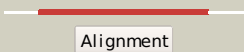
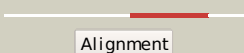
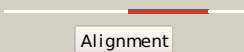
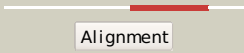
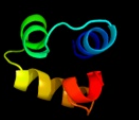
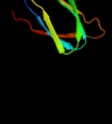
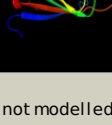


# Phyre2

|               |                             |
|---------------|-----------------------------|
| Email         | I.a.kelley@imperial.ac.uk   |
| Description   | A4UR80                      |
| Date          | Thu Jan 5 10:55:08 GMT 2012 |
| Unique Job ID | 8923b57e530990e2            |

Detailed template information

| #  | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                                                   |
|----|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c3gbgA_</a> | <br>Alignment   |    | 100.0      | 13     | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> tcp pilus virulence regulatory protein;<br><b>PDBTitle:</b> crystal structure of toxT from vibrio cholerae o395                                                                                                    |
| 2  | <a href="#">c1d5yD_</a> | <br>Alignment   |    | 99.9       | 22     | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> D: <b>PDB Molecule:</b> rob transcription factor;<br><b>PDBTitle:</b> crystal structure of the e. coli rob transcription factor2 in complex with dna                                                                                             |
| 3  | <a href="#">c3oouA_</a> | <br>Alignment   |    | 99.9       | 28     | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> lin2118 protein;<br><b>PDBTitle:</b> the structure of a protein with unkown function from listeria innocua                                                                                           |
| 4  | <a href="#">c3oioA_</a> | <br>Alignment   |   | 99.9       | 21     | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (arac-type dna-binding domain-<br><b>PDBTitle:</b> crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum     |
| 5  | <a href="#">c1bl0A_</a> | <br>Alignment |  | 99.9       | 20     | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (multiple antibiotic resistance protein);<br><b>PDBTitle:</b> multiple antibiotic resistance protein (mara)/dna complex                                                                                          |
| 6  | <a href="#">c3mklB_</a> | <br>Alignment |  | 99.9       | 20     | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator gadx;<br><b>PDBTitle:</b> crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12                                                           |
| 7  | <a href="#">c2k9sA_</a> | <br>Alignment |  | 99.9       | 17     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> arabinose operon regulatory protein;<br><b>PDBTitle:</b> solution structure of dna binding domain of e. coli arac                                                                                                            |
| 8  | <a href="#">c3mn2B_</a> | <br>Alignment |  | 99.9       | 21     | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable arac family transcriptional regulator;<br><b>PDBTitle:</b> the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009                              |
| 9  | <a href="#">c3lsgD_</a> | <br>Alignment |  | 99.8       | 22     | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> D: <b>PDB Molecule:</b> two-component response regulator yesn;<br><b>PDBTitle:</b> the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586 |
| 10 | <a href="#">d1d5ya2</a> | <br>Alignment |  | 99.5       | 31     | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> AraC type transcriptional activator                                                                                                                                                            |
| 11 | <a href="#">d1bl0a2</a> | <br>Alignment |  | 99.5       | 23     | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> AraC type transcriptional activator                                                                                                                                                            |

|    |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                                                                                           |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">d2arca_</a> | Alignment |     | 98.9 | 14 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> Regulatory protein AraC<br><b>Family:</b> Regulatory protein AraC                                                                                                                                                                          |
| 13 | <a href="#">d1bl0a1</a> | Alignment |    | 98.8 | 19 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> AraC type transcriptional activator                                                                                                                                                               |
| 14 | <a href="#">d1d5ya1</a> | Alignment |    | 98.8 | 15 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> AraC type transcriptional activator                                                                                                                                                               |
| 15 | <a href="#">c3ibmB_</a> | Alignment |    | 98.8 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein;<br><b>PDBTitle:</b> crystal structure of cupin 2 domain-containing protein hha1_0468 from2 halorhodospira halophila                                           |
| 16 | <a href="#">c1zgwA_</a> | Alignment |    | 98.7 | 19 | <b>PDB header:</b> transcription regulator/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> ada polypprotein;<br><b>PDBTitle:</b> nmr structure of e. coli ada protein in complex with dna                                                                                                                    |
| 17 | <a href="#">c3kgzA_</a> | Alignment |   | 98.6 | 21 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein;<br><b>PDBTitle:</b> crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris                                            |
| 18 | <a href="#">c3h7yA_</a> | Alignment |  | 98.6 | 11 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> bacilysin biosynthesis protein bacb;<br><b>PDBTitle:</b> crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form                                                                       |
| 19 | <a href="#">c3jzvA_</a> | Alignment |  | 98.6 | 21 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rru_a2000;<br><b>PDBTitle:</b> crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.                                                                    |
| 20 | <a href="#">d1vj2a_</a> | Alignment |  | 98.5 | 17 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> TM1459-like                                                                                                                                                                                             |
| 21 | <a href="#">d1yfua1</a> | Alignment | not modelled                                                                        | 98.5 | 20 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> 3-hydroxyanthranilic acid dioxygenase-like                                                                                                                                                              |
| 22 | <a href="#">c3fjsC_</a> | Alignment | not modelled                                                                        | 98.5 | 16 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein with rmlc-like cupin fold;<br><b>PDBTitle:</b> crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution |
| 23 | <a href="#">c2ozjB_</a> | Alignment | not modelled                                                                        | 98.4 | 11 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel;<br><b>PDBTitle:</b> crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution                                                      |
| 24 | <a href="#">c3cewA_</a> | Alignment | not modelled                                                                        | 98.4 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized cupin protein;<br><b>PDBTitle:</b> crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205                     |
| 25 | <a href="#">d1y9qa2</a> | Alignment | not modelled                                                                        | 98.4 | 16 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Probable transcriptional regulator VC1968, C-terminal domain                                                                                                                                            |
| 26 | <a href="#">c3d82A_</a> | Alignment | not modelled                                                                        | 98.4 | 16 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein;<br><b>PDBTitle:</b> crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution                        |
| 27 | <a href="#">d1y3ta1</a> | Alignment | not modelled                                                                        | 98.4 | 18 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins                                                                                                                                                                                                                           |

|    |                         |           |                                                                                   |      |                                                                                                                                                                                                                                                                                                               |
|----|-------------------------|-----------|-----------------------------------------------------------------------------------|------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                         |           |                                                                                   |      | <b>Family:</b> Quercetin 2,3-dioxygenase-like                                                                                                                                                                                                                                                                 |
| 28 | <a href="#">dlsefa_</a> | Alignment | not modelled                                                                      | 98.3 | 14<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> YlbA-like                                                                                                                                                                                             |
| 29 | <a href="#">clsefA_</a> | Alignment | not modelled                                                                      | 98.3 | 14<br><b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein;<br><b>PDBTitle:</b> crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis                                                                      |
| 30 | <a href="#">c2gu9B_</a> | Alignment | not modelled                                                                      | 98.3 | 14<br><b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> tetracenomycin polyketide synthesis protein;<br><b>PDBTitle:</b> crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure |
| 31 | <a href="#">c2pfwB_</a> | Alignment | not modelled                                                                      | 98.3 | 21<br><b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein;<br><b>PDBTitle:</b> crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution                                             |
| 32 | <a href="#">dl04ta_</a> | Alignment | not modelled                                                                      | 98.3 | 25<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> TM1287-like                                                                                                                                                                                           |
| 33 | <a href="#">c2o8qA_</a> | Alignment | not modelled                                                                      | 98.3 | 23<br><b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> crystal structure of a protein with a cupin-like fold and unknown2 function (bxo_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution                            |
| 34 | <a href="#">dlsq4a_</a> | Alignment | not modelled                                                                      | 98.3 | 14<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> YlbA-like                                                                                                                                                                                             |
| 35 | <a href="#">c3rnsA_</a> | Alignment | not modelled                                                                      | 98.3 | 18<br><b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein;<br><b>PDBTitle:</b> cupin 2 conserved barrel domain protein from leptotrichia buccalis                                                                       |
| 36 | <a href="#">dl1r5a_</a> | Alignment |  | 98.2 | 18<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                        |
| 37 | <a href="#">dl1sfa_</a> | Alignment | not modelled                                                                      | 98.2 | 10<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> YlbA-like                                                                                                                                                                                             |
| 38 | <a href="#">c3bu7A_</a> | Alignment | not modelled                                                                      | 98.2 | 15<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gentisate 1,2-dioxygenase;<br><b>PDBTitle:</b> crystal structure and biochemical characterization of glosp,2 a gentisate 1,2-dioxygenase from silicibacter pomeroyi                                                          |
| 39 | <a href="#">d3bu7a1</a> | Alignment | not modelled                                                                      | 98.2 | 15<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Gentisate 1,2-dioxygenase-like                                                                                                                                                                        |
| 40 | <a href="#">dluika1</a> | Alignment | not modelled                                                                      | 98.2 | 15<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                        |
| 41 | <a href="#">c2d40C_</a> | Alignment | not modelled                                                                      | 98.2 | 16<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative gentisate 1,2-dioxygenase;<br><b>PDBTitle:</b> crystal structure of z3393 from escherichia coli o157:h7                                                                                                             |
| 42 | <a href="#">dlv70a_</a> | Alignment | not modelled                                                                      | 98.2 | 21<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> TM1287-like                                                                                                                                                                                           |
| 43 | <a href="#">d2d40a1</a> | Alignment | not modelled                                                                      | 98.2 | 10<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Gentisate 1,2-dioxygenase-like                                                                                                                                                                        |
| 44 | <a href="#">d2b8ma1</a> | Alignment | not modelled                                                                      | 98.2 | 11<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> MJ0764-like                                                                                                                                                                                           |
| 45 | <a href="#">d2phda1</a> | Alignment | not modelled                                                                      | 98.2 | 16<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Gentisate 1,2-dioxygenase-like                                                                                                                                                                        |
| 46 | <a href="#">dlvhfa1</a> | Alignment | not modelled                                                                      | 98.2 | 15<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> TM1287-like                                                                                                                                                                                           |
| 47 | <a href="#">c3i7dB_</a> | Alignment | not modelled                                                                      | 98.1 | 21<br><b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> sugar phosphate isomerase;<br><b>PDBTitle:</b> crystal structure of sugar phosphate isomerase from a cupin2 superfamily spo2919 from silicibacter pomeroyi (yp_168127.1) from3 silicibacter pomeroyi dss-3 at 2.30 a resolution   |
| 48 | <a href="#">c3l2hD_</a> | Alignment | not modelled                                                                      | 98.1 | 23<br><b>PDB header:</b> isomerase<br><b>Chain:</b> D: <b>PDB Molecule:</b> putative sugar phosphate isomerase;<br><b>PDBTitle:</b> crystal structure of putative sugar phosphate isomerase (afe_0303)2 from acidithiobacillus ferrooxidans atcc 23270 at 1.85 a resolution                                   |
| 49 | <a href="#">dluija1</a> | Alignment | not modelled                                                                      | 98.1 | 17<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                        |
| 50 | <a href="#">dlrc6a_</a> | Alignment | not modelled                                                                      | 98.1 | 14<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> YlbA-like                                                                                                                                                                                             |
| 51 | <a href="#">d2f4pa1</a> | Alignment | not modelled                                                                      | 98.1 | 24<br><b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> TM1287-like                                                                                                                                                                                           |

|    |                          |           |              |      |    |                                                                                                                                                                                                                                                                                                                                                                            |
|----|--------------------------|-----------|--------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 52 | <a href="#">c2oa2A_</a>  | Alignment | not modelled | 98.1 | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> bh2720 protein;<br><b>PDBTitle:</b> crystal structure of bh2720 (10175341) from bacillus halodurans at2 1.41 a resolution                                                                                                                                                |
| 53 | <a href="#">c2i45C_</a>  | Alignment | not modelled | 98.1 | 21 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> crystal structure of protein nmb1881 from neisseria meningitidis                                                                                                                                                               |
| 54 | <a href="#">dlzvfa1</a>  | Alignment | not modelled | 98.1 | 15 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> 3-hydroxyanthranilic acid dioxygenase-like                                                                                                                                                                                                                               |
| 55 | <a href="#">c3bcwB_</a>  | Alignment | not modelled | 98.0 | 15 | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution                                                                                                     |
| 56 | <a href="#">c2vpvA_</a>  | Alignment | not modelled | 98.0 | 13 | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein mif2;<br><b>PDBTitle:</b> dimerization domain of mif2p                                                                                                                                                                                                                                      |
| 57 | <a href="#">c3h8uA_</a>  | Alignment | not modelled | 98.0 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein with double-stranded<br><b>PDBTitle:</b> crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution |
| 58 | <a href="#">c3ht2A_</a>  | Alignment | not modelled | 98.0 | 25 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> remf protein;<br><b>PDBTitle:</b> zink containing polyketide cyclase remf from streptomyces2 resistomycificus                                                                                                                                                                                            |
| 59 | <a href="#">dljuha_</a>  | Alignment | not modelled | 97.9 | 22 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Quercetin 2,3-dioxygenase-like                                                                                                                                                                                                                                           |
| 60 | <a href="#">c3lwcA_</a>  | Alignment | not modelled | 97.9 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of structural genomics, unknown function2 (yp_766765.1) from rhizobium leguminosarum bv. viciae 3841 at 1.40 a3 resolution                                                                                |
| 61 | <a href="#">dlzrra1</a>  | Alignment | not modelled | 97.9 | 16 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Acireductone dioxygenase                                                                                                                                                                                                                                                 |
| 62 | <a href="#">dl dgwa_</a> | Alignment | not modelled | 97.8 | 17 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                                                                           |
| 63 | <a href="#">dlj58a_</a>  | Alignment | not modelled | 97.8 | 24 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                                                                           |
| 64 | <a href="#">dlx82a_</a>  | Alignment | not modelled | 97.8 | 21 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Glucose-6-phosphate isomerase, GPI                                                                                                                                                                                                                                       |
| 65 | <a href="#">c2q30C_</a>  | Alignment | not modelled | 97.7 | 14 | <b>PDB header:</b> unknown function<br><b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution                                                                                                                          |
| 66 | <a href="#">dlj3pa_</a>  | Alignment | not modelled | 97.7 | 21 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Glucose-6-phosphate isomerase, GPI                                                                                                                                                                                                                                       |
| 67 | <a href="#">c1y9qA_</a>  | Alignment | not modelled | 97.7 | 16 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family;<br><b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae                                                                                                                                         |
| 68 | <a href="#">c2vqaC_</a>  | Alignment | not modelled | 97.7 | 19 | <b>PDB header:</b> metal-binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> sll1358 protein;<br><b>PDBTitle:</b> protein-folding location can regulate mn versus cu- or zn-2 binding. crystal structure of mnca.                                                                                                                                                     |
| 69 | <a href="#">c2fqpD_</a>  | Alignment | not modelled | 97.6 | 18 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein bp2299;<br><b>PDBTitle:</b> crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution                                                                                                                                   |
| 70 | <a href="#">dl o5ua_</a> | Alignment | not modelled | 97.6 | 22 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Hypothetical protein TM1112                                                                                                                                                                                                                                              |
| 71 | <a href="#">c3es1A_</a>  | Alignment | not modelled | 97.5 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein;<br><b>PDBTitle:</b> crystal structure of protein with a cupin-like fold and unknown2 function (yp_001165807.1) from novosphingobium aromaticivorans dsm3 12444 at 1.91 a resolution                                            |
| 72 | <a href="#">d2et1a1</a>  | Alignment | not modelled | 97.5 | 24 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                                                                           |
| 73 | <a href="#">c2eaaB_</a>  | Alignment | not modelled | 97.4 | 18 | <b>PDB header:</b> plant protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> 7s globulin-3;<br><b>PDBTitle:</b> crystal structure of adzuki bean 7s globulin-3                                                                                                                                                                                                                |
| 74 | <a href="#">d2bnma2</a>  | Alignment | not modelled | 97.4 | 19 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> TM1459-like                                                                                                                                                                                                                                                              |
| 75 | <a href="#">dlfxza1</a>  | Alignment | not modelled | 97.4 | 13 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                                                                           |
| 76 | <a href="#">d2pyta1</a>  | Alignment | not modelled | 97.4 | 19 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> EutQ-like                                                                                                                                                                                                                                                                |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                                                                             |
|-----|-------------------------|-----------|--------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 77  | <a href="#">c2oziA</a>  | Alignment | not modelled | 97.4 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rpa4178;<br><b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodospseudomonas palustris cga009                                                                                       |
| 78  | <a href="#">c1uijA</a>  | Alignment | not modelled | 97.4 | 17 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta subunit of beta conglycinin;<br><b>PDBTitle:</b> crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)                                                                                                                                        |
| 79  | <a href="#">c1cauB</a>  | Alignment | not modelled | 97.4 | 19 | <b>PDB header:</b> seed storage protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> canavalin;<br><b>PDBTitle:</b> determination of three crystal structures of canavalin by molecular2 replacement                                                                                                                                                            |
| 80  | <a href="#">d2phla1</a> | Alignment | not modelled | 97.3 | 15 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                                                            |
| 81  | <a href="#">d2phla2</a> | Alignment | not modelled | 97.3 | 13 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                                                            |
| 82  | <a href="#">d1fxza2</a> | Alignment | not modelled | 97.3 | 9  | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                                                            |
| 83  | <a href="#">c2opkC</a>  | Alignment | not modelled | 97.2 | 14 | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein;<br><b>PDBTitle:</b> crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution                                                                                                             |
| 84  | <a href="#">c3s7eB</a>  | Alignment | not modelled | 97.1 | 16 | <b>PDB header:</b> allergen<br><b>Chain:</b> B: <b>PDB Molecule:</b> allergen ara h 1, clone p41b;<br><b>PDBTitle:</b> crystal structure of ara h 1                                                                                                                                                                                                         |
| 85  | <a href="#">d1od5a2</a> | Alignment | not modelled | 97.1 | 12 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                                                            |
| 86  | <a href="#">c2cauA</a>  | Alignment | not modelled | 97.0 | 16 | <b>PDB header:</b> plant protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (canavalin);<br><b>PDBTitle:</b> canavalin from jack bean                                                                                                                                                                                                                 |
| 87  | <a href="#">d1od5a1</a> | Alignment | not modelled | 97.0 | 14 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                                                            |
| 88  | <a href="#">c1fxzC</a>  | Alignment | not modelled | 97.0 | 14 | <b>PDB header:</b> plant protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> glycinin g1;<br><b>PDBTitle:</b> crystal structure of soybean proglycinin a1ab1b homotrimer                                                                                                                                                                                       |
| 89  | <a href="#">c3kglB</a>  | Alignment | not modelled | 96.9 | 10 | <b>PDB header:</b> plant protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> cruciferin;<br><b>PDBTitle:</b> crystal structure of procruciferin, 11s globulin from2 brassica napus                                                                                                                                                                             |
| 90  | <a href="#">d1uika2</a> | Alignment | not modelled | 96.8 | 13 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                                                            |
| 91  | <a href="#">c3ebrA</a>  | Alignment | not modelled | 96.8 | 8  | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized rmlc-like cupin;<br><b>PDBTitle:</b> crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution                                                                                                         |
| 92  | <a href="#">c2bnoA</a>  | Alignment | not modelled | 96.8 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase;<br><b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.                                                                                                                                                                      |
| 93  | <a href="#">c3kscD</a>  | Alignment | not modelled | 96.8 | 12 | <b>PDB header:</b> plant protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> lega class;<br><b>PDBTitle:</b> crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.                                                                                                                                                                  |
| 94  | <a href="#">d1vr3a1</a> | Alignment | not modelled | 96.8 | 19 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Ac1reductone dioxygenase                                                                                                                                                                                                                                  |
| 95  | <a href="#">c3myxA</a>  | Alignment | not modelled | 96.7 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pspto_0244;<br><b>PDBTitle:</b> crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution                     |
| 96  | <a href="#">c3es4B</a>  | Alignment | not modelled | 96.6 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein duf861 with a rmlc-like cupin fold;<br><b>PDBTitle:</b> crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution |
| 97  | <a href="#">d1uija2</a> | Alignment | not modelled | 96.5 | 13 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Germin/Seed storage 7S protein                                                                                                                                                                                                                            |
| 98  | <a href="#">c3qacA</a>  | Alignment | not modelled | 96.5 | 17 | <b>PDB header:</b> plant protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 11s globulin seed storage protein;<br><b>PDBTitle:</b> structure of amaranth 11s proglobulin seed storage protein from2 amaranthus hypochondriacus l.                                                                                                                             |
| 99  | <a href="#">c3o14B</a>  | Alignment | not modelled | 96.5 | 21 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> B: <b>PDB Molecule:</b> anti-ecfsigma factor, chrr;<br><b>PDBTitle:</b> crystal structure of an anti-ecfsigma factor, chrr (magu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution                                                                                                            |
| 100 | <a href="#">c2d5fB</a>  | Alignment | not modelled | 96.5 | 20 | <b>PDB header:</b> plant protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> glycinin a3b4 subunit;<br><b>PDBTitle:</b> crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly                                                                                |
| 101 | <a href="#">c2e9qA</a>  | Alignment | not modelled | 96.4 | 20 | <b>PDB header:</b> plant protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 11s globulin subunit beta;<br><b>PDBTitle:</b> recombinant pro-11s globulin of pumpkin                                                                                                                                                                                            |
|     |                         |           |              |      |    | <b>PDB header:</b> allergen                                                                                                                                                                                                                                                                                                                                 |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                 |
|-----|-------------------------|-----------|--------------|------|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 102 | <a href="#">c3c3vA_</a> | Alignment | not modelled | 96.3 | 12 | <b>Chain:</b> A: <b>PDB Molecule:</b> arachin arah3 isoform;<br><b>PDBTitle:</b> crystal structure of peanut major allergen ara h 3                                                                                                                                                             |
| 103 | <a href="#">c3balB_</a> | Alignment | not modelled | 96.0 | 9  | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetylacetone-cleaving enzyme;<br><b>PDBTitle:</b> crystal structure of an acetylacetone dioxygenase from2 acinetobacter johnsonii                                                                                   |
| 104 | <a href="#">c3ehkC_</a> | Alignment | not modelled | 96.0 | 15 | <b>PDB header:</b> plant protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> prunin;<br><b>PDBTitle:</b> crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis                                                                                                            |
| 105 | <a href="#">d2hsga1</a> | Alignment | not modelled | 95.8 | 16 | <b>Fold:</b> lambda repressor-like DNA-binding domains<br><b>Superfamily:</b> lambda repressor-like DNA-binding domains<br><b>Family:</b> GalR/LacI-like bacterial regulator                                                                                                                    |
| 106 | <a href="#">d2bjca1</a> | Alignment | not modelled | 95.6 | 16 | <b>Fold:</b> lambda repressor-like DNA-binding domains<br><b>Superfamily:</b> lambda repressor-like DNA-binding domains<br><b>Family:</b> GalR/LacI-like bacterial regulator                                                                                                                    |
| 107 | <a href="#">d1efaa1</a> | Alignment | not modelled | 95.3 | 16 | <b>Fold:</b> lambda repressor-like DNA-binding domains<br><b>Superfamily:</b> lambda repressor-like DNA-binding domains<br><b>Family:</b> GalR/LacI-like bacterial regulator                                                                                                                    |
| 108 | <a href="#">d2o1qa1</a> | Alignment | not modelled | 95.3 | 8  | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Acetylacetone-cleaving enzyme-like                                                                                                                                                            |
| 109 | <a href="#">c3cxE_</a>  | Alignment | not modelled | 95.2 | 13 | <b>PDB header:</b> unknown function<br><b>Chain:</b> E: <b>PDB Molecule:</b> protein of unknown function with a cupin-like fold;<br><b>PDBTitle:</b> crystal structure of a protein of unknown function with a cupin-like fold (reut_b4571) from ralstonia eutropha jmp134 at 2.60 a resolution |
| 110 | <a href="#">d1sgma1</a> | Alignment | not modelled | 95.2 | 10 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> Homeodomain-like<br><b>Family:</b> Tetracyclin repressor-like, N-terminal domain                                                                                                                                           |
| 111 | <a href="#">c2qnkA_</a> | Alignment | not modelled | 95.1 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyanthranilate 3,4-dioxygenase;<br><b>PDBTitle:</b> crystal structure of human 3-hydroxyanthranilate 3,4-dioxygenase                                                                                          |
| 112 | <a href="#">d1qpza1</a> | Alignment | not modelled | 95.1 | 19 | <b>Fold:</b> lambda repressor-like DNA-binding domains<br><b>Superfamily:</b> lambda repressor-like DNA-binding domains<br><b>Family:</b> GalR/LacI-like bacterial regulator                                                                                                                    |
| 113 | <a href="#">c1vi0B_</a> | Alignment | not modelled | 94.9 | 6  | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of a transcriptional regulator                                                                                                                       |
| 114 | <a href="#">c2xlfA_</a> | Alignment | not modelled | 94.9 | 14 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sll1785 protein;<br><b>PDBTitle:</b> structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)                                                                               |
| 115 | <a href="#">c3on4D_</a> | Alignment | not modelled | 94.7 | 4  | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, tetr family;<br><b>PDBTitle:</b> crystal structure of tetr transcriptional regulator from legionella2 pneumophila                                                                          |
| 116 | <a href="#">d1eyba_</a> | Alignment | not modelled | 94.7 | 12 | <b>Fold:</b> Double-stranded beta-helix<br><b>Superfamily:</b> RmlC-like cupins<br><b>Family:</b> Homogentisate dioxygenase                                                                                                                                                                     |
| 117 | <a href="#">c1sgmA_</a> | Alignment | not modelled | 94.7 | 11 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator yxaf;<br><b>PDBTitle:</b> crystal structure of hypothetical protein yxaf                                                                                                  |
| 118 | <a href="#">c3fx3A_</a> | Alignment | not modelled | 94.6 | 13 | <b>PDB header:</b> camp-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cyclic nucleotide-binding protein;<br><b>PDBTitle:</b> structure of a putative camp-binding regulatory protein from2 silicibacter pomeroyi dss-3                                                               |
| 119 | <a href="#">c1ey2A_</a> | Alignment | not modelled | 94.5 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> homogentisate 1,2-dioxygenase;<br><b>PDBTitle:</b> human homogentisate dioxygenase with fe(ii)                                                                                                                       |
| 120 | <a href="#">c3h5tA_</a> | Alignment | not modelled | 94.4 | 21 | <b>PDB header:</b> transcription regulator<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family;<br><b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum                                          |