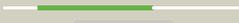
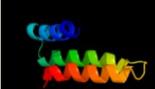
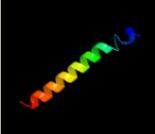
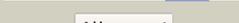
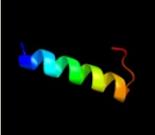
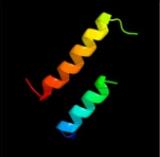
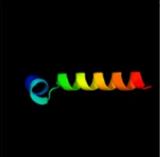
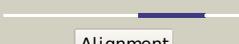
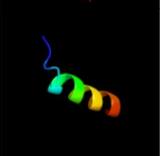
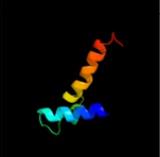


Phyre2

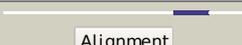
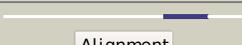
| | |
|---------------|-----------------------------|
| Email | I.a.kelley@imperial.ac.uk |
| Description | P77354 |
| Date | Thu Jan 5 12:28:05 GMT 2012 |
| Unique Job ID | 366dabe3c7782112 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c1ciiA_ |  Alignment |  | 66.2 | 14 | PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia; PDBTitle: colicin ia |
| 2 | c3fewX_ |  Alignment |  | 59.7 | 17 | PDB header: immune system Chain: X; PDB Molecule: colicin s4; PDBTitle: structure and function of colicin s4, a colicin with a2 duplicated receptor binding domain |
| 3 | dlyqga1 |  Alignment |  | 51.0 | 12 | Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like |
| 4 | d1cola_ |  Alignment |  | 45.0 | 17 | Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin |
| 5 | d1rh1a2 |  Alignment |  | 44.9 | 10 | Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin |
| 6 | c1rh1A_ |  Alignment |  | 28.1 | 10 | PDB header: antibiotic Chain: A; PDB Molecule: colicin b; PDBTitle: crystal structure of the cytotoxic bacterial protein2 colicin b at 2.5 a resolution |
| 7 | d1luxa_ |  Alignment |  | 27.5 | 18 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 8 | c2ag8A_ |  Alignment |  | 21.6 | 12 | PDB header: oxidoreductase Chain: A; PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis |
| 9 | c3mb2J_ |  Alignment |  | 20.4 | 26 | PDB header: isomerase Chain: J; PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - beta subunit; PDBTitle: kinetic and structural characterization of a heterohexameric 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily |
| 10 | c3qwmA_ |  Alignment |  | 17.5 | 20 | PDB header: signaling protein Chain: A; PDB Molecule: iq motif and sec7 domain-containing protein 1; PDBTitle: crystal structure of gep100, the plectrin homology domain of iq motif2 and sec7 domain-containing protein 1 isoform a |
| 11 | c3m8jA_ |  Alignment |  | 16.2 | 33 | PDB header: transcription Chain: A; PDB Molecule: focb protein; PDBTitle: crystal structure of e.coli focb at 1.4 a resolution |

| | | | | | | |
|----|-------------------------|---|---|------|----|--|
| 12 | c1a87A_ |  Alignment |  | 15.8 | 25 | PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n |
| 13 | d1a87a_ |  Alignment |  | 15.8 | 25 | Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin |
| 14 | c3h0dB_ |  Alignment |  | 14.2 | 22 | PDB header: transcription/dna Chain: B: PDB Molecule: ctsr; PDBTitle: crystal structure of ctsr in complex with a 26bp dna duplex |
| 15 | d2ahra1 |  Alignment |  | 13.5 | 21 | Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like |
| 16 | c2izzE_ |  Alignment |  | 9.7 | 19 | PDB header: oxidoreductase Chain: E: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate2 reductase |
| 17 | c1s7cA_ |  Alignment |  | 9.4 | 22 | PDB header: structural genomics, oxidoreductase Chain: A: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase a; PDBTitle: crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli |
| 18 | c2i5pO_ |  Alignment |  | 8.9 | 11 | PDB header: oxidoreductase Chain: O: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase 1; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase isoform 1 from k. marxianus |
| 19 | c3gtyS_ |  Alignment |  | 8.9 | 10 | PDB header: chaperone/ribosomal protein Chain: S: PDB Molecule: 30s ribosomal protein s7; PDBTitle: promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone |
| 20 | c3h9eA_ |  Alignment | | 8.4 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: PDBTitle: crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate |
| 21 | c1hdgO_ |  Alignment | not modelled | 8.3 | 11 | PDB header: oxidoreductase (aldehy(d)-nad(a)) Chain: O: PDB Molecule: holo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: the crystal structure of holo-glyceraldehyde-3-phosphate dehydrogenase2 from the hyperthermophilic bacterium thermotoga maritima at 2.53 angstroms resolution |
| 22 | c3ci9B_ |  Alignment | not modelled | 8.3 | 21 | PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1 |
| 23 | c3b20R_ |  Alignment | not modelled | 8.2 | 9 | PDB header: oxidoreductase Chain: R: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase (nadp+); PDBTitle: crystal structure analysis of dehydrogenase complexed with nad |
| 24 | c3hq4R_ |  Alignment | not modelled | 8.1 | 11 | PDB header: oxidoreductase Chain: R: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase 1; PDBTitle: crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution |
| 25 | c3hjaB_ |  Alignment | not modelled | 8.0 | 11 | PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase from borrelia burgdorferi |
| 26 | c1ihxD_ |  Alignment | not modelled | 7.9 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of two d-glyceraldehyde-3-phosphate2 dehydrogenase complexes: a case of asymmetry |
| | |  Alignment | | | | PDB header: oxidoreductase Chain: O: PDB Molecule: glyceraldehyde 3-phosphate |

| | | | | | | |
|----|-------------------------|-----------|--------------|-----|----|--|
| 27 | c2d2iO_ | Alignment | not modelled | 7.9 | 11 | dehydrogenase; PDBTitle: crystal structure of nadp-dependent glyceraldehyde-3-2 phosphate dehydrogenase from synechococcus sp. complexed3 with nadp+ |
| 28 | d1k6ka_ | Alignment | not modelled | 7.6 | 16 | Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif |
| 29 | c2x5kO_ | Alignment | not modelled | 7.4 | 6 | PDB header: oxidoreductase Chain: O: PDB Molecule: d-erythrose-4-phosphate dehydrogenase; PDBTitle: structure of an active site mutant of the d-erythrose-4-phosphate2 dehydrogenase from e. coli |
| 30 | c1qvrB_ | Alignment | not modelled | 7.4 | 18 | PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb |
| 31 | c2ep7B_ | Alignment | not modelled | 7.2 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: structural study of project id aq_1065 from aquifex aeolicus vf5 |
| 32 | d1u94a2 | Alignment | not modelled | 7.2 | 19 | Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain |
| 33 | d2bida_ | Alignment | not modelled | 7.1 | 9 | Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death |
| 34 | c2pkrl_ | Alignment | not modelled | 7.1 | 11 | PDB header: oxidoreductase Chain: I: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase aor; PDBTitle: crystal structure of (a+cte)4 chimeric form of2 photosynthetic glyceraldehyde-3-phosphate dehydrogenase,3 complexed with nadp |
| 35 | c3docD_ | Alignment | not modelled | 7.0 | 11 | PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of trka glyceraldehyde-3-phosphate2 dehydrogenase from brucella melitensis |
| 36 | c1rm4O_ | Alignment | not modelled | 6.9 | 11 | PDB header: oxidoreductase Chain: O: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase a; PDBTitle: crystal structure of recombinant photosynthetic glyceraldehyde-3-2 phosphate dehydrogenase a4 isoform, complexed with nadp |
| 37 | c2fs1A_ | Alignment | not modelled | 6.9 | 15 | PDB header: protein binding Chain: A: PDB Molecule: psd-1; PDBTitle: solution structure of psd-1 |
| 38 | d1xp8a2 | Alignment | not modelled | 6.9 | 20 | Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain |
| 39 | c2b4rO_ | Alignment | not modelled | 6.8 | 11 | PDB header: oxidoreductase Chain: Q: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falci parum at 2.25 angstrom resolution reveals intriguing3 extra electron density in the active site |
| 40 | c1i32D_ | Alignment | not modelled | 6.8 | 13 | PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors |
| 41 | c1cerC_ | Alignment | not modelled | 6.6 | 6 | PDB header: oxidoreductase (aldehyde(d)-nad(a)) Chain: C: PDB Molecule: holo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: determinants of enzyme thermostability observed in the2 molecular structure of thermus aquaticus d-glyceraldehyde-3 3-phosphate dehydrogenase at 2.5 angstroms resolution |
| 42 | d1mo6a2 | Alignment | not modelled | 6.5 | 16 | Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain |
| 43 | d1ubea2 | Alignment | not modelled | 6.4 | 16 | Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain |
| 44 | c3cieC_ | Alignment | not modelled | 6.3 | 17 | PDB header: oxidoreductase Chain: C: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum |
| 45 | c1obfO_ | Alignment | not modelled | 6.2 | 11 | PDB header: glycolytic pathway Chain: O: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: the crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from alcaligenes xylooxidans at 1.73 resolution. |
| 46 | d2c42a4 | Alignment | not modelled | 6.1 | 18 | Fold: Pyruvate-ferredoxin oxidoreductase, PFOR, domain III Superfamily: Pyruvate-ferredoxin oxidoreductase, PFOR, domain III Family: Pyruvate-ferredoxin oxidoreductase, PFOR, domain III |
| 47 | d1gjsa_ | Alignment | not modelled | 6.1 | 23 | Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: GA module, an albumin-binding domain |
| 48 | c2i88A_ | Alignment | not modelled | 6.1 | 15 | PDB header: membrane protein Chain: A: PDB Molecule: colicin-e1; PDBTitle: crystal structure of the channel-forming domain of colicin2 e1 |
| 49 | d1v9va1 | Alignment | not modelled | 6.1 | 17 | Fold: Bromodomain-like Superfamily: MAST3 pre-PK domain-like Family: MAST3 pre-PK domain-like |

| | | | | | | |
|----|-------------------------|---|--------------|-----|----|--|
| 50 | c3sthA_ |  Alignment | not modelled | 5.6 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from <i>Toxoplasma gondii</i> |
| 51 | c2y69Z_ |  Alignment | not modelled | 5.5 | 17 | PDB header: electron transport Chain: Z: PDB Molecule: cytochrome c oxidase polypeptide 8h; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen |
| 52 | c1g92A_ |  Alignment | not modelled | 5.4 | 67 | PDB header: toxin Chain: A: PDB Molecule: poneratoxin; PDBTitle: solution structure of poneratoxin |
| 53 | c2po3B_ |  Alignment | not modelled | 5.3 | 22 | PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its 2 tdp-sugar product |
| 54 | c2gd1P_ |  Alignment | not modelled | 5.1 | 11 | PDB header: oxidoreductase(aldehyde(d)-nad(a)) Chain: P: PDB Molecule: apo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: coenzyme-induced conformational changes in glyceraldehyde-3-phosphate dehydrogenase from <i>Bacillus stearothermophilus</i> |
| 55 | d1hula_ |  Alignment | not modelled | 5.1 | 17 | Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines |