

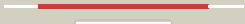
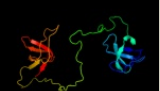
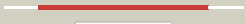
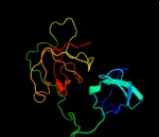
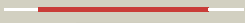




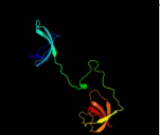












Phyre2

| | |
|---------------|------------------------------|
| Email | l.a.kelley@imperial.ac.uk |
| Description | Q9CX99 |
| Date | Tue Jul 30 12:56:35 BST 2013 |
| Unique Job ID | 1b9aac585807dbbb |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c1griA_ |  Alignment |  | 100.0 | 57 | PDB header: signal transduction adaptor Chain: A: PDB Molecule: growth factor bound protein 2; PDBTitle: grb2 |
| 2 | c2lqnA_ |  Alignment |  | 100.0 | 21 | PDB header: signaling protein Chain: A: PDB Molecule: crk-like protein; PDBTitle: solution structure of crkl |
| 3 | c2l3sA_ |  Alignment |  | 100.0 | 24 | PDB header: structural protein Chain: A: PDB Molecule: autoinhibited crk protein; PDBTitle: structure of the autoinhibited crk |
| 4 | c2eyzA_ |  Alignment |  | 100.0 | 22 | PDB header: signaling protein Chain: A: PDB Molecule: v-crk sarcoma virus ct10 oncogene homolog PDBTitle: ct10-regulated kinase isoform ii |
| 5 | c1ng2A_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase activator Chain: A: PDB Molecule: neutrophil cytosolic factor 1; PDBTitle: structure of autoinhibited p47phox |
| 6 | c1ov3A_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase activator Chain: A: PDB Molecule: neutrophil cytosol factor 1; PDBTitle: structure of the p22phox-p47phox complex |
| 7 | c2eyvA_ |  Alignment |  | 99.9 | 25 | PDB header: signaling protein Chain: A: PDB Molecule: v-crk sarcoma virus ct10 oncogene homolog PDBTitle: ct10-regulated kinase isoform i |
| 8 | c1k9aB_ |  Alignment |  | 99.9 | 29 | PDB header: transferase Chain: B: PDB Molecule: carboxyl-terminal src kinase; PDBTitle: crystal structure analysis of full-length carboxyl-terminal2 src kinase at 2.5 a resolution |
| 9 | c1mv3A_ |  Alignment |  | 99.8 | 18 | PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: myc box dependent interacting protein 1; PDBTitle: nmr structure of the tumor suppressor bin1: alternative2 splicing in melanoma and interaction with c-myc |
| 10 | c1oplA_ |  Alignment |  | 99.8 | 35 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase; PDBTitle: structural basis for the auto-inhibition of c-abl tyrosine2 kinase |
| 11 | c2fo0A_ |  Alignment |  | 99.8 | 34 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase abl1 (1b isoform); PDBTitle: organization of the sh3-sh2 unit in active and inactive forms of the2 c-abl tyrosine kinase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 12 | c3qwxX_ | Alignment | | 99.8 | 25 | PDB header: signaling protein Chain: X: PDB Molecule: cell death abnormality protein 2; PDBTitle: ced-2 1-174 |
| 13 | c3qwyA_ | Alignment | | 99.8 | 24 | PDB header: signaling protein Chain: A: PDB Molecule: cell death abnormality protein 2; PDBTitle: ced-2 |
| 14 | c2dvjA_ | Alignment | | 99.8 | 28 | PDB header: signaling protein Chain: A: PDB Molecule: v-crk sarcoma virus ct10 oncogene homolog, PDBTitle: phosphorylated crk-ii |
| 15 | c2ablA_ | Alignment | | 99.8 | 36 | PDB header: transferase Chain: A: PDB Molecule: abl tyrosine kinase; PDBTitle: sh3-sh2 domain fragment of human bcr-abl tyrosine kinase |
| 16 | c1y57A_ | Alignment | | 99.8 | 28 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase src; PDBTitle: structure of unphosphorylated c-src in complex with an inhibitor |
| 17 | d1ng2a2 | Alignment | | 99.8 | 23 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 18 | c2h8hA_ | Alignment | | 99.8 | 31 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase src; PDBTitle: src kinase in complex with a quinazoline inhibitor |
| 19 | c2dx1A_ | Alignment | | 99.8 | 32 | PDB header: signaling protein Chain: A: PDB Molecule: rho guanine nucleotide exchange factor 4; PDBTitle: crystal structure of rhogef protein asef |
| 20 | c2dybA_ | Alignment | | 99.8 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: neutrophil cytosol factor 4; PDBTitle: the crystal structure of human p40(phox) |
| 21 | c1x27F_ | Alignment | not modelled | 99.8 | 35 | PDB header: signaling protein Chain: F: PDB Molecule: proto-oncogene tyrosine-protein kinase lck; PDBTitle: crystal structure of lck sh2-sh3 with sh2 binding site of p130cas |
| 22 | c2c0iA_ | Alignment | not modelled | 99.7 | 32 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase hck; PDBTitle: src family kinase hck with bound inhibitor a-420983 |
| 23 | c2ed0A_ | Alignment | not modelled | 99.7 | 25 | PDB header: signaling protein Chain: A: PDB Molecule: abl interactor 2; PDBTitle: solution structure of the sh3 domain of abl interactor 22 (abelson interactor 2) |
| 24 | c3nmzD_ | Alignment | not modelled | 99.7 | 25 | PDB header: cell adhesion/cell cycle Chain: D: PDB Molecule: rho guanine nucleotide exchange factor 4; PDBTitle: crytal structure of apc complexed with asef |
| 25 | c3nhnA_ | Alignment | not modelled | 99.7 | 32 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase hck; PDBTitle: crystal structure of the src-family kinase hck sh3-sh2-linker2 regulatory region |
| 26 | c2cubA_ | Alignment | not modelled | 99.7 | 28 | PDB header: signaling protein Chain: A: PDB Molecule: cytoplasmic protein nck1; PDBTitle: solution structure of the sh3 domain of the human2 cytoplasmic protein nck1 |
| 27 | c2xmfA_ | Alignment | not modelled | 99.7 | 32 | PDB header: motor protein Chain: A: PDB Molecule: myosin 1e sh3; PDBTitle: myosin 1e sh3 |
| 28 | c2lj0A_ | Alignment | not modelled | 99.7 | 35 | PDB header: signaling protein Chain: A: PDB Molecule: sorbin and sh3 domain-containing protein 1; PDBTitle: the third sh3 domain of r85fl |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c1x2qA | Alignment | not modelled | 99.7 | 24 | PDB header: signaling protein Chain: A: PDB Molecule: signal transducing adapter molecule 2; PDBTitle: solution structure of the sh3 domain of the signal2 transducing adaptor molecule 2 |
| 30 | c2dmoA | Alignment | not modelled | 99.7 | 25 | PDB header: signaling protein Chain: A: PDB Molecule: neutrophil cytosol factor 2; PDBTitle: refined solution structure of the 1st sh3 domain from human2 neutrophil cytosol factor 2 (ncf-2) |
| 31 | d1ov3a2 | Alignment | not modelled | 99.7 | 24 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 32 | c2df6A | Alignment | not modelled | 99.7 | 33 | PDB header: signaling protein Chain: A: PDB Molecule: rho guanine nucleotide exchange factor 7; PDBTitle: crystal structure of the sh3 domain of betapix in complex2 with a high affinity peptide from pak2 |
| 33 | d1sema | Alignment | not modelled | 99.7 | 40 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 34 | c4glmD | Alignment | not modelled | 99.7 | 27 | PDB header: signaling protein Chain: D: PDB Molecule: dynamamin-binding protein; PDBTitle: crystal structure of the sh3 domain of dnmbp protein [homo sapiens] |
| 35 | d1gcqa | Alignment | not modelled | 99.7 | 46 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 36 | d1utia | Alignment | not modelled | 99.7 | 43 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 37 | c2yuoA | Alignment | not modelled | 99.7 | 32 | PDB header: signaling protein Chain: A: PDB Molecule: run and tbc1 domain containing 3; PDBTitle: solution structure of the sh3 domain of mouse run and tbc12 domain containing 3 |
| 38 | d1pwta | Alignment | not modelled | 99.7 | 24 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 39 | d1gria2 | Alignment | not modelled | 99.7 | 45 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 40 | c1zx6A | Alignment | not modelled | 99.7 | 36 | PDB header: protein binding Chain: A: PDB Molecule: ypr154wp; PDBTitle: high-resolution crystal structure of yeast pin3 sh3 domain |
| 41 | c2yunA | Alignment | not modelled | 99.7 | 34 | PDB header: protein transport Chain: A: PDB Molecule: nostrin; PDBTitle: solution structure of the sh3 domain of human nostrin |
| 42 | c2kymA | Alignment | not modelled | 99.7 | 25 | PDB header: signaling protein Chain: A: PDB Molecule: bud emergence protein 1; PDBTitle: solution structure of the bem1p sh3-ci domain from l.elongisporus in2 complex with ste20p peptide |
| 43 | c1g83A | Alignment | not modelled | 99.7 | 31 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase fyn; PDBTitle: crystal structure of fyn sh3-sh2 |
| 44 | d1wlpb2 | Alignment | not modelled | 99.7 | 28 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 45 | d1uuea | Alignment | not modelled | 99.7 | 26 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 46 | c2drmB | Alignment | not modelled | 99.7 | 29 | PDB header: contractile protein Chain: B: PDB Molecule: acanthamoeba myosin ib; PDBTitle: acanthamoeba myosin i sh3 domain bound to acan125 |
| 47 | c2dbkA | Alignment | not modelled | 99.7 | 25 | PDB header: signaling protein Chain: A: PDB Molecule: crk-like protein; PDBTitle: solution structures of the sh3 domain of human crk-like2 protein |
| 48 | c2nwmA | Alignment | not modelled | 99.7 | 44 | PDB header: cell adhesion Chain: A: PDB Molecule: vinexin; PDBTitle: solution structure of the first sh3 domain of human vinexin2 and its interaction with the peptides from vinculin |
| 49 | c2ysqA | Alignment | not modelled | 99.7 | 23 | PDB header: signaling protein Chain: A: PDB Molecule: rho guanine nucleotide exchange factor 9; PDBTitle: solution structure of the sh3 domain from rho guanine2 nucleotide exchange factor 9 |
| 50 | c2djqa | Alignment | not modelled | 99.7 | 26 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sh3 domain containing ring finger 2; PDBTitle: the solution structure of the first sh3 domain of mouse sh32 domain containing ring finger 2 |
| 51 | c2epdA | Alignment | not modelled | 99.7 | 29 | PDB header: protein binding Chain: A: PDB Molecule: rho gtpase-activating protein 4; PDBTitle: solution structure of sh3 domain in rho-gtpase-activating2 protein 4 |
| 52 | d1oeba | Alignment | not modelled | 99.7 | 39 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 53 | c2csqA | Alignment | not modelled | 99.7 | 25 | PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: rim binding protein 2; PDBTitle: solution structure of the second sh3 domain of human rim-2 binding protein 2 |
| 54 | d1e6ga | Alignment | not modelled | 99.7 | 22 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 55 | c1w70A | Alignment | not modelled | 99.7 | 31 | PDB header: sh3 domain Chain: A: PDB Molecule: neutrophil cytosol factor 4; PDBTitle: sh3 domain of p40phox complexed with c-terminal |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | polyproline2 region of p47phox |
| 56 | c2azsA | Alignment | not modelled | 99.7 | 59 | PDB header: signaling protein Chain: A: PDB Molecule: sh2-sh3 adapter protein drk; PDBTitle: nmr structure of the n-terminal sh3 domain of drk2 (calculated without noe restraints) |
| 57 | c2dl4A | Alignment | not modelled | 99.7 | 33 | PDB header: signaling protein Chain: A: PDB Molecule: protein stac; PDBTitle: solution structure of the first sh3 domain of stac protein |
| 58 | d1udla | Alignment | not modelled | 99.7 | 26 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 59 | c2d1xD | Alignment | not modelled | 99.7 | 36 | PDB header: cell invasion Chain: D: PDB Molecule: cortactin isoform a; PDBTitle: the crystal structure of the cortactin-sh3 domain and amap1-2 peptide complex |
| 60 | c4iqzA | Alignment | not modelled | 99.7 | 40 | PDB header: protein binding Chain: A: PDB Molecule: sorbin and sh3 domain-containing protein 2; PDBTitle: crystal structure of the sh3 domain of human sorbin and sh3 domain-2 containing protein 2 |
| 61 | c2dlpA | Alignment | not modelled | 99.7 | 33 | PDB header: structural protein Chain: A: PDB Molecule: kiaa1783 protein; PDBTitle: solution structure of the sh3 domain of human kiaa17832 protein |
| 62 | c2bz8B | Alignment | not modelled | 99.7 | 35 | PDB header: sh3 domain Chain: B: PDB Molecule: sh3-domain kinase binding protein 1; PDBTitle: n-terminal sh3 domain of cin85 bound to cbl-b peptide |
| 63 | c2yt6A | Alignment | not modelled | 99.7 | 23 | PDB header: cell cycle Chain: A: PDB Molecule: adult male urinary bladder cdna, riken full- PDBTitle: solution structure of the sh3_1 domain of yamaguchi sarcoma2 viral (v-yes) oncogene homolog 1 |
| 64 | d1k4us | Alignment | not modelled | 99.7 | 26 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 65 | d1u06a1 | Alignment | not modelled | 99.7 | 25 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 66 | c2cudA | Alignment | not modelled | 99.7 | 23 | PDB header: signaling protein Chain: A: PDB Molecule: src-like-adapter; PDBTitle: solution structure of the sh3 domain of the human src-like2 adopter protein (slap) |
| 67 | c1x69A | Alignment | not modelled | 99.7 | 28 | PDB header: signaling protein Chain: A: PDB Molecule: cortactin isoform a; PDBTitle: solution structures of the sh3 domain of human src2 substrate cortactin |
| 68 | c2pqhA | Alignment | not modelled | 99.7 | 25 | PDB header: structural protein Chain: A: PDB Molecule: spectrin alpha chain, brain; PDBTitle: structure of sh3 chimera with a type ii ligand linked to the chain c-2 terminal |
| 69 | c2ebpA | Alignment | not modelled | 99.7 | 25 | PDB header: cell adhesion Chain: A: PDB Molecule: sam and sh3 domain-containing protein 1; PDBTitle: solution structure of the sh3 domain from human sam and sh32 domain containing protein 1 |
| 70 | c2yupA | Alignment | not modelled | 99.7 | 29 | PDB header: cell adhesion Chain: A: PDB Molecule: vinexin; PDBTitle: solution structure of the second sh3 domain of human vinexin |
| 71 | c2oi3A | Alignment | not modelled | 99.7 | 23 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase hck; PDBTitle: nmr structure analysis of the hematopoietic cell kinase sh32 domain complexed with an artificial high affinity ligand3 (pd1) |
| 72 | c2dl3A | Alignment | not modelled | 99.7 | 39 | PDB header: cell adhesion, signaling protein Chain: A: PDB Molecule: sorbin and sh3 domain-containing protein 1; PDBTitle: solution structure of the first sh3 domain of human sorbin2 and sh3 domain-containing protein 1 |
| 73 | c2eyxA | Alignment | not modelled | 99.7 | 25 | PDB header: signaling protein Chain: A: PDB Molecule: v-crk sarcoma virus ct10 oncogene homolog PDBTitle: c-terminal sh3 domain of ct10-regulated kinase |
| 74 | c2fpeB | Alignment | not modelled | 99.7 | 24 | PDB header: signaling protein Chain: B: PDB Molecule: c-jun-amino-terminal kinase interacting protein PDBTitle: conserved dimerization of the ib1 src-homology 3 domain |
| 75 | c2l0aA | Alignment | not modelled | 99.7 | 29 | PDB header: signaling protein Chain: A: PDB Molecule: signal transducing adapter molecule 1; PDBTitle: solution nmr structure of signal transducing adapter molecule 1 stam-12 from homo sapiens, northeast structural genomics consortium target3 hr4479e |
| 76 | c1zukA | Alignment | not modelled | 99.7 | 26 | PDB header: contractile protein Chain: A: PDB Molecule: myosin tail region-interacting protein mt1; PDBTitle: yeast bbc1 sh3 domain complexed with a peptide from las17 |
| 77 | c2j6kE | Alignment | not modelled | 99.7 | 23 | PDB header: protein binding Chain: E: PDB Molecule: cd2-associated protein; PDBTitle: n-terminal sh3 domain of cms (cd2ap human homolog) |
| 78 | c2rqrA | Alignment | not modelled | 99.7 | 18 | PDB header: protein binding Chain: A: PDB Molecule: engulfment and cell motility protein 1, linker, dedicator PDBTitle: the solution structure of human dock2 sh3 domain - elmo1 peptide2 chimera complex |
| 79 | d1uj0a | Alignment | not modelled | 99.7 | 29 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 80 | c2ekhA | Alignment | not modelled | 99.7 | 24 | PDB header: signaling protein Chain: A: PDB Molecule: sh3 and px domain-containing protein 2a; PDBTitle: solution structures of the sh3 domain of human kiaa0418 |

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|-----|------------------------|-----------|--------------|------|----|--|
| 81 | c1negA | Alignment | not modelled | 99.7 | 25 | PDB header: structural protein Chain: A: PDB Molecule: spectrin alpha chain, brain; PDBTitle: crystal structure analysis of sh3-2 domain of alpha-chicken spectrin |
| 82 | d1nega | Alignment | not modelled | 99.7 | 25 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 83 | d1e6ha | Alignment | not modelled | 99.7 | 20 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 84 | d1oota | Alignment | not modelled | 99.7 | 36 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 85 | c1x43A | Alignment | not modelled | 99.7 | 22 | PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: sh3 domain grb2-like protein b1; PDBTitle: solution structure of the sh3 domain of endophilin b12 (sh3g1b1) |
| 86 | c2dl8A | Alignment | not modelled | 99.7 | 25 | PDB header: signaling protein Chain: A: PDB Molecule: slit-robo rho gtpase-activating protein 2; PDBTitle: solution structure of the sh3 domain of human slit-robo rho2 gtpase-activating protein 2 |
| 87 | c1zlmA | Alignment | not modelled | 99.7 | 30 | PDB header: signaling protein Chain: A: PDB Molecule: osteoclast stimulating factor 1; PDBTitle: crystal structure of the sh3 domain of human osteoclast2 stimulating factor |
| 88 | c2i0nA | Alignment | not modelled | 99.7 | 29 | PDB header: structural protein Chain: A: PDB Molecule: class vii unconventional myosin; PDBTitle: structure of dictyostelium discoideum myosin vii sh3 domain2 with adjacent proline rich region |
| 89 | c4esrB | Alignment | not modelled | 99.7 | 31 | PDB header: protein binding Chain: B: PDB Molecule: jouberin; PDBTitle: molecular and structural characterization of the sh3 domain of ahi-12 in regulation of cellular resistance of bcr-abl+ chronic myeloid3 leukemia cells to tyrosine kinase inhibitors |
| 90 | d1h8ka | Alignment | not modelled | 99.7 | 21 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 91 | c1wi7A | Alignment | not modelled | 99.7 | 31 | PDB header: protein binding Chain: A: PDB Molecule: sh3-domain kinase binding protein 1; PDBTitle: solution structure of the sh3 domain of sh3-domain kinase2 binding protein 1 |
| 92 | c2dilA | Alignment | not modelled | 99.7 | 35 | PDB header: cell adhesion Chain: A: PDB Molecule: proline-serine-threonine phosphatase-interacting PDBTitle: solution structure of the sh3 domain of the human proline-2 serine-threonine phosphatase-interacting protein 1 |
| 93 | c1x6bA | Alignment | not modelled | 99.7 | 23 | PDB header: signaling protein Chain: A: PDB Molecule: rho guanine exchange factor (gef) 16; PDBTitle: solution structures of the sh3 domain of human rho guanine2 exchange factor (gef) 16 |
| 94 | c1x6gA | Alignment | not modelled | 99.7 | 18 | PDB header: signaling protein Chain: A: PDB Molecule: megakaryocyte-associated tyrosine-protein kinase; PDBTitle: solution structures of the sh3 domain of human2 megakaryocyte-associated tyrosine-protein kinase. |
| 95 | c2dbmA | Alignment | not modelled | 99.7 | 31 | PDB header: transferase, signaling protein Chain: A: PDB Molecule: sh3-containing grb2-like protein 2; PDBTitle: solution structures of the sh3 domain of human sh3-2 containing grb2-like protein 2 |
| 96 | c2ed1A | Alignment | not modelled | 99.7 | 26 | PDB header: signaling protein Chain: A: PDB Molecule: 130 kda phosphatidylinositol 4,5-biphosphate- PDBTitle: solution structure of the sh3 domain of 130 kda2 phosphatidylinositol 4,5-biphosphate-dependent arf1 gtpase-3 activating protein |
| 97 | c2ct3A | Alignment | not modelled | 99.7 | 33 | PDB header: signaling protein Chain: A: PDB Molecule: vinexin; PDBTitle: solution structure of the sh3 domain of the vinexin protein |
| 98 | c2dnuA | Alignment | not modelled | 99.7 | 23 | PDB header: structural genomics, structural protein Chain: A: PDB Molecule: sh3 multiple domains 1; PDBTitle: solution structure of rsgi ruh-061, a sh3 domain from human |
| 99 | d1ue9a | Alignment | not modelled | 99.7 | 30 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 100 | c2jxbA | Alignment | not modelled | 99.7 | 14 | PDB header: signaling protein complex Chain: A: PDB Molecule: t-cell surface glycoprotein cd3 epsilon chain, PDBTitle: structure of cd3epsilon-nck2 first sh3 domain complex |
| 101 | d1ujya | Alignment | not modelled | 99.7 | 32 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 102 | c1wyxA | Alignment | not modelled | 99.7 | 33 | PDB header: cell adhesion Chain: A: PDB Molecule: crk-associated substrate; PDBTitle: the crystal structure of the p130cas sh3 domain at 1.1 a2 resolution |
| 103 | c2krnA | Alignment | not modelled | 99.7 | 33 | PDB header: signaling protein Chain: A: PDB Molecule: cd2-associated protein; PDBTitle: high resolution structure of the second sh3 domain of cd2ap |
| 104 | d1jo8a | Alignment | not modelled | 99.7 | 30 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 105 | c1bb9A | Alignment | not modelled | 99.7 | 31 | PDB header: transferase Chain: A: PDB Molecule: amphiphysin 2; PDBTitle: crystal structure of the sh3 domain from rat amphiphysin 2 |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 106 | d1bb9a_ | Alignment | not modelled | 99.7 | 31 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 107 | c1x2pA_ | Alignment | not modelled | 99.7 | 28 | PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 2; PDBTitle: solution structure of the sh3 domain of the protein2 arginine n-methyltransferase 2 |
| 108 | d1gbra_ | Alignment | not modelled | 99.7 | 60 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 109 | c2dl7A_ | Alignment | not modelled | 99.7 | 32 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: kiaa0769 protein; PDBTitle: solution structure of the second sh3 domain of human2 kiaa0769 protein |
| 110 | c2e5kA_ | Alignment | not modelled | 99.7 | 20 | PDB header: protein binding Chain: A: PDB Molecule: suppressor of t-cell receptor signaling 1; PDBTitle: solution structure of sh3 domain in suppressor of t-cell2 receptor signaling 1 |
| 111 | d1ov3a1 | Alignment | not modelled | 99.7 | 27 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 112 | c2js0A_ | Alignment | not modelled | 99.7 | 36 | PDB header: signaling protein Chain: A: PDB Molecule: cytoplasmic protein nck1; PDBTitle: solution structure of second sh3 domain of adaptor nck |
| 113 | d2v1ra1 | Alignment | not modelled | 99.7 | 34 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 114 | d1uhfa_ | Alignment | not modelled | 99.7 | 31 | Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain |
| 115 | c2j06B_ | Alignment | not modelled | 99.7 | 16 | PDB header: signal transduction Chain: B: PDB Molecule: ras gtpase-activating protein 1; PDBTitle: crystal structure of the rasgap sh3 domain at 1.8 angstrom2 resolution |
| 116 | c2egaA_ | Alignment | not modelled | 99.7 | 24 | PDB header: signaling protein Chain: A: PDB Molecule: sh3 and px domain-containing protein 2a; PDBTitle: solution structure of the first sh3 domain from human2 kiaa0418 protein |
| 117 | c2kbtA_ | Alignment | not modelled | 99.7 | 42 | PDB header: signaling protein Chain: A: PDB Molecule: chimera of proto-oncogene vav, linker, PDBTitle: attachment of an nmr-invisible solubility enhancement tag2 (inset) using a sortase-mediated protein ligation method |
| 118 | c3rnjA_ | Alignment | not modelled | 99.7 | 24 | PDB header: protein binding Chain: A: PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: crystal structure of the sh3 domain from irsp53 (baiap2) |
| 119 | c2rf0D_ | Alignment | not modelled | 99.7 | 44 | PDB header: transferase Chain: D: PDB Molecule: mitogen-activated protein kinase kinase kinase 10; PDBTitle: crystal structure of human mixed lineage kinase map3k10 sh3 domain |
| 120 | c3cqtA_ | Alignment | not modelled | 99.7 | 28 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase fyn; PDBTitle: n53i v55l mutant of fyn sh3 domain |