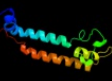
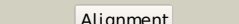
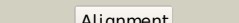
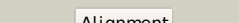
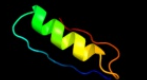
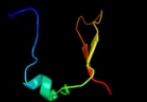
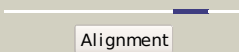
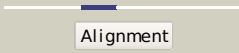
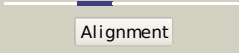
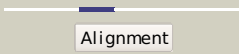
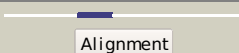
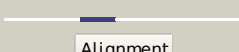
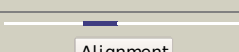
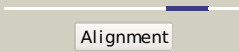
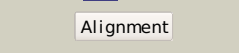
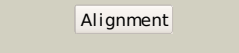


| #  | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                |
|----|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c3ftjA_</a> | <br>Alignment   |    | 99.0       | 14     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein<br><b>PDBTitle:</b> crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans              |
| 2  | <a href="#">c3is6A_</a> | <br>Alignment   |    | 97.5       | 10     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative permease protein, abc transporter;<br><b>PDBTitle:</b> the crystal structure of a domain of a putative permease protein from2 porphyromonas gingivalis to 2a |
| 3  | <a href="#">c1ciiA_</a> | <br>Alignment   |    | 85.2       | 15     | <b>PDB header:</b> transmembrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia;<br><b>PDBTitle:</b> colicin ia                                                                                                                        |
| 4  | <a href="#">c3ltiA_</a> | <br>Alignment   |    | 25.2       | 31     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta;<br><b>PDBTitle:</b> crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-beta4 domains                    |
| 5  | <a href="#">d2r6gg1</a> | <br>Alignment |  | 15.8       | 13     | <b>Fold:</b> MetI-like<br><b>Superfamily:</b> MetI-like<br><b>Family:</b> MetI-like                                                                                                                                                                 |
| 6  | <a href="#">d1cola_</a> | <br>Alignment |  | 15.0       | 9      | <b>Fold:</b> Toxins' membrane translocation domains<br><b>Superfamily:</b> Colicin<br><b>Family:</b> Colicin                                                                                                                                        |
| 7  | <a href="#">d1mvfd_</a> | <br>Alignment |  | 13.4       | 17     | <b>Fold:</b> Double-split beta-barrel<br><b>Superfamily:</b> AbrB/MazE/MraZ-like<br><b>Family:</b> Kis/PemI addiction antidote                                                                                                                      |
| 8  | <a href="#">c3k07A_</a> | <br>Alignment |  | 13.3       | 13     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cation efflux system protein cusa;<br><b>PDBTitle:</b> crystal structure of cusa                                                                                      |
| 9  | <a href="#">c2yvxD_</a> | <br>Alignment |  | 12.1       | 14     | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> mg2+ transporter mgte;<br><b>PDBTitle:</b> crystal structure of magnesium transporter mgte                                                                            |
| 10 | <a href="#">d1g8ka1</a> | <br>Alignment |  | 12.0       | 11     | <b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain                                                                                                       |
| 11 | <a href="#">d1ub4c_</a> | <br>Alignment |  | 11.6       | 17     | <b>Fold:</b> Double-split beta-barrel<br><b>Superfamily:</b> AbrB/MazE/MraZ-like<br><b>Family:</b> Kis/PemI addiction antidote                                                                                                                      |

|    |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                                       |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">d2yvxa3</a> | Alignment |    | 11.4 | 18 | <b>Fold:</b> MgtE membrane domain-like<br><b>Superfamily:</b> MgtE membrane domain-like<br><b>Family:</b> MgtE membrane domain-like                                                                                                                   |
| 13 | <a href="#">c2jsxA</a>  | Alignment |    | 11.3 | 11 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein napd;<br><b>PDBTitle:</b> solution structure of the e. coli tat proofreading2 chaperone protein napd                                                                    |
| 14 | <a href="#">d1ogya1</a> | Alignment |    | 10.5 | 11 | <b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain                                                                                                         |
| 15 | <a href="#">d2jioa1</a> | Alignment |    | 10.4 | 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                                                                                                         |
| 16 | <a href="#">d1scjb</a>  | Alignment |    | 10.4 | 20 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> Protease propeptides/inhibitors<br><b>Family:</b> Subtilase propeptides/inhibitors                                                                                                                |
| 17 | <a href="#">c2cwbA</a>  | Alignment |    | 9.9  | 16 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> chimera of immunoglobulin g binding protein g<br><b>PDBTitle:</b> solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin |
| 18 | <a href="#">c2a8vA</a>  | Alignment |  | 9.6  | 21 | <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                                                                  |
| 19 | <a href="#">c2l66B</a>  | Alignment |  | 9.6  | 24 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, abrb family;<br><b>PDBTitle:</b> the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.     |
| 20 | <a href="#">c2pmwA</a>  | Alignment |  | 9.6  | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9;<br><b>PDBTitle:</b> the crystal structure of proprotein convertase subtilisin2 kexin type 9 (pcsk9)                              |
| 21 | <a href="#">c2w2mP</a>  | Alignment | not modelled                                                                        | 9.6  | 15 | <b>PDB header:</b> hydrolase/receptor<br><b>Chain:</b> P: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9;<br><b>PDBTitle:</b> wt pcsk9-deltac bound to wt egf-a of ldlr                                                           |
| 22 | <a href="#">c2p4eP</a>  | Alignment | not modelled                                                                        | 9.6  | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> P: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9;<br><b>PDBTitle:</b> crystal structure of pcsk9                                                                                   |
| 23 | <a href="#">d2vbua1</a> | Alignment | not modelled                                                                        | 9.5  | 27 | <b>Fold:</b> Reductase/isomerase/elongation factor common domain<br><b>Superfamily:</b> Riboflavin kinase-like<br><b>Family:</b> CTP-dependent riboflavin kinase-like                                                                                 |
| 24 | <a href="#">c1wr1B</a>  | Alignment | not modelled                                                                        | 9.3  | 12 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like protein dsk2;<br><b>PDBTitle:</b> the complex sturcture of dsk2p uba with ubiquitin                                                                      |
| 25 | <a href="#">d2dnaa1</a> | Alignment | not modelled                                                                        | 9.3  | 12 | <b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                                 |
| 26 | <a href="#">d1o8ba2</a> | Alignment | not modelled                                                                        | 9.2  | 7  | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain<br><b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain                                                                             |
| 27 | <a href="#">d1a62a2</a> | Alignment | not modelled                                                                        | 9.1  | 21 | <b>Fold:</b> OB-fold<br><b>Superfamily:</b> Nucleic acid-binding proteins<br><b>Family:</b> Cold shock DNA-binding domain-like                                                                                                                        |
| 28 | <a href="#">d1spbp</a>  | Alignment | not modelled                                                                        | 9.1  | 20 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> Protease propeptides/inhibitors<br><b>Family:</b> Subtilase propeptides/inhibitors                                                                                                                |
| 29 | <a href="#">c2w1tB</a>  | Alignment | not modelled                                                                        | 9.0  | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> stage v sporulation protein t;                                                                                                                                              |

|    |                         |           |              |     |                                                                                                                                                                                                                                                          |
|----|-------------------------|-----------|--------------|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                         |           |              |     | <b>PDBTitle:</b> crystal structure of b. subtilis spovt                                                                                                                                                                                                  |
| 30 | <a href="#">d2bwba1</a> | Alignment | not modelled | 9.0 | 12<br><b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                              |
| 31 | <a href="#">c2dahA</a>  | Alignment | not modelled | 9.0 | 12<br><b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquilin-3;<br><b>PDBTitle:</b> solution structure of the c-terminal uba domain in the2 human ubiquilin 3                                       |
| 32 | <a href="#">d1vlfm1</a> | Alignment | not modelled | 8.7 | 13<br><b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain                                                                                                      |
| 33 | <a href="#">d1veja1</a> | Alignment | not modelled | 8.6 | 12<br><b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                              |
| 34 | <a href="#">c2dnaA</a>  | Alignment | not modelled | 8.5 | 12<br><b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> unnamed protein product;<br><b>PDBTitle:</b> solution structure of rsgi ruh-056, a uba domain from mouse2 cdna                                   |
| 35 | <a href="#">c3fewX</a>  | Alignment | not modelled | 8.5 | 9<br><b>PDB header:</b> immune system<br><b>Chain:</b> X: <b>PDB Molecule:</b> colicin s4;<br><b>PDBTitle:</b> structure and function of colicin s4, a colicin with a2 duplicated receptor binding domain                                                |
| 36 | <a href="#">d1y5ia1</a> | Alignment | not modelled | 8.5 | 17<br><b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain                                                                                                      |
| 37 | <a href="#">d1h0ha1</a> | Alignment | not modelled | 8.4 | 17<br><b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain                                                                                                      |
| 38 | <a href="#">d1m0sa2</a> | Alignment | not modelled | 8.3 | 14<br><b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain<br><b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain                                                                          |
| 39 | <a href="#">d1uj4a2</a> | Alignment | not modelled | 8.2 | 14<br><b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain<br><b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain                                                                          |
| 40 | <a href="#">d2daha1</a> | Alignment | not modelled | 8.2 | 12<br><b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                              |
| 41 | <a href="#">c2e74E</a>  | Alignment | not modelled | 8.1 | 8<br><b>PDB header:</b> photosynthesis<br><b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6;<br><b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from m.laminosus                                                  |
| 42 | <a href="#">c1vf5E</a>  | Alignment | not modelled | 8.1 | 8<br><b>PDB header:</b> photosynthesis<br><b>Chain:</b> E: <b>PDB Molecule:</b> protein pet l;<br><b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus                                                                          |
| 43 | <a href="#">d2e74e1</a> | Alignment | not modelled | 8.1 | 8<br><b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> PetL subunit of the cytochrome b6f complex<br><b>Family:</b> PetL subunit of the cytochrome b6f complex                                                                              |
| 44 | <a href="#">c1vf5R</a>  | Alignment | not modelled | 8.1 | 8<br><b>PDB header:</b> photosynthesis<br><b>Chain:</b> R: <b>PDB Molecule:</b> protein pet l;<br><b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus                                                                          |
| 45 | <a href="#">c2e75E</a>  | Alignment | not modelled | 8.1 | 8<br><b>PDB header:</b> photosynthesis<br><b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6;<br><b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus |
| 46 | <a href="#">c2e76E</a>  | Alignment | not modelled | 8.1 | 8<br><b>PDB header:</b> photosynthesis<br><b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6;<br><b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus               |
| 47 | <a href="#">d1lk5a2</a> | Alignment | not modelled | 8.0 | 14<br><b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain<br><b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain                                                                          |
| 48 | <a href="#">c3hzqA</a>  | Alignment | not modelled | 7.9 | 8<br><b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> large-conductance mechanosensitive channel;<br><b>PDBTitle:</b> structure of a tetrameric mscl in an expanded intermediate2 state                                      |
| 49 | <a href="#">d1tmoa1</a> | Alignment | not modelled | 7.9 | 18<br><b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain                                                                                                      |
| 50 | <a href="#">d1dv0a</a>  | Alignment | not modelled | 7.9 | 21<br><b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                              |
| 51 | <a href="#">d2fy9a1</a> | Alignment | not modelled | 7.6 | 14<br><b>Fold:</b> Double-split beta-barrel<br><b>Superfamily:</b> AbrB/MazE/MraZ-like<br><b>Family:</b> AbrB N-terminal domain-like                                                                                                                     |
| 52 | <a href="#">c2k21A</a>  | Alignment | not modelled | 7.5 | 17<br><b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e<br><b>PDBTitle:</b> nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c                              |
| 53 | <a href="#">d1dmra1</a> | Alignment | not modelled | 7.4 | 16<br><b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain                                                                                                      |
| 54 | <a href="#">c3d31D</a>  | Alignment | not modelled | 7.4 | 15<br><b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> sulfate/molybdate abc transporter, permease<br><b>PDBTitle:</b> modbc from methanosarcina acetivorans                                                                |
| 55 | <a href="#">d3d31c1</a> | Alignment | not modelled | 7.4 | 15<br><b>Fold:</b> MetI-like<br><b>Superfamily:</b> MetI-like                                                                                                                                                                                            |

|    |                         |           |              |     |    |                                                                                                                                                                                                                                                                                                                               |
|----|-------------------------|-----------|--------------|-----|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                         |           |              |     |    | <b>Family:</b> MetH-like                                                                                                                                                                                                                                                                                                      |
| 56 | <a href="#">d2iv2x1</a> | Alignment | not modelled | 7.3 | 11 | <b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain                                                                                                                                                                                 |
| 57 | <a href="#">d1yfba1</a> | Alignment | not modelled | 7.2 | 15 | <b>Fold:</b> Double-split beta-barrel<br><b>Superfamily:</b> AbrB/MazE/MraZ-like<br><b>Family:</b> AbrB N-terminal domain-like                                                                                                                                                                                                |
| 58 | <a href="#">d1kqfa1</a> | Alignment | not modelled | 7.2 | 19 | <b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain                                                                                                                                                                                 |
| 59 | <a href="#">c2jy5A</a>  | Alignment | not modelled | 7.1 | 8  | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquilin-1;<br><b>PDBTitle:</b> nmr structure of ubiquilin 1 uba domain                                                                                                                                                                        |
| 60 | <a href="#">c2kncA</a>  | Alignment | not modelled | 7.1 | 17 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB;<br><b>PDBTitle:</b> platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex                                                                                                                                    |
| 61 | <a href="#">c3idwA</a>  | Alignment | not modelled | 7.0 | 44 | <b>PDB header:</b> endocytosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> actin cytoskeleton-regulatory complex protein sla1;<br><b>PDBTitle:</b> crystal structure of sla1 homology domain 2                                                                                                                                   |
| 62 | <a href="#">c2glwA</a>  | Alignment | not modelled | 7.0 | 26 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> 92aa long hypothetical protein;<br><b>PDBTitle:</b> the solution structure of phs018 from pyrococcus horikoshii                                                                                                                                     |
| 63 | <a href="#">c1eu1A</a>  | Alignment | not modelled | 6.9 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dimethyl sulfoxide reductase;<br><b>PDBTitle:</b> the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.                                                         |
| 64 | <a href="#">c2kncB</a>  | Alignment | not modelled | 6.8 | 6  | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3;<br><b>PDBTitle:</b> platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex                                                                                                                                       |
| 65 | <a href="#">d1eu1a1</a> | Alignment | not modelled | 6.6 | 18 | <b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain                                                                                                                                                                                 |
| 66 | <a href="#">c2iv2X</a>  | Alignment | not modelled | 6.5 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> X: <b>PDB Molecule:</b> formate dehydrogenase h;<br><b>PDBTitle:</b> reinterpretation of reduced form of formate dehydrogenase h2 from e. coli                                                                                                                             |
| 67 | <a href="#">c1wlfa</a>  | Alignment | not modelled | 6.4 | 15 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> peroxisome biogenesis factor 1;<br><b>PDBTitle:</b> structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain                                                                               |
| 68 | <a href="#">c2jpcA</a>  | Alignment | not modelled | 6.2 | 14 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> ssrb;<br><b>PDBTitle:</b> ssrb dna binding protein                                                                                                                                                                                            |
| 69 | <a href="#">c1h5nC</a>  | Alignment | not modelled | 6.1 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> dmsO reductase;<br><b>PDBTitle:</b> dmsO reductase modified by the presence of dms and air                                                                                                                                                         |
| 70 | <a href="#">c2ki8A</a>  | Alignment | not modelled | 6.1 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase,<br><b>PDBTitle:</b> solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7                   |
| 71 | <a href="#">d1e32a1</a> | Alignment | not modelled | 6.0 | 10 | <b>Fold:</b> Double psi beta-barrel<br><b>Superfamily:</b> ADC-like<br><b>Family:</b> Cdc48 N-terminal domain-like                                                                                                                                                                                                            |
| 72 | <a href="#">d1q08a</a>  | Alignment | not modelled | 5.9 | 25 | <b>Fold:</b> Putative DNA-binding domain<br><b>Superfamily:</b> Putative DNA-binding domain<br><b>Family:</b> DNA-binding N-terminal domain of transcription activators                                                                                                                                                       |
| 73 | <a href="#">c3kwmC</a>  | Alignment | not modelled | 5.9 | 7  | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a;<br><b>PDBTitle:</b> crystal structure of ribose-5-isomerase a                                                                                                                                                           |
| 74 | <a href="#">c2k29A</a>  | Alignment | not modelled | 5.6 | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin relB;<br><b>PDBTitle:</b> structure of the dbd domain of e. coli antitoxin relB                                                                                                                                                           |
| 75 | <a href="#">d1oqya2</a> | Alignment | not modelled | 5.5 | 22 | <b>Fold:</b> RuvA C-terminal domain-like<br><b>Superfamily:</b> UBA-like<br><b>Family:</b> UBA domain                                                                                                                                                                                                                         |
| 76 | <a href="#">d1ijwc</a>  | Alignment | not modelled | 5.4 | 25 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> Recombinase DNA-binding domain                                                                                                                                                                                        |
| 77 | <a href="#">c2v45A</a>  | Alignment | not modelled | 5.4 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic nitrate reductase;<br><b>PDBTitle:</b> a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand |
| 78 | <a href="#">d1m56d</a>  | Alignment | not modelled | 5.4 | 12 | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> Bacterial aa3 type cytochrome c oxidase subunit IV<br><b>Family:</b> Bacterial aa3 type cytochrome c oxidase subunit IV                                                                                                                                        |
| 79 | <a href="#">d1ygya3</a> | Alignment | not modelled | 5.3 | 3  | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> ACT-like<br><b>Family:</b> Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain                                                                                                                                                                                 |
| 80 | <a href="#">c1lkzB</a>  | Alignment | not modelled | 5.3 | 7  | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ribose 5-phosphate isomerase a;<br><b>PDBTitle:</b> crystal structure of d-ribose-5-phosphate isomerase (rpiA)2 from escherichia coli.                                                                                                                  |

|    |                         |                                                                                             |              |     |    |                                                                                                                                                                                                                                                                   |
|----|-------------------------|---------------------------------------------------------------------------------------------|--------------|-----|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 81 | <a href="#">c2rmzA_</a> |  Alignment  | not modelled | 5.3 | 14 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> integrin beta-3;<br><b>PDBTitle:</b> bicelle-embedded integrin beta3 transmembrane segment                                                                                              |
| 82 | <a href="#">c2nyaF_</a> |  Alignment | not modelled | 5.3 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> F: <b>PDB Molecule:</b> periplasmic nitrate reductase;<br><b>PDBTitle:</b> crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli                                                 |
| 83 | <a href="#">c1zc1A_</a> |  Alignment | not modelled | 5.3 | 20 | <b>PDB header:</b> protein turnover<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin fusion degradation protein 1;<br><b>PDBTitle:</b> ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites                                         |
| 84 | <a href="#">c2ro5B_</a> |  Alignment | not modelled | 5.3 | 19 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> stage v sporulation protein t;<br><b>PDBTitle:</b> rdc-refined solution structure of the n-terminal dna2 recognition domain of the bacillus subtilis transition-3 state regulator spovt |
| 85 | <a href="#">c2yujA_</a> |  Alignment | not modelled | 5.3 | 20 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin fusion degradation 1-like;<br><b>PDBTitle:</b> solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1                                             |
| 86 | <a href="#">c2ivfA_</a> |  Alignment | not modelled | 5.3 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ethylbenzene dehydrogenase alpha-subunit;<br><b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum                                                                   |
| 87 | <a href="#">d1dzfa2</a> |  Alignment | not modelled | 5.2 | 29 | <b>Fold:</b> RPB5-like RNA polymerase subunit<br><b>Superfamily:</b> RPB5-like RNA polymerase subunit<br><b>Family:</b> RPB5                                                                                                                                      |
| 88 | <a href="#">c1lk5C_</a> |  Alignment | not modelled | 5.1 | 14 | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> d-ribose-5-phosphate isomerase;<br><b>PDBTitle:</b> structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii                                                             |
| 89 | <a href="#">c2kr6A_</a> |  Alignment | not modelled | 5.0 | 26 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> presenilin-1;<br><b>PDBTitle:</b> solution structure of presenilin-1 ctf subunit                                                                                                            |
| 90 | <a href="#">d1hmja_</a> |  Alignment | not modelled | 5.0 | 18 | <b>Fold:</b> RPB5-like RNA polymerase subunit<br><b>Superfamily:</b> RPB5-like RNA polymerase subunit<br><b>Family:</b> RPB5                                                                                                                                      |
| 91 | <a href="#">c1g8jC_</a> |  Alignment | not modelled | 5.0 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> arsenite oxidase;<br><b>PDBTitle:</b> crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis                                                                        |