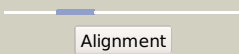

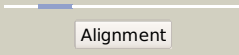

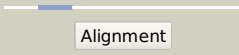

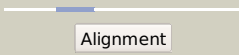

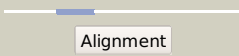

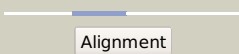
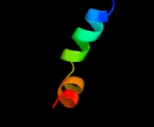
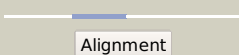

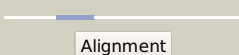
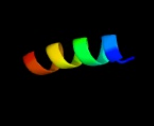

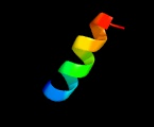
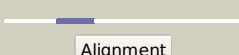

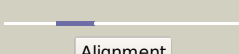



Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2342_(-)_2620282_2620539 |
| Date | Mon Aug 5 13:25:49 BST 2019 |
| Unique Job ID | 3b9697f8c99f115e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4cz5D_ |  Alignment |  | 28.3 | 40 | PDB header: cell cycle Chain: D: PDB Molecule: cellular tumor antigen p53; PDBTitle: truncated tetramerization domain of zebrafish p53 (crystal form i) |
| 2 | c1q90M_ |  Alignment |  | 26.7 | 33 | PDB header: photosynthesis Chain: M: PDB Molecule: cytochrome b6f complex subunit petm; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii |
| 3 | d1q90m_ |  Alignment |  | 26.7 | 33 | Fold: Single transmembrane helix Superfamily: PetM subunit of the cytochrome b6f complex Family: PetM subunit of the cytochrome b6f complex |
| 4 | c4a9zD_ |  Alignment |  | 22.6 | 33 | PDB header: transcription Chain: D: PDB Molecule: tumor protein 63; PDBTitle: crystal structure of human p63 tetramerization domain |
| 5 | c3zy1A_ |  Alignment |  | 22.6 | 33 | PDB header: transcription Chain: A: PDB Molecule: tumor protein 63; PDBTitle: crystal structure of the human p63 tetramerization domain |
| 6 | d1zcba1 |  Alignment |  | 21.7 | 19 | Fold: Transducin (alpha subunit), insertion domain Superfamily: Transducin (alpha subunit), insertion domain Family: Transducin (alpha subunit), insertion domain |
| 7 | d2bcjq1 |  Alignment |  | 20.8 | 10 | Fold: Transducin (alpha subunit), insertion domain Superfamily: Transducin (alpha subunit), insertion domain Family: Transducin (alpha subunit), insertion domain |
| 8 | c4a9zC_ |  Alignment |  | 20.0 | 33 | PDB header: transcription Chain: C: PDB Molecule: tumor protein 63; PDBTitle: crystal structure of human p63 tetramerization domain |
| 9 | d1hs5a_ |  Alignment |  | 19.7 | 47 | Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain |
| 10 | c4d1mE_ |  Alignment |  | 19.7 | 40 | PDB header: transcription Chain: E: PDB Molecule: cellular tumor antigen p53; PDBTitle: tetramerization domain of zebrafish p53 (crystal form ii) |
| 11 | c5hobB_ |  Alignment |  | 18.9 | 33 | PDB header: transcription Chain: B: PDB Molecule: tumor protein p73; PDBTitle: p73 homo-tetramerization domain mutant i |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | d3saka_ | Alignment | | 18.8 | 40 | Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain |
| 13 | c5h75B_ | Alignment | | 18.6 | 21 | PDB header: lyase Chain: B: PDB Molecule: mersacidin decarboxylase,immunoglobulin g-binding protein PDBTitle: crystal structure of the mrsd-protein a fusion protein |
| 14 | d1zcaal | Alignment | | 18.1 | 14 | Fold: Transducin (alpha subunit), insertion domain Superfamily: Transducin (alpha subunit), insertion domain Family: Transducin (alpha subunit), insertion domain |
| 15 | c5w8sA_ | Alignment | | 17.9 | 14 | PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations |
| 16 | d1aztal | Alignment | | 17.1 | 19 | Fold: Transducin (alpha subunit), insertion domain Superfamily: Transducin (alpha subunit), insertion domain Family: Transducin (alpha subunit), insertion domain |
| 17 | d1a1ua_ | Alignment | | 15.4 | 47 | Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain |
| 18 | d1tadal | Alignment | | 14.6 | 5 | Fold: Transducin (alpha subunit), insertion domain Superfamily: Transducin (alpha subunit), insertion domain Family: Transducin (alpha subunit), insertion domain |
| 19 | d1cipal | Alignment | | 14.5 | 11 | Fold: Transducin (alpha subunit), insertion domain Superfamily: Transducin (alpha subunit), insertion domain Family: Transducin (alpha subunit), insertion domain |
| 20 | c3j9eD_ | Alignment | | 14.4 | 5 | PDB header: viral protein Chain: D: PDB Molecule: vp5; PDBTitle: atomic structure of a non-enveloped virus reveals ph sensors for a2 coordinated process of cell entry |
| 21 | c3tsaA_ | Alignment | not modelled | 12.6 | 17 | PDB header: transferase Chain: A: PDB Molecule: ndp-rhamnosyltransferase; PDBTitle: spinosyn rhamnosyltransferase spng |
| 22 | d1g5qa_ | Alignment | not modelled | 12.3 | 20 | Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD |
| 23 | c2wtth_ | Alignment | not modelled | 11.5 | 16 | PDB header: transcription Chain: H: PDB Molecule: tumor protein p73; PDBTitle: structure of the human p73 tetramerization domain (crystal form ii) |
| 24 | c2wttn_ | Alignment | not modelled | 11.3 | 27 | PDB header: transcription Chain: N: PDB Molecule: tumor protein p73; PDBTitle: structure of the human p73 tetramerization domain (crystal form ii) |
| 25 | c2j10B_ | Alignment | not modelled | 10.9 | 40 | PDB header: transcription Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k |
| 26 | c2j10D_ | Alignment | not modelled | 10.9 | 40 | PDB header: transcription Chain: D: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k |
| 27 | c2j10A_ | Alignment | not modelled | 10.9 | 40 | PDB header: transcription Chain: A: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k |
| 28 | d1aiea_ | Alignment | not modelled | 10.7 | 40 | Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain |
| | | | | | | PDB header: oxidoreductase |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c6gcsj_ | Alignment | not modelled | 10.7 | 35 | Chain: J: PDB Molecule: nujm subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica |
| 30 | c6jlsA_ | Alignment | not modelled | 10.6 | 17 | PDB header: biosynthetic protein Chain: A: PDB Molecule: putative flavoprotein decarboxylase; PDBTitle: crystal structure of fmn-dependent cysteine decarboxylases tvaf from2 thioviridamide biosynthesis |
| 31 | c2qjhH_ | Alignment | not modelled | 10.4 | 3 | PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate |
| 32 | c2rjbD_ | Alignment | not modelled | 10.4 | 10 | PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein ydcj (sf1787) from2 shigella flexneri which includes domain duf1338. northeast structural3 genomics consortium target sfr276 |
| 33 | c4rieB_ | Alignment | not modelled | 10.0 | 20 | PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase homolog; PDBTitle: landomycin glycosyltransferase langt2 |
| 34 | c6cfwL_ | Alignment | not modelled | 10.0 | 35 | PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase |
| 35 | c4leiB_ | Alignment | not modelled | 9.8 | 20 | PDB header: transferase Chain: B: PDB Molecule: ndp-forosamyltransferase; PDBTitle: spinosyn forosaminyltransferase spnp |
| 36 | d1n2aa1 | Alignment | not modelled | 9.5 | 14 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 37 | c2j11D_ | Alignment | not modelled | 9.4 | 40 | PDB header: transcription Chain: D: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant y327s t329g q331g |
| 38 | c2kegA_ | Alignment | not modelled | 9.4 | 36 | PDB header: antimicrobial protein Chain: A: PDB Molecule: plnk; PDBTitle: nmr structure of plantaricin k in dpc-micelles |
| 39 | c2wttL_ | Alignment | not modelled | 9.1 | 27 | PDB header: transcription Chain: L: PDB Molecule: tumor protein p73; PDBTitle: structure of the human p73 tetramerization domain (crystal form ii) |
| 40 | c1flcB_ | Alignment | not modelled | 8.2 | 38 | PDB header: hydrolase Chain: B: PDB Molecule: haemagglutinin-esterase-fusion glycoprotein; PDBTitle: x-ray structure of the haemagglutinin-esterase-fusion glycoprotein of2 influenza c virus |
| 41 | d1p3y1_ | Alignment | not modelled | 8.2 | 19 | Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD |
| 42 | d1f2ea1 | Alignment | not modelled | 7.9 | 10 | Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain |
| 43 | c4fzrA_ | Alignment | not modelled | 7.9 | 9 | PDB header: transferase Chain: A: PDB Molecule: ssfs6; PDBTitle: crystal structure of ssfs6, streptomyces sp. sf25752 glycosyltransferase |
| 44 | c2ls4A_ | Alignment | not modelled | 7.6 | 46 | PDB header: metal transport Chain: A: PDB Molecule: high affinity copper uptake protein 1; PDBTitle: 1h chemical shift assignments for the third transmembrane domain from2 the human copper transport 1 |
| 45 | c2j6yB_ | Alignment | not modelled | 7.5 | 26 | PDB header: hydrolase Chain: B: PDB Molecule: phosphoserine phosphatase rsbu; PDBTitle: structural and functional characterisation of partner switching2 regulating the environmental stress response in bacillus subtilis |
| 46 | c6g2jY_ | Alignment | not modelled | 7.3 | 24 | PDB header: oxidoreductase Chain: Y: PDB Molecule: mcg5603; PDBTitle: mouse mitochondrial complex i in the active state |
| 47 | c4zbbD_ | Alignment | not modelled | 7.3 | 9 | PDB header: transferase Chain: D: PDB Molecule: pcure2p8; PDBTitle: crystal structure of the glutathione transferase ure2p8 from2 phanerochaete chrysosporium complexed with glutathionyl-s-3 dinitrobenzene. |
| 48 | c5ldwY_ | Alignment | not modelled | 7.0 | 24 | PDB header: oxidoreductase Chain: Y: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class1 |
| 49 | d2tpta3 | Alignment | not modelled | 6.9 | 32 | Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain |
| 50 | c3gndC_ | Alignment | not modelled | 6.8 | 11 | PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate |
| 51 | c4hfgB_ | Alignment | not modelled | 6.8 | 20 | PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of udp-x diphosphatase |
| 52 | c3wadA_ | Alignment | not modelled | 6.6 | 14 | PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicanistatin |
| 53 | c4onxB_ | Alignment | not modelled | 5.9 | 8 | PDB header: transferase Chain: B: PDB Molecule: sensor histidine kinase; PDBTitle: 2.8 angstrom crystal structure of sensor domain of histidine kinase2 from clostridium perfringens. PDB header: viral protein |

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|----|-------------------------|-----------|--------------|-----|----|---|
| 54 | c2imuA_ | Alignment | not modelled | 5.6 | 29 | Chain: A; PDB Molecule: structural polyprotein (pp) p1; PDBTitle: nmr structure of pep46 from the infectious bursal disease2 virus (ibdv) in dodecylphosphocholin (dpc). |
| 55 | c4isdA_ | Alignment | not modelled | 5.6 | 7 | PDB header: transferase Chain: A; PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of glutathione transferase homolog from burkholderia2 gl bgr1, target efi-501803, with bound glutathione |
| 56 | c1p58E_ | Alignment | not modelled | 5.5 | 24 | PDB header: virus Chain: E; PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2.9.5 angstrom cryo-em reconstruction |