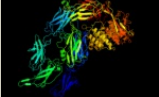
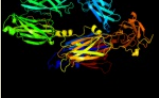
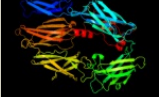
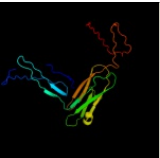
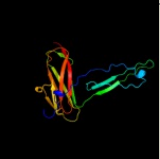
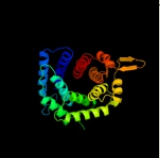
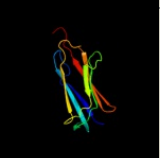
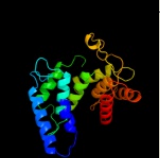
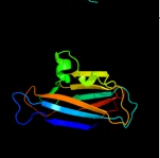


# Phyre2

|               |                              |
|---------------|------------------------------|
| Email         | l.a.kelley@imperial.ac.uk    |
| Description   | P76464                       |
| Date          | Wed Jan 25 15:21:08 GMT 2012 |
| Unique Job ID | 169b609148868c42             |

Detailed template information

| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c3cu7A_</a> |  Alignment   |    | 100.0      | 14     | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> complement c5;<br><b>PDBTitle:</b> human complement component 5                                           |
| 2  | <a href="#">c2b39B_</a> |  Alignment   |    | 100.0      | 14     | <b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> c3;<br><b>PDBTitle:</b> structure of mammalian c3 with an intact thioester at 3a resolution               |
| 3  | <a href="#">c2pn5A_</a> |  Alignment   |    | 100.0      | 13     | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> thioester-containing protein i;<br><b>PDBTitle:</b> crystal structure of tep1r                            |
| 4  | <a href="#">c3pvmB_</a> |  Alignment   |   | 100.0      | 16     | <b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> cobra venom factor;<br><b>PDBTitle:</b> structure of complement c5 in complex with cvf                    |
| 5  | <a href="#">c2a73B_</a> |  Alignment |  | 100.0      | 13     | <b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> complement c3;<br><b>PDBTitle:</b> human complement component c3                                          |
| 6  | <a href="#">c3g6jB_</a> |  Alignment |  | 100.0      | 13     | <b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> complement c3 alpha chain;<br><b>PDBTitle:</b> c3b in complex with a c3b specific fab                     |
| 7  | <a href="#">c3hrzA_</a> |  Alignment |  | 100.0      | 18     | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> cobra venom factor;<br><b>PDBTitle:</b> cobra venom factor (cvf) in complex with human factor b           |
| 8  | <a href="#">c2qkiA_</a> |  Alignment |  | 100.0      | 15     | <b>PDB header:</b> immune system/hydrolase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> complement c3;<br><b>PDBTitle:</b> human c3c in complex with the inhibitor compstatin |
| 9  | <a href="#">d1hzfa_</a> |  Alignment |  | 100.0      | 18     | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases<br><b>Family:</b> Complement components                                        |
| 10 | <a href="#">c1hzfa_</a> |  Alignment |  | 100.0      | 18     | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> complement factor c4a;<br><b>PDBTitle:</b> c4adg fragment of human complement factor c4a                  |
| 11 | <a href="#">d1c3da_</a> |  Alignment |  | 100.0      | 14     | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases<br><b>Family:</b> Complement components                                        |

|    |                          |           |                                                                                     |       |    |                                                                                                                                                                                                                                             |
|----|--------------------------|-----------|-------------------------------------------------------------------------------------|-------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c3hs0B_</a>  | Alignment |     | 100.0 | 15 | <b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> cobra venom factor;<br><b>PDBTitle:</b> cobra venom factor (cvf) in complex with human factor b                                                                   |
| 13 | <a href="#">c2a74B_</a>  | Alignment |    | 99.9  | 15 | <b>PDB header:</b> immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> complement component c3c;<br><b>PDBTitle:</b> human complement component c3c                                                                                      |
| 14 | <a href="#">d1qqfa_</a>  | Alignment |    | 99.9  | 12 | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases<br><b>Family:</b> Complement components                                                                                                |
| 15 | <a href="#">c2p9rA_</a>  | Alignment |    | 99.8  | 19 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-2-macroglobulin;<br><b>PDBTitle:</b> human alpha2-macroglobulin is composed of multiple domains,2 as predicted by homology with complement component c3 |
| 16 | <a href="#">d3es6b1</a>  | Alignment |    | 98.9  | 11 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> SVA-like                                                                                                                              |
| 17 | <a href="#">c1o79A_</a>  | Alignment |   | 98.5  | 12 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> squalene--hopene cyclase;<br><b>PDBTitle:</b> structures of human oxidosqualene cyclase inhibitors bound2 to a homologous enzyme                                      |
| 18 | <a href="#">c3hrzC_</a>  | Alignment |  | 98.4  | 6  | <b>PDB header:</b> immune system<br><b>Chain:</b> C: <b>PDB Molecule:</b> cobra venom factor;<br><b>PDBTitle:</b> cobra venom factor (cvf) in complex with human factor b                                                                   |
| 19 | <a href="#">c1w6ka_</a>  | Alignment |  | 98.1  | 11 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lanosterol synthase;<br><b>PDBTitle:</b> structure of human osc in complex with lanosterol                                                                            |
| 20 | <a href="#">d1ledya_</a> | Alignment |  | 98.0  | 12 | <b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f<br><b>Superfamily:</b> Alpha-macroglobulin receptor domain<br><b>Family:</b> Alpha-macroglobulin receptor domain                                            |
| 21 | <a href="#">d2sqca1</a>  | Alignment | not modelled                                                                        | 97.9  | 13 | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases<br><b>Family:</b> Terpene synthases                                                                                                    |
| 22 | <a href="#">c2qkiC_</a>  | Alignment | not modelled                                                                        | 97.9  | 8  | <b>PDB header:</b> immune system/hydrolase inhibitor<br><b>Chain:</b> C: <b>PDB Molecule:</b> complement c3;<br><b>PDBTitle:</b> human c3c in complex with the inhibitor compstatin                                                         |
| 23 | <a href="#">d1bv8a_</a>  | Alignment | not modelled                                                                        | 97.9  | 11 | <b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f<br><b>Superfamily:</b> Alpha-macroglobulin receptor domain<br><b>Family:</b> Alpha-macroglobulin receptor domain                                            |
| 24 | <a href="#">d1ayoa_</a>  | Alignment | not modelled                                                                        | 97.8  | 13 | <b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f<br><b>Superfamily:</b> Alpha-macroglobulin receptor domain<br><b>Family:</b> Alpha-macroglobulin receptor domain                                            |
| 25 | <a href="#">d2sqca2</a>  | Alignment | not modelled                                                                        | 97.7  | 20 | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases<br><b>Family:</b> Terpene synthases                                                                                                    |
| 26 | <a href="#">d1w6ka1</a>  | Alignment | not modelled                                                                        | 97.6  | 10 | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases<br><b>Family:</b> Terpene synthases                                                                                                    |
| 27 | <a href="#">c1cwvA_</a>  | Alignment | not modelled                                                                        | 97.2  | 14 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> invasin;<br><b>PDBTitle:</b> crystal structure of invasins: a bacterial integrin-binding protein                                                             |
| 28 | <a href="#">d1w6ka2</a>  | Alignment | not modelled                                                                        | 96.6  | 15 | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases<br><b>Family:</b> Terpene synthases                                                                                                    |
| 29 | <a href="#">c1w6ka</a>   | Alignment | not modelled                                                                        | 96.2  | 11 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> gelation factor;                                                                                                                                             |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                 |
|----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">c1wma</a>   | Alignment | not modelled | 96.3 | 11 | <b>PDBTitle:</b> molecular structure of the rod domain of dictyostelium2 filamin<br><b>PDB header:</b> cell adhesion                                                                                                                                                            |
| 30 | <a href="#">c2pz4A</a>  | Alignment | not modelled | 96.2 | 14 | <b>Chain:</b> A: <b>PDB Molecule:</b> protein gbs052;<br><b>PDBTitle:</b> crystal structure of spab (gbs52), the minor pilin in gram-positive2 pathogen streptococcus agalactiae                                                                                                |
| 31 | <a href="#">c3e8vA</a>  | Alignment | not modelled | 96.0 | 19 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> possible transglutaminase-family protein;<br><b>PDBTitle:</b> crystal structure of a possible transglutaminase-family2 protein proteolytic fragment from bacteroides fragilis |
| 32 | <a href="#">c3qvaB</a>  | Alignment | not modelled | 95.9 | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> transthyretin-like protein;<br><b>PDBTitle:</b> structure of klebsiella pneumoniae 5-hydroxyisourate hydrolase                                                                                            |
| 33 | <a href="#">c2k7pA</a>  | Alignment | not modelled | 95.7 | 15 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> filamin-a;<br><b>PDBTitle:</b> filamin a ig-like domains 16-17                                                                                                                                   |
| 34 | <a href="#">dlr76a</a>  | Alignment | not modelled | 95.7 | 14 | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Family 10 polysaccharide lyase<br><b>Family:</b> Family 10 polysaccharide lyase                                                                                                                                          |
| 35 | <a href="#">d1gxma</a>  | Alignment | not modelled | 95.5 | 9  | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Family 10 polysaccharide lyase<br><b>Family:</b> Family 10 polysaccharide lyase                                                                                                                                          |
| 36 | <a href="#">c2zxcA</a>  | Alignment | not modelled | 95.3 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> neutral ceramidase;<br><b>PDBTitle:</b> seramidase complexed with c2                                                                                                                                      |
| 37 | <a href="#">d2dj4a1</a> | Alignment | not modelled | 95.0 | 22 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                               |
| 38 | <a href="#">d2dmba1</a> | Alignment | not modelled | 94.8 | 17 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                               |
| 39 | <a href="#">d1vjja1</a> | Alignment | not modelled | 94.7 | 16 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Transglutaminase N-terminal domain                                                                                                                                        |
| 40 | <a href="#">d2bp3a1</a> | Alignment | not modelled | 94.6 | 19 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                               |
| 41 | <a href="#">d2d7ma1</a> | Alignment | not modelled | 94.6 | 22 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                               |
| 42 | <a href="#">c2gpzC</a>  | Alignment | not modelled | 94.6 | 28 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> transthyretin-like protein;<br><b>PDBTitle:</b> transthyretin-like protein from salmonella dublin                                                                                                         |
| 43 | <a href="#">d1qfha1</a> | Alignment | not modelled | 94.5 | 11 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                               |
| 44 | <a href="#">d1kgia</a>  | Alignment | not modelled | 94.5 | 21 | <b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Transthyretin (synonym: prealbumin)<br><b>Family:</b> Transthyretin (synonym: prealbumin)                                                                                                                                   |
| 45 | <a href="#">d1ttaa</a>  | Alignment | not modelled | 94.2 | 23 | <b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Transthyretin (synonym: prealbumin)<br><b>Family:</b> Transthyretin (synonym: prealbumin)                                                                                                                                   |
| 46 | <a href="#">d2dica1</a> | Alignment | not modelled | 94.2 | 19 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                               |
| 47 | <a href="#">d2h6fb1</a> | Alignment | not modelled | 94.1 | 14 | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases<br><b>Family:</b> Protein prenyltransferases                                                                                                                               |
| 48 | <a href="#">c2h0eA</a>  | Alignment | not modelled | 94.0 | 13 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> transthyretin-like protein pucm;<br><b>PDBTitle:</b> crystal structure of pucm in the absence of substrate                                                                                                |
| 49 | <a href="#">d1v05a</a>  | Alignment | not modelled | 94.0 | 16 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                               |
| 50 | <a href="#">d1f86a</a>  | Alignment | not modelled | 93.9 | 23 | <b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Transthyretin (synonym: prealbumin)<br><b>Family:</b> Transthyretin (synonym: prealbumin)                                                                                                                                   |
| 51 | <a href="#">d1qfha2</a> | Alignment | not modelled | 93.7 | 10 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                               |
| 52 | <a href="#">c3kptA</a>  | Alignment | not modelled | 93.7 | 17 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> collagen adhesion protein;<br><b>PDBTitle:</b> crystal structure of bcpa, the major pilin subunit of2 bacillus cereus                                                                                 |
| 53 | <a href="#">d1w8oa1</a> | Alignment | not modelled | 93.6 | 20 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> E-set domains of sugar-utilizing enzymes                                                                                                                                  |
| 54 | <a href="#">c3e37B</a>  | Alignment | not modelled | 93.6 | 14 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein farnesyltransferase subunit beta;<br><b>PDBTitle:</b> protein farnesyltransferase complexed with bisubstrate2 ethylenediamine scaffold inhibitor 5                                              |
| 55 | <a href="#">d3dssb1</a> | Alignment | not modelled | 93.6 | 5  | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases<br><b>Family:</b> Protein prenyltransferases                                                                                                                               |
| 56 | <a href="#">d2e9ia1</a> | Alignment | not modelled | 93.6 | 21 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains                                                                                                                                                                                             |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                     |
|----|-------------------------|-----------|--------------|------|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |                         |           |              |      |    | <b>Family:</b> Filamin repeat (rod domain)                                                                                                                                                                                                                          |
| 57 | <a href="#">c1l9mB</a>  | Alignment | not modelled | 93.4 | 13 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein-glutamine glutamyltransferase e3;<br><b>PDBTitle:</b> three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation |
| 58 | <a href="#">d2di8a1</a> | Alignment | not modelled | 93.3 | 17 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                   |
| 59 | <a href="#">c3irpX</a>  | Alignment | not modelled | 93.2 | 18 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> X: <b>PDB Molecule:</b> uro-adherence factor a;<br><b>PDBTitle:</b> crystal structure of functional region of uafa from staphylococcus2 saprophyticus at 1.50 angstrom resolution                                 |
| 60 | <a href="#">c3osvC</a>  | Alignment | not modelled | 93.2 | 12 | <b>PDB header:</b> structural protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> flagellar basal-body rod modification protein flgd;<br><b>PDBTitle:</b> the crytsal structure of flgd from p. aeruginosa                                                             |
| 61 | <a href="#">c2ee6A</a>  | Alignment | not modelled | 93.2 | 14 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> filamin-b;<br><b>PDBTitle:</b> solution structure of the 21th filamin domain from human2 filamin-b                                                                                   |
| 62 | <a href="#">c3iswA</a>  | Alignment | not modelled | 93.1 | 16 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> filamin-a;<br><b>PDBTitle:</b> crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cfr                                                   |
| 63 | <a href="#">d1oo2a</a>  | Alignment | not modelled | 92.9 | 26 | <b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Transthyretin (synonym: prealbumin)<br><b>Family:</b> Transthyretin (synonym: prealbumin)                                                                                                                       |
| 64 | <a href="#">c2ds4A</a>  | Alignment | not modelled | 92.8 | 14 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> tripartite motif protein 45;<br><b>PDBTitle:</b> solution structure of the filamin domain from human2 tripartite motif protein 45                                                       |
| 65 | <a href="#">c2h1xB</a>  | Alignment | not modelled | 92.7 | 26 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 5-hydroxyisourate hydrolase (formerly known as<br><b>PDBTitle:</b> crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)                   |
| 66 | <a href="#">d1h8la1</a> | Alignment | not modelled | 92.7 | 7  | <b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Carboxypeptidase regulatory domain-like<br><b>Family:</b> Carboxypeptidase regulatory domain                                                                                                                    |
| 67 | <a href="#">c3isyA</a>  | Alignment | not modelled | 92.7 | 18 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> intracellular proteinase inhibitor;<br><b>PDBTitle:</b> crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution         |
| 68 | <a href="#">c3cnkB</a>  | Alignment | not modelled | 92.3 | 17 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> filamin-a;<br><b>PDBTitle:</b> crystal structure of the dimerization domain of human2 filamin a                                                                                      |
| 69 | <a href="#">d2diaa1</a> | Alignment | not modelled | 92.2 | 19 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                   |
| 70 | <a href="#">c2fauA</a>  | Alignment | not modelled | 92.2 | 19 | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting 26;<br><b>PDBTitle:</b> crystal structure of human vps26                                                                                                     |
| 71 | <a href="#">c3c12A</a>  | Alignment | not modelled | 92.0 | 17 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein;<br><b>PDBTitle:</b> crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly                    |
| 72 | <a href="#">c2e9jA</a>  | Alignment | not modelled | 92.0 | 19 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> filamin-b;<br><b>PDBTitle:</b> solution structure of the 14th filamin domain from human2 filamin-b                                                                                   |
| 73 | <a href="#">c2brqB</a>  | Alignment | not modelled | 91.6 | 14 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> filamin a;<br><b>PDBTitle:</b> crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide                                              |
| 74 | <a href="#">d2d7pa1</a> | Alignment | not modelled | 91.4 | 11 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                   |
| 75 | <a href="#">d2d7na1</a> | Alignment | not modelled | 91.3 | 14 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                   |
| 76 | <a href="#">d2diba1</a> | Alignment | not modelled | 91.0 | 21 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                   |
| 77 | <a href="#">d1wlha1</a> | Alignment | not modelled | 90.7 | 12 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                   |
| 78 | <a href="#">d1cwva1</a> | Alignment | not modelled | 90.5 | 11 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Invasin/intimin cell-adhesion fragments<br><b>Family:</b> Invasin/intimin cell-adhesion fragments                                                                                             |
| 79 | <a href="#">c1tnuL</a>  | Alignment | not modelled | 90.4 | 5  | <b>PDB header:</b> transferase<br><b>Chain:</b> L: <b>PDB Molecule:</b> geranylgeranyl transferase type i beta subunit;<br><b>PDBTitle:</b> rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a gcincckvl peptide derived from rhob    |
| 80 | <a href="#">d1n4qb</a>  | Alignment | not modelled | 90.3 | 5  | <b>Fold:</b> alpha/alpha toroid<br><b>Superfamily:</b> Terpenoid cyclases/Protein prenyltransferases<br><b>Family:</b> Protein prenyltransferases                                                                                                                   |
| 81 | <a href="#">d2dmca1</a> | Alignment | not modelled | 89.7 | 17 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                   |
|    |                         |           |              |      |    | <b>Fold:</b> Immunoglobulin-like beta-sandwich                                                                                                                                                                                                                      |

|     |                         |           |              |      |    |                                                                                                                                                                                                                                                                                         |
|-----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 82  | <a href="#">d2d7oa1</a> | Alignment | not modelled | 89.0 | 14 | <b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                                                                                         |
| 83  | <a href="#">c2ww8A_</a> | Alignment | not modelled | 88.9 | 11 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> cell wall surface anchor family protein;<br><b>PDBTitle:</b> structure of the pilus adhesin (rrga) from streptococcus2 pneumoniae                                                                             |
| 84  | <a href="#">c2pmvB_</a> | Alignment | not modelled | 88.8 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> gastric intrinsic factor;<br><b>PDBTitle:</b> crystal structure of human intrinsic factor- cobalamin complex at 2.62 a resolution                                                                         |
| 85  | <a href="#">d3pccm_</a> | Alignment | not modelled | 88.8 | 17 | <b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Aromatic compound dioxygenase<br><b>Family:</b> Aromatic compound dioxygenase                                                                                                                                                       |
| 86  | <a href="#">d2w0pa1</a> | Alignment | not modelled | 88.8 | 14 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                                       |
| 87  | <a href="#">c3n9tA_</a> | Alignment | not modelled | 88.3 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pnpc;<br><b>PDBTitle:</b> cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dli-e4                                                                                                 |
| 88  | <a href="#">c3draB_</a> | Alignment | not modelled | 88.3 | 7  | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> geranylgeranyltransferase type i beta subunit;<br><b>PDBTitle:</b> candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp                                                                    |
| 89  | <a href="#">c3rghA_</a> | Alignment | not modelled | 88.0 | 17 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> filamin-a;<br><b>PDBTitle:</b> structure of filamin a immunoglobulin-like repeat 10 from homo sapiens                                                                                                         |
| 90  | <a href="#">d2burb1</a> | Alignment | not modelled | 87.9 | 20 | <b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Aromatic compound dioxygenase<br><b>Family:</b> Aromatic compound dioxygenase                                                                                                                                                       |
| 91  | <a href="#">d1f00i1</a> | Alignment | not modelled | 87.9 | 20 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Invasin/intimin cell-adhesion fragments<br><b>Family:</b> Invasin/intimin cell-adhesion fragments                                                                                                                 |
| 92  | <a href="#">c2j3sB_</a> | Alignment | not modelled | 87.7 | 15 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> filamin-a;<br><b>PDBTitle:</b> crystal structure of the human filamin a ig domains 19 to2 21                                                                                                             |
| 93  | <a href="#">d1ex0a1</a> | Alignment | not modelled | 87.6 | 10 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Transglutaminase N-terminal domain                                                                                                                                                |
| 94  | <a href="#">c2kl6A_</a> | Alignment | not modelled | 87.6 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a |
| 95  | <a href="#">c1qfhB_</a> | Alignment | not modelled | 87.6 | 12 | <b>PDB header:</b> actin binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein (gelation factor);<br><b>PDBTitle:</b> dimerization of gelation factor from dictyostelium2 discoideum: crystal structure of rod domains 5 and 6                                               |
| 96  | <a href="#">c2r5oA_</a> | Alignment | not modelled | 87.3 | 12 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative atp binding component of abc-<br><b>PDBTitle:</b> crystal structure of the c-terminal domain of wzt                                                                                              |
| 97  | <a href="#">c2brqA_</a> | Alignment | not modelled | 86.9 | 16 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> filamin a;<br><b>PDBTitle:</b> crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide                                                                  |
| 98  | <a href="#">c2w0pB_</a> | Alignment | not modelled | 86.9 | 16 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> B: <b>PDB Molecule:</b> filamin-a;<br><b>PDBTitle:</b> crystal structure of the filamin a repeat 21 complexed with2 the migfilin peptide                                                                                              |
| 99  | <a href="#">c3iswB_</a> | Alignment | not modelled | 86.9 | 16 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> filamin-a;<br><b>PDBTitle:</b> crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cfr                                                                       |
| 100 | <a href="#">d2q3za1</a> | Alignment | not modelled | 86.8 | 21 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Transglutaminase N-terminal domain                                                                                                                                                |
| 101 | <a href="#">d2nqca1</a> | Alignment | not modelled | 86.2 | 17 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Filamin repeat (rod domain)                                                                                                                                                       |
| 102 | <a href="#">c2nqcA_</a> | Alignment | not modelled | 86.2 | 17 | <b>PDB header:</b> immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> filamin-c;<br><b>PDBTitle:</b> crystal structure of ig-like domain 23 from human filamin c                                                                                                                    |
| 103 | <a href="#">c2jflA_</a> | Alignment | not modelled | 85.9 | 14 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> filamin-a;<br><b>PDBTitle:</b> crystal structure of the filamin a repeat 21 complexed with2 the integrin beta2 cytoplasmic tail peptide                                                                       |
| 104 | <a href="#">c3q7aB_</a> | Alignment | not modelled | 85.3 | 14 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> B: <b>PDB Molecule:</b> farnesyltransferase beta subunit;<br><b>PDBTitle:</b> cryptococcus neoformans protein farnesyltransferase in complex with2 fpp and l-778,123                                              |
| 105 | <a href="#">c1ksrA_</a> | Alignment | not modelled | 84.5 | 12 | <b>PDB header:</b> actin binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> gelation factor;<br><b>PDBTitle:</b> the repeating segments of the f-actin cross-linking2 gelation factor (abp-120) have an immunoglobulin fold, nmr,3 20 structures                                  |
| 106 | <a href="#">c1uwyA_</a> | Alignment | not modelled | 84.5 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> carboxypeptidase m;<br><b>PDBTitle:</b> crystal structure of human carboxypeptidase m                                                                                                                             |
| 107 | <a href="#">c2xsuA_</a> | Alignment | not modelled | 84.4 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> catechol 1,2 dioxygenase;<br><b>PDBTitle:</b> crystal structure of the a72g mutant of acinetobacter2 radioresistens catechol 1,2 dioxygenase                                                                 |

|     |                         |           |                                                                                    |      |    |                                                                                                                                                                                                                                                                 |
|-----|-------------------------|-----------|------------------------------------------------------------------------------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 108 | <a href="#">d1cwva2</a> | Alignment | not modelled                                                                       | 84.3 | 21 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Invasin/intimin cell-adhesion fragments<br><b>Family:</b> Invasin/intimin cell-adhesion fragments                                                                                         |
| 109 | <a href="#">c3mn8A_</a> | Alignment | not modelled                                                                       | 84.2 | 12 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lp15968p;<br><b>PDBTitle:</b> structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short                                                                                   |
| 110 | <a href="#">d2bura1</a> | Alignment | not modelled                                                                       | 84.2 | 22 | <b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Aromatic compound dioxygenase<br><b>Family:</b> Aromatic compound dioxygenase                                                                                                                               |
| 111 | <a href="#">d1uwya1</a> | Alignment | not modelled                                                                       | 84.0 | 18 | <b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Carboxypeptidase regulatory domain-like<br><b>Family:</b> Carboxypeptidase regulatory domain                                                                                                                |
| 112 | <a href="#">c2k7qA_</a> | Alignment | not modelled                                                                       | 83.2 | 15 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> filamin-a;<br><b>PDBTitle:</b> filamin a ig-like domains 18-19                                                                                                                   |
| 113 | <a href="#">d3pcca_</a> | Alignment | not modelled                                                                       | 81.7 | 20 | <b>Fold:</b> Prealbumin-like<br><b>Superfamily:</b> Aromatic compound dioxygenase<br><b>Family:</b> Aromatic compound dioxygenase                                                                                                                               |
| 114 | <a href="#">c2v3nA_</a> | Alignment | not modelled                                                                       | 80.9 | 11 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcobalamin-2;<br><b>PDBTitle:</b> crystallographic analysis of upper axial ligand2 substitutions in cobalamin bound to transcobalamin                                         |
| 115 | <a href="#">c1h8lA_</a> | Alignment | not modelled                                                                       | 79.8 | 13 | <b>PDB header:</b> carboxypeptidase<br><b>Chain:</b> A: <b>PDB Molecule:</b> carboxypeptidase gp180 residues 503-882;<br><b>PDBTitle:</b> duck carboxypeptidase d domain ii in complex with gema                                                                |
| 116 | <a href="#">c2x5pA_</a> | Alignment | not modelled                                                                       | 78.9 | 11 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> fibronectin binding protein;<br><b>PDBTitle:</b> crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b                                                |
| 117 | <a href="#">c2di7A_</a> | Alignment | not modelled                                                                       | 78.0 | 9  | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> bk158_1;<br><b>PDBTitle:</b> solution structure of the filamin domain from human bk158_12 protein                                                                                |
| 118 | <a href="#">c3ottB_</a> | Alignment |  | 76.8 | 17 | <b>PDB header:</b> transcription<br><b>Chain:</b> B: <b>PDB Molecule:</b> two-component system sensor histidine kinase;<br><b>PDBTitle:</b> crystal structure of the extracellular domain of the putative one2 component system bt4673 from b. thetaiotaomicron |
| 119 | <a href="#">c1ayrA_</a> | Alignment | not modelled                                                                       | 76.6 | 16 | <b>PDB header:</b> sensory transduction<br><b>Chain:</b> A: <b>PDB Molecule:</b> arrestin;<br><b>PDBTitle:</b> arrestin from bovine rod outer segments                                                                                                          |
| 120 | <a href="#">d1g0da1</a> | Alignment | not modelled                                                                       | 76.1 | 13 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> E set domains<br><b>Family:</b> Transglutaminase N-terminal domain                                                                                                                        |