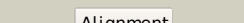
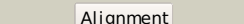
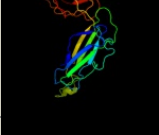
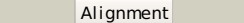
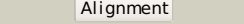
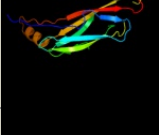
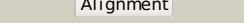
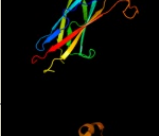
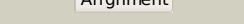
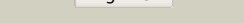
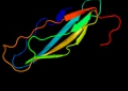


| #  | Template                | Alignment Coverage                                                                               | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                         |
|----|-------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c1qpxA_</a> | <br>Alignment   |    | 100.0      | 20     | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> papd chaperone;<br><b>PDBTitle:</b> crystal structures of self-capping papd chaperone homodimers                                                       |
| 2  | <a href="#">c1z9sA_</a> | <br>Alignment   |    | 100.0      | 15     | <b>PDB header:</b> chaperone/immune system<br><b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein caf1m;<br><b>PDBTitle:</b> crystal structure of the native chaperone:subunit:subunit2 caf1m:caf1:caf1 complex          |
| 3  | <a href="#">c2co7B_</a> | <br>Alignment   |    | 100.0      | 17     | <b>PDB header:</b> fibril protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative fimbriae assembly chaperone;<br><b>PDBTitle:</b> salmonella enterica safp pilin in complex with the safb2 chaperone (type ii)            |
| 4  | <a href="#">c1qunA_</a> | <br>Alignment   |   | 100.0      | 12     | <b>PDB header:</b> chaperone/structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> papd-like chaperone fimc;<br><b>PDBTitle:</b> x-ray structure of the fimc-fimh chaperone adhesin complex2 from uropathogenic e.coli |
| 5  | <a href="#">c3q48B_</a> | <br>Alignment |  | 100.0      | 19     | <b>PDB header:</b> chaperone<br><b>Chain:</b> B: <b>PDB Molecule:</b> chaperone cupb2;<br><b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa cupb2 chaperone                                                       |
| 6  | <a href="#">c1l4iA_</a> | <br>Alignment |  | 100.0      | 15     | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> sfae protein;<br><b>PDBTitle:</b> crystal structure of the periplasmic chaperone sfae                                                                  |
| 7  | <a href="#">c3f6iB_</a> | <br>Alignment |  | 99.9       | 15     | <b>PDB header:</b> chaperone<br><b>Chain:</b> B: <b>PDB Molecule:</b> chaperone protein faee;<br><b>PDBTitle:</b> structure of the semet labeled f4 fibrial chaperone faee                                                   |
| 8  | <a href="#">d1p5va1</a> | <br>Alignment |  | 99.9       | 17     | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> PapD-like<br><b>Family:</b> Pilus chaperone                                                                                                            |
| 9  | <a href="#">d2co7b1</a> | <br>Alignment |  | 99.9       | 20     | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> PapD-like<br><b>Family:</b> Pilus chaperone                                                                                                            |
| 10 | <a href="#">d2j2za1</a> | <br>Alignment |  | 99.9       | 19     | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> PapD-like<br><b>Family:</b> Pilus chaperone                                                                                                            |
| 11 | <a href="#">d3bwuc1</a> | <br>Alignment |  | 99.9       | 13     | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> PapD-like<br><b>Family:</b> Pilus chaperone                                                                                                            |

|    |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                                                                              |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">dl14ia1</a> | Alignment |    | 99.9 | 17 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> PapD-like<br><b>Family:</b> Pilus chaperone                                                                                                                                                                            |
| 13 | <a href="#">c2qsvA</a>  | Alignment |    | 97.9 | 17 | <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 protein of unknown function from porphyromonas2 gingivalis w83                                                           |
| 14 | <a href="#">dlrowa</a>  | Alignment |    | 97.3 | 14 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> PapD-like<br><b>Family:</b> MSP-like                                                                                                                                                                                   |
| 15 | <a href="#">dlmlsa</a>  | Alignment |    | 97.0 | 10 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> PapD-like<br><b>Family:</b> MSP-like                                                                                                                                                                                   |
| 16 | <a href="#">d2j2za2</a> | Alignment |    | 97.0 | 19 | <b>Fold:</b> C2 domain-like<br><b>Superfamily:</b> Periplasmic chaperone C-domain<br><b>Family:</b> Periplasmic chaperone C-domain                                                                                                                                                           |
| 17 | <a href="#">c3qisA</a>  | Alignment |   | 96.3 | 13 | <b>PDB header:</b> hydrolase/protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> inositol polyphosphate 5-phosphatase ocr1-1;<br><b>PDBTitle:</b> recognition of the f&h motif by the lowe syndrome protein ocr1                                                                        |
| 18 | <a href="#">c3o0lB</a>  | Alignment |  | 96.1 | 10 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution                                  |
| 19 | <a href="#">dlgrwa</a>  | Alignment |  | 95.7 | 12 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> PapD-like<br><b>Family:</b> MSP-like                                                                                                                                                                                   |
| 20 | <a href="#">c1z9oB</a>  | Alignment |  | 95.6 | 8  | <b>PDB header:</b> protein binding/lipid binding protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> vesicle-associated membrane protein-associated protein a;<br><b>PDBTitle:</b> 1.9 angstrom crystal structure of the rat vap-a msp homology domain in2 complex with the rat orp1 ffat motif |
| 21 | <a href="#">c2e6jA</a>  | Alignment | not modelled                                                                        | 95.4 | 9  | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hydin protein;<br><b>PDBTitle:</b> solution structure of the c-terminal papd-like domain from2 human hydin protein                                                                         |
| 22 | <a href="#">dlmspa</a>  | Alignment | not modelled                                                                        | 95.4 | 10 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> PapD-like<br><b>Family:</b> MSP-like                                                                                                                                                                                   |
| 23 | <a href="#">dlwica</a>  | Alignment | not modelled                                                                        | 94.9 | 14 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> PapD-like<br><b>Family:</b> MSP-like                                                                                                                                                                                   |
| 24 | <a href="#">c2ys4A</a>  | Alignment | not modelled                                                                        | 94.8 | 15 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> hydrocephalus-inducing protein homolog;<br><b>PDBTitle:</b> solution structure of the n-terminal papd-like domain of2 hydin protein from human                                             |
| 25 | <a href="#">d3bwuc2</a> | Alignment | not modelled                                                                        | 94.8 | 10 | <b>Fold:</b> C2 domain-like<br><b>Superfamily:</b> Periplasmic chaperone C-domain<br><b>Family:</b> Periplasmic chaperone C-domain                                                                                                                                                           |
| 26 | <a href="#">c3qbth</a>  | Alignment | not modelled                                                                        | 94.4 | 11 | <b>PDB header:</b> protein transport/hydrolase<br><b>Chain:</b> H: <b>PDB Molecule:</b> inositol polyphosphate 5-phosphatase ocr1-1;<br><b>PDBTitle:</b> crystal structure of ocr1 540-678 in complex with rab8a:gppnhp                                                                      |
| 27 | <a href="#">dlp5va2</a> | Alignment | not modelled                                                                        | 92.3 | 10 | <b>Fold:</b> C2 domain-like<br><b>Superfamily:</b> Periplasmic chaperone C-domain<br><b>Family:</b> Periplasmic chaperone C-domain                                                                                                                                                           |
| 28 | <a href="#">dlw8oa1</a> | Alignment | not modelled                                                                        | 91.4 | 16 | <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                                                                                                                                               |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                         |
|----|-------------------------|-----------|--------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">d2co7b2</a> | Alignment | not modelled | 89.9 | 13 | <b>Fold:</b> C2 domain-like<br><b>Superfamily:</b> Periplasmic chaperone C-domain<br><b>Family:</b> Periplasmic chaperone C-domain                                                                                                                                                      |
| 30 | <a href="#">c2jwyA</a>  | Alignment | not modelled | 89.8 | 9  | <b>PDB header:</b> lipoprotein<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized lipoprotein yaji;<br><b>PDBTitle:</b> solution nmr structure of uncharacterized lipoprotein yaji from2 escherichia coli. northeast structural genomics target er540                             |
| 31 | <a href="#">d2vza2</a>  | Alignment | not modelled | 89.1 | 13 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> beta-Galactosidase/glucuronidase domain<br><b>Family:</b> beta-Galactosidase/glucuronidase domain                                                                                                                 |
| 32 | <a href="#">c1l9mB</a>  | Alignment | not modelled | 88.9 | 12 | <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                     |
| 33 | <a href="#">d1l4ia2</a> | Alignment | not modelled | 85.4 | 16 | <b>Fold:</b> C2 domain-like<br><b>Superfamily:</b> Periplasmic chaperone C-domain<br><b>Family:</b> Periplasmic chaperone C-domain                                                                                                                                                      |
| 34 | <a href="#">c3cfuA</a>  | Alignment | not modelled | 80.9 | 12 | <b>PDB header:</b> lipoprotein<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized lipoprotein yjha;<br><b>PDBTitle:</b> crystal structure of the yjha protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr562                                     |
| 35 | <a href="#">d1exha</a>  | Alignment | not modelled | 79.4 | 12 | <b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f<br><b>Superfamily:</b> Carbohydrate-binding domain<br><b>Family:</b> Cellulose-binding domain family II                                                                                                 |
| 36 | <a href="#">c3ac0B</a>  | Alignment | not modelled | 76.9 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase i;<br><b>PDBTitle:</b> crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose                                                                               |
| 37 | <a href="#">c2r39A</a>  | Alignment | not modelled | 75.6 | 10 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> fixg-related protein;<br><b>PDBTitle:</b> crystal structure of fixg-related protein from vibrio parahaemolyticus                                                                      |
| 38 | <a href="#">c2kl6A</a>  | Alignment | not modelled | 72.8 | 12 | <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 |
| 39 | <a href="#">c2x41A</a>  | Alignment | not modelled | 72.7 | 23 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase;<br><b>PDBTitle:</b> structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose                                                                                       |
| 40 | <a href="#">c3isyA</a>  | Alignment | not modelled | 59.7 | 15 | <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                             |
| 41 | <a href="#">c2je8B</a>  | Alignment | not modelled | 58.9 | 11 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> beta-mannosidase;<br><b>PDBTitle:</b> structure of a beta-mannosidase from bacteroides2 thetaiotaomicron                                                                                                          |
| 42 | <a href="#">d1yq2a1</a> | Alignment | not modelled | 53.5 | 7  | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> beta-Galactosidase/glucuronidase domain<br><b>Family:</b> beta-Galactosidase/glucuronidase domain                                                                                                                 |
| 43 | <a href="#">c3jt0B</a>  | Alignment | not modelled | 47.9 | 13 | <b>PDB header:</b> structural protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> lamin-b1;<br><b>PDBTitle:</b> crystal structure of the c-terminal fragment (426-558)2 lamin-b1 from homo sapiens, northeast structural genomics3 consortium target hr5546a                               |
| 44 | <a href="#">d1ex0a2</a> | Alignment | not modelled | 44.9 | 13 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Transglutaminase, two C-terminal domains<br><b>Family:</b> Transglutaminase, two C-terminal domains                                                                                                               |
| 45 | <a href="#">c3rgbA</a>  | Alignment | not modelled | 44.1 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> methane monooxygenase subunit b2;<br><b>PDBTitle:</b> crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)                                                           |
| 46 | <a href="#">d1vjja2</a> | Alignment | not modelled | 43.7 | 11 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Transglutaminase, two C-terminal domains<br><b>Family:</b> Transglutaminase, two C-terminal domains                                                                                                               |
| 47 | <a href="#">d1ejxb</a>  | Alignment | not modelled | 43.3 | 12 | <b>Fold:</b> beta-clip<br><b>Superfamily:</b> Urease, beta-subunit<br><b>Family:</b> Urease, beta-subunit                                                                                                                                                                               |
| 48 | <a href="#">c1yewl</a>  | Alignment | not modelled | 42.2 | 14 | <b>PDB header:</b> oxidoreductase, membrane protein<br><b>Chain:</b> I: <b>PDB Molecule:</b> particulate methane monooxygenase, b subunit;<br><b>PDBTitle:</b> crystal structure of particulate methane monooxygenase                                                                   |
| 49 | <a href="#">d4ubpb</a>  | Alignment | not modelled | 40.1 | 12 | <b>Fold:</b> beta-clip<br><b>Superfamily:</b> Urease, beta-subunit<br><b>Family:</b> Urease, beta-subunit                                                                                                                                                                               |
| 50 | <a href="#">c2lIIA</a>  | Alignment | not modelled | 39.5 | 16 | <b>PDB header:</b> structural protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> lamin-b2;<br><b>PDBTitle:</b> solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a                                          |
| 51 | <a href="#">d1ufga</a>  | Alignment | not modelled | 38.8 | 16 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Lamin A/C globular tail domain<br><b>Family:</b> Lamin A/C globular tail domain                                                                                                                                   |
| 52 | <a href="#">d1xvsa</a>  | Alignment | not modelled | 38.0 | 6  | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> ApaG-like<br><b>Family:</b> ApaG-like                                                                                                                                                                             |
| 53 | <a href="#">d1g0da2</a> | Alignment | not modelled | 37.2 | 19 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Transglutaminase, two C-terminal domains<br><b>Family:</b> Transglutaminase, two C-terminal domains                                                                                                               |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                  |
|----|-------------------------|-----------|--------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 54 | <a href="#">d1v10a2</a> | Alignment | not modelled | 34.3 | 15 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Multidomain cupredoxins                                                                                                                                                                                        |
| 55 | <a href="#">c3nrfa_</a> | Alignment | not modelled | 32.3 | 28 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> apag protein;<br><b>PDBTitle:</b> crystal structure of an apag protein (pa1934) from pseudomonas2 aeruginosa pao1 at 1.50 a resolution                                                         |
| 56 | <a href="#">d1e9ya1</a> | Alignment | not modelled | 32.1 | 15 | <b>Fold:</b> beta-clip<br><b>Superfamily:</b> Urease, beta-subunit<br><b>Family:</b> Urease, beta-subunit                                                                                                                                                                                        |
| 57 | <a href="#">c2kutA_</a> | Alignment | not modelled | 31.4 | 14 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a                              |
| 58 | <a href="#">c3ndyG_</a> | Alignment | not modelled | 30.9 | 13 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> G: <b>PDB Molecule:</b> endoglucanase d;<br><b>PDBTitle:</b> the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans                                                                     |
| 59 | <a href="#">c3qgaD_</a> | Alignment | not modelled | 30.1 | 13 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> fusion of urease beta and gamma subunits;<br><b>PDBTitle:</b> 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae                                                                                    |
| 60 | <a href="#">c2f1eA_</a> | Alignment | not modelled | 30.0 | 16 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein apag;<br><b>PDBTitle:</b> solution structure of apag protein                                                                                                                           |
| 61 | <a href="#">d3pmga4</a> | Alignment | not modelled | 29.9 | 9  | <b>Fold:</b> TBP-like<br><b>Superfamily:</b> Phosphoglucomutase, C-terminal domain<br><b>Family:</b> Phosphoglucomutase, C-terminal domain                                                                                                                                                       |
| 62 | <a href="#">c2l0dA_</a> | Alignment | not modelled | 29.7 | 14 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> cell surface protein;<br><b>PDBTitle:</b> solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a |
| 63 | <a href="#">c2x3bB_</a> | Alignment | not modelled | 26.8 | 13 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> toxic extracellular endopeptidase;<br><b>PDBTitle:</b> asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase                                                                                      |
| 64 | <a href="#">d1xq4a_</a> | Alignment | not modelled | 26.2 | 14 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> ApaG-like<br><b>Family:</b> ApaG-like                                                                                                                                                                                      |
| 65 | <a href="#">d2q3za2</a> | Alignment | not modelled | 25.2 | 16 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Transglutaminase, two C-terminal domains<br><b>Family:</b> Transglutaminase, two C-terminal domains                                                                                                                        |
| 66 | <a href="#">c3rfrl_</a> | Alignment | not modelled | 24.7 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> I: <b>PDB Molecule:</b> pmob;<br><b>PDBTitle:</b> crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m                                                                                              |
| 67 | <a href="#">d1kyaa2</a> | Alignment | not modelled | 24.2 | 11 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Multidomain cupredoxins                                                                                                                                                                                        |
| 68 | <a href="#">c1e9zA_</a> | Alignment | not modelled | 22.0 | 15 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> urease subunit alpha;<br><b>PDBTitle:</b> crystal structure of helicobacter pylori urease                                                                                                                                  |
| 69 | <a href="#">d2cj3a1</a> | Alignment | not modelled | 20.4 | 25 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                                                                                       |
| 70 | <a href="#">c3se6A_</a> | Alignment | not modelled | 20.4 | 10 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 2;<br><b>PDBTitle:</b> crystal structure of the human endoplasmic reticulum aminopeptidase 2                                                                                          |
| 71 | <a href="#">d1bqka_</a> | Alignment | not modelled | 19.7 | 26 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                                                                                       |
| 72 | <a href="#">d1hfua2</a> | Alignment | not modelled | 19.7 | 9  | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Multidomain cupredoxins                                                                                                                                                                                        |
| 73 | <a href="#">c3cc1B_</a> | Alignment | not modelled | 18.3 | 10 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-n-acetyl galactosaminidase;<br><b>PDBTitle:</b> crystal structure of a putative alpha-n-acetyl galactosaminidase2 (bh1870) from bacillus halodurans c-125 at 2.00 a resolution                              |
| 74 | <a href="#">c1f13A_</a> | Alignment | not modelled | 18.3 | 12 | <b>PDB header:</b> coagulation factor<br><b>Chain:</b> A: <b>PDB Molecule:</b> cellular coagulation factor xiii zymogen;<br><b>PDBTitle:</b> recombinant human cellular coagulation factor xiii                                                                                                  |
| 75 | <a href="#">d1tzaa_</a> | Alignment | not modelled | 17.1 | 10 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> ApaG-like<br><b>Family:</b> ApaG-like                                                                                                                                                                                      |
| 76 | <a href="#">d1plaa_</a> | Alignment | not modelled | 17.0 | 36 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                                                                                       |
| 77 | <a href="#">d1lifr_</a> | Alignment | not modelled | 16.2 | 18 | <b>Fold:</b> Immunoglobulin-like beta-sandwich<br><b>Superfamily:</b> Lamin A/C globular tail domain<br><b>Family:</b> Lamin A/C globular tail domain                                                                                                                                            |
| 78 | <a href="#">c2qv2A_</a> | Alignment | not modelled | 16.0 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> inositol polyphosphate 5-phosphatase ocrl-1;<br><b>PDBTitle:</b> a role of the lowe syndrome protein ocrl in early steps of2 the endocytic pathway                                                                         |
|    |                         |           |              |      |    | <b>Fold:</b> Immunoglobulin-like beta-sandwich                                                                                                                                                                                                                                                   |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                  |
|----|-------------------------|-----------|--------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 79 | <a href="#">d1lvtA_</a> | Alignment | not modelled | 15.5 | 18 | <b>Superfamily:</b> Lamin A/C globular tail domain<br><b>Family:</b> Lamin A/C globular tail domain                                                                                                                              |
| 80 | <a href="#">d1hmja_</a> | Alignment | not modelled | 14.7 | 16 | <b>Fold:</b> RPB5-like RNA polymerase subunit<br><b>Superfamily:</b> RPB5-like RNA polymerase subunit<br><b>Family:</b> RPB5                                                                                                     |
| 81 | <a href="#">d1bxua_</a> | Alignment | not modelled | 14.2 | 26 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |
| 82 | <a href="#">d1adwa_</a> | Alignment | not modelled | 14.0 | 19 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |
| 83 | <a href="#">d1plca_</a> | Alignment | not modelled | 13.2 | 33 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |
| 84 | <a href="#">c3rx9A_</a> | Alignment | not modelled | 13.2 | 18 | <b>PDB header:</b> lipid binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> 3d structure of scin from an escherichia coli patotype                                   |
| 85 | <a href="#">d1pmya_</a> | Alignment | not modelled | 12.9 | 26 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |
| 86 | <a href="#">d1paza_</a> | Alignment | not modelled | 12.8 | 19 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |
| 87 | <a href="#">c3ppsD_</a> | Alignment | not modelled | 12.5 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> laccase;<br><b>PDBTitle:</b> crystal structure of an ascomycete fungal laccase from thielavia2 arenaria                                               |
| 88 | <a href="#">d1bypa_</a> | Alignment | not modelled | 12.1 | 33 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |
| 89 | <a href="#">d9pcya_</a> | Alignment | not modelled | 12.1 | 30 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |
| 90 | <a href="#">d1pcsa_</a> | Alignment | not modelled | 12.0 | 32 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |
| 91 | <a href="#">d2q5ba1</a> | Alignment | not modelled | 11.9 | 21 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |
| 92 | <a href="#">c2zoeA_</a> | Alignment | not modelled | 11.2 | 13 | <b>PDB header:</b> toxin<br><b>Chain:</b> A: <b>PDB Molecule:</b> hemagglutinin components ha3;<br><b>PDBTitle:</b> ha3 subcomponent of clostridium botulinum type c progenitor2 toxin, complex with n-acetylneuramic acid       |
| 93 | <a href="#">d7pcya_</a> | Alignment | not modelled | 10.8 | 37 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |
| 94 | <a href="#">d1qbaa2</a> | Alignment | not modelled | 10.2 | 10 | <b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f<br><b>Superfamily:</b> Carbohydrate-binding domain<br><b>Family:</b> Bacterial chitinase, n-terminal domain                                      |
| 95 | <a href="#">c3qnfa_</a> | Alignment | not modelled | 10.1 | 13 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 1;<br><b>PDBTitle:</b> crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1     |
| 96 | <a href="#">d2jxma1</a> | Alignment | not modelled | 9.8  | 22 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |
| 97 | <a href="#">c2zv4O_</a> | Alignment | not modelled | 9.4  | 15 | <b>PDB header:</b> structural protein<br><b>Chain:</b> O: <b>PDB Molecule:</b> major vault protein;<br><b>PDBTitle:</b> the structure of rat liver vault at 3.5 angstrom resolution                                              |
| 98 | <a href="#">c2xdtA_</a> | Alignment | not modelled | 9.3  | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic reticulum aminopeptidase 1;<br><b>PDBTitle:</b> crystal structure of the soluble domain of human2 endoplasmic reticulum aminopeptidase 1 erap1 |
| 99 | <a href="#">d1ag6a_</a> | Alignment | not modelled | 8.9  | 33 | <b>Fold:</b> Cupredoxin-like<br><b>Superfamily:</b> Cupredoxins<br><b>Family:</b> Plastocyanin/azurin-like                                                                                                                       |