    |                         |           |              |     |    |  |
|----|-------------------------|-----------|--------------|-----|----|--|
|    |                         |           |              |     |    | melanogaster   |
| 29 | <a href="#">c2kptA</a>  | Alignment | not modelled | 8.5 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted protein;<br><b>PDBTitle:</b> solution nmr structure of the n-terminal domain of cg24962 protein from corynebacterium glutamicum. northeast3 structural genomics consortium target cgr26a |
| 30 | <a href="#">c2jtvA</a>  | Alignment | not modelled | 8.5 | 67 | <b>PDB header:</b> structural genomics<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function;<br><b>PDBTitle:</b> solution structure of protein rpa3401, northeast structural genomics2 consortium target rpt7, ontario center for structural proteomics3 target rp3384                       |
| 31 | <a href="#">c5cwwB</a>  | Alignment | not modelled | 8.4 | 21 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> nucleoporin nup82;<br><b>PDBTitle:</b> crystal structure of the chaetomium thermophilum heterotrimeric nup82 ntd-nup159 tail-nup145n apd complex   |
| 32 | <a href="#">c2lmrA</a>  | Alignment | not modelled | 8.3 | 40 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin repeat and sam domain-containing protein 1a;<br><b>PDBTitle:</b> solution structure of the first sam domain of odin  |
| 33 | <a href="#">d1zbx1</a>  | Alignment | not modelled | 8.3 | 48 | <b>Fold:</b> ORC1-binding domain<br><b>Superfamily:</b> ORC1-binding domain<br><b>Family:</b> ORC1-binding domain  |
| 34 | <a href="#">c5j8yC</a>  | Alignment | not modelled | 8.1 | 21 | <b>PDB header:</b> nuclear protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> polycomb protein sfmbt;<br><b>PDBTitle:</b> crystal structure of the scm-sam and sfmbt-sam heterodimer   |
| 35 | <a href="#">c2ke7A</a>  | Alignment | not modelled | 7.8 | 42 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> ankyrin repeat and sterile alpha motif domain-<br><b>PDBTitle:</b> nmr structure of the first sam domain from aida1  |
| 36 | <a href="#">d1tf5a4</a> | Alignment | not modelled | 7.7 | 55 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Tandem AAA-ATPase domain   |
| 37 | <a href="#">c6a8yA</a>  | Alignment | not modelled | 7.7 | 75 | <b>PDB header:</b> antimicrobial protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> yr26_sds;<br><b>PDBTitle:</b> yr26_sds   |
| 38 | <a href="#">c2dl0A</a>  | Alignment | not modelled | 7.6 | 50 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sam and sh3 domain-containing protein 1;<br><b>PDBTitle:</b> solution structure of the sam-domain of the sam and sh32 domain containing protein 1  |
| 39 | <a href="#">c2b6gA</a>  | Alignment | not modelled | 7.6 | 21 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> vts1p;<br><b>PDBTitle:</b> rna recognition by the vts1 sam domain  |
| 40 | <a href="#">c5zrzB</a>  | Alignment | not modelled | 7.6 | 27 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> sterile alpha motif domain-containing protein 5;<br><b>PDBTitle:</b> crystal structure of epha5/samd5 complex  |
| 41 | <a href="#">c2eseA</a>  | Alignment | not modelled | 7.5 | 15 | <b>PDB header:</b> protein/rna complex<br><b>Chain:</b> A: <b>PDB Molecule:</b> vts1p;<br><b>PDBTitle:</b> structure of the sam domain of vts1p in complex with rna  |
| 42 | <a href="#">c1xtkA</a>  | Alignment | not modelled | 7.3 | 42 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase p47;<br><b>PDBTitle:</b> structure of decd to dead mutation of human uap56   |
| 43 | <a href="#">c1ow5A</a>  | Alignment | not modelled | 7.3 | 40 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase ste11;<br><b>PDBTitle:</b> nmr structure of the saccharomyces cerevisiae sam (sterile2 alpha motif) domain   |
| 44 | <a href="#">d1ow5a</a>  | Alignment | not modelled | 7.3 | 40 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> SAM/Pointed domain<br><b>Family:</b> SAM (sterile alpha motif) domain  |
| 45 | <a href="#">c4nhoA</a>  | Alignment | not modelled | 7.3 | 58 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx23;<br><b>PDBTitle:</b> structure of the spliceosomal dead-box protein prp28  |
| 46 | <a href="#">c3pbpD</a>  | Alignment | not modelled | 7.3 | 15 | <b>PDB header:</b> transport protein,structural protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> nucleoporin nup82;<br><b>PDBTitle:</b> structure of the yeast heterotrimeric nup82-nup159-nup116 nucleoporin2 complex   |
| 47 | <a href="#">d1oh1a</a>  | Alignment | not modelled | 7.1 | 33 | <b>Fold:</b> Streptavidin-like<br><b>Superfamily:</b> beta-Barrel protease inhibitors<br><b>Family:</b> Staphostatin   |
| 48 | <a href="#">c5supB</a>  | Alignment | not modelled | 7.0 | 50 | <b>PDB header:</b> hydrolase/rna<br><b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna helicase sub2;<br><b>PDBTitle:</b> structure of mrna export factors  |
| 49 | <a href="#">c1s2mA</a>  | Alignment | not modelled | 7.0 | 55 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative atp-dependent rna helicase dhh1;<br><b>PDBTitle:</b> crystal structure of the dead box protein dhh1p  |
| 50 | <a href="#">c3k1rB</a>  | Alignment | not modelled | 6.9 | 27 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> usher syndrome type-1g protein;<br><b>PDBTitle:</b> structure of harmonin npd21 in complex with the sam-pbm of2 sans  |
| 51 | <a href="#">c2db3D</a>  | Alignment | not modelled | 6.9 | 50 | <b>PDB header:</b> hydrolase/rna<br><b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent rna helicase vasa;<br><b>PDBTitle:</b> structural basis for rna unwinding by the dead-box protein2 drosophila vasa   |
| 52 | <a href="#">c4ct4B</a>  | Alignment | not modelled | 6.7 | 50 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx6;<br><b>PDBTitle:</b> cnot1 mif4g domain - ddx6 complex  |
| 53 | <a href="#">c4w7sA</a>  | Alignment | not modelled | 6.6 | 42 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing atp-dependent rna helicase prp28;<br><b>PDBTitle:</b> crystal structure of the yeast dead-box splicing factor prp28 at 2.542 angstroms resolution  |
|    |                         |           |              |     |    | <b>Fold:</b> SAM domain-like   |

|    |                         |           |              |     |    |  |
|----|-------------------------|-----------|--------------|-----|----|--|
| 54 | <a href="#">d1rg6a_</a> | Alignment | not modelled | 6.5 | 36 | <b>Superfamily:</b> SAM/Pointed domain<br><b>Family:</b> SAM (sterile alpha motif) domain  |
| 55 | <a href="#">c5lcsA_</a> | Alignment | not modelled | 6.5 | 56 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> gallinacin-7;<br><b>PDBTitle:</b> nmr structure of chicken avbd7 defensin  |
| 56 | <a href="#">c3fhtA_</a> | Alignment | not modelled | 6.5 | 50 | <b>PDB header:</b> hydrolase/rna<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx19b;<br><b>PDBTitle:</b> crystal structure of human dbp5 in complex with amppnp and rna  |
| 57 | <a href="#">c4rqmC_</a> | Alignment | not modelled | 6.4 | 21 | <b>PDB header:</b> protein binding<br><b>Chain:</b> C: <b>PDB Molecule:</b> protein bicaudal c homolog 1;<br><b>PDBTitle:</b> crystal structure of the semet bicc1 sam domain r924e mutant   |
| 58 | <a href="#">d1t5ia_</a> | Alignment | not modelled | 6.4 | 56 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Tandem AAA-ATPase domain   |
| 59 | <a href="#">c4z8vA_</a> | Alignment | not modelled | 6.3 | 42 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> avrrxo1-orf1;<br><b>PDBTitle:</b> crystal structure of avrrxo1-orf1:-orf2 complex, native.   |
| 60 | <a href="#">c3eiqD_</a> | Alignment | not modelled | 6.2 | 67 | <b>PDB header:</b> hydrolase/antitumor protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> eukaryotic initiation factor 4a-i;<br><b>PDBTitle:</b> crystal structure of pcdc4-eif4a  |
| 61 | <a href="#">c4pxaA_</a> | Alignment | not modelled | 6.1 | 50 | <b>PDB header:</b> translation, rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase ddx3x;<br><b>PDBTitle:</b> dead-box rna helicase ddx3x cancer-associated mutant d354v  |
| 62 | <a href="#">c5zryB_</a> | Alignment | not modelled | 6.0 | 23 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> ankyrin repeat and sam domain-containing protein 1a, ephrin<br><b>PDBTitle:</b> crystal structure of epha6/odin complex  |
| 63 | <a href="#">c2eanA_</a> | Alignment | not modelled | 5.9 | 20 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> connector enhancer of kinase suppressor of ras 2;<br><b>PDBTitle:</b> solution structure of the n-terminal sam-domain of human2 kiaa0902 protein (connector enhancer of kinase suppressor3 of ras 2)     |
| 64 | <a href="#">c3r7gB_</a> | Alignment | not modelled | 5.9 | 78 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> formin-2;<br><b>PDBTitle:</b> crystal structure of spire kind domain in complex with the tail of2 fmn2   |
| 65 | <a href="#">c2hivB_</a> | Alignment | not modelled | 5.8 | 55 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna helicase dbpa;<br><b>PDBTitle:</b> structure of the second domain (residues 207-368) of the2 bacillus subtilis yxin protein  |
| 66 | <a href="#">c4kbfA_</a> | Alignment | not modelled | 5.7 | 58 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> heat resistant rna dependent atpase;<br><b>PDBTitle:</b> two different open conformations of the helicase core of the rna2 helicase hera   |
| 67 | <a href="#">c5mntD_</a> | Alignment | not modelled | 5.7 | 31 | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> a2 maturation protein;<br><b>PDBTitle:</b> bacteriophage qbeta maturation protein  |
| 68 | <a href="#">c6c4qA_</a> | Alignment | not modelled | 5.7 | 29 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> polyketide synthase pks13;<br><b>PDBTitle:</b> 1.16 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1-100) of polyketide synthase pks13 from3 mycobacterium tuberculosis |
| 69 | <a href="#">c2eaoA_</a> | Alignment | not modelled | 5.4 | 50 | <b>PDB header:</b> signaling protein, transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-b receptor 1;<br><b>PDBTitle:</b> solution structure of the c-terminal sam-domain of mouse2 ephrin type-b receptor 1 precursor (ec 2.7.1.112)                                   |
| 70 | <a href="#">c2kr5A_</a> | Alignment | not modelled | 5.4 | 17 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> afatoxin biosynthesis polyketide synthase;<br><b>PDBTitle:</b> solution structure of an acyl carrier protein domain from fungal type2 i polyketide synthase  |
| 71 | <a href="#">c2e8nA_</a> | Alignment | not modelled | 5.3 | 50 | <b>PDB header:</b> transferase, signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 2;<br><b>PDBTitle:</b> solution structure of the c-terminal sam-domain of ephaa2:2 ephrin type-a receptor 2 precursor (ec 2.7.10.1)                                  |
| 72 | <a href="#">d1sr2a_</a> | Alignment | not modelled | 5.3 | 17 | <b>Fold:</b> Four-helical up-and-down bundle<br><b>Superfamily:</b> Histidine-containing phosphotransfer domain, HPT domain<br><b>Family:</b> Sensor-like histidine kinase YojN, C-terminal domain   |
| 73 | <a href="#">c6c4lC_</a> | Alignment | not modelled | 5.3 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> yersinopine dehydrogenase;<br><b>PDBTitle:</b> yersinopine dehydrogenase (ypodh) - apo  |
| 74 | <a href="#">c4b2uA_</a> | Alignment | not modelled | 5.3 | 80 | <b>PDB header:</b> toxin<br><b>Chain:</b> A: <b>PDB Molecule:</b> s67;<br><b>PDBTitle:</b> s67, a spider venom toxin peptide from sicarius dolichocephalus   |
| 75 | <a href="#">c5y3tA_</a> | Alignment | not modelled | 5.2 | 42 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ranbp-type and c3hc4-type zinc finger-containing protein 1;<br><b>PDBTitle:</b> crystal structure of hetero-trimeric core of lubac: hoip double-uba2 complexed with hoil-1l ubl and sharpin ubl                     |
| 76 | <a href="#">c4d25A_</a> | Alignment | not modelled | 5.2 | 50 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> bmvlg protein;<br><b>PDBTitle:</b> crystal structure of the bombyx mori vasa helicase (e339q)2 in complex with rna and amppnp  |
| 77 | <a href="#">d3buxb3</a> | Alignment | not modelled | 5.2 | 35 | <b>Fold:</b> SH2-like<br><b>Superfamily:</b> SH2 domain<br><b>Family:</b> SH2 domain   |