Phyre2

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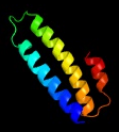
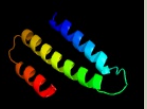
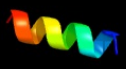
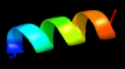
| Email | tim.levine@ucl.ac.uk |
| Description | Ice2____ |
| Date | Fri Feb 12 18:45:40 GMT 2021 |
| Unique Job ID | a721a0f25048fc30 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c6sp2E_ | Alignment | | 87.4 | 14 | **PDB header:**membrane protein<br>**Chain:** E: **PDB Molecule:**membrane protein tms1d;<br>**PDBTitle:** cryoem structure of serinc from drosophila melanogaster |
| 2 | c6sp2F_ | Alignment | | 87.4 | 14 | **PDB header:**membrane protein<br>**Chain:** F: **PDB Molecule:**membrane protein tms1d;<br>**PDBTitle:** cryoem structure of serinc from drosophila melanogaster |
| 3 | c6cfwB_ | Alignment | | 56.7 | 15 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**monovalent cation/h+ antiporter subunit f;<br>**PDBTitle:** cryoem structure of a respiratory membrane-bound hydrogenase |
| 4 | c7d3uF_ | Alignment |  | 53.2 | 18 | **PDB header:**membrane protein<br>**Chain:** F: **PDB Molecule:**monovalent na+/h+ antiporter subunit f;<br>**PDBTitle:** structure of mrp complex from dietzia sp. dq12-45-1b |
| 5 | c6ly5l_ | Alignment |  | 44.2 | 39 | **PDB header:**photosynthesis<br>**Chain:** L: **PDB Molecule:**fcpi-14;<br>**PDBTitle:** organization and energy transfer in a huge diatom psi-fcpi2 supercomplex |
| 6 | c6z16F_ | Alignment |  | 38.3 | 11 | **PDB header:**membrane protein<br>**Chain:** F: **PDB Molecule:**multisubunit na+/h+ antiporter, f subunit;<br>**PDBTitle:** structure of the mrp antiporter complex |
| 7 | c6u8yb_ | Alignment | | 32.0 | 14 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**monovalent cation/h+ antiporter subunit f;<br>**PDBTitle:** structure of the membrane-bound sulfane sulfur reductase (mbs), an2 archaeal respiratory membrane complex |
| 8 | c4dhxA_ | Alignment | | 26.4 | 21 | **PDB header:**transport protein/dna binding protein<br>**Chain:** A: **PDB Molecule:**80 kda mcm3-associated protein;<br>**PDBTitle:** eny2:ganp complex |
| 9 | d1rzhh2 | Alignment |  | 23.9 | 36 | **Fold:**Single transmembrane helix<br>**Superfamily:**Photosystem II reaction centre subunit H, transmembrane region<br>**Family:**Photosystem II reaction centre subunit H, transmembrane region |
| 10 | d1l9bh2 | Alignment |  | 22.0 | 36 | **Fold:**Single transmembrane helix<br>**Superfamily:**Photosystem II reaction centre subunit H, transmembrane region<br>**Family:**Photosystem II reaction centre subunit H, transmembrane region |
| 11 | c1yodB_ | Alignment | | 21.7 | 47 | **PDB header:**de novo protein<br>**Chain:** B: **PDB Molecule:**water-solublized phospholamban;<br>**PDBTitle:** crystal structure of a water soluble analog of phospholamban |

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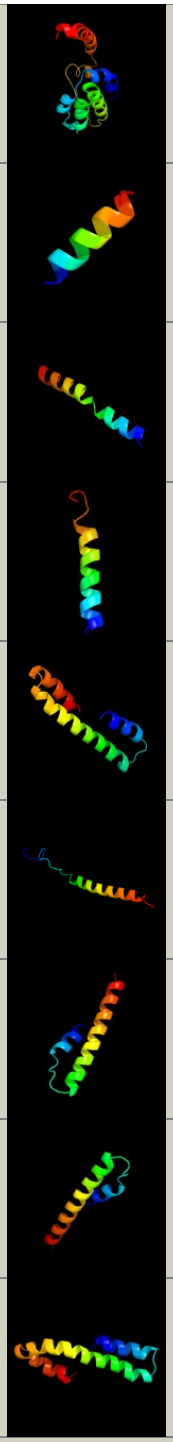
| 12 | c4nqkD_ | Alignment |  | 21.3 | 13 | **PDB header:**hydrolase/apoptosis<br>**Chain:** D: **PDB Molecule:**probable atp-dependent rna helicase ddx58;<br>**PDBTitle:** structure of an ubiquitin complex |
| 13 | c1yodA_ | Alignment | | 21.0 | 47 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**water-solublized phospholamban;<br>**PDBTitle:** crystal structure of a water soluble analog of phospholamban |
| 14 | c4dhxD_ | Alignment | | 19.5 | 21 | **PDB header:**transport protein/dna binding protein<br>**Chain:** D: **PDB Molecule:**80 kda mcm3-associated protein;<br>**PDBTitle:** eny2:ganp complex |
| 15 | c6pnjL_ | Alignment | | 19.0 | 16 | **PDB header:**photosynthesis<br>**Chain:** L: **PDB Molecule:**photosystem i reaction center protein subunit xi;<br>**PDBTitle:** structure of photosystem i acclimated to far-red light |
| 16 | d2ra7a1 | Alignment | | 16.7 | 18 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**FAT domain of focal adhesion kinase<br>**Family:**FAT domain of focal adhesion kinase |
| 17 | c6t0br_ | Alignment | | 16.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** R: **PDB Molecule:**cytochrome b-c1 complex subunit 7;<br>**PDBTitle:** the iii2-iv(5b)2 respiratory supercomplex from s. cerevisiae |
| 18 | c6xdcB_ | Alignment | | 14.4 | 25 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**orf3a protein;<br>**PDBTitle:** cryo-em structure of sars-cov-2 orf3a |
| 19 | c6xdcA_ | Alignment | | 14.4 | 25 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**orf3a protein;<br>**PDBTitle:** cryo-em structure of sars-cov-2 orf3a |
| 20 | d1qvxa_ | Alignment | | 14.4 | 20 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**FAT domain of focal adhesion kinase<br>**Family:**FAT domain of focal adhesion kinase |
| 21 | c5ghwP_ | Alignment | not modelled | 14.2 | 71 | **PDB header:**immune system<br>**Chain:** P: **PDB Molecule:**endogenous retrovirus group k member 8 env polyprotein;<br>**PDBTitle:** crystal structure of broad neutralizing antibody 10e8 with long2 epitope bound |
| 22 | d2rcrh2 | Alignment | not modelled | 14.2 | 38 | **Fold:**Single transmembrane helix<br>**Superfamily:**Photosystem II reaction centre subunit H, transmembrane region<br>**Family:**Photosystem II reaction centre subunit H, transmembrane region |
| 23 | d1uf2c1 | Alignment | not modelled | 14.1 | 41 | **Fold:**A virus capsid protein alpha-helical domain<br>**Superfamily:**A virus capsid protein alpha-helical domain<br>**Family:**Phytoreovirus capsid |
| 24 | c2lq0A_ | Alignment | not modelled | 13.1 | 41 | **PDB header:**antifreeze protein<br>**Chain:** A: **PDB Molecule:**de novo designed antifreeze peptide 1m;<br>**PDBTitle:** solution structure of de novo designed antifreeze peptide 1m |
| 25 | c3gm1A_ | Alignment | not modelled | 12.4 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein tyrosine kinase 2 beta;<br>**PDBTitle:** crystal structure of the focal adhesion targeting (fat)2 domain of pyk2 in complex with paxillin ld4 motif-derived3 peptides |
| 26 | c2l6fA_ | Alignment | not modelled | 12.3 | 20 | **PDB header:**transferase,cell adhesion<br>**Chain:** A: **PDB Molecule:**focal adhesion kinase 1, linker1, paxillin, linker2,<br>**PDBTitle:** nmr solution structure of fat domain of fak complexed with ld2 and ld42 motifs of paxillin |
| 27 | c2gypB_ | Alignment | not modelled | 12.2 | 44 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**hepatocyte nuclear factor 1-alpha;<br>**PDBTitle:** diabetes mellitus due to a frustrated schellman motif in hnf-1a |
| | | | | | | **PDB header:**transcription regulator |

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| 28 | c2gypA_ | Alignment | not modelled | 12.2 | 44 | **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** diabetes mellitus due to a frustrated schellman motif in hnf-1a |
| 29 | d1k04a_ | Alignment | not modelled | 12.0 | 18 | **Fold:**Four-helical up-and-down bundle **Superfamily:**FAT domain of focal adhesion kinase **Family:**FAT domain of focal adhesion kinase |
| 30 | c6igzL_ | Alignment | not modelled | 11.5 | 25 | **PDB header:**plant protein **Chain:** L: **PDB Molecule:**psaI; **PDBTitle:** structure of psi-lhci |
| 31 | c2l6hA_ | Alignment | not modelled | 11.3 | 20 | **PDB header:**transferase,cell adhesion **Chain:** A: **PDB Molecule:**focal adhesion kinase 1, linker, paxillin; **PDBTitle:** fat domain of focal adhesion kinase tethered to ld4 motif of paxillin2 via ggs linker |
| 32 | c5zghL_ | Alignment | not modelled | 11.0 | 36 | **PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**psaI; **PDBTitle:** cryo-em structure of the red algal psi-lhcr |
| 33 | d1iv0a_ | Alignment | not modelled | 10.8 | 27 | **Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX |
| 34 | c5j12A_ | Alignment | not modelled | 10.5 | 20 | **PDB header:**signaling protein **Chain:** A: **PDB Molecule:**thymic stromal lymphopoietin; **PDBTitle:** structure of human tslp:tslpr in complex with mouse il-7ralpha |
| 35 | d1jb0l_ | Alignment | not modelled | 10.5 | 32 | **Fold:**Photosystem I reaction center subunit XI, PsaL **Superfamily:**Photosystem I reaction center subunit XI, PsaL **Family:**Photosystem I reaction center subunit XI, PsaL |
| 36 | c3h01A_ | Alignment | not modelled | 10.1 | 54 | **PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** structure of the c-terminal domain of a putative hiv-1 gp41 fusion2 intermediate |
| 37 | c2kjgA_ | Alignment | not modelled | 9.9 | 17 | **PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**archaeal protein sso6904; **PDBTitle:** solution structure of an archaeal protein sso6904 from2 hyperthermophilic sulfolobus solfataricus |
| 38 | c1uf2F_ | Alignment | not modelled | 9.8 | 41 | **PDB header:**virus **Chain:** F: **PDB Molecule:**outer capsid protein p8; **PDBTitle:** the atomic structure of rice dwarf virus (rdv) |
| 39 | d2i5nh2 | Alignment | not modelled | 9.7 | 22 | **Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region |
| 40 | d3buxb1 | Alignment | not modelled | 9.3 | 27 | **Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins |
| 41 | c6ijoL_ | Alignment | not modelled | 9.3 | 29 | **PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**psaI; **PDBTitle:** photosystem i of chlamydomonas reinhardtii |
| 42 | c2l6gA_ | Alignment | not modelled | 8.6 | 20 | **PDB header:**transferase,cell adhesion **Chain:** A: **PDB Molecule:**focal adhesion kinase 1, linker, paxillin; **PDBTitle:** fat-ld2 double labeled construct with free ld4 peptide |
| 43 | c3k9aA_ | Alignment | not modelled | 7.6 | 50 | **PDB header:**viral protein **Chain:** A: **PDB Molecule:**hiv glycoprotein gp41; **PDBTitle:** crystal structure of hiv gp41 with mper |
| 44 | d1nu0a_ | Alignment | not modelled | 7.3 | 20 | **Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX |
| 45 | d1vhxa_ | Alignment | not modelled | 7.2 | 13 | **Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX |
| 46 | c5u3mA_ | Alignment | not modelled | 6.9 | 44 | **PDB header:**immune system/viral protein **Chain:** A: **PDB Molecule:**gp41 mper peptide; **PDBTitle:** crystal structure of dh511.11p fab in complex with hiv-1 gp41 mper2 peptide |
| 47 | c1g2zB_ | Alignment | not modelled | 6.9 | 71 | **PDB header:**transcription **Chain:** B: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** dimerization domain of hnf-1alpha with a leu 13 selenomethionine2 substitution |
| 48 | d1utca2 | Alignment | not modelled | 6.9 | 50 | **Fold:**7-bladed beta-propeller **Superfamily:**Clathrin heavy-chain terminal domain **Family:**Clathrin heavy-chain terminal domain |
| 49 | c1jb6A_ | Alignment | not modelled | 6.8 | 71 | **PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of dimerization domain (1-33) of hnf-1alpha |
| 50 | c5u3kP_ | Alignment | not modelled | 6.8 | 44 | **PDB header:**immune system/viral protein **Chain:** P: **PDB Molecule:**gp41 mper peptide; **PDBTitle:** crystal structure of dh511.2 fab in complex with hiv-1 gp41 mper 662-2 683 peptide |
| 51 | c1g2zA_ | Alignment | not modelled | 6.7 | 71 | **PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** dimerization domain of hnf-1alpha with a leu 13 selenomethionine2 substitution |
| 52 | d1g2za_ | Alignment | not modelled | 6.7 | 71 | **Fold:**Dimerisation interlock **Superfamily:**Dimerization cofactor of HNF-1 alpha **Family:**Dimerization cofactor of HNF-1 alpha |
| 53 | c1c9lA_ | Alignment | not modelled | 6.5 | 50 | **PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**clathrin; **PDBTitle:** peptide-in-groove interactions link target proteins to the b-propeller2 of clathrin |
| 54 | c6humE_ | Alignment | not modelled | 6.3 | 22 | **PDB header:**proton transport **Chain:** E: **PDB Molecule:**nad(p)h-quinone oxidoreductase subunit 4l; **PDBTitle:** structure of the photosynthetic complex i from |

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| | | | | | | thermosynechococcus2 elongatus |
| 55 | c6hu9e_ | Alignment | not modelled | 6.2 | 14 | **PDB header:**oxidoreductase/electron transport<br>**Chain:** E: **PDB Molecule:**cytochrome b-c1 complex subunit rieske, mitochondrial;<br>**PDBTitle:** iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae |
| 56 | c2wscL_ | Alignment | not modelled | 6.0 | 40 | **PDB header:**photosynthesis<br>**Chain:** L: **PDB Molecule:**photosystem i reaction center subunit xi, chloroplastic;<br>**PDBTitle:** improved model of plant photosystem i |
| 57 | c1zy5B_ | Alignment | not modelled | 5.9 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**serine/threonine-protein kinase gcn2;<br>**PDBTitle:** crystal structure of eif2alpha protein kinase gcn2: r794g2 hyperactivating mutant complexed with ampppnp. |
| 58 | c5u3nA_ | Alignment | not modelled | 5.7 | 44 | **PDB header:**immune system/viral protein<br>**Chain:** A: **PDB Molecule:**gp41 mper peptide;<br>**PDBTitle:** crystal structure of dh511.12p fab in complex with hiv-1 gp41 mper2 peptide |
| 59 | c6hv97_ | Alignment | not modelled | 5.7 | 17 | **PDB header:**dna binding protein<br>**Chain:** 7: **PDB Molecule:**dna replication licensing factor mcm7;<br>**PDBTitle:** s. cerevisiae cmg-pol epsilon-dna |
| 60 | c2w02A_ | Alignment | not modelled | 5.6 | 12 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**acsd;<br>**PDBTitle:** co-complex structure of achromobactin synthetase protein d (acsd) with2 atp from pectobacterium chrysanthemi |
| 61 | c6k61l_ | Alignment | not modelled | 5.4 | 30 | **PDB header:**photosynthesis<br>**Chain:** L: **PDB Molecule:**photosystem i reaction center subunit xi;<br>**PDBTitle:** cryo-em structure of the tetrameric photosystem i from a heterocyst-2 forming cyanobacterium anabaena sp. pcc7120 |
| 62 | c1javA_ | Alignment | not modelled | 5.4 | 56 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**transmembrane glycoprotein (gp41);<br>**PDBTitle:** average nmr solution structure of the trp-rich peptide of2 hiv gp41 bound to dpc micelles |
| 63 | c2pv6A_ | Alignment | not modelled | 5.4 | 63 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**envelope glycoprotein;<br>**PDBTitle:** hiv-1 gp41 membrane proximal ectodomain region peptide in2 dpc micelle |
| 64 | c6al5A_ | Alignment | not modelled | 5.3 | 67 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**b-lymphocyte antigen cd19;<br>**PDBTitle:** complex between cd19 (n138q mutant) and b43 fab |
| 65 | c6gcsc_ | Alignment | not modelled | 5.2 | 18 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**49-kda protein (nucm);<br>**PDBTitle:** cryo-em structure of respiratory complex i from yarrowia lipolytica |
| 66 | d1jb0f_ | Alignment | not modelled | 5.1 | 43 | **Fold:**Single transmembrane helix<br>**Superfamily:**Subunit III of photosystem I reaction centre, PsaF<br>**Family:**Subunit III of photosystem I reaction centre, PsaF |
| 67 | c4y2iA_ | Alignment | not modelled | 5.1 | 25 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**putative metal-binding transport protein;<br>**PDBTitle:** gold ion bound to golb |