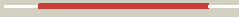

























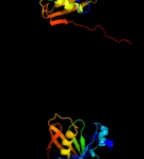

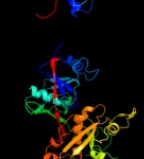

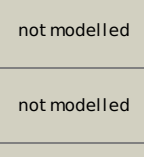


| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">c3g7kD_</a> |  Alignment   |    | 100.0      | 38     | <b>PDB header:</b> isomerase<br><b>Chain:</b> D: <b>PDB Molecule:</b> 3-methylitaconate isomerase;<br><b>PDBTitle:</b> crystal structure of methylitaconate-delta-isomerase   |
| 2  | <a href="#">c2pw0A_</a> |  Alignment   |    | 100.0      | 39     | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> prpf methylaconitate isomerase;<br><b>PDBTitle:</b> crystal structure of trans-aconitate bound to methylaconitate2 isomerase prpf from shewanella oneidensis                       |
| 3  | <a href="#">d2h9fa1</a> |  Alignment   |    | 100.0      | 42     | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> PA0793-like   |
| 4  | <a href="#">d2h9fa2</a> |  Alignment   |    | 100.0      | 30     | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> PA0793-like   |
| 5  | <a href="#">c1w62B_</a> |  Alignment |  | 99.4       | 18     | <b>PDB header:</b> racemase<br><b>Chain:</b> B: <b>PDB Molecule:</b> b-cell mitogen;<br><b>PDBTitle:</b> proline racemase in complex with one molecule of pyrrole-2-2 carboxylic acid (hemi form)   |
| 6  | <a href="#">d1tm0a_</a> |  Alignment |  | 98.5       | 26     | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> Proline racemase  |
| 7  | <a href="#">c2gkjA_</a> |  Alignment |  | 98.4       | 16     | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate epimerase;<br><b>PDBTitle:</b> crystal structure of diaminopimelate epimerase in complex2 with an irreversible inhibitor dl-azidap  |
| 8  | <a href="#">c3ednB_</a> |  Alignment |  | 98.1       | 18     | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> phenazine biosynthesis protein, phzf family;<br><b>PDBTitle:</b> crystal structure of the bacillus anthracis phenazine2 biosynthesis protein, phzf family                      |
| 9  | <a href="#">c3ekmE_</a> |  Alignment |  | 98.0       | 16     | <b>PDB header:</b> isomerase<br><b>Chain:</b> E: <b>PDB Molecule:</b> diaminopimelate epimerase, chloroplastic;<br><b>PDBTitle:</b> crystal structure of diaminopimelate epimerase form2 arabidopsis thaliana in complex with irreversible inhibitor3 dl-azidap |
| 10 | <a href="#">c1ym5A_</a> |  Alignment |  | 97.4       | 13     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 32.6 kda protein in dap2-slt2<br><b>PDBTitle:</b> crystal structure of yhi9, the yeast member of the2 phenazine biosynthesis phzf enzyme superfamily.                   |
| 11 | <a href="#">d1xuba1</a> |  Alignment |  | 97.3       | 18     | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> PhzC/PhzF-like  |

|    |                         |           |   |      |    |  |
|----|-------------------------|-----------|---|------|----|--|
| 12 | <a href="#">c1u1wA_</a> | Alignment |     | 97.2 | 18 | <b>PDB header:</b> isomerase, lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phenazine biosynthesis protein phzf;<br><b>PDBTitle:</b> structure and function of phenazine-biosynthesis protein phzf from2 pseudomonas fluorescens 2-79 |
| 13 | <a href="#">d1qy9a1</a> | Alignment |    | 96.4 | 18 | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> PhzC/PhzF-like   |
| 14 | <a href="#">d1s7ja_</a> | Alignment |    | 95.9 | 13 | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> PhzC/PhzF-like   |
| 15 | <a href="#">c1qy9B_</a> | Alignment |    | 95.6 | 16 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ydde;<br><b>PDBTitle:</b> crystal structure of e. coli se-met protein ydde   |
| 16 | <a href="#">d1xuba2</a> | Alignment |    | 95.2 | 18 | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> PhzC/PhzF-like   |
| 17 | <a href="#">d1qy9a2</a> | Alignment |   | 95.2 | 16 | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> PhzC/PhzF-like   |
| 18 | <a href="#">c3fveA_</a> | Alignment |  | 95.1 | 18 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate epimerase;<br><b>PDBTitle:</b> crystal structure of diaminopimelate epimerase mycobacterium2 tuberculosis dapf                                   |
| 19 | <a href="#">c2otnB_</a> | Alignment |  | 94.8 | 21 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelate epimerase;<br><b>PDBTitle:</b> crystal structure of the catalytically active form of diaminopimelate2 epimerase from bacillus anthracis          |
| 20 | <a href="#">d1u0ka1</a> | Alignment |  | 93.4 | 10 | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> PhzC/PhzF-like   |
| 21 | <a href="#">d2gkea1</a> | Alignment | not modelled  | 93.3 | 17 | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> Diaminopimelate epimerase  |
| 22 | <a href="#">d2gkea2</a> | Alignment | not modelled  | 90.2 | 16 | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> Diaminopimelate epimerase  |
| 23 | <a href="#">c2azpA_</a> | Alignment | not modelled  | 87.6 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa1268;<br><b>PDBTitle:</b> crystal structure of pa1268 solved by sulfur sad                                    |
| 24 | <a href="#">c1u0kA_</a> | Alignment | not modelled  | 83.8 | 8  | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> gene product pa4716;<br><b>PDBTitle:</b> the structure of a predicted epimerase pa4716 from pseudomonas2 aeruginosa                  |
| 25 | <a href="#">c1pyuD_</a> | Alignment | not modelled  | 61.1 | 21 | <b>PDB header:</b> lyase<br><b>Chain:</b> D: <b>PDB Molecule:</b> aspartate 1-decarboxylase alfa chain;<br><b>PDBTitle:</b> processed aspartate decarboxylase mutant with ser25 mutated to cys   |
| 26 | <a href="#">c3ougA_</a> | Alignment | not modelled  | 58.5 | 36 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartate 1-decarboxylase;<br><b>PDBTitle:</b> crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis                             |
| 27 | <a href="#">c1vc3B_</a> | Alignment | not modelled  | 57.5 | 25 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> l-aspartate-alpha-decarboxylase heavy chain;<br><b>PDBTitle:</b> crystal structure of l-aspartate-alpha-decarboxylase  |
| 28 | <a href="#">c1pt1B_</a> | Alignment | not modelled  | 56.1 | 21 | <b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> aspartate 1-decarboxylase;<br><b>PDBTitle:</b> unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine                          |
|    |                         |           |   |      |    | <b>Fold:</b> Double psi beta-barrel  |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 29 | <a href="#">d1ppya_</a> | Alignment | not modelled | 55.7 | 21 | <b>Superfamily:</b> ADC-like<br><b>Family:</b> Pyruvoyl dependent aspartate decarboxylase, ADC  |
| 30 | <a href="#">c2c45F_</a> | Alignment | not modelled | 51.5 | 32 | <b>PDB header:</b> lyase<br><b>Chain:</b> F: <b>PDB Molecule:</b> aspartate 1-decarboxylase precursor;<br><b>PDBTitle:</b> native precursor of pyruvoyl dependent aspartate2 decarboxylase  |
| 31 | <a href="#">d1bk8a_</a> | Alignment | not modelled | 39.2 | 31 | <b>Fold:</b> Knottins (small inhibitors, toxins, lectins)<br><b>Superfamily:</b> Scorpion toxin-like<br><b>Family:</b> Plant defensins  |
| 32 | <a href="#">d1yq2a1</a> | Alignment | not modelled | 36.4 | 13 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> beta-Galactosidase/glucuronidase domain<br><b>Family:</b> beta-Galactosidase/glucuronidase domain   |
| 33 | <a href="#">d1kl7a_</a> | Alignment | not modelled | 25.5 | 44 | <b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes<br><b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes<br><b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes |
| 34 | <a href="#">d1jz8a2</a> | Alignment | not modelled | 25.1 | 12 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> beta-Galactosidase/glucuronidase domain<br><b>Family:</b> beta-Galactosidase/glucuronidase domain   |
| 35 | <a href="#">d1h6ua1</a> | Alignment | not modelled | 24.7 | 32 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Internalin Ig-like domain   |
| 36 | <a href="#">d2omza1</a> | Alignment | not modelled | 23.6 | 26 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Internalin Ig-like domain   |
| 37 | <a href="#">c3opwA_</a> | Alignment | not modelled | 21.7 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> dna damage-responsive transcriptional repressor rph1;<br><b>PDBTitle:</b> crystal structure of the rph1 catalytic core   |
| 38 | <a href="#">d1h6ta1</a> | Alignment | not modelled | 21.2 | 21 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Internalin Ig-like domain   |
| 39 | <a href="#">c2wh7A_</a> | Alignment | not modelled | 17.5 | 36 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hyaluronidase-phage associated;<br><b>PDBTitle:</b> the partial structure of a group a streptococcal phage-2 encoded tail fibre hyaluronate lyase hylp2             |
| 40 | <a href="#">d1w5sa1</a> | Alignment | not modelled | 16.7 | 46 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Helicase DNA-binding domain  |
| 41 | <a href="#">d1xhja_</a> | Alignment | not modelled | 14.3 | 18 | <b>Fold:</b> Alpha-lytic protease prodomain-like<br><b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like<br><b>Family:</b> NifU C-terminal domain-like  |
| 42 | <a href="#">d1ayja_</a> | Alignment | not modelled | 13.8 | 23 | <b>Fold:</b> Knottins (small inhibitors, toxins, lectins)<br><b>Superfamily:</b> Scorpion toxin-like<br><b>Family:</b> Plant defensins  |
| 43 | <a href="#">c4proD_</a> | Alignment | not modelled | 12.8 | 22 | <b>PDB header:</b> serine protease<br><b>Chain:</b> D: <b>PDB Molecule:</b> alpha-lytic protease;<br><b>PDBTitle:</b> alpha-lytic protease complexed with pro region  |
| 44 | <a href="#">d1yuaa1</a> | Alignment | not modelled | 12.7 | 29 | <b>Fold:</b> Rubredoxin-like<br><b>Superfamily:</b> Zinc beta-ribbon<br><b>Family:</b> Prokaryotic DNA topoisomerase I, a C-terminal fragment   |
| 45 | <a href="#">d1xpma2</a> | Alignment | not modelled | 12.4 | 27 | <b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Chalcone synthase-like  |
| 46 | <a href="#">c2qj8B_</a> | Alignment | not modelled | 12.4 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> mlr6093 protein;<br><b>PDBTitle:</b> crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution       |
| 47 | <a href="#">d1ee0a2</a> | Alignment | not modelled | 12.2 | 36 | <b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Chalcone synthase-like  |
| 48 | <a href="#">d1u0ka2</a> | Alignment | not modelled | 12.0 | 23 | <b>Fold:</b> Diaminopimelate epimerase-like<br><b>Superfamily:</b> Diaminopimelate epimerase-like<br><b>Family:</b> PhzC/PhzF-like  |
| 49 | <a href="#">c1yuA_</a>  | Alignment | not modelled | 11.1 | 29 | <b>PDB header:</b> dna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase i;<br><b>PDBTitle:</b> c-terminal domain of escherichia coli topoisomerase i  |
| 50 | <a href="#">c3tsyA_</a> | Alignment | not modelled | 11.0 | 31 | <b>PDB header:</b> ligase, transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein 4-coumarate--coa ligase 1, resveratrol<br><b>PDBTitle:</b> 4-coumaroyl-coa ligase::stilbene synthase fusion protein                        |
| 51 | <a href="#">c3muwU_</a> | Alignment | not modelled | 10.9 | 15 | <b>PDB header:</b> virus<br><b>Chain:</b> U: <b>PDB Molecule:</b> structural polyprotein;<br><b>PDBTitle:</b> pseudo-atomic structure of the e2-e1 protein shell in sindbis virus   |
| 52 | <a href="#">d1bi5a2</a> | Alignment | not modelled | 10.3 | 36 | <b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Chalcone synthase-like  |
| 53 | <a href="#">d1u0ua2</a> | Alignment | not modelled | 10.3 | 36 | <b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Chalcone synthase-like  |
| 54 | <a href="#">d1xafa_</a> | Alignment | not modelled | 9.7  | 20 | <b>Fold:</b> CNF1/YfiH-like putative cysteine hydrolases<br><b>Superfamily:</b> CNF1/YfiH-like putative cysteine hydrolases<br><b>Family:</b> YfiH-like   |
| 55 | <a href="#">d1gpqa_</a> | Alignment | not modelled | 9.1  | 36 | <b>Fold:</b> Inhibitor of vertebrate lysozyme, Ivy<br><b>Superfamily:</b> Inhibitor of vertebrate lysozyme, Ivy   |

|    |                         |           |              |     |   |
|----|-------------------------|-----------|--------------|-----|---|
|    |                         |           |              |     | <b>Family:</b> Inhibitor of vertebrate lysozyme, lvy  |
| 56 | <a href="#">d1tbxa_</a> | Alignment | not modelled | 8.9 | 19<br><b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> F93-like   |
| 57 | <a href="#">d2b59b2</a> | Alignment | not modelled | 8.5 | 33<br><b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Carboxypeptidase regulatory domain-like<br><b>Family:</b> Pre-dockerin domain   |
| 58 | <a href="#">c2klxA_</a> | Alignment | not modelled | 8.5 | 18<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin;<br><b>PDBTitle:</b> solution structure of glutaredoxin from bartonella henselae str.2 houston  |
| 59 | <a href="#">c2bs5A_</a> | Alignment | not modelled | 8.2 | 29<br><b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> fucose-binding lectin protein;<br><b>PDBTitle:</b> lectin from ralstonia solanacearum complexed with 2-2 fucosyllactose   |
| 60 | <a href="#">c1uheA_</a> | Alignment | not modelled | 8.0 | 25<br><b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> aspartate 1-decarboxylase alpha chain;<br><b>PDBTitle:</b> crystal structure of aspartate decarboxylase, isoasparagine complex  |
| 61 | <a href="#">c3a5iB_</a> | Alignment | not modelled | 7.6 | 37<br><b>PDB header:</b> protein transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> flagellar biosynthesis protein flha;<br><b>PDBTitle:</b> structure of the cytoplasmic domain of flha  |
| 62 | <a href="#">d1rv9a_</a> | Alignment | not modelled | 7.5 | 20<br><b>Fold:</b> CNF1/YfiH-like putative cysteine hydrolases<br><b>Superfamily:</b> CNF1/YfiH-like putative cysteine hydrolases<br><b>Family:</b> YfiH-like   |
| 63 | <a href="#">c3mixA_</a> | Alignment | not modelled | 7.5 | 45<br><b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> flagellar biosynthesis protein flha;<br><b>PDBTitle:</b> crystal structure of the cytosolic domain of b. subtilis flha  |
| 64 | <a href="#">c2d3mA_</a> | Alignment | not modelled | 7.1 | 25<br><b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pentaketide chromone synthase;<br><b>PDBTitle:</b> pentaketide chromone synthase complexed with coenzyme a  |
| 65 | <a href="#">c1xtB_</a>  | Alignment | not modelled | 7.0 | 27<br><b>PDB header:</b> lyase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxy-3-methylglutaryl-coa synthase;<br><b>PDBTitle:</b> staphylococcus aureus 3-hydroxy-3-methylglutaryl-coa2 synthase   |
| 66 | <a href="#">d1gmia_</a> | Alignment | not modelled | 6.8 | 11<br><b>Fold:</b> C2 domain-like<br><b>Superfamily:</b> C2 domain (Calcium/lipid-binding domain, CaLB)<br><b>Family:</b> PLC-like (P variant)  |
| 67 | <a href="#">d2ckca1</a> | Alignment | not modelled | 6.6 | 35<br><b>Fold:</b> GYF/BRK domain-like<br><b>Superfamily:</b> BRK domain-like<br><b>Family:</b> BRK domain-like   |
| 68 | <a href="#">c2ckcA_</a> | Alignment | not modelled | 6.6 | 35<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> chromodomain-helicase-dna-binding protein 7;<br><b>PDBTitle:</b> solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction |
| 69 | <a href="#">c3o6xC_</a> | Alignment | not modelled | 6.6 | 20<br><b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> glutamine synthetase;<br><b>PDBTitle:</b> crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis  |
| 70 | <a href="#">d1ueba1</a> | Alignment | not modelled | 6.3 | 19<br><b>Fold:</b> SH3-like barrel<br><b>Superfamily:</b> Translation proteins SH3-like domain<br><b>Family:</b> eIF5a N-terminal domain-like   |
| 71 | <a href="#">d1t8ha_</a> | Alignment | not modelled | 6.2 | 25<br><b>Fold:</b> CNF1/YfiH-like putative cysteine hydrolases<br><b>Superfamily:</b> CNF1/YfiH-like putative cysteine hydrolases<br><b>Family:</b> YfiH-like   |
| 72 | <a href="#">d1u0ma2</a> | Alignment | not modelled | 6.2 | 31<br><b>Fold:</b> Thiolase-like<br><b>Superfamily:</b> Thiolase-like<br><b>Family:</b> Chalcone synthase-like  |
| 73 | <a href="#">c2ht9A_</a> | Alignment | not modelled | 6.0 | 19<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin-2;<br><b>PDBTitle:</b> the structure of dimeric human glutaredoxin 2  |
| 74 | <a href="#">d2yvxa3</a> | Alignment | not modelled | 5.9 | 19<br><b>Fold:</b> MgtE membrane domain-like<br><b>Superfamily:</b> MgtE membrane domain-like<br><b>Family:</b> MgtE membrane domain-like   |
| 75 | <a href="#">c3brcA_</a> | Alignment | not modelled | 5.9 | 28<br><b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein of unknown function;<br><b>PDBTitle:</b> crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum  |
| 76 | <a href="#">c2xfbl_</a> | Alignment | not modelled | 5.9 | 20<br><b>PDB header:</b> virus<br><b>Chain:</b> I: <b>PDB Molecule:</b> e2 envelope glycoprotein;<br><b>PDBTitle:</b> the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map   |
| 77 | <a href="#">c2zunB_</a> | Alignment | not modelled | 5.9 | 28<br><b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 458aa long hypothetical endo-1,4-beta-glucanase;<br><b>PDBTitle:</b> functional analysis of hyperthermophilic endocellulase from2 the archaeon pyrococcus horikoshii  |
| 78 | <a href="#">d2v0ea1</a> | Alignment | not modelled | 5.8 | 35<br><b>Fold:</b> GYF/BRK domain-like<br><b>Superfamily:</b> BRK domain-like<br><b>Family:</b> BRK domain-like   |
| 79 | <a href="#">c3izcG_</a> | Alignment | not modelled | 5.8 | 17<br><b>PDB header:</b> ribosome<br><b>Chain:</b> G: <b>PDB Molecule:</b> 60s ribosomal protein rpl6 (l6e);<br><b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome  |
| 80 | <a href="#">c3n43B_</a> | Alignment | not modelled | 5.8 | 20<br><b>PDB header:</b> viral protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> e2 envelope glycoprotein;<br><b>PDBTitle:</b> crystal structures of the mature envelope glycoprotein complex2 (trypsin cleavage) of chikungunya virus.  |
|    |                         |           |              |     | <b>PDB header:</b> viral protein  |

|    |                         |           |              |     |    |   |
|----|-------------------------|-----------|--------------|-----|----|---|
| 81 | <a href="#">c3n40P_</a> | Alignment | not modelled | 5.7 | 18 | <b>Chain:</b> P: <b>PDB Molecule:</b> p62 envelope glycoprotein;<br><b>PDBTitle:</b> crystal structure of the immature envelope glycoprotein complex of2 chikungunya virus.   |
| 82 | <a href="#">d1rw0a_</a> | Alignment | not modelled | 5.5 | 23 | <b>Fold:</b> CNF1/YfiH-like putative cysteine hydrolases<br><b>Superfamily:</b> CNF1/YfiH-like putative cysteine hydrolases<br><b>Family:</b> YfiH-like   |
| 83 | <a href="#">d1b24a2</a> | Alignment | not modelled | 5.3 | 43 | <b>Fold:</b> Homing endonuclease-like<br><b>Superfamily:</b> Homing endonucleases<br><b>Family:</b> Group I mobile intron endonuclease  |
| 84 | <a href="#">d1a77a1</a> | Alignment | not modelled | 5.2 | 23 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> 5' to 3' exonuclease, C-terminal subdomain<br><b>Family:</b> 5' to 3' exonuclease, C-terminal subdomain   |
| 85 | <a href="#">c3mydA_</a> | Alignment | not modelled | 5.1 | 32 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> flagellar biosynthesis protein flha;<br><b>PDBTitle:</b> structure of the cytoplasmic domain of flha from helicobacter pylori                                     |
| 86 | <a href="#">c2xm5A_</a> | Alignment | not modelled | 5.1 | 29 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cloq;<br><b>PDBTitle:</b> structural and mechanistic analysis of the magnesium-2 independent aromatic prenyltransferase cloq from the3 clorobiocin biosynthetic pathway |
| 87 | <a href="#">c2p8uB_</a> | Alignment | not modelled | 5.1 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa synthase, cytoplasmic;<br><b>PDBTitle:</b> crystal structure of human 3-hydroxy-3-methylglutaryl coa synthase i                               |
| 88 | <a href="#">c3lehA_</a> | Alignment | not modelled | 5.1 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative hydroxymethylglutaryl-coa synthase;<br><b>PDBTitle:</b> the crystal structure of smu.943c from streptococcus mutans ua159                                      |