# Phyre$^2$

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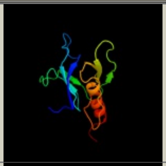
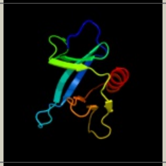
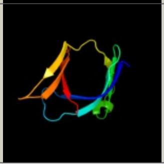
| Email | l.a.kelley@imperial.ac.uk |
| Description | Q53GA4 |
| Date | Fri May 25 10:06:09 BST 2012 |
| Unique Job ID | 27fbdd852cf88224 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1plsa_ | Alignment |  | 98.1 | 21 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 2 | c2dkpA_ | Alignment |  | 98.0 | 17 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**pleckstrin homology domain-containing family a<br>**PDBTitle:** solution structure of the ph domain of pleckstrin homology2 domain-containing protein family a member 5 from human |
| 3 | d1upqa_ | Alignment |  | 97.9 | 20 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 4 | c1faoA_ | Alignment |  | 97.8 | 16 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**dual adaptor of phosphotyrosine and 3-<br>**PDBTitle:** structure of the pleckstrin homology domain from2 dapp1/phish in complex with inositol 1,3,4,5-3 tetrakisphosphate |
| 5 | d1faoa_ | Alignment |  | 97.8 | 16 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 6 | c2yryA_ | Alignment |  | 97.8 | 21 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**pleckstrin homology domain-containing family a<br>**PDBTitle:** solution structure of the ph domain of pleckstrin homology2 domain-containing family a member 6 from human |
| 7 | c1u5fA_ | Alignment |  | 97.7 | 23 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**src-associated adaptor protein;<br>**PDBTitle:** crystal structure of the ph domain of skap-hom with 8 vector-derived2 n-terminal residues |
| 8 | d1eaza_ | Alignment |  | 97.7 | 16 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 9 | d1u5fa1 | Alignment |  | 97.7 | 22 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 10 | d1xx0a1 | Alignment |  | 97.6 | 22 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 11 | d1baka_ | Alignment |  | 97.6 | 14 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |

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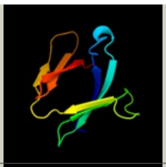
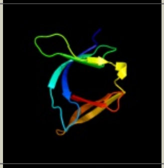
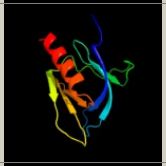
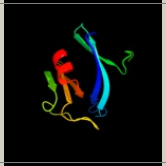
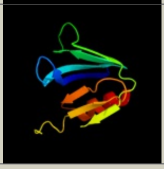
| 12 | d2i5fa1 | Alignment |  | 97.6 | 19 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 13 | c2rloA_ | Alignment |  | 97.6 | 31 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**centaurin-gamma 1;<br>**PDBTitle:** split ph domain of pi3-kinase enhancer |
| 14 | d2bcja2 | Alignment |  | 97.5 | 16 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 15 | c2dn6A_ | Alignment |  | 97.5 | 15 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**kiaa0640 protein;<br>**PDBTitle:** solution structure of the ph domain of kiaa0640 protein2 from human |
| 16 | d1x1ga1 | Alignment |  | 97.4 | 27 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 17 | d1u5ea1 | Alignment |  | 97.4 | 23 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 18 | c2dhkA_ | Alignment |  | 97.4 | 13 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**tbc1 domain family member 2;<br>**PDBTitle:** solution structure of the ph domain of tbc1 domain family2 member 2 protein from human |
| 19 | c2d9vA_ | Alignment |  | 97.3 | 17 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**pleckstrin homology domain-containing protein<br>**PDBTitle:** solution structure of the ph domain of pleckstrin homology2 domain-containing protein family b member 1 from mouse |
| 20 | d1u5da1 | Alignment |  | 97.3 | 23 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 21 | c2dhiA_ | Alignment | not modelled | 97.3 | 20 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**pleckstrin homology domain-containing family b<br>**PDBTitle:** solution structure of the ph domain of evectin-2 from mouse |
| 22 | d2coda1 | Alignment | not modelled | 97.3 | 18 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 23 | d1wi1a_ | Alignment | not modelled | 97.2 | 16 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 24 | d1u29a1 | Alignment | not modelled | 97.2 | 26 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 25 | c2kcjA_ | Alignment | not modelled | 97.1 | 13 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**pleckstrin homology domain-containing family a<br>**PDBTitle:** solution structure of fapp1 ph domain |
| 26 | d1wgqa_ | Alignment | not modelled | 97.1 | 17 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 27 | d2coaa1 | Alignment | not modelled | 97.1 | 29 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 28 | d1wg7a_ | Alignment | not modelled | 97.0 | 17 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
|  |  |  |  |  |  | **Fold:**PH domain-like barrel |

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| 29 | d1w1ha_ | Alignment | not modelled | 96.9 | 17 | **Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 30 | c2d9wA_ | Alignment | not modelled | 96.9 | 23 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**docking protein 2;<br>**PDBTitle:** solution structure of the ph domain of docking protein 22 from human |
| 31 | d1unqa_ | Alignment | not modelled | 96.9 | 20 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 32 | d1x1fa1 | Alignment | not modelled | 96.8 | 13 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 33 | c2da0A_ | Alignment | not modelled | 96.8 | 17 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**130-kda phosphatidylinositol 4,5-biphosphate-<br>**PDBTitle:** solution structure of the ph domain of pip2-dependent arf12 gtpase-activating protein from human |
| 34 | c3cxbB_ | Alignment | not modelled | 96.8 | 18 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**pleckstrin homology domain-containing family m<br>**PDBTitle:** crystal structure of sifa and skip |
| 35 | d1btka_ | Alignment | not modelled | 96.7 | 20 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 36 | c3nsuA_ | Alignment | not modelled | 96.7 | 21 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**phosphatidylinositol 4,5-bisphosphate-binding protein slm1;<br>**PDBTitle:** a systematic screen for protein-lipid interactions in saccharomyces2 cerevisiae |
| 37 | c2d9xA_ | Alignment | not modelled | 96.6 | 15 | **PDB header:**lipid transport<br>**Chain:** A: **PDB Molecule:**oxysterol binding protein-related protein 11;<br>**PDBTitle:** solution structure of the ph domain of oxysterol binding2 protein-related protein 11 from human |
| 38 | c2ys3A_ | Alignment | not modelled | 96.6 | 19 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**unc-112-related protein 2;<br>**PDBTitle:** solution structure of the ph domain of kindlin-3 from human |
| 39 | d1v89a_ | Alignment | not modelled | 96.5 | 14 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 40 | d1p6sa_ | Alignment | not modelled | 96.5 | 21 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 41 | d1wjma_ | Alignment | not modelled | 96.4 | 22 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 42 | d2dyna_ | Alignment | not modelled | 96.4 | 25 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 43 | d1v88a_ | Alignment | not modelled | 96.4 | 11 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 44 | c2lkoA_ | Alignment | not modelled | 96.3 | 15 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**fermitin family homolog 2;<br>**PDBTitle:** structural basis of phosphoinositide binding to kindlin-2 pleckstrin2 homology domain in regulating integrin activation |
| 45 | d2fjla1 | Alignment | not modelled | 96.3 | 14 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 46 | c2p0fA_ | Alignment | not modelled | 96.3 | 22 | **PDB header:**ligand binding protein<br>**Chain:** A: **PDB Molecule:**rho gtpase-activating protein 9;<br>**PDBTitle:** arhgap9 ph domain in complex with ins(1,3,5)p3 |
| 47 | c2d9zA_ | Alignment | not modelled | 96.2 | 25 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**protein kinase c, nu type;<br>**PDBTitle:** solution structure of the ph domain of protein kinase c, nu2 type from human |
| 48 | d1fgya_ | Alignment | not modelled | 96.2 | 22 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 49 | d1v5ua_ | Alignment | not modelled | 96.2 | 21 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 50 | c3o96A_ | Alignment | not modelled | 96.1 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**rac-alpha serine/threonine-protein kinase;<br>**PDBTitle:** crystal structure of human akt1 with an allosteric inhibitor |
| 51 | d2cofa1 | Alignment | not modelled | 95.9 | 12 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 52 | d1droa_ | Alignment | not modelled | 95.8 | 13 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 53 | c3pp2A_ | Alignment | not modelled | 95.3 | 20 | **PDB header:**hydrolase activator<br>**Chain:** A: **PDB Molecule:**rho gtpase-activating protein 27;<br>**PDBTitle:** crystal structure of the pleckstrin homology domain of arhgap27 |
| 54 | c2r09A_ | Alignment | not modelled | 95.3 | 23 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**cytohesin-3;<br>**PDBTitle:** crystal structure of autoinhibited form of grp1 arf gtpase exchange2 factor |
|  |  |  |  |  |  | **Fold:**PH domain-like barrel |

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| 55 | d2j59m1 | Alignment | not modelled | 95.2 | 23 | **Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 56 | d2elba2 | Alignment | not modelled | 95.2 | 11 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 57 | c2j59O_ | Alignment | not modelled | 94.9 | 21 | **PDB header:**hydrolase<br>**Chain:** O: **PDB Molecule:**rho-gtpase activating protein 10;<br>**PDBTitle:** crystal structure of the arf1:arhgap21-arfbd complex |
| 58 | d1btna_ | Alignment | not modelled | 94.8 | 20 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 59 | c3tfmA_ | Alignment | not modelled | 94.7 | 16 | **PDB header:**motor protein<br>**Chain:** A: **PDB Molecule:**myosin x;<br>**PDBTitle:** myosin x ph1n-ph2-ph1c tandem |
| 60 | c3a8qB_ | Alignment | not modelled | 94.6 | 26 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**t-lymphoma invasion and metastasis-inducing<br>**PDBTitle:** low-resolution crystal structure of the tiam2 phccex domain |
| 61 | d1qqga1 | Alignment | not modelled | 94.3 | 18 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Phosphotyrosine-binding domain (PTB) |
| 62 | c1qqgA_ | Alignment | not modelled | 93.7 | 19 | **PDB header:**signal transduction<br>**Chain:** A: **PDB Molecule:**insulin receptor substrate 1;<br>**PDBTitle:** crystal structure of the ph-ptb targeting region of irs-1 |
| 63 | d2coca1 | Alignment | not modelled | 93.6 | 14 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 64 | c2q13A_ | Alignment | not modelled | 93.4 | 14 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**dcc-interacting protein 13 alpha;<br>**PDBTitle:** crystal structure of bar-ph domain of appl1 |
| 65 | c2dtcB_ | Alignment | not modelled | 93.0 | 12 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**ral guanine nucleotide exchange factor ralgps1a;<br>**PDBTitle:** crystal structure of ms0666 |
| 66 | d1v5pa_ | Alignment | not modelled | 92.7 | 11 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 67 | c2k2jA_ | Alignment | not modelled | 92.1 | 22 | **PDB header:**hydrolase, signaling protein<br>**Chain:** A: **PDB Molecule:**1-phosphatidylinositol-4,5-bisphosphate<br>**PDBTitle:** nmr solution structure of the split ph domain from2 phospholipase c gamma 2 |
| 68 | c3fehA_ | Alignment | not modelled | 91.6 | 27 | **PDB header:**hydrolase activator<br>**Chain:** A: **PDB Molecule:**centaurin-alpha-1;<br>**PDBTitle:** crystal structure of full length centaurin alpha-1 |
| 69 | c3a8nA_ | Alignment | not modelled | 89.8 | 24 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**t-lymphoma invasion and metastasis-inducing<br>**PDBTitle:** crystal structure of the tiam1 phccex domain |
| 70 | c2rovA_ | Alignment | not modelled | 88.9 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**rho-associated protein kinase 2;<br>**PDBTitle:** the split ph domain of rock ii |
| 71 | d1ki1b2 | Alignment | not modelled | 87.5 | 20 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 72 | c3ml4D_ | Alignment | not modelled | 85.6 | 21 | **PDB header:**signaling protein<br>**Chain:** D: **PDB Molecule:**protein dok-7;<br>**PDBTitle:** crystal structure of a complex between dok7 ph-ptb and the musk2 juxtamembrane region |
| 73 | c2y7bA_ | Alignment | not modelled | 85.3 | 22 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**actin-binding protein anillin;<br>**PDBTitle:** crystal structure of the ph domain of human actin-binding2 protein anillin anln |
| 74 | d1zc3b1 | Alignment | not modelled | 79.1 | 15 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 75 | c3hk0B_ | Alignment | not modelled | 73.7 | 24 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**growth factor receptor-bound protein 10;<br>**PDBTitle:** crystal structure of the ra and ph domains of grb10 |
| 76 | d2dfka2 | Alignment | not modelled | 67.2 | 14 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 77 | d1omwa2 | Alignment | not modelled | 58.6 | 16 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 78 | c3dcaC_ | Alignment | not modelled | 31.1 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**rpa0582;<br>**PDBTitle:** crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target |
| 79 | d3bida1 | Alignment | not modelled | 28.5 | 20 | **Fold:**YegP-like<br>**Superfamily:**YegP-like<br>**Family:**YegP-like |
| 80 | d1tdza2 | Alignment | not modelled | 25.0 | 28 | **Fold:**N-terminal domain of MutM-like DNA repair proteins<br>**Superfamily:**N-terminal domain of MutM-like DNA repair proteins<br>**Family:**N-terminal domain of MutM-like DNA repair proteins |
| 81 | d1rj2a2 | Alignment | not modelled | 24.3 | 7 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |

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| 82 | d1maia_ | Alignment | not modelled | 23.9 | 15 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 83 | d1ee8a2 | Alignment | not modelled | 23.7 | 24 | **Fold:**N-terminal domain of MutM-like DNA repair proteins<br>**Superfamily:**N-terminal domain of MutM-like DNA repair proteins<br>**Family:**N-terminal domain of MutM-like DNA repair proteins |
| 84 | c3djmA_ | Alignment | not modelled | 21.6 | 20 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein duf427;<br>**PDBTitle:** crystal structure of a protein of unknown function from duf427 family2 (rsph17029_0682) from rhodobacter sphaeroides 2.4.1 at 2.51 a3 resolution |
| 85 | d1txda2 | Alignment | not modelled | 20.9 | 19 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 86 | c2bw2A_ | Alignment | not modelled | 20.9 | 20 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**bypass of forespore c;<br>**PDBTitle:** bofc from bacillus subtilis |
| 87 | c3gypA_ | Alignment | not modelled | 19.1 | 14 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**histone chaperone rtt106;<br>**PDBTitle:** rtt106p |
| 88 | d1tp6a_ | Alignment | not modelled | 18.8 | 33 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**PA1314-like |
| 89 | d1xcga2 | Alignment | not modelled | 17.8 | 16 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 90 | c3pvlA_ | Alignment | not modelled | 17.2 | 19 | **PDB header:**motor protein/protein transport<br>**Chain:** A: **PDB Molecule:**myosin viia isoform 1;<br>**PDBTitle:** structure of myosin viia myth4-ferm-sh3 in complex with the cen1 of2 sans |
| 91 | d1ok8a2 | Alignment | not modelled | 17.2 | 18 | **Fold:**Viral glycoprotein, central and dimerisation domains<br>**Superfamily:**Viral glycoprotein, central and dimerisation domains<br>**Family:**Viral glycoprotein, central and dimerisation domains |
| 92 | c3fssA_ | Alignment | not modelled | 17.0 | 16 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**histone chaperone rtt106;<br>**PDBTitle:** structure of the tandem ph domains of rtt106 |
| 93 | c1xdvB_ | Alignment | not modelled | 15.9 | 26 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**son of sevenless protein homolog 1;<br>**PDBTitle:** experimentally phased structure of human the son of2 sevenless protein at 4.1 ang. |
| 94 | d1v5ma_ | Alignment | not modelled | 13.5 | 28 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 95 | c1p58C_ | Alignment | not modelled | 12.1 | 19 | **PDB header:**virus<br>**Chain:** C: **PDB Molecule:**major envelope protein e;<br>**PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction |
| 96 | d3ctaa1 | Alignment | not modelled | 11.4 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**MarR-like transcriptional regulators |
| 97 | d2rnrb1 | Alignment | not modelled | 11.3 | 15 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**TFIIH domain |
| 98 | c2xetB_ | Alignment | not modelled | 10.9 | 24 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein;<br>**PDBTitle:** conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly |
| 99 | c3uajA_ | Alignment | not modelled | 10.9 | 16 | **PDB header:**viral protein/immune system<br>**Chain:** A: **PDB Molecule:**envelope protein;<br>**PDBTitle:** crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab fragment of the chimpanzee3 monoclonal antibody 5h2 |