

















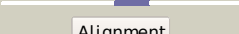

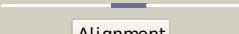
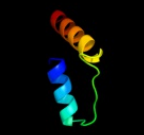
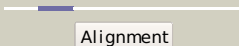
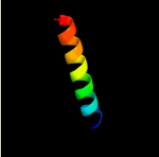

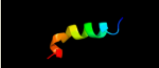

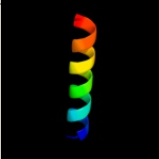
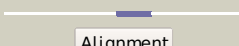

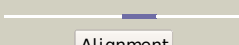
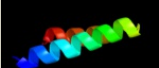
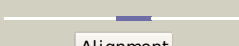
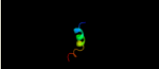
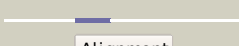





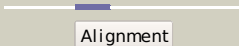
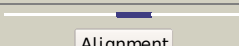

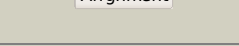
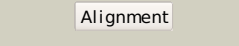

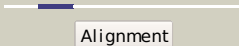



Phyre2

| | |
|---------------|------------------------------|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P52078 |
| Date | Tue Jul 17 17:05:11 BST 2012 |
| Unique Job ID | 91020c197ee4e477 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c3okzB_ |  Alignment |  | 100.0 | 27 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative uncharacterized protein gbs0355; PDBTitle: crystal structure of protein gbs0355 from streptococcus agalactiae,2 northeast structural genomics consortium target sar127 |
| 2 | c3pe5B_ |  Alignment |  | 100.0 | 22 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: three-dimensional structure of protein a7vv38_9clot from clostridium2 leptum dsm 753, northeast structural genomics consortium target3 qlr103 |
| 3 | c3qfiA_ |  Alignment |  | 100.0 | 31 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of transcriptional regulator (ef0465) from2 enterococcus faecalis, northeast structural genomics consortium3 target efr190 |
| 4 | c3mejA_ |  Alignment |  | 100.0 | 40 | PDB header: transcriptional regulator Chain: A: PDB Molecule: transcriptional regulator ywtf; PDBTitle: crystal structure of putative transcriptional regulator ywtf from2 bacillus subtilis, northeast structural genomics consortium target3 sr736 |
| 5 | c3owqB_ |  Alignment |  | 100.0 | 34 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lin1025 protein; PDBTitle: x-ray structure of lin1025 protein from listeria innocua, northeast2 structural genomics consortium target lkr164 |
| 6 | c3nroA_ |  Alignment |  | 100.0 | 33 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo1026 protein; PDBTitle: crystal structure of putative transcriptional factor lmo1026 from2 listeria monocytogenes (fragment 52-321), northeast structural3 genomics consortium target lmr194 |
| 7 | c3nxhA_ |  Alignment |  | 100.0 | 36 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator yvhj; PDBTitle: crystal structure of the transcriptional regulator yvhj from bacillus2 subtilis. northeast structural genomics consortium target sr735. |
| 8 | d1ny8a_ |  Alignment |  | 20.3 | 14 | Fold: Alpha-lytic protease prodomain-like Superfamily: BolA-like Family: BolA-like |
| 9 | c3bpjD_ |  Alignment |  | 18.3 | 13 | PDB header: translation Chain: D: PDB Molecule: eukaryotic translation initiation factor 3 subunit j; PDBTitle: crystal structure of human translation initiation factor 3, subunit 12 alpha |
| 10 | c3tr3A_ |  Alignment |  | 16.8 | 17 | PDB header: unknown function Chain: A: PDB Molecule: bola; PDBTitle: structure of a bola protein homologue from coxiella burnetii |
| 11 | c3rgqA_ |  Alignment |  | 15.6 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptptm1 in complex with pi(5)p |

| | | | | | | |
|----|-------------------------|---|---|------|----|---|
| 12 | c3vmtA_ |  |  | 14.3 | 21 | PDB header: transferase Chain: A: PDB Molecule: monofunctional glycosyltransferase; PDBTitle: crystal structure of staphylococcus aureus membrane-bound2 transglycosylase in complex with a lipid ii analog |
| 13 | c2dhmA_ |  |  | 13.9 | 10 | PDB header: protein binding Chain: A: PDB Molecule: protein bola; PDBTitle: solution structure of the bola protein from escherichia coli |
| 14 | d1m56d_ |  |  | 13.5 | 10 | Fold: Single transmembrane helix Superfamily: Bacterial aa3 type cytochrome c oxidase subunit IV Family: Bacterial aa3 type cytochrome c oxidase subunit IV |
| 15 | c3o2eA_ |  |  | 13.5 | 10 | PDB header: unknown function Chain: A: PDB Molecule: bola-like protein; PDBTitle: crystal structure of a bol-like protein from babesia bovis |
| 16 | c2wl8D_ |  |  | 13.3 | 11 | PDB header: protein transport Chain: D: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: x-ray crystal structure of pex19p |
| 17 | c1v60A_ |  |  | 12.2 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: riken cdna 1810037g04; PDBTitle: solution structure of bola1 protein from mus musculus |
| 18 | c2pjuD_ |  |  | 12.0 | 24 | PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon2 regulatory protein prp |
| 19 | c4ddpA_ |  |  | 11.1 | 14 | PDB header: membrane protein Chain: A: PDB Molecule: beclin-1; PDBTitle: crystal structure of beclin 1 evolutionarily conserved domain(ecd) |
| 20 | d1fpza_ |  |  | 11.0 | 11 | Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like |
| 21 | d2pjuA1 |  | not modelled | 10.5 | 24 | Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like |
| 22 | c1xs3A_ |  | not modelled | 8.8 | 10 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein xc975; PDBTitle: solution structure analysis of the xc975 protein |
| 23 | c3vp7A_ |  | not modelled | 8.6 | 19 | PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: crystal structure of the beta-alpha repeated, autophagy-specific2 (bara) domain of vps30/atg6 |
| 24 | c1oheA_ |  | not modelled | 8.6 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand |
| 25 | d1jhfa1 |  | not modelled | 8.5 | 16 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain |
| 26 | c3jycA_ |  | not modelled | 8.3 | 20 | PDB header: metal transport Chain: A: PDB Molecule: inward-rectifier k+ channel kir2.2; PDBTitle: crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution |
| 27 | d1stza1 |  | not modelled | 8.2 | 13 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain |
| 28 | c2q5cA_ |  | not modelled | 7.7 | 14 | PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|--|
| 29 | c1spfA_ | Alignment | not modelled | 7.5 | 33 | PDB header: lipoprotein(surface film) Chain: A; PDB Molecule: pulmonary surfactant-associated polypeptide c; PDBTitle: the nmr structure of the pulmonary surfactant-associated2 polypeptide sp-c in an apolar solvent contains a valyl-3 rich alpha-helix |
| 30 | d1gwya_ | Alignment | not modelled | 6.9 | 12 | Fold: Cytolysin/lectin Superfamily: Cytolysin/lectin Family: Anemone pore-forming cytolysin |
| 31 | c3i7aA_ | Alignment | not modelled | 6.3 | 13 | PDB header: hydrolase Chain: A; PDB Molecule: putative metal-dependent phosphohydrolase; PDBTitle: crystal structure of putative metal-dependent phosphohydrolase2 (yp_926882.1) from shewanella amazonensis sb2b at 2.06 a resolution |
| 32 | c3df0C_ | Alignment | not modelled | 6.0 | 23 | PDB header: hydrolase Chain: C; PDB Molecule: calpastatin; PDBTitle: calcium-dependent complex between m-calpain and calpastatin |
| 33 | d1v9ja_ | Alignment | not modelled | 5.8 | 17 | Fold: Alpha-lytic protease prodomain-like Superfamily: BolA-like Family: BolA-like |
| 34 | c3aygA_ | Alignment | not modelled | 5.7 | 26 | PDB header: oxidoreductase Chain: A; PDB Molecule: nitric oxide reductase; PDBTitle: crystal structure of nitric oxide reductase complex with hqno |
| 35 | d1p5dx4 | Alignment | not modelled | 5.6 | 11 | Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain |
| 36 | c2kwpA_ | Alignment | not modelled | 5.3 | 13 | PDB header: transcription Chain: A; PDB Molecule: transcription elongation protein nusa; PDBTitle: solution structure of the aminoterminal domain of e. coli nusa |
| 37 | d1vc2a1 | Alignment | not modelled | 5.3 | 33 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 38 | c2kz0A_ | Alignment | not modelled | 5.3 | 17 | PDB header: transcription Chain: A; PDB Molecule: bola family protein; PDBTitle: solution structure of a bola protein (ech_0303) from ehrlichia2 chaffeensis. seattle structural genomics center for infectious3 disease target ehcha.10365.a |
| 39 | c2e0tA_ | Alignment | not modelled | 5.2 | 11 | PDB header: hydrolase Chain: A; PDB Molecule: dual specificity phosphatase 26; PDBTitle: crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens |
| 40 | d1xza1 | Alignment | not modelled | 5.1 | 17 | Fold: Four-helical up-and-down bundle Superfamily: TrmE connector domain Family: TrmE connector domain |
| 41 | d1vh4a_ | Alignment | not modelled | 5.1 | 17 | Fold: Single-stranded right-handed beta-helix Superfamily: Stabilizer of iron transporter SufD Family: Stabilizer of iron transporter SufD |
| 42 | d1ohea2 | Alignment | not modelled | 5.0 | 15 | Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like |