

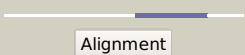

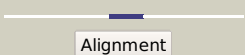



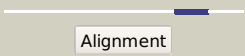

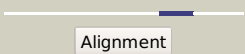

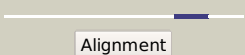

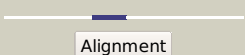



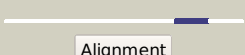

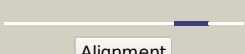



Phyre2

| | |
|---------------|------------------------------|
| Email | I.a.kelley@imperial.ac.uk |
| Description | Q5BN45 |
| Date | Tue Jul 30 13:19:44 BST 2013 |
| Unique Job ID | 2c34026662aeb7fe |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4gafA_ |  Alignment |  | 12.8 | 18 | PDB header: signaling protein Chain: A; PDB Molecule: ebi-005; PDBTitle: crystal structure of ebi-005, a chimera of human il-1beta and il-1ra,2 bound to human interleukin-1 receptor type 1 |
| 2 | c2cw1A_ |  Alignment |  | 12.3 | 31 | PDB header: de novo protein Chain: A; PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein |
| 3 | c1s21A_ |  Alignment |  | 9.8 | 35 | PDB header: chaperone Chain: A; PDB Molecule: orf2; PDBTitle: crystal structure of avrpvh orf2, a type iii effector from2 p. syringae |
| 4 | d1s21a_ |  Alignment |  | 9.8 | 35 | Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: AvrPphF ORF2, a type III effector |
| 5 | c3dv0L_ |  Alignment |  | 9.6 | 20 | PDB header: oxidoreductase/transferase Chain: I; PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex |
| 6 | c4a4yA_ |  Alignment |  | 9.4 | 43 | PDB header: protein binding Chain: A; PDB Molecule: protein mxig; PDBTitle: structure of the cytosolic domain of the shigella t3s2 component mxig |
| 7 | c2dt7A_ |  Alignment |  | 9.1 | 33 | PDB header: rna binding protein Chain: A; PDB Molecule: splicing factor 3a subunit 3; PDBTitle: solution structure of the second surp domain of human2 splicing factor sf3a120 in complex with a fragment of3 human splicing factor sf3a60 |
| 8 | d1v0da_ |  Alignment |  | 8.9 | 50 | Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: Caspase-activated DNase, CAD (DffB, DFF40) |
| 9 | c1v0dA_ |  Alignment |  | 8.9 | 50 | PDB header: hydrolase Chain: A; PDB Molecule: dna fragmentation factor 40 kda subunit; PDBTitle: crystal structure of caspase-activated dnase (cad) |
| 10 | d1w4ha1 |  Alignment |  | 8.8 | 20 | Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex |
| 11 | d1bala_ |  Alignment |  | 8.6 | 20 | Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|---|
| 12 | c3ka5A_ | Alignment | | 8.3 | 24 | PDB header: chaperone Chain: A: PDB Molecule: ribosome-associated protein y (psrp-1); PDBTitle: crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a |
| 13 | d1v58a2 | Alignment | | 8.2 | 32 | Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like |
| 14 | c3aa6C_ | Alignment | | 8.2 | 83 | PDB header: protein binding Chain: C: PDB Molecule: 23mer peptide from cd2-associated protein; PDBTitle: crystal structure of actin capping protein in complex with the cp-2 binding motif derived from cd2ap |
| 15 | c3k2tA_ | Alignment | | 7.7 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2511 protein; PDBTitle: crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a |
| 16 | d1sfua_ | Alignment | | 7.5 | 50 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain |
| 17 | c3w0dA_ | Alignment | | 6.9 | 39 | PDB header: hydrolase inhibitor Chain: A: PDB Molecule: elastase inhibitor afuei; PDBTitle: structure of elastase inhibitor afuei (cyrstal form i) |
| 18 | c2eq8C_ | Alignment | | 6.8 | 28 | PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp |
| 19 | c2cooA_ | Alignment | | 6.7 | 32 | PDB header: transferase Chain: A: PDB Molecule: lipoamide acyltransferase component of branched- PDBTitle: solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase |
| 20 | d1w85i_ | Alignment | | 6.5 | 20 | Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex |
| 21 | d2choa2 | Alignment | not modelled | 6.0 | 11 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain |
| 22 | d8i1ba_ | Alignment | not modelled | 5.5 | 23 | Fold: beta-Trefoil Superfamily: Cytokine Family: Interleukin-1 (IL-1) |
| 23 | d1ubdc1 | Alignment | not modelled | 5.4 | 17 | Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2 |
| 24 | c1w3dA_ | Alignment | not modelled | 5.4 | 20 | PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p |