# Phyre$^2$

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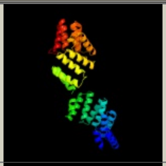
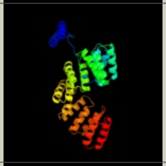
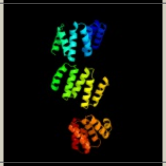
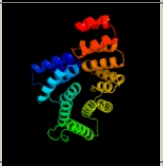
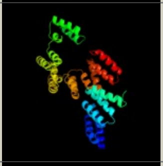
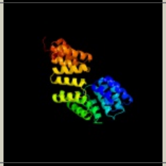
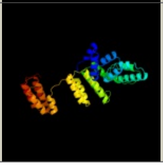
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0ACB7 |
| Date | Thu Jan 5 11:17:50 GMT 2012 |
| Unique Job ID | 0432c4151738a211 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1w3ba_ | Alignment |  | 100.0 | 17 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 2 | c2xpiA_ | Alignment |  | 100.0 | 12 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**anaphase-promoting complex subunit cut9;<br>**PDBTitle:** crystal structure of apc/c hetero-tetramer cut9-hcn1 |
| 3 | c3iegB_ | Alignment |  | 100.0 | 15 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 3;<br>**PDBTitle:** crystal structure of p58(ipk) tpr domain at 2.5 a |
| 4 | c3fp4A_ | Alignment |  | 100.0 | 10 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**tpr repeat-containing protein yhr117w;<br>**PDBTitle:** crystal structure of tom71 complexed with ssa1 c-terminal2 fragment |
| 5 | c2y4tA_ | Alignment |  | 100.0 | 13 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3;<br>**PDBTitle:** crystal structure of the human co-chaperone p58(ipk) |
| 6 | c3cvpA_ | Alignment |  | 100.0 | 12 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**peroxisome targeting signal 1 receptor pex5;<br>**PDBTitle:** structure of peroxisomal targeting signal 1 (pts1) binding2 domain of trypanosoma brucei peroxin 5 (tbpex5)complexed3 to pts1 peptide (10-skl) |
| 7 | d1fcha_ | Alignment |  | 100.0 | 17 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 8 | c1fchB_ | Alignment |  | 100.0 | 17 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**peroxisomal targeting signal 1 receptor;<br>**PDBTitle:** crystal structure of the pts1 complexed to the tpr region2 of human pex5 |
| 9 | c2gw1A_ | Alignment |  | 100.0 | 13 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**mitochondrial precursor proteins import receptor;<br>**PDBTitle:** crystal structure of the yeast tom70 |
| 10 | c3hymB_ | Alignment |  | 100.0 | 12 | **PDB header:**cell cycle, ligase<br>**Chain:** B: **PDB Molecule:**cell division cycle protein 16 homolog;<br>**PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure |
| 11 | c2uy1A_ | Alignment |  | 99.9 | 13 | **PDB header:**rna-binding protein<br>**Chain:** A: **PDB Molecule:**cleavage stimulation factor 77;<br>**PDBTitle:** crystal structure of cstf-77 |

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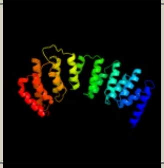
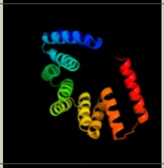
|---|---|---|---|---|---|---|
| 12 | d2ooea1 | Alignment |  | 99.9 | 11 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**HAT/Suf repeat |
| 13 | c3mkrA_ | Alignment |  | 99.9 | 12 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**coatomer subunit epsilon;<br>**PDBTitle:** crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat |
| 14 | d1hz4a_ | Alignment |  | 99.9 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Transcription factor MalT domain III |
| 15 | d1dcea1 | Alignment |  | 99.9 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Protein prenylyltransferase<br>**Family:**Protein prenylyltransferase |
| 16 | d1qsaa1 | Alignment |  | 99.9 | 14 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Bacterial muramidases<br>**Family:**Bacterial muramidases |
| 17 | c3pe3D_ | Alignment |  | 99.9 | 18 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n-<br>**PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate |
| 18 | c2ho1B_ | Alignment |  | 99.9 | 16 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**type 4 fimbrial biogenesis protein pilf;<br>**PDBTitle:** functional characterization of pseudomonas aeruginosa pilf |
| 19 | c2vq2A_ | Alignment |  | 99.9 | 16 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**putative fimbrial biogenesis and twitching<br>**PDBTitle:** crystal structure of pilw, widely conserved type iv pilus2 biogenesis factor |
| 20 | c3draA_ | Alignment |  | 99.9 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein<br>**PDBTitle:** candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp |
| 21 | d1xnfa_ | Alignment | not modelled | 99.8 | 12 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 22 | c3q75A_ | Alignment | not modelled | 99.8 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**farnesyltransferase alpha subunit;<br>**PDBTitle:** cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide |
| 23 | c2q7fA_ | Alignment | not modelled | 99.8 | 10 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**yrrb protein;<br>**PDBTitle:** crystal structure of yrrb: a tpr protein with an unusual peptide-2 binding site |
| 24 | c3mv3B_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**protein transport<br>**Chain:** B: **PDB Molecule:**coatomer subunit epsilon;<br>**PDBTitle:** crystal structure of a-cop in complex with e-cop |
| 25 | c3q15A_ | Alignment | not modelled | 99.8 | 11 | **PDB header:**hydrolase/kinase<br>**Chain:** A: **PDB Molecule:**response regulator aspartate phosphatase h;<br>**PDBTitle:** crystal structure of raph complexed with spo0f |
| 26 | d1d8da_ | Alignment | not modelled | 99.8 | 10 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Protein prenylyltransferase<br>**Family:**Protein prenylyltransferase |
| 27 | d2h6fa1 | Alignment | not modelled | 99.8 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Protein prenylyltransferase<br>**Family:**Protein prenylyltransferase |
| 28 | c3sf4B_ | Alignment | not modelled | 99.8 | 12 | **PDB header:**signaling protein/protein binding<br>**Chain:** B: **PDB Molecule:**g-protein-signaling modulator 2;<br>**PDBTitle:** crystal structure of the complex between the conserved cell polarity2 proteins inscuteable and lgn |
| | | | | | | **PDB header:**transferase |

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| 29 | c1tnoI_ | Alignment | not modelled | 99.8 | 11 | **Chain:** I: **PDB Molecule:**geranylgeranyltransferase type i alpha subunit;<br>**PDBTitle:** rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a kkksktkcvim peptide derived from k-3 ras4b |
| 30 | c3as5A_ | Alignment | not modelled | 99.8 | 23 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**mama;<br>**PDBTitle:** mama amb-1 p212121 |
| 31 | c2r5sB_ | Alignment | not modelled | 99.7 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein vp0806;<br>**PDBTitle:** the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633 |
| 32 | c3urzB_ | Alignment | not modelled | 99.7 | 11 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a hypothetical protein (bacova_03105) from2 bacteroides ovatus atcc 8483 at 2.19 a resolution |
| 33 | c2pl2A_ | Alignment | not modelled | 99.7 | 23 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**hypothetical conserved protein ttc0263;<br>**PDBTitle:** crystal structure of ttc0263: a thermophilic tpr protein in thermus2 thermophilus hb27 |
| 34 | d1hh8a_ | Alignment | not modelled | 99.7 | 16 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 35 | c1slyA_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**glycosyltransferase<br>**Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase;<br>**PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a |
| 36 | c3ulqA_ | Alignment | not modelled | 99.7 | 10 | **PDB header:**gene regulation/transcription activator<br>**Chain:** A: **PDB Molecule:**response regulator aspartate phosphatase f;<br>**PDBTitle:** crystal structure of the anti-activator rapf complexed with the2 response regulator coma dna binding domain |
| 37 | c2ifuA_ | Alignment | not modelled | 99.6 | 14 | **PDB header:**endocytosis/exocytosis<br>**Chain:** A: **PDB Molecule:**gamma-snap;<br>**PDBTitle:** crystal structure of a gamma-snap from danio rerio |
| 38 | c2hyzA_ | Alignment | not modelled | 99.6 | 18 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**synthetic consensus tpr protein;<br>**PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix2 (orthorombic crystal form) |
| 39 | c2c2lD_ | Alignment | not modelled | 99.6 | 11 | **PDB header:**chaperone<br>**Chain:** D: **PDB Molecule:**carboxy terminus of hsp70-interacting protein;<br>**PDBTitle:** crystal structure of the chip u-box e3 ubiquitin ligase |
| 40 | c1wao4_ | Alignment | not modelled | 99.6 | 15 | **PDB header:**hydrolase<br>**Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5;<br>**PDBTitle:** pp5 structure |
| 41 | d2c2la1 | Alignment | not modelled | 99.6 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 42 | c1xi4D_ | Alignment | not modelled | 99.6 | 16 | **PDB header:**endocytosis/exocytosis<br>**Chain:** D: **PDB Molecule:**clathrin heavy chain;<br>**PDBTitle:** clathrin d6 coat |
| 43 | d2onda1 | Alignment | not modelled | 99.6 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**HAT/Suf repeat |
| 44 | c3nf1A_ | Alignment | not modelled | 99.6 | 9 | **PDB header:**motor protein, transport protein<br>**Chain:** A: **PDB Molecule:**kinesin light chain 1;<br>**PDBTitle:** crystal structure of the tpr domain of kinesin light chain 1 |
| 45 | c3gw4B_ | Alignment | not modelled | 99.6 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of uncharacterized protein from deinococcus2 radiodurans. northeast structural genomics consortium target drr162b. |
| 46 | c2katA_ | Alignment | not modelled | 99.6 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution structure of protein bpp2914 from bordetella2 parapertussis. northeast structural genomics consortium3 target bpr206 |
| 47 | c2xcbA_ | Alignment | not modelled | 99.6 | 10 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**regulatory protein pcrh;<br>**PDBTitle:** crystal structure of pcrh in complex with the chaperone2 binding region of popd |
| 48 | c2kckA_ | Alignment | not modelled | 99.6 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**tpr repeat;<br>**PDBTitle:** nmr solution structure of the northeast structural genomics2 consortium (nesg) target mrr121a |
| 49 | d1hxia_ | Alignment | not modelled | 99.6 | 21 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 50 | c3gyzB_ | Alignment | not modelled | 99.6 | 13 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**chaperone protein ipgc;<br>**PDBTitle:** crystal structure of ipgc from shigella flexneri |
| 51 | c2yhcA_ | Alignment | not modelled | 99.5 | 11 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**upf0169 lipoprotein yfio;<br>**PDBTitle:** structure of bamd from e. coli |
| 52 | c3ly8A_ | Alignment | not modelled | 99.5 | 11 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**transcriptional activator cadc;<br>**PDBTitle:** crystal structure of mutant d471e of the periplasmic domain of cadc |
| 53 | c3qkyA_ | Alignment | not modelled | 99.5 | 10 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane assembly lipoprotein yfio;<br>**PDBTitle:** crystal structure of rhodothermus marinus bamd |
| | | | | | | **PDB header:**oxidoreductase |

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| 54 | c3qdnA_ | Alignment | not modelled | 99.5 | 14 | **Chain:** A: **PDB Molecule:**putative thioredoxin protein;<br>**PDBTitle:** putative thioredoxin protein from salmonella typhimurium |
| 55 | d1elwa_ | Alignment | not modelled | 99.5 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 56 | c2vyiA_ | Alignment | not modelled | 99.5 | 15 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**sgta protein;<br>**PDBTitle:** crystal structure of the tpr domain of human sgt |
| 57 | c2e2eA_ | Alignment | not modelled | 99.4 | 10 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**formate-dependent nitrite reductase complex nrfg subunit;<br>**PDBTitle:** tpr domain of nrfg mediates the complex formation between heme lyase2 and formate-dependent nitrite reductase in escherichia coli o157:h7 |
| 58 | d1a17a_ | Alignment | not modelled | 99.4 | 17 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 59 | c2kcvA_ | Alignment | not modelled | 99.4 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**tetratricopeptide repeat domain protein;<br>**PDBTitle:** solution nmr structure of tetratricopeptide repeat domain2 protein sru_0103 from salinibacter ruber, northeast3 structural genomics consortium (nesg) target srr115c |
| 60 | c3q49B_ | Alignment | not modelled | 99.4 | 14 | **PDB header:**ligase/chaperone<br>**Chain:** B: **PDB Molecule:**stip1 homology and u box-containing protein 1;<br>**PDBTitle:** crystal structure of the tpr domain of chip complexed with hsp70-c2 peptide |
| 61 | c3sz7A_ | Alignment | not modelled | 99.4 | 12 | **PDB header:**chaperone regulator<br>**Chain:** A: **PDB Molecule:**hsc70 cochaperone (sgt);<br>**PDBTitle:** crystal structure of the sgt2 tpr domain from aspergillus fumigatus |
| 62 | d2buga1 | Alignment | not modelled | 99.4 | 16 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 63 | c3k9iA_ | Alignment | not modelled | 99.4 | 19 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**bh0479 protein;<br>**PDBTitle:** crystal structure of putative protein binding protein (np_241345.1)2 from bacillus halodurans at 2.71 a resolution |
| 64 | d1kt1a1 | Alignment | not modelled | 99.3 | 10 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 65 | c2vsnB_ | Alignment | not modelled | 99.3 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**xcogt;<br>**PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation |
| 66 | d1qqea_ | Alignment | not modelled | 99.3 | 14 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 67 | d1zu2a1 | Alignment | not modelled | 99.3 | 18 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 68 | d1elra_ | Alignment | not modelled | 99.3 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 69 | c3ceqB_ | Alignment | not modelled | 99.3 | 12 | **PDB header:**motor protein, transport protein<br>**Chain:** B: **PDB Molecule:**kinesin light chain 2;<br>**PDBTitle:** the tpr domain of human kinesin light chain 2 (hklc2) |
| 70 | d1pc2a_ | Alignment | not modelled | 99.3 | 15 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 71 | d1nzna_ | Alignment | not modelled | 99.3 | 14 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 72 | d1iyga_ | Alignment | not modelled | 99.3 | 14 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 73 | c2dbaA_ | Alignment | not modelled | 99.3 | 13 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**smooth muscle cell associated protein-1, isoform<br>**PDBTitle:** the solution structure of the tetratrico peptide repeat of2 human smooth muscle cell associated protein-1, isoform 2 |
| 74 | c2if4A_ | Alignment | not modelled | 99.3 | 13 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**atfkbp42;<br>**PDBTitle:** crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana |
| 75 | d1p5qa1 | Alignment | not modelled | 99.3 | 19 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 76 | c3rkvA_ | Alignment | not modelled | 99.3 | 11 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**putative peptidylprolyl isomerase;<br>**PDBTitle:** c-terminal domain of protein c56c10.10, a putative peptidylprolyl2 isomerase, from caenorhabditis elegans |
| 77 | c1kt0A_ | Alignment | not modelled | 99.3 | 20 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**51 kda fk506-binding protein;<br>**PDBTitle:** structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes |
| 78 | c2xevB_ | Alignment | not modelled | 99.2 | 12 | **PDB header:**metal binding<br>**Chain:** B: **PDB Molecule:**ybgf;<br>**PDBTitle:** crystal structure of the tpr domain of xanthomonas2 campestris ybgf |
| | | | | | | **PDB header:**isomerase |

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| 79 | c1ihgA_ | Alignment | not modelled | 99.2 | 12 | **Chain:** A: **PDB Molecule:**cyclophilin 40;<br>**PDBTitle:** bovine cyclophilin 40, monoclinic form |
| 80 | c2vgxA_ | Alignment | not modelled | 99.2 | 10 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**chaperone sycd;<br>**PDBTitle:** structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd |
| 81 | d2hr2a1 | Alignment | not modelled | 99.2 | 16 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**CT2138-like |
| 82 | c2fbnA_ | Alignment | not modelled | 99.2 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**70 kda peptidylprolyl isomerase, putative;<br>**PDBTitle:** plasmodium falciparum putative fk506-binding protein2 pfl2275c, c-terminal tpr-containing domain |
| 83 | d2fbna1 | Alignment | not modelled | 99.2 | 11 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 84 | c1na3A_ | Alignment | not modelled | 99.2 | 18 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**designed protein ctpr2;<br>**PDBTitle:** design of stable alpha-helical arrays from an idealized tpr2 motif |
| 85 | c2avpA_ | Alignment | not modelled | 99.2 | 25 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**synthetic consensus tpr protein;<br>**PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix |
| 86 | c2l6jA_ | Alignment | not modelled | 99.2 | 17 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**tpr repeat-containing protein associated with hsp90;<br>**PDBTitle:** tah1 complexed by meevd |
| 87 | d1ihga1 | Alignment | not modelled | 99.2 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 88 | d1zbpa1 | Alignment | not modelled | 99.1 | 13 | **Fold:**ImpE-like<br>**Superfamily:**ImpE-like<br>**Family:**ImpE-like |
| 89 | c1qz2B_ | Alignment | not modelled | 99.1 | 19 | **PDB header:**isomerase/chaperone<br>**Chain:** B: **PDB Molecule:**fk506-binding protein 4;<br>**PDBTitle:** crystal structure of fkbp52 c-terminal domain complex with2 the c-terminal peptide meevd of hsp90 |
| 90 | c2kc7A_ | Alignment | not modelled | 99.0 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**bfr218_protein;<br>**PDBTitle:** solution nmr structure of bacteroides fragilis protein2 bf1650. northeast structural genomics consortium target3 bfr218 |
| 91 | d1tjca_ | Alignment | not modelled | 99.0 | 18 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 92 | c3beeB_ | Alignment | not modelled | 98.9 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative yfre protein;<br>**PDBTitle:** crystal structure of putative yfre protein from vibrio2 parahaemolyticus |
| 93 | d1y8ma1 | Alignment | not modelled | 98.9 | 15 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 94 | c3fflC_ | Alignment | not modelled | 98.9 | 15 | **PDB header:**cell cycle<br>**Chain:** C: **PDB Molecule:**anaphase-promoting complex subunit 7;<br>**PDBTitle:** crystal structure of the n-terminal domain of anaphase-2 promoting complex subunit 7 |
| 95 | c1ltxA_ | Alignment | not modelled | 98.8 | 10 | **PDB header:**transferase/protein binding<br>**Chain:** A: **PDB Molecule:**rab geranylgeranyltransferase alpha subunit;<br>**PDBTitle:** structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid |
| 96 | d1ouva_ | Alignment | not modelled | 98.8 | 7 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**HCP-like<br>**Family:**HCP-like |
| 97 | c3n71A_ | Alignment | not modelled | 98.7 | 15 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**histone lysine methyltransferase smyd1;<br>**PDBTitle:** crystal structure of cardiac specific histone methyltransferase smyd1 |
| 98 | d2ff4a2 | Alignment | not modelled | 98.7 | 12 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**BTAD-like |
| 99 | c2xm6A_ | Alignment | not modelled | 98.7 | 13 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**protein corresponding to locus c5321 from cft073 e.coli<br>**PDBTitle:** crystal structure of the protein corresponding to locus c5321 from2 cft073 e.coli strain |
| 100 | d2pqrb1 | Alignment | not modelled | 98.5 | 12 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 101 | c3q3hA_ | Alignment | not modelled | 98.4 | 7 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hmw1c-like glycosyltransferase;<br>**PDBTitle:** crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc |
| 102 | c3qwvA_ | Alignment | not modelled | 98.4 | 8 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**set and mynd domain-containing protein 2;<br>**PDBTitle:** crystal structure of histone lysine methyltransferase smyd2 in complex2 with the cofactor product adohcy |
| 103 | c2qfcB_ | Alignment | not modelled | 98.4 | 11 | **PDB header:**transcription regulation<br>**Chain:** B: **PDB Molecule:**plcr protein;<br>**PDBTitle:** crystal structure of bacillus thuringiensis plcr complexed with papr |
| 104 | c3mekA_ | Alignment | not modelled | 98.3 | 9 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**set and mynd domain-containing protein 3; |

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| 104 |  | Alignment | not modelled |  | 9 | **PDBTitle:** crystal structure of human histone-lysine n-2 methyltransferase smyd3 in complex with s-adenosyl-l-3 methionine |
| 105 | c3oxgA_ | Alignment | not modelled | 98.2 | 9 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**set and mynd domain-containing protein 3;<br>**PDBTitle:** human lysine methyltransferase smyd3 in complex with adohcy (form iii) |
| 106 | c3e4bD_ | Alignment | not modelled | 97.9 | 16 | **PDB header:**protein binding<br>**Chain:** D: **PDB Molecule:**algk;<br>**PDBTitle:** crystal structure of algk from pseudomonas fluorescens wcs374r |
| 107 | c3txmA_ | Alignment | not modelled | 97.9 | 12 | **PDB header:**hydrolase, protein binding<br>**Chain:** A: **PDB Molecule:**26s proteasome regulatory complex subunit p42b;<br>**PDBTitle:** crystal structure of rpn6 from drosophila melanogaster, gd(3+) complex |
| 108 | c2ff4B_ | Alignment | not modelled | 97.4 | 11 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**probable regulatory protein embr;<br>**PDBTitle:** mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide |
| 109 | c3lvhA_ | Alignment | not modelled | 97.3 | 13 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**clathrin heavy chain 1;<br>**PDBTitle:** crystal structure of a clathrin heavy chain and clathrin light chain2 complex |
| 110 | d1iipa1 | Alignment | not modelled | 96.3 | 8 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 111 | d1ya0a1 | Alignment | not modelled | 96.1 | 14 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 112 | c3eslA_ | Alignment | not modelled | 96.1 | 14 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**checkpoint serine/threonine-protein kinase bub1;<br>**PDBTitle:** crystal structure of the conserved n-terminal domain of the2 mitotic checkpoint component bub1 |
| 113 | c2wviA_ | Alignment | not modelled | 95.7 | 8 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**mitotic checkpoint serine/threonine-protein<br>**PDBTitle:** crystal structure of the n-terminal domain of bubr1 |
| 114 | c2lahA_ | Alignment | not modelled | 95.7 | 10 | **PDB header:**cell cycle, apoptosis<br>**Chain:** A: **PDB Molecule:**mitotic checkpoint serine/threonine-protein kinase bub1;<br>**PDBTitle:** solution nmr structure of mitotic checkpoint serine/threonine-protein2 kinase bub1 n-terminal domain from homo sapiens, northeast structural3 genomics consortium target hr5460a (methods development) |
| 115 | c3mkqA_ | Alignment | not modelled | 95.1 | 9 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**coatomer beta'-subunit;<br>**PDBTitle:** crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat |
| 116 | c3rjvA_ | Alignment | not modelled | 94.0 | 12 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**putative sel1 repeat protein;<br>**PDBTitle:** crystal structure of a putative sel1 repeat protein (kpn_04481) from2 klebsiella pneumoniae subsp. pneumoniae at 1.65 a resolution |
| 117 | c3kaeC_ | Alignment | not modelled | 92.6 | 19 | **PDB header:**protein binding<br>**Chain:** C: **PDB Molecule:**possible protein of nuclear scaffold;<br>**PDBTitle:** cdc27 n-terminus |
| 118 | c3mkqB_ | Alignment | not modelled | 91.9 | 9 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**coatomer subunit alpha;<br>**PDBTitle:** crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat |
| 119 | d1klxa_ | Alignment | not modelled | 88.0 | 14 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**HCP-like<br>**Family:**HCP-like |
| 120 | c2dl1A_ | Alignment | not modelled | 84.3 | 20 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**spartin;<br>**PDBTitle:** solution structure of the mit domain from human spartin |