



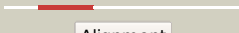














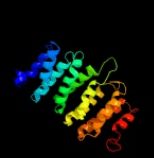




Phyre2

| | |
|---------------|-----------------------------|
| Email | rachel.harding@utoronto.ca |
| Description | Full-length_HTT |
| Date | Wed Mar 2 01:07:03 GMT 2016 |
| Unique Job ID | Occb2c2f556874ba |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | d1b3ua_ |  Alignment |  | 99.1 | 14 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HEAT repeat |
| 2 | d1u6gc_ |  Alignment |  | 99.0 | 12 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HEAT repeat |
| 3 | c4a0cB_ |  Alignment |  | 98.9 | 13 | PDB header: cell cycle Chain: B: PDB Molecule: cullin-associated nedd8-dissociated protein 1; PDBTitle: structure of the cand1-cul4b-rbx1 complex |
| 4 | c3c5wA_ |  Alignment |  | 98.6 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: pp2a a subunit; PDBTitle: complex between pp2a-specific methyltransferase pme-1 and pp2a core2 enzyme |
| 5 | d1gw5b_ |  Alignment |  | 98.6 | 15 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Clathrin adaptor core protein |
| 6 | c1m5nS_ |  Alignment |  | 98.1 | 23 | PDB header: protein transport Chain: S: PDB Molecule: importin beta-1 subunit; PDBTitle: crystal structure of heat repeats (1-11) of importin b2 bound to the non-classical nls(67-94) of pthrp |
| 7 | c4r10A_ |  Alignment |  | 98.0 | 13 | PDB header: cell adhesion/protein binding Chain: A: PDB Molecule: protein humpback-2; PDBTitle: a conserved phosphorylation switch controls the interaction between2 cadherin and beta-catenin in vitro and in vivo |
| 8 | c4g3aA_ |  Alignment |  | 98.0 | 17 | PDB header: cell cycle Chain: A: PDB Molecule: clip-associating protein; PDBTitle: crystal structure of mast/orbit n-terminal domain |
| 9 | c1w63A_ |  Alignment |  | 98.0 | 17 | PDB header: endocytosis Chain: A: PDB Molecule: adapter-related protein complex 1 gamma 1 PDBTitle: ap1 clathrin adaptor core |
| 10 | c5dn7A_ |  Alignment |  | 97.9 | 13 | PDB header: structural protein Chain: A: PDB Molecule: protein fam179b; PDBTitle: crescerin uses a tog domain array to regulate microtubules in the2 primary cilium |
| 11 | c3w3zA_ |  Alignment |  | 97.9 | 18 | PDB header: protein transport/nuclear protein Chain: A: PDB Molecule: importin subunit beta-3; PDBTitle: crystal structure of kap121p bound to rangtp |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c4qmjA_ | Alignment | | 97.8 | 15 | PDB header: protein binding Chain: A: PDB Molecule: cytoskeleton-associated protein 5; PDBTitle: the xmap215 family drives microtubule polymerization using a2 structurally diverse tog array |
| 13 | c2qk2A_ | Alignment | | 97.7 | 18 | PDB header: protein binding Chain: A: PDB Molecule: lp04448p; PDBTitle: structural basis of microtubule plus end tracking by xmap215, clip-1702 and eb1 |
| 14 | c4qmhA_ | Alignment | | 97.7 | 19 | PDB header: protein binding Chain: A: PDB Molecule: lp04448p; PDBTitle: the xmap215 family drives microtubule polymerization using a2 structurally diverse tog array |
| 15 | d1qbkB_ | Alignment | | 97.6 | 15 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 16 | c2qk1A_ | Alignment | | 97.6 | 15 | PDB header: protein binding Chain: A: PDB Molecule: protein stu2; PDBTitle: structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1 |
| 17 | c2db0B_ | Alignment | | 97.6 | 16 | PDB header: protein binding Chain: B: PDB Molecule: 253aa long hypothetical protein; PDBTitle: crystal structure of ph0542 |
| 18 | c4db9A_ | Alignment | | 97.5 | 14 | PDB header: de novo protein Chain: A: PDB Molecule: armadillo repeat protein, yiiim3aiii; PDBTitle: designed armadillo repeat protein (yiiim3aiii) |
| 19 | c2z6hA_ | Alignment | | 97.5 | 14 | PDB header: cell adhesion Chain: A: PDB Molecule: catenin beta-1; PDBTitle: crystal structure of beta-catenin armadillo repeat region2 and its c-terminal domain |
| 20 | d1jdha_ | Alignment | | 97.4 | 14 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 21 | c3wozA_ | Alignment | not modelled | 97.2 | 16 | PDB header: structural protein Chain: A: PDB Molecule: clip-associating protein 2; PDBTitle: crystal structure of claspt2 tog domain (tog3) |
| 22 | c4xrkA_ | Alignment | not modelled | 97.2 | 13 | PDB header: transport protein Chain: A: PDB Molecule: importin beta; PDBTitle: crystal structure of importin beta in a polyethylene glycol condition |
| 23 | c2iw3B_ | Alignment | not modelled | 97.1 | 17 | PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp |
| 24 | d2bpta1 | Alignment | not modelled | 97.0 | 15 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 25 | c4y5IA_ | Alignment | not modelled | 97.0 | 16 | PDB header: protein binding Chain: A: PDB Molecule: mini spindles tog3; PDBTitle: drosophila melanogaster mini spindles tog3 |
| 26 | c4hxtA_ | Alignment | not modelled | 96.9 | 14 | PDB header: de novo protein Chain: A: PDB Molecule: de novo protein or329; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or329 |
| 27 | c4d4eA_ | Alignment | not modelled | 96.9 | 15 | PDB header: de novo protein Chain: A: PDB Molecule: armadillo repeat protein arm00016; PDBTitle: crystal structure of computationally designed armadillo2 repeat proteins for modular peptide recognition. |
| 28 | c4nl6C_ | Alignment | not modelled | 96.8 | 33 | PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients |
| | | | | | | PDB header: protein transport |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c1pjmB | Alignment | not modelled | 96.8 | 15 | Chain: B: PDB Molecule: importin alpha-2 subunit; PDBTitle: mouse importin alpha-bipartite nls from human2 retinoblastoma protein complex |
| 30 | d1ee4a | Alignment | not modelled | 96.8 | 11 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 31 | c3oqsA | Alignment | not modelled | 96.6 | 15 | PDB header: protein transport Chain: A: PDB Molecule: importin subunit alpha-2; PDBTitle: crystal structure of importin-alpha bound to a clic4 nls peptide |
| 32 | c5ewpA | Alignment | not modelled | 96.5 | 17 | PDB header: protein binding Chain: A: PDB Molecule: aro (armadillo repeats only protein); PDBTitle: aro (armadillo repeats only protein) from plasmodium falciparum |
| 33 | c4plrA | Alignment | not modelled | 96.5 | 16 | PDB header: peptide binding protein Chain: A: PDB Molecule: arm00008; PDBTitle: crystal structures of designed armadillo repeat proteins: implications2 of construct design and crystallization conditions on overall3 structure. |
| 34 | c4k92B | Alignment | not modelled | 96.5 | 12 | PDB header: structural protein Chain: B: PDB Molecule: clip-associating protein 1; PDBTitle: a cryptic tog domain with a distinct architecture underlies clasp-2 dependent bipolar spindle formation |
| 35 | c2c1tA | Alignment | not modelled | 96.5 | 12 | PDB header: protein transport/membrane protein Chain: A: PDB Molecule: importin alpha subunit; PDBTitle: structure of the kap60p:nup2 complex |
| 36 | d1xqra1 | Alignment | not modelled | 96.5 | 11 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: HspBP1 domain |
| 37 | c4ffbC | Alignment | not modelled | 96.5 | 18 | PDB header: hydrolase Chain: C: PDB Molecule: protein stu2; PDBTitle: a tog:alpha/beta-tubulin complex structure reveals conformation-based2 mechanisms for a microtubule polymerase |
| 38 | d1ibrb | Alignment | not modelled | 96.4 | 14 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 39 | c1wa5B | Alignment | not modelled | 96.3 | 15 | PDB header: nuclear transport Chain: B: PDB Molecule: importin alpha subunit; PDBTitle: crystal structure of the exportin cse1p complexed with its2 cargo (kap60p) and rangtp |
| 40 | d1wa5b | Alignment | not modelled | 96.3 | 15 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 41 | c1xqrA | Alignment | not modelled | 96.3 | 12 | PDB header: chaperone Chain: A: PDB Molecule: hspbp1 protein; PDBTitle: crystal structure of the hspbp1 core domain |
| 42 | c3b2aA | Alignment | not modelled | 96.2 | 10 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the archaeal heat-like repeats protein ton_19372 from thermococcus onnurineus na1 |
| 43 | c5a1vG | Alignment | not modelled | 96.2 | 19 | PDB header: transport protein Chain: G: PDB Molecule: coatomer subunit beta'; PDBTitle: the structure of the copi coat linkage i |
| 44 | c3ltjA | Alignment | not modelled | 96.2 | 19 | PDB header: protein binding Chain: A: PDB Molecule: alpharep-4; PDBTitle: structure of a new family of artificial alpha helicoidal repeat2 proteins (alpha-rep) based on thermostable heat-like repeats |
| 45 | d1qgra | Alignment | not modelled | 96.2 | 14 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 46 | c3slaE | Alignment | not modelled | 96.1 | 11 | PDB header: signaling protein Chain: E: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin |
| 47 | c3u0rA | Alignment | not modelled | 96.1 | 15 | PDB header: apoptosis inhibitor Chain: A: PDB Molecule: apoptosis inhibitor 5; PDBTitle: helical repeat structure of apoptosis inhibitor 5 reveals protein-2 protein interaction modules |
| 48 | c4db8B | Alignment | not modelled | 96.0 | 17 | PDB header: de novo protein Chain: B: PDB Molecule: armadillo-repeat protein; PDBTitle: designed armadillo-repeat protein |
| 49 | c4gmnA | Alignment | not modelled | 95.9 | 19 | PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structural basis of rpl5 recognition by syo1 |
| 50 | c4d50A | Alignment | not modelled | 95.9 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: deoxyhypusine hydroxylase; PDBTitle: structure of human deoxyhypusine hydroxylase |
| 51 | c2j dqB | Alignment | not modelled | 95.8 | 16 | PDB header: protein transport Chain: B: PDB Molecule: importin alpha-1 subunit; PDBTitle: c-terminal domain of influenza a virus polymerase pb22 subunit in complex with human importin alpha5 |
| 52 | c3sl9B | Alignment | not modelled | 95.8 | 11 | PDB header: signaling protein, protein binding Chain: B: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bc19 |
| 53 | c4xl5C | Alignment | not modelled | 95.7 | 21 | PDB header: protein binding Chain: C: PDB Molecule: bgfp-a; PDBTitle: x-ray structure of bgfp-a / egfp complex |
| 54 | c4xriA | Alignment | not modelled | 95.7 | 14 | PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of importin beta in an ammonium sulfate condition |
| | | | | | | PDB header: signaling protein, protein binding |

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|----|-------------------------|-----------|--------------|------|----|---|
| 55 | c3sl9E_ | Alignment | not modelled | 95.7 | 11 | Chain: E: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9 |
| 56 | c3slaD_ | Alignment | not modelled | 95.6 | 11 | PDB header: signaling protein Chain: D: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin |
| 57 | c3sl9A_ | Alignment | not modelled | 95.6 | 11 | PDB header: signaling protein, protein binding Chain: A: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9 |
| 58 | c3ifqB_ | Alignment | not modelled | 95.6 | 15 | PDB header: cell adhesion Chain: B: PDB Molecule: plakoglobin; PDBTitle: interction of plakoglobin and beta-catenin with desmosomal2 cadherins |
| 59 | c3gb8A_ | Alignment | not modelled | 95.5 | 14 | PDB header: transport protein Chain: A: PDB Molecule: exportin-1; PDBTitle: crystal structure of crm1/snurportin-1 complex |
| 60 | c2ot8B_ | Alignment | not modelled | 95.4 | 14 | PDB header: transport protein Chain: B: PDB Molecule: transportin-1; PDBTitle: karyopherin beta2/transportin-hnrnp nls complex |
| 61 | d1q1sc_ | Alignment | not modelled | 95.4 | 15 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 62 | c3l9tA_ | Alignment | not modelled | 95.2 | 14 | PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein smu.31; PDBTitle: the crystal structure of smu.31 from streptococcus mutans ua159 |
| 63 | c3nowA_ | Alignment | not modelled | 95.2 | 13 | PDB header: protein binding Chain: A: PDB Molecule: unc-45 protein, sd10334p; PDBTitle: unc-45 from drosophila melanogaster |
| 64 | d1te4a_ | Alignment | not modelled | 95.1 | 21 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: PBS lyase HEAT-like repeat |
| 65 | c2w3cA_ | Alignment | not modelled | 95.1 | 12 | PDB header: transport protein Chain: A: PDB Molecule: general vesicular transport factor p115; PDBTitle: globular head region of the human general vesicular2 transport factor p115 |
| 66 | c2of3A_ | Alignment | not modelled | 95.1 | 12 | PDB header: structural protein, cell cycle Chain: A: PDB Molecule: zyg-9; PDBTitle: tog domain structure from c.elegans zyg9 |
| 67 | c3sl9G_ | Alignment | not modelled | 94.9 | 9 | PDB header: signaling protein, protein binding Chain: G: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of beta catenin in complex with bcl9 |
| 68 | c2qnaA_ | Alignment | not modelled | 94.3 | 14 | PDB header: transport protein Chain: A: PDB Molecule: importin subunit beta-1; PDBTitle: crystal structure of human importin-beta (127-876) in complex with the2 ibb-domain of snurportin1 (1-65) |
| 69 | c3slaB_ | Alignment | not modelled | 94.1 | 12 | PDB header: signaling protein Chain: B: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin |
| 70 | c3m1iC_ | Alignment | not modelled | 94.1 | 10 | PDB header: protein transport Chain: C: PDB Molecule: exportin-1; PDBTitle: crystal structure of yeast crm1 (xpo1p) in complex with yeast ranbp12 (yrb1p) and yeast rangtp (gsp1pgtp) |
| 71 | c4uaeA_ | Alignment | not modelled | 94.0 | 14 | PDB header: protein transport Chain: A: PDB Molecule: importin subunit alpha-3; PDBTitle: importin alpha 3 delta ibb in complex with influenza pb2 nuclear2 localization domain |
| 72 | d1wa5c_ | Alignment | not modelled | 94.0 | 12 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 73 | c4rxhB_ | Alignment | not modelled | 93.9 | 12 | PDB header: transport protein Chain: B: PDB Molecule: importin subunit alpha; PDBTitle: crystal structure of importin-alpha from neurospora crassa complexed2 with sv40nls |
| 74 | c4rv1F_ | Alignment | not modelled | 92.8 | 14 | PDB header: de novo protein Chain: F: PDB Molecule: engineered protein or497; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium (nesg) target or497. |
| 75 | c4c0pD_ | Alignment | not modelled | 92.2 | 9 | PDB header: transport protein Chain: D: PDB Molecule: transportin-3; PDBTitle: unliganded transportin 3 |
| 76 | c2x19B_ | Alignment | not modelled | 91.5 | 10 | PDB header: nuclear transport Chain: B: PDB Molecule: importin-13; PDBTitle: crystal structure of importin13 - rangtp complex |
| 77 | c2z6gA_ | Alignment | not modelled | 91.5 | 14 | PDB header: cell adhesion Chain: A: PDB Molecule: b-catenin; PDBTitle: crystal structure of a full-length zebrafish beta-catenin |
| 78 | c3nmwA_ | Alignment | not modelled | 91.4 | 16 | PDB header: cell adhesion/cell cycle Chain: A: PDB Molecule: apc variant protein; PDBTitle: crytal structure of armadillo repeats domain of apc |
| 79 | c3gq2B_ | Alignment | not modelled | 89.4 | 11 | PDB header: transport protein Chain: B: PDB Molecule: general vesicular transport factor p115; PDBTitle: crystal structure of the dimer of the p115 tether globular head domain |
| 80 | c3gjxD_ | Alignment | not modelled | 88.6 | 14 | PDB header: protein transport Chain: D: PDB Molecule: exportin-1; PDBTitle: crystal structure of the nuclear export complex crm1-2 snurportin1-rangtp |
| 81 | c3v6aA_ | Alignment | not modelled | 88.4 | 16 | PDB header: apoptosis inhibitor Chain: A: PDB Molecule: apoptosis inhibitor 5; PDBTitle: helical repeat structure of apoptosis inhibitor 5 reveals protein-2 protein interaction modules |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 82 | c4fgvA | Alignment | not modelled | 88.1 | 16 | PDB header: transport protein Chain: A: PDB Molecule: chromosome region maintenance 1 (crm1) or exportin 1 PDBTitle: crystal structure of free crm1 (crystal form 1) |
| 83 | c3slaA | Alignment | not modelled | 87.0 | 10 | PDB header: signaling protein Chain: A: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin |
| 84 | c5a1yM | Alignment | not modelled | 85.7 | 13 | PDB header: transport protein Chain: M: PDB Molecule: coatomer subunit gamma-1; PDBTitle: the structure of the copi coat linkage iv |
| 85 | d1lrva | Alignment | not modelled | 83.4 | 15 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Leucine-rich repeat variant |
| 86 | c2d3fC | Alignment | not modelled | 82.8 | 48 | PDB header: structural protein Chain: C: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4 |
| 87 | c1x1kE | Alignment | not modelled | 82.8 | 48 | PDB header: structural protein Chain: E: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4 |
| 88 | c2d3fB | Alignment | not modelled | 82.8 | 48 | PDB header: structural protein Chain: B: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4 |
| 89 | c2d3fA | Alignment | not modelled | 82.8 | 48 | PDB header: structural protein Chain: A: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4 |
| 90 | c2ynsA | Alignment | not modelled | 82.7 | 10 | PDB header: transport protein Chain: A: PDB Molecule: importin subunit alpha-1a; PDBTitle: rimp_alpha_b54nls |
| 91 | c2jkrL | Alignment | not modelled | 82.3 | 14 | PDB header: endocytosis Chain: L: PDB Molecule: ap-2 complex subunit alpha-2; PDBTitle: ap2 clathrin adaptor core with dileucine peptide rm(2 phosphos)qikrllse |
| 92 | c1x1kA | Alignment | not modelled | 82.2 | 48 | PDB header: structural protein Chain: A: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4 |
| 93 | c1x1kD | Alignment | not modelled | 82.2 | 48 | PDB header: structural protein Chain: D: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4 |
| 94 | c2d3fE | Alignment | not modelled | 82.2 | 48 | PDB header: structural protein Chain: E: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4 |
| 95 | c2d3fD | Alignment | not modelled | 82.2 | 48 | PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4 |
| 96 | c2d3fF | Alignment | not modelled | 82.2 | 48 | PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4 |
| 97 | c1x1kC | Alignment | not modelled | 82.2 | 48 | PDB header: structural protein Chain: C: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4 |
| 98 | c1x1kB | Alignment | not modelled | 82.2 | 48 | PDB header: structural protein Chain: B: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4 |
| 99 | c4imiA | Alignment | not modelled | 82.1 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: symplekin; PDBTitle: novel modifications on c-terminal domain of rna polymerase ii can2 fine- tune the phosphatase activity of ssu72. |
| 100 | d1v18a1 | Alignment | not modelled | 79.7 | 10 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Armadillo repeat |
| 101 | c2cuoA | Alignment | not modelled | 79.6 | 50 | PDB header: structural protein Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9 |
| 102 | c2cuoD | Alignment | not modelled | 79.6 | 50 | PDB header: structural protein Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9 |
| 103 | c2cuoE | Alignment | not modelled | 79.6 | 50 | PDB header: structural protein Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9 |
| 104 | c2cuoB | Alignment | not modelled | 79.6 | 50 | PDB header: structural protein Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9 |
| 105 | c2cuoF | Alignment | not modelled | 79.0 | 50 | PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: collagen model peptide (pro-pro-gly)9 |
| 106 | c2cuoC_ | Alignment | not modelled | 79.0 | 50 | PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9 |
| 107 | d1ho8a_ | Alignment | not modelled | 78.9 | 17 | Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Regulatory subunit H of the V-type ATPase |
| 108 | c3slaC_ | Alignment | not modelled | 77.9 | 11 | PDB header: signaling protein Chain: C: PDB Molecule: catenin beta-1; PDBTitle: x-ray structure of first four repeats of human beta-catenin |
| 109 | c1x1kF_ | Alignment | not modelled | 77.8 | 52 | PDB header: structural protein Chain: F: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4 |
| 110 | c3abnA_ | Alignment | not modelled | 77.6 | 44 | PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro- gly)4 at 1.022 a |
| 111 | c3admD_ | Alignment | not modelled | 77.5 | 44 | PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro- gly)4 |
| 112 | c3ah9C_ | Alignment | not modelled | 77.1 | 52 | PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution |
| 113 | c3ah9E_ | Alignment | not modelled | 77.1 | 52 | PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution |
| 114 | c3ah9B_ | Alignment | not modelled | 77.1 | 52 | PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution |
| 115 | c2l1IB_ | Alignment | not modelled | 76.9 | 15 | PDB header: nuclear protein Chain: B: PDB Molecule: exportin-1; PDBTitle: nmr solution structure of the phi0 pki nes peptide in complex with2 crm1-rangtp |
| 116 | c3a19E_ | Alignment | not modelled | 76.9 | 50 | PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal |
| 117 | c3a19C_ | Alignment | not modelled | 76.9 | 50 | PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal |
| 118 | c3nmzB_ | Alignment | not modelled | 76.8 | 18 | PDB header: cell adhesion/cell cycle Chain: B: PDB Molecule: apc variant protein; PDBTitle: crytal structure of apc complexed with asef |
| 119 | c3admE_ | Alignment | not modelled | 76.7 | 44 | PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro- gly)4 |
| 120 | c3admB_ | Alignment | not modelled | 76.7 | 44 | PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro- gly)4 |