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| Email | I.a.kelley@imperial.ac.uk |
| Description | Q96IW2 |
| Date | Sat Jun 16 10:30:30 BST 2012 |
| Unique Job ID | 9730485162c2534d |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c2eo6A_ |  Alignment |  | 100.0 | 23 | PDB header: signaling protein Chain: A: PDB Molecule: b-cell linker protein; PDBTitle: solution structure of the sh2 domain from mouse b-cell2 linker protein blnk |
| 2 | c2y3aB_ |  Alignment |  | 99.9 | 28 | PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit beta; PDBTitle: crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941 |
| 3 | d1pica_ |  Alignment |  | 99.9 | 28 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 4 | c2crhA_ |  Alignment |  | 99.9 | 23 | PDB header: signaling protein Chain: A: PDB Molecule: vav proto-oncogene; PDBTitle: solution structure of the sh2 domain of human proto-2 oncogene protein vav1 |
| 5 | d3c7ia1 |  Alignment |  | 99.9 | 31 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 6 | c2lqnA_ |  Alignment |  | 99.9 | 24 | PDB header: signaling protein Chain: A: PDB Molecule: crk-like protein; PDBTitle: solution structure of crkl |
| 7 | c3hizB_ |  Alignment |  | 99.9 | 29 | PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit PDBTitle: crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha |
| 8 | c2eo3A_ |  Alignment |  | 99.9 | 24 | PDB header: signaling protein Chain: A: PDB Molecule: crk-like protein; PDBTitle: solution structure of the sh2 domain from human crk-like2 protein |
| 9 | c2c9wA_ |  Alignment |  | 99.9 | 26 | PDB header: transcription regulation Chain: A: PDB Molecule: suppressor of cytokine signaling 2; PDBTitle: crystal structure of socs-2 in complex with elongin-b and2 elongin-c at 1.9a resolution |
| 10 | d2oq1a1 |  Alignment |  | 99.9 | 27 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 11 | c2gsbA_ |  Alignment |  | 99.9 | 29 | PDB header: signaling protein Chain: A: PDB Molecule: ras gtpase-activating protein 1; PDBTitle: solution structure of the second sh2 domain of human ras2 gtpase-activating protein 1 |

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|----|-------------------------|-----------|---|------|----|---|
| 12 | c2dlzA_ | Alignment |  | 99.9 | 25 | PDB header: signaling protein Chain: A: PDB Molecule: protein vav-2; PDBTitle: solution structure of the sh2 domain of human protein vav-2 |
| 13 | d1fhsa_ | Alignment |  | 99.9 | 30 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 14 | c2fo0A_ | Alignment |  | 99.9 | 33 | 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 |
| 15 | c2oq1A_ | Alignment |  | 99.9 | 27 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase zap-70; PDBTitle: tandem sh2 domains of zap-70 with 19-mer zeta1 peptide |
| 16 | c2dlyA_ | Alignment |  | 99.9 | 29 | PDB header: transferase Chain: A: PDB Molecule: fyn-related kinase; PDBTitle: solution structure of the sh2 domain of murine fyn-related2 kinase |
| 17 | c2vifA_ | Alignment |  | 99.9 | 30 | PDB header: signaling protein Chain: A: PDB Molecule: suppressor of cytokine signalling 6; PDBTitle: crystal structure of socs3 sh2 domain in complex with a c-kit2 phosphopeptide |
| 18 | d2shpa2 | Alignment |  | 99.9 | 30 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 19 | c2ablA_ | Alignment |  | 99.9 | 35 | PDB header: transferase Chain: A: PDB Molecule: abl tyrosine kinase; PDBTitle: sh3-sh2 domain fragment of human bcr-abl tyrosine kinase |
| 20 | c2kk6A_ | Alignment |  | 99.9 | 29 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase fer; PDBTitle: solution structure of sh2 domain of proto-oncogene tyrosine-2 protein kinase fer from homo sapiens, northeast structural3 genomics consortium (nesg) target hr3461d |
| 21 | c1ka6A_ | Alignment | not modelled | 99.9 | 24 | PDB header: immune system Chain: A: PDB Molecule: sh2 domain protein 1a; PDBTitle: sap/sh2d1a bound to peptide n-py |
| 22 | c2hmbA_ | Alignment | not modelled | 99.9 | 22 | PDB header: cytokine regulator Chain: A: PDB Molecule: suppressor of cytokine signaling 3; PDBTitle: crystal structure of socs3 in complex with gp130(pyr757)2 phosphopeptide. |
| 23 | c1x6cA_ | Alignment | not modelled | 99.9 | 28 | PDB header: signaling protein Chain: A: PDB Molecule: tyrosine-protein phosphatase, non-receptor type PDBTitle: solution structures of the sh2 domain of human protein-2 tyrosine phosphatase shp-1 |
| 24 | c2shpA_ | Alignment | not modelled | 99.9 | 31 | PDB header: tyrosine phosphatase Chain: A: PDB Molecule: shp-2; PDBTitle: tyrosine phosphatase shp-2 |
| 25 | c2lctA_ | Alignment | not modelled | 99.9 | 25 | PDB header: signaling protein Chain: A: PDB Molecule: proto-oncogene vav; PDBTitle: solution structure of the vav1 sh2 domain complexed with a syk-derived2 doubly phosphorylated peptide |
| 26 | d1qada_ | Alignment | not modelled | 99.9 | 29 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 27 | c2eobA_ | Alignment | not modelled | 99.9 | 29 | PDB header: hydrolase Chain: A: PDB Molecule: 1-phosphatidylinositol-4,5-bisphosphate PDBTitle: solution structure of the second sh2 domain from rat plc2 gamma-2 |
| 28 | c2dcrA_ | Alignment | not modelled | 99.9 | 29 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase fes/fps; PDBTitle: fully automated solution structure determination of the |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | fes2 sh2 domain |
| 29 | d1ayaa_ | Alignment | not modelled | 99.9 | 31 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 30 | d1a81e1 | Alignment | not modelled | 99.9 | 21 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 31 | d1blja_ | Alignment | not modelled | 99.9 | 34 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 32 | c2b3oA_ | Alignment | not modelled | 99.9 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase, non-receptor type PDBTitle: crystal structure of human tyrosine phosphatase shp-1 |
| 33 | d2izva2 | Alignment | not modelled | 99.9 | 25 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 34 | d1opka2 | Alignment | not modelled | 99.9 | 35 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 35 | c2izvA_ | Alignment | not modelled | 99.9 | 25 | PDB header: transcription Chain: A: PDB Molecule: suppressor of cytokine signaling 4; PDBTitle: crystal structure of socs-4 in complex with elongin-b and2 elongin-c at 2.55a resolution |
| 36 | d1a81e2 | Alignment | not modelled | 99.9 | 26 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 37 | d1r1qa_ | Alignment | not modelled | 99.9 | 31 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 38 | d1rjaa_ | Alignment | not modelled | 99.9 | 33 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 39 | d1k9aa2 | Alignment | not modelled | 99.9 | 28 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 40 | d1d4ta_ | Alignment | not modelled | 99.9 | 24 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 41 | d1mila_ | Alignment | not modelled | 99.9 | 35 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 42 | c2ci8A_ | Alignment | not modelled | 99.9 | 34 | PDB header: translation Chain: A: PDB Molecule: cytoplasmic protein nck1; PDBTitle: sh2 domain of human nck1 adaptor protein - uncomplexed |
| 43 | c2ysxA_ | Alignment | not modelled | 99.9 | 27 | PDB header: signaling protein Chain: A: PDB Molecule: signaling inositol polyphosphate phosphatase PDBTitle: solution structure of the human ship sh2 domain |
| 44 | d1a81a1 | Alignment | not modelled | 99.9 | 21 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 45 | c1oplA_ | Alignment | not modelled | 99.9 | 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 |
| 46 | d2shpa3 | Alignment | not modelled | 99.9 | 38 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 47 | d1lkka_ | Alignment | not modelled | 99.9 | 35 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 48 | c3gqiB_ | Alignment | not modelled | 99.9 | 31 | PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: phospholipase c-gamma-1; PDBTitle: crystal structure of activated receptor tyrosine kinase in complex2 with substrates |
| 49 | d1g83a2 | Alignment | not modelled | 99.9 | 30 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 50 | d2oq1a2 | Alignment | not modelled | 99.9 | 21 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 51 | d2cs0a1 | Alignment | not modelled | 99.9 | 25 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 52 | d1fu6a_ | Alignment | not modelled | 99.9 | 28 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 53 | d1jwoa_ | Alignment | not modelled | 99.9 | 26 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 54 | d1a81a2 | Alignment | not modelled | 99.9 | 26 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 55 | d2eyva1 | Alignment | not modelled | 99.9 | 32 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |

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| 56 | d1csya_ | Alignment | not modelled | 99.9 | 25 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 57 | c2ozoA_ | Alignment | not modelled | 99.9 | 26 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase zap-70; PDBTitle: autoinhibited intact human zap-70 |
| 58 | c2knoA_ | Alignment | not modelled | 99.9 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: tensin-like c1 domain-containing phosphatase; PDBTitle: nmr solution structure of sh2 domain of the human tensin like c12 domain containing phosphatase (tenc1) |
| 59 | d1luia_ | Alignment | not modelled | 99.9 | 28 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 60 | d1jyra_ | Alignment | not modelled | 99.9 | 32 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 61 | c3ps5A_ | Alignment | not modelled | 99.9 | 22 | PDB header: hydrolase, signaling protein Chain: A: PDB Molecule: tyrosine-protein phosphatase non-receptor type 6; PDBTitle: crystal structure of the full-length human protein tyrosine2 phosphatase shp-1 |
| 62 | d1nrva_ | Alignment | not modelled | 99.9 | 22 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 63 | c2ge9A_ | Alignment | not modelled | 99.9 | 26 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase btk; PDBTitle: solution structures of the sh2 domain of bruton's tyrosine2 kinase |
| 64 | d1i3za_ | Alignment | not modelled | 99.9 | 25 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 65 | d2c9wa2 | Alignment | not modelled | 99.9 | 22 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 66 | c3nhnA_ | Alignment | not modelled | 99.9 | 30 | 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 |
| 67 | c1y57A_ | Alignment | not modelled | 99.9 | 26 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase src; PDBTitle: structure of unphosphorylated c-src in complex with an inhibitor |
| 68 | d1o48a_ | Alignment | not modelled | 99.9 | 25 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 69 | c2ekxA_ | Alignment | not modelled | 99.9 | 29 | PDB header: signaling protein Chain: A: PDB Molecule: cytoplasmic tyrosine-protein kinase bmx; PDBTitle: solution structure of the human bmx sh2 domain |
| 70 | d1qcfa2 | Alignment | not modelled | 99.9 | 31 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 71 | c1x27F_ | Alignment | not modelled | 99.9 | 34 | 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 of2 p130cas |
| 72 | d1xa6a2 | Alignment | not modelled | 99.9 | 25 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 73 | d2qmsa1 | Alignment | not modelled | 99.9 | 26 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 74 | c1k9aB_ | Alignment | not modelled | 99.9 | 28 | 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 |
| 75 | d1f2fa_ | Alignment | not modelled | 99.9 | 26 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 76 | d1bkla_ | Alignment | not modelled | 99.9 | 27 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 77 | c2c0iA_ | Alignment | not modelled | 99.9 | 31 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase hck; PDBTitle: src family kinase hck with bound inhibitor a-420983 |
| 78 | d2fcia1 | Alignment | not modelled | 99.9 | 29 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 79 | c3mazA_ | Alignment | not modelled | 99.9 | 15 | PDB header: signaling protein Chain: A: PDB Molecule: signal-transducing adaptor protein 1; PDBTitle: crystal structure of the human brdg1/stap-1 sh2 domain in complex with2 the ntal tyr136 peptide |
| 80 | c1a81E_ | Alignment | not modelled | 99.9 | 20 | PDB header: complex (transferase/peptide) Chain: E: PDB Molecule: syk kinase; PDBTitle: crystal structure of the tandem sh2 domain of the syk kinase bound to2 a dually tyrosine-phosphorylated itam |
| 81 | c2el8A_ | Alignment | not modelled | 99.9 | 22 | PDB header: signaling protein Chain: A: PDB Molecule: signal-transducing adaptor protein 2; PDBTitle: solution structure of the human stap2 sh2 domain |

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| 82 | c1g83A | Alignment | not modelled | 99.9 | 31 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase fyn; PDBTitle: crystal structure of fyn sh3-sh2 |
| 83 | c2h8hA | Alignment | not modelled | 99.9 | 27 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase src; PDBTitle: src kinase in complex with a quinazoline inhibitor |
| 84 | c2dm0A | Alignment | not modelled | 99.9 | 24 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase btk; PDBTitle: solution structure of the sh2 domain of human tyrosine-2 protein kinase btk |
| 85 | d1rpya | Alignment | not modelled | 99.9 | 33 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 86 | c1rqgC | Alignment | not modelled | 99.9 | 34 | PDB header: transferase/signaling protein Chain: C: PDB Molecule: adaptor protein aps; PDBTitle: crystal structure of the insulin receptor kinase in complex2 with the sh2 domain of aps |
| 87 | d1cwea | Alignment | not modelled | 99.9 | 35 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 88 | c3gxxB | Alignment | not modelled | 99.8 | 15 | PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt6; PDBTitle: structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b |
| 89 | c2eyzA | Alignment | not modelled | 99.8 | 30 | PDB header: signaling protein Chain: A: PDB Molecule: v-crk sarcoma virus ct10 oncogene homolog PDBTitle: ct10-regulated kinase isoform ii |
| 90 | c2cr4A | Alignment | not modelled | 99.8 | 24 | PDB header: signaling protein Chain: A: PDB Molecule: sh3 domain-binding protein 2; PDBTitle: solution structure of the sh2 domain of human sh3bp2 protein |
| 91 | c2dviA | Alignment | not modelled | 99.8 | 31 | PDB header: signaling protein Chain: A: PDB Molecule: v-crk sarcoma virus ct10 oncogene homolog, PDBTitle: phosphorylated crk-ii |
| 92 | c2eyyA | Alignment | not modelled | 99.8 | 30 | PDB header: signaling protein Chain: A: PDB Molecule: v-crk sarcoma virus ct10 oncogene homolog PDBTitle: ct10-regulated kinase isoform i |
| 93 | c3qwxX | Alignment | not modelled | 99.8 | 29 | PDB header: signaling protein Chain: X: PDB Molecule: cell death abnormality protein 2; PDBTitle: ced-2 1-174 |
| 94 | c3qwyA | Alignment | not modelled | 99.8 | 26 | PDB header: signaling protein Chain: A: PDB Molecule: cell death abnormality protein 2; PDBTitle: ced-2 |
| 95 | c2dx0B | Alignment | not modelled | 99.8 | 37 | PDB header: hydrolase Chain: B: PDB Molecule: phospholipase c, gamma 2; PDBTitle: crystal structure of the n-terminal sh2 domain of mouse2 phospholipase c-gamma 2 |
| 96 | c3or8A | Alignment | not modelled | 99.7 | 16 | PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: a tandem sh2 domain in transcription elongation factor spt6 |
| 97 | c2xp1A | Alignment | not modelled | 99.6 | 17 | PDB header: transcription Chain: A: PDB Molecule: spt6; PDBTitle: structure of the tandem sh2 domains from antonospora locustae2 transcription elongation factor spt6 |
| 98 | c1xa6A | Alignment | not modelled | 99.6 | 27 | PDB header: signaling protein Chain: A: PDB Molecule: beta2-chimaerin; PDBTitle: crystal structure of the human beta2-chimaerin |
| 99 | d1uura3 | Alignment | not modelled | 99.6 | 13 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 100 | d1bf5a3 | Alignment | not modelled | 99.5 | 17 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 101 | d1bg1a3 | Alignment | not modelled | 99.4 | 19 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 102 | c3cblA | Alignment | not modelled | 99.2 | 36 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase fes/fps; PDBTitle: crystal structure of human feline sarcoma viral oncogene homologue (v-2 fes) in complex with staurosporine and a consensus peptide |
| 103 | c1yvlB | Alignment | not modelled | 98.5 | 18 | PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1 |
| 104 | c1uusA | Alignment | not modelled | 98.4 | 20 | PDB header: signal transduction Chain: A: PDB Molecule: stat protein; PDBTitle: structure of an activated dictyostelium stat in its2 dna-unbound form |
| 105 | c1bf5A | Alignment | not modelled | 98.3 | 18 | PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: tyrosine phosphorylated stat-1/dna complex |
| 106 | c2cblA | Alignment | not modelled | 98.2 | 26 | PDB header: complex (proto-oncogene/peptide) Chain: A: PDB Molecule: proto-oncogene cbl; PDBTitle: n-terminal domain of cbl in complex with its binding site2 on zap-70 |
| 107 | c3bunB | Alignment | not modelled | 98.2 | 26 | PDB header: ligase/signaling protein Chain: B: PDB Molecule: e3 ubiquitin-protein ligase cbl; PDBTitle: crystal structure of c-cbl-tkb domain complexed with its2 |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | binding motif in sprouty4 |
| 108 | c1y1uA | Alignment | not modelled | 98.2 | 22 | PDB header: signaling protein Chain: A: PDB Molecule: signal transducer and activator of transcription 5a; PDBTitle: structure of unphosphorylated stat5a |
| 109 | c1bg1A | Alignment | not modelled | 98.1 | 18 | PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex |
| 110 | c3cwqA | Alignment | not modelled | 96.7 | 20 | PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment |
| 111 | c1fbvA | Alignment | not modelled | 93.4 | 26 | PDB header: ligase Chain: A: PDB Molecule: signal transduction protein cbl; PDBTitle: structure of a cbl-ubch7 complex: ring domain function in2 ubiquitin-protein ligases |
| 112 | c1griA | Alignment | not modelled | 93.4 | 36 | PDB header: signal transduction adaptor Chain: A: PDB Molecule: growth factor bound protein 2; PDBTitle: grb2 |
| 113 | d3buxb3 | Alignment | not modelled | 90.5 | 26 | Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain |
| 114 | c3op0B | Alignment | not modelled | 85.9 | 28 | PDB header: signaling protein/signaling protein regu Chain: B: PDB Molecule: signal transduction protein cbl-c; PDBTitle: crystal structure of cbl-c (cbl-3) tkb domain in complex with egfr2 py1069 peptide |
| 115 | c2yt6A | Alignment | not modelled | 68.7 | 37 | 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 |
| 116 | d2d7na1 | Alignment | not modelled | 63.2 | 17 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain) |
| 117 | d2e9ia1 | Alignment | not modelled | 62.3 | 14 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain) |
| 118 | d1wlha1 | Alignment | not modelled | 62.1 | 17 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain) |
| 119 | d1qfha1 | Alignment | not modelled | 58.9 | 10 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain) |
| 120 | d2di9a1 | Alignment | not modelled | 58.3 | 17 | Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain) |