Phyre$^2$

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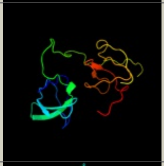
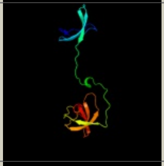
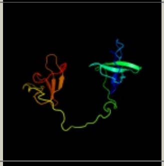
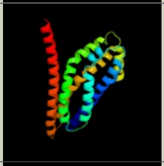
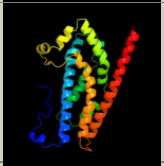
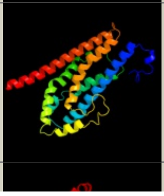
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | Q6XZF7 |
| Date | Thu Apr 26 09:30:42 BST 2012 |
| Unique Job ID | 56338b38252c9db8 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2dx1A_ | Alignment |  | 100.0 | 39 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 4;<br>**PDBTitle:** crystal structure of rhogef protein asef |
| 2 | c1griA_ | Alignment |  | 100.0 | 23 | **PDB header:**signal transduction adaptor<br>**Chain:** A: **PDB Molecule:**growth factor bound protein 2;<br>**PDBTitle:** grb2 |
| 3 | c3ky9B_ | Alignment |  | 100.0 | 25 | **PDB header:**apoptosis<br>**Chain:** B: **PDB Molecule:**proto-oncogene vav;<br>**PDBTitle:** autoinhibited vav1 |
| 4 | c1ng2A_ | Alignment |  | 99.9 | 27 | **PDB header:**oxidoreductase activator<br>**Chain:** A: **PDB Molecule:**neutrophil cytosolic factor 1;<br>**PDBTitle:** structure of autoinhibited p47phox |
| 5 | c2l3sA_ | Alignment |  | 99.9 | 24 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**autoinhibited crk protein;<br>**PDBTitle:** structure of the autoinhibited crk |
| 6 | c1ov3A_ | Alignment |  | 99.9 | 27 | **PDB header:**oxidoreductase activator<br>**Chain:** A: **PDB Molecule:**neutrophil cytosol factor 1;<br>**PDBTitle:** structure of the p22phox-p47phox complex |
| 7 | c2eyzA_ | Alignment |  | 99.9 | 20 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog<br>**PDBTitle:** ct10-regulated kinase isoform ii |
| 8 | c2vrwB_ | Alignment |  | 99.9 | 26 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**proto-oncogene vav;<br>**PDBTitle:** critical structural role for the ph and c1 domains of the2 vav1 exchange factor |
| 9 | c3ksyA_ | Alignment |  | 99.9 | 20 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**son of sevenless homolog 1;<br>**PDBTitle:** crystal structure of the histone domain, dh-ph unit, and2 catalytic unit of the ras activator son of sevenless (sos) |
| 10 | c3odoA_ | Alignment |  | 99.9 | 22 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 1;<br>**PDBTitle:** crystal structure of the dh/ph domains of p115-rhogef |
| 11 | c1xcgA_ | Alignment |  | 99.9 | 20 | **PDB header:**signaling protein activator/signaling pr<br>**Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 11;<br>**PDBTitle:** crystal structure of human rhoa in complex with dh/ph2 fragment of pdzrhogef |

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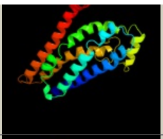
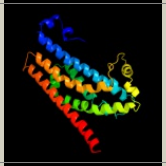
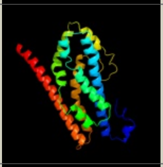
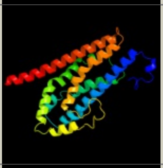
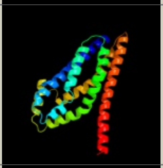
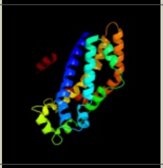
|---|---|---|---|---|---|---|
| 12 | c1foeA_ | Alignment |  | 99.9 | 29 | **PDB header:**signaling protein, immune system/signali<br>**Chain:** A: **PDB Molecule:**t-lymphoma invasion and metastasis inducing<br>**PDBTitle:** crystal structure of rac1 in complex with the guanine2 nucleotide exchange region of tiam1 |
| 13 | c1x86A_ | Alignment |  | 99.9 | 19 | **PDB header:**signaling protein/membrane protein<br>**Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 12;<br>**PDBTitle:** crystal structure of the dh/ph domains of leukemia-associated rhogef2 in complex with rhoa |
| 14 | c3t06E_ | Alignment |  | 99.9 | 20 | **PDB header:**signaling protein<br>**Chain:** E: **PDB Molecule:**rho guanine nucleotide exchange factor 11;<br>**PDBTitle:** crystal structure of the dh/ph fragment of pdzrhogef with n-terminal2 regulatory elements in complex with human rhoa |
| 15 | d1xcga1 | Alignment |  | 99.9 | 20 | **Fold:**DBL homology domain (DH-domain)<br>**Superfamily:**DBL homology domain (DH-domain)<br>**Family:**DBL homology domain (DH-domain) |
| 16 | c2dfkA_ | Alignment |  | 99.9 | 29 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**collybistin ii;<br>**PDBTitle:** crystal structure of the cdc42-collybistin ii complex |
| 17 | c3bjiA_ | Alignment |  | 99.9 | 25 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**proto-oncogene vav;<br>**PDBTitle:** structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1 |
| 18 | c1xdvB_ | Alignment |  | 99.9 | 20 | **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. |
| 19 | d1txda1 | Alignment |  | 99.9 | 20 | **Fold:**DBL homology domain (DH-domain)<br>**Superfamily:**DBL homology domain (DH-domain)<br>**Family:**DBL homology domain (DH-domain) |
| 20 | c2z0qA_ | Alignment |  | 99.9 | 32 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 3;<br>**PDBTitle:** crystal structure of dh-ph domain of rhogef3(xpln) |
| 21 | c1ki1B_ | Alignment | not modelled | 99.9 | 26 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**intersectin long form;<br>**PDBTitle:** guanine nucleotide exchange region of intersectin in2 complex with cdc42 |
| 22 | d1dbha1 | Alignment | not modelled | 99.9 | 20 | **Fold:**DBL homology domain (DH-domain)<br>**Superfamily:**DBL homology domain (DH-domain)<br>**Family:**DBL homology domain (DH-domain) |
| 23 | c1lb1C_ | Alignment | not modelled | 99.9 | 29 | **PDB header:**signaling protein<br>**Chain:** C: **PDB Molecule:**guanine nucleotide exchange factor dbs;<br>**PDBTitle:** crystal structure of the dbl and pleckstrin homology2 domains of dbs in complex with rhoa |
| 24 | d2dfka1 | Alignment | not modelled | 99.9 | 31 | **Fold:**DBL homology domain (DH-domain)<br>**Superfamily:**DBL homology domain (DH-domain)<br>**Family:**DBL homology domain (DH-domain) |
| 25 | c2rgnB_ | Alignment | not modelled | 99.9 | 26 | **PDB header:**signaling protein complex<br>**Chain:** B: **PDB Molecule:**rhoa/rac/cdc42 exchange factor;<br>**PDBTitle:** crystal structure of p63rhogef complex with galpha-q and rhoa |
| 26 | c3odwB_ | Alignment | not modelled | 99.9 | 22 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**rho guanine nucleotide exchange factor 1;<br>**PDBTitle:** crystal structure of the linker-dh/ph domains of p115-rhogef |
| 27 | c1dbhA_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**protein (human sos 1);<br>**PDBTitle:** dbl and pleckstrin homology domains from hsos1 |
| 28 | d1foea1 | Alignment | not modelled | 99.9 | 32 | **Fold:**DBL homology domain (DH-domain)<br>**Superfamily:**DBL homology domain (DH-domain)<br>**Family:**DBL homology domain (DH-domain) |
|  |  |  |  |  |  | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor |

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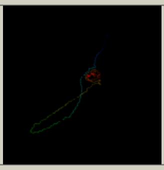
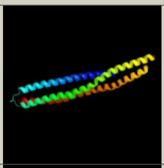
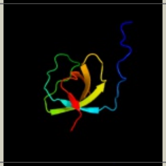
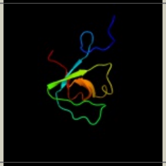
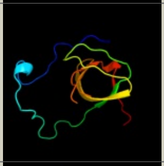
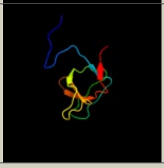
| 29 | c3odxA_ | Alignment | not modelled | 99.9 | 22 | 1;<br>**PDBTitle:** crystal structure of an n-terminally truncated linker-dh/ph domains of2 p115-rhogef |
| 30 | d1ki1b1 | Alignment | not modelled | 99.9 | 25 | **Fold:**DBL homology domain (DH-domain)<br>**Superfamily:**DBL homology domain (DH-domain)<br>**Family:**DBL homology domain (DH-domain) |
| 31 | d1by1a_ | Alignment | not modelled | 99.9 | 24 | **Fold:**DBL homology domain (DH-domain)<br>**Superfamily:**DBL homology domain (DH-domain)<br>**Family:**DBL homology domain (DH-domain) |
| 32 | c3mpxA_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**lipid binding protein<br>**Chain:** A: **PDB Molecule:**fyve, rhogef and ph domain-containing protein 5;<br>**PDBTitle:** crystal structure of the dh and ph-1 domains of human fgd5 |
| 33 | d1kz7a1 | Alignment | not modelled | 99.9 | 27 | **Fold:**DBL homology domain (DH-domain)<br>**Superfamily:**DBL homology domain (DH-domain)<br>**Family:**DBL homology domain (DH-domain) |
| 34 | c3eo2A_ | Alignment | not modelled | 99.8 | 31 | **PDB header:**splicing<br>**Chain:** A: **PDB Molecule:**neuroepithelial cell-transforming gene 1 protein;<br>**PDBTitle:** crystal structure of the rhogef domain of human neuroepithelial cell-2 transforming gene 1 protein |
| 35 | c1ntyA_ | Alignment | not modelled | 99.8 | 25 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**triple functional domain protein;<br>**PDBTitle:** crystal structure of the first dh/ph domain of trio to 1.7 a |
| 36 | d1ntya1 | Alignment | not modelled | 99.8 | 25 | **Fold:**DBL homology domain (DH-domain)<br>**Superfamily:**DBL homology domain (DH-domain)<br>**Family:**DBL homology domain (DH-domain) |
| 37 | d1f5xa_ | Alignment | not modelled | 99.8 | 25 | **Fold:**DBL homology domain (DH-domain)<br>**Superfamily:**DBL homology domain (DH-domain)<br>**Family:**DBL homology domain (DH-domain) |
| 38 | c1mv3A_ | Alignment |  | 99.8 | 7 | **PDB header:**endocytosis/exocytosis<br>**Chain:** A: **PDB Molecule:**myc box dependent interacting protein 1;<br>**PDBTitle:** nmr structure of the tumor suppressor bin1: alternative2 splicing in melanoma and interaction with c-myc |
| 39 | c3gf9A_ | Alignment | not modelled | 99.8 | 29 | **PDB header:**endocytosis<br>**Chain:** A: **PDB Molecule:**intersectin 2;<br>**PDBTitle:** crystal structure of human intersectin 2 rhogef domain |
| 40 | c2dybA_ | Alignment | not modelled | 99.7 | 31 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**neutrophil cytosol factor 4;<br>**PDBTitle:** the crystal structure of human p40(phox) |
| 41 | c2ficA_ | Alignment |  | 99.7 | 22 | **PDB header:**endocytosis/exocytosis, membrane protein<br>**Chain:** A: **PDB Molecule:**bridging integrator 1;<br>**PDBTitle:** the crystal structure of the bar domain from human bin1/amphiphysin ii2 and its implications for molecular recognition |
| 42 | d1ng2a2 | Alignment |  | 99.6 | 20 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 43 | c2e5kA_ | Alignment |  | 99.6 | 17 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**suppressor of t-cell receptor signaling 1;<br>**PDBTitle:** solution structure of sh3 domain in suppressor of t-cell2 receptor signaling 1 |
| 44 | c2rqrA_ | Alignment |  | 99.6 | 19 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**engulfment and cell motility protein 1, linker, dedicator<br>**PDBTitle:** the solution structure of human dock2 sh3 domain - elmo1 peptide2 chimera complex |
| 45 | d1uhca_ | Alignment |  | 99.6 | 94 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 46 | d1udla_ | Alignment | not modelled | 99.6 | 23 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 47 | d1ug1a_ | Alignment | not modelled | 99.6 | 20 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 48 | c2jxbA_ | Alignment | not modelled | 99.6 | 19 | **PDB header:**signaling protein complex<br>**Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd3 epsilon chain,<br>**PDBTitle:** structure of cd3epsilon-nck2 first sh3 domain complex |
| | | | | | | **Fold:**SH3-like barrel |

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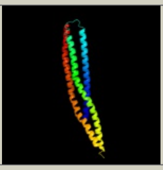
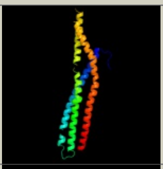
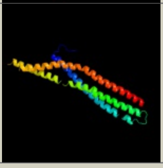
| 49 | d1ov3a2 | Alignment | not modelled | 99.6 | 20 | **Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 50 | c2dlpA_ | Alignment | not modelled | 99.6 | 18 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**kiaa1783 protein;<br>**PDBTitle:** solution structure of the sh3 domain of human kiaa17832 protein |
| 51 | c2jmcA_ | Alignment | not modelled | 99.6 | 17 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**spectrin alpha chain, brain and p41 peptide<br>**PDBTitle:** chimer between spc-sh3 and p41 |
| 52 | c1x6gA_ | Alignment | not modelled | 99.6 | 17 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**megakaryocyte-associated tyrosine-protein kinase;<br>**PDBTitle:** solution structures of the sh3 domain of human2 megakaryocyte-associated tyrosine-protein kinase. |
| 53 | c2csqA_ | Alignment | not modelled | 99.5 | 21 | **PDB header:**endocytosis/exocytosis<br>**Chain:** A: **PDB Molecule:**rim binding protein 2;<br>**PDBTitle:** solution structure of the second sh3 domain of human rim-2 binding protein 2 |
| 54 | c3nmzD_ | Alignment | not modelled | 99.5 | 15 | **PDB header:**cell adhesion/cell cycle<br>**Chain:** D: **PDB Molecule:**rho guanine nucleotide exchange factor 4;<br>**PDBTitle:** crytal structure of apc complexed with asef |
| 55 | d1i1ja_ | Alignment | not modelled | 99.5 | 18 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 56 | c3sogA_ | Alignment |  | 99.5 | 24 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**amphiphysin;<br>**PDBTitle:** crystal structure of the bar domain of human amphiphysin, isoform 1 |
| 57 | c1x43A_ | Alignment | not modelled | 99.5 | 26 | **PDB header:**endocytosis/exocytosis<br>**Chain:** A: **PDB Molecule:**sh3 domain grb2-like protein b1;<br>**PDBTitle:** solution structure of the sh3 domain of endophilin b12 (sh3g1b1) |
| 58 | d1urua_ | Alignment |  | 99.5 | 23 | **Fold:**BAR/IMD domain-like<br>**Superfamily:**BAR/IMD domain-like<br>**Family:**BAR domain |
| 59 | c1uruA_ | Alignment |  | 99.5 | 23 | **PDB header:**endocytosis<br>**Chain:** A: **PDB Molecule:**amphiphysin;<br>**PDBTitle:** amphiphysin bar domain from drosophila |
| 60 | c2cubA_ | Alignment | not modelled | 99.5 | 25 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**cytoplasmic protein nck1;<br>**PDBTitle:** solution structure of the sh3 domain of the human2 cytoplasmic protein nck1 |
| 61 | c2egeA_ | Alignment | not modelled | 99.5 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein kiaa1666;<br>**PDBTitle:** solution structure of the third sh3 domain from human2 kiaa1666 protein |
| 62 | c2yuoA_ | Alignment | not modelled | 99.5 | 25 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**run and tbc1 domain containing 3;<br>**PDBTitle:** solution structure of the sh3 domain of mouse run and tbc12 domain containing 3 |
| 63 | c1x2qA_ | Alignment | not modelled | 99.5 | 23 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**signal transducing adapter molecule 2;<br>**PDBTitle:** solution structure of the sh3 domain of the signal2 transducing adaptor molecule 2 |
| 64 | c2ysqA_ | Alignment | not modelled | 99.5 | 23 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 9;<br>**PDBTitle:** solution structure of the sh3 domain from rho guanine2 nucleotide exchange factor 9 |
| 65 | c2dl7A_ | Alignment | not modelled | 99.5 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**kiaa0769 protein;<br>**PDBTitle:** solution structure of the second sh3 domain of human2 kiaa0769 protein |
| 66 | d1wlpb2 | Alignment | not modelled | 99.5 | 18 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 67 | c1zlmA_ | Alignment | not modelled | 99.5 | 36 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**osteoclast stimulating factor 1;<br>**PDBTitle:** crystal structure of the sh3 domain of human osteoclast2 stimulating factor |
| 68 | c2ekhA_ | Alignment | not modelled | 99.5 | 24 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**sh3 and px domain-containing protein 2a;<br>**PDBTitle:** solution structures of the sh3 domain of human kiaa0418 |
| 69 | d1bb9a_ | Alignment | not modelled | 99.5 | 17 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 70 | c1bb9A_ | Alignment | not modelled | 99.5 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**amphiphysin 2;<br>**PDBTitle:** crystal structure of the sh3 domain from rat amphiphysin 2 |
| 71 | d1uuea_ | Alignment | not modelled | 99.5 | 32 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |

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|---|---|---|---|---|---|---|
| 72 | d2v1ra1 | Alignment | not modelled | 99.5 | 33 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 73 | d1ycsb2 | Alignment | not modelled | 99.5 | 32 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 74 | c2yt6A_ | Alignment | not modelled | 99.5 | 26 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**adult male urinary bladder cdna, riken full-<br>**PDBTitle:** solution structure of the sh3_1 domain of yamaguchi sarcoma2 viral (v-yes) oncogene homolog 1 |
| 75 | c2eyyA_ | Alignment | not modelled | 99.5 | 20 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog<br>**PDBTitle:** ct10-regulated kinase isoform i |
| 76 | c2djqA_ | Alignment | not modelled | 99.5 | 31 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**sh3 domain containing ring finger 2;<br>**PDBTitle:** the solution structure of the first sh3 domain of mouse sh32 domain containing ring finger 2 |
| 77 | c1x2pA_ | Alignment | not modelled | 99.5 | 30 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 2;<br>**PDBTitle:** solution structure of the sh3 domain of the protein2 arginine n-methyltransferase 2 |
| 78 | d1jqqa_ | Alignment | not modelled | 99.5 | 26 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 79 | c2oi3A_ | Alignment | not modelled | 99.5 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**tyrosine-protein kinase hck;<br>**PDBTitle:** nmr structure analysis of the hematopoetic cell kinase sh32 domain complexed with an artificial high affinity ligand3 (pd1) |
| 80 | c2epdA_ | Alignment | not modelled | 99.5 | 30 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**rho gtpase-activating protein 4;<br>**PDBTitle:** solution structure of sh3 domain in rho-gtpase-activating2 protein 4 |
| 81 | c2ed1A_ | Alignment | not modelled | 99.5 | 30 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**130 kda phosphatidylinositol 4,5-biphosphate-<br>**PDBTitle:** solution structure of the sh3 domain of 130 kda2 phosphatidylinositol 4,5-biphosphate-dependent arf1 gtpase-3 activating protein |
| 82 | c1wyxA_ | Alignment | not modelled | 99.5 | 32 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**crk-associated substrate;<br>**PDBTitle:** the crystal structure of the p130cas sh3 domain at 1.1 a2 resolution |
| 83 | d1ujya_ | Alignment | not modelled | 99.5 | 30 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 84 | c1x69A_ | Alignment | not modelled | 99.5 | 24 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**cortactin isoform a;<br>**PDBTitle:** solution structures of the sh3 domain of human src2 substrate cortactin |
| 85 | c2csiA_ | Alignment | not modelled | 99.5 | 28 | **PDB header:**endocytosis/exocytosis<br>**Chain:** A: **PDB Molecule:**rim binding protein 2;<br>**PDBTitle:** solution structure of the third sh3 domain of human rim-2 binding protein 2 |
| 86 | c2pqhA_ | Alignment | not modelled | 99.5 | 23 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**spectrin alpha chain, brain;<br>**PDBTitle:** structure of sh3 chimera with a type ii ligand linked to the chain c-2 terminal |
| 87 | d1k4us_ | Alignment | not modelled | 99.5 | 41 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 88 | c2dnuA_ | Alignment | not modelled | 99.5 | 21 | **PDB header:**structural genomics, structural protein<br>**Chain:** A: **PDB Molecule:**sh3 multiple domains 1;<br>**PDBTitle:** solution structure of rsgi ruh-061, a sh3 domain from human |
| 89 | c2yupA_ | Alignment | not modelled | 99.5 | 23 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**vinexin;<br>**PDBTitle:** solution structure of the second sh3 domain of human vinexin |
| 90 | c2d1xD_ | Alignment | not modelled | 99.5 | 25 | **PDB header:**cell invasion<br>**Chain:** D: **PDB Molecule:**cortactin isoform a;<br>**PDBTitle:** the crystal structure of the cortactin-sh3 domain and amap1-2 peptide complex |
| 91 | c2dilA_ | Alignment | not modelled | 99.5 | 29 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**proline-serine-threonine phosphatase-interacting<br>**PDBTitle:** solution structure of the sh3 domain of the human proline-2 serine-threonine phosphatase-interacting protein 1 |
| 92 | c3rnjA_ | Alignment | not modelled | 99.5 | 21 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**brain-specific angiogenesis inhibitor 1-associated protein<br>**PDBTitle:** crystal structure of the sh3 domain from irsp53 (baiap2) |
| 93 | c2bz8B_ | Alignment | not modelled | 99.5 | 24 | **PDB header:**sh3 domain<br>**Chain:** B: **PDB Molecule:**sh3-domain kinase binding protein 1;<br>**PDBTitle:** n-terminal sh3 domain of cin85 bound to cbl-b peptide |
| 94 | c2dl4A_ | Alignment | not modelled | 99.5 | 37 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**protein stac;<br>**PDBTitle:** solution structure of the first sh3 domain of stac protein |
| 95 | c2ebpA_ | Alignment | not modelled | 99.5 | 12 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1;<br>**PDBTitle:** solution structure of the sh3 domain from human sam and sh32 domain containing protein 1 |
| 96 | d1u06a1 | Alignment | not modelled | 99.5 | 31 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |

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| 97 | c2cudA_ | Alignment | not modelled | 99.5 | 16 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**src-like-adapter;<br>**PDBTitle:** solution structure of the sh3 domain of the human src-like2 adopter protein (slap) |
| 98 | c2dbmA_ | Alignment | not modelled | 99.5 | 36 | **PDB header:**transferase, signaling protein<br>**Chain:** A: **PDB Molecule:**sh3-containing grb2-like protein 2;<br>**PDBTitle:** solution structures of the sh3 domain of human sh3-2 containing grb2-like protein 2 |
| 99 | c2kbtA_ | Alignment | not modelled | 99.5 | 36 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**chimera of proto-oncogene vav, linker,<br>**PDBTitle:** attachment of an nmr-invisible solubility enhancement tag2 (inset) using a sortase-mediated protein ligation method |
| 100 | c2creA_ | Alignment | not modelled | 99.5 | 26 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hef-like protein;<br>**PDBTitle:** solution structure of rsgi ruh-036, an sh3 domain from2 human cdna |
| 101 | d1e6ga_ | Alignment | not modelled | 99.5 | 29 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 102 | c2fpeB_ | Alignment | not modelled | 99.5 | 23 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**c-jun-amino-terminal kinase interacting protein<br>**PDBTitle:** conserved dimerization of the ib1 src-homology 3 domain |
| 103 | d1gria2 | Alignment | not modelled | 99.5 | 21 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 104 | d1oeba_ | Alignment | not modelled | 99.5 | 26 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 105 | c2dmoA_ | Alignment | not modelled | 99.5 | 31 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**neutrophil cytosol factor 2;<br>**PDBTitle:** refined solution structure of the 1st sh3 domain from human2 neutrophil cytosol factor 2 (ncf-2) |
| 106 | c2egcA_ | Alignment | not modelled | 99.5 | 26 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**sh3 and px domain-containing protein 2a;<br>**PDBTitle:** solution structure of the fifth sh3 domain from human2 kiaa0418 protein |
| 107 | d1e6ha_ | Alignment | not modelled | 99.5 | 28 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 108 | d1uffa_ | Alignment | not modelled | 99.5 | 32 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 109 | d1utia_ | Alignment | not modelled | 99.5 | 27 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 110 | c1wx6A_ | Alignment | not modelled | 99.5 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**cytoplasmic protein nck2;<br>**PDBTitle:** solution structure of the sh3 domain of the human2 cytoplasmic protein nck2 |
| 111 | c1wi7A_ | Alignment | not modelled | 99.5 | 39 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**sh3-domain kinase binding protein 1;<br>**PDBTitle:** solution structure of the sh3 domain of sh3-domain kinase2 binding protein 1 |
| 112 | c2yunA_ | Alignment | not modelled | 99.5 | 26 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**nostrin;<br>**PDBTitle:** solution structure of the sh3 domain of human nostrin |
| 113 | c2nwmA_ | Alignment | not modelled | 99.5 | 35 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**vinexin;<br>**PDBTitle:** solution structure of the first sh3 domain of human vinexin2 and its interaction with the peptides from vinculin |
| 114 | d1uj0a_ | Alignment | not modelled | 99.5 | 29 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 115 | c2df6A_ | Alignment | not modelled | 99.5 | 40 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 7;<br>**PDBTitle:** crystal structure of the sh3 domain of betapix in complex2 with a high affinity peptide from pak2 |
| 116 | d1oota_ | Alignment | not modelled | 99.5 | 29 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 117 | c2dl3A_ | Alignment | not modelled | 99.5 | 35 | **PDB header:**cell adhesion, signaling protein<br>**Chain:** A: **PDB Molecule:**sorbin and sh3 domain-containing protein 1;<br>**PDBTitle:** solution structure of the first sh3 domain of human sorbin2 and sh3 domain-containing protein 1 |
| 118 | c2ed0A_ | Alignment | not modelled | 99.5 | 35 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**abl interactor 2;<br>**PDBTitle:** solution structure of the sh3 domain of abl interactor 22 (abelson interactor 2) |
| 119 | d1wiea_ | Alignment | not modelled | 99.5 | 24 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 120 | c2js0A_ | Alignment | not modelled | 99.5 | 27 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**cytoplasmic protein nck1;<br>**PDBTitle:** solution structure of second sh3 domain of adaptor nck |