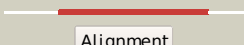

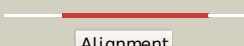

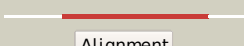

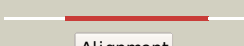


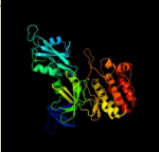







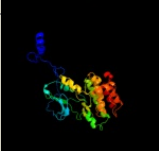






Phyre2

| | |
|---------------|-----------------------------|
| Email | l.a.kelley@imperial.ac.uk |
| Description | Q08881 |
| Date | Tue Apr 3 14:36:05 BST 2012 |
| Unique Job ID | cdf2a639be697450 |


Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c2fo0A_ |  Alignment |  | 100.0 | 36 | 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 |
| 2 | c1y57A_ |  Alignment |  | 100.0 | 38 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase src; PDBTitle: structure of unphosphorylated c-src in complex with an inhibitor |
| 3 | c1oplA_ |  Alignment |  | 100.0 | 36 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase; PDBTitle: structural basis for the auto-inhibition of c-abl tyrosine2 kinase |
| 4 | c2h8hA_ |  Alignment |  | 100.0 | 38 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase src; PDBTitle: src kinase in complex with a quinazoline inhibitor |
| 5 | c1k9aB_ |  Alignment |  | 100.0 | 37 | 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 |
| 6 | c2c0iA_ |  Alignment |  | 100.0 | 37 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase hck; PDBTitle: src family kinase hck with bound inhibitor a-420983 |
| 7 | c2ozoA_ |  Alignment |  | 100.0 | 32 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase zap-70; PDBTitle: autoinhibited intact human zap-70 |
| 8 | c3cblA_ |  Alignment |  | 100.0 | 41 | 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 |
| 9 | c2j0kB_ |  Alignment |  | 100.0 | 33 | PDB header: transferase Chain: B: PDB Molecule: focal adhesion kinase 1; PDBTitle: crystal structure of a fragment of focal adhesion kinase2 containing the ferm and kinase domains. |
| 10 | d1qcfa3 |  Alignment |  | 100.0 | 39 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 11 | d1lopja |  Alignment |  | 100.0 | 41 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |

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|----|-------------------------|-----------|--------------|-------|-----|---|
| 12 | d1qpca_ | Alignment | | 100.0 | 40 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 13 | c3zzwA_ | Alignment | | 100.0 | 36 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase transmembrane receptor ror2; PDBTitle: crystal structure of the kinase domain of ror2 |
| 14 | d1k2pa_ | Alignment | | 100.0 | 59 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 15 | d1u59a_ | Alignment | | 100.0 | 36 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 16 | c2ivsA_ | Alignment | | 100.0 | 35 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase receptor PDBTitle: crystal structure of non-phosphorylated ret tyrosine kinase2 domain |
| 17 | c3g0eA_ | Alignment | | 100.0 | 34 | PDB header: transferase Chain: A: PDB Molecule: mast/stem cell growth factor receptor; PDBTitle: kit kinase domain in complex with sunitinib |
| 18 | c3pfgA_ | Alignment | | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: protein kinase c beta type; PDBTitle: crystal structure and allosteric activation of protein kinase c beta2 ii |
| 19 | c2acxB_ | Alignment | | 100.0 | 22 | PDB header: transferase Chain: B: PDB Molecule: g protein-coupled receptor kinase 6; PDBTitle: crystal structure of g protein coupled receptor kinase 6 bound to2 amppnp |
| 20 | c1lufA_ | Alignment | | 100.0 | 38 | PDB header: transferase Chain: A: PDB Molecule: muscle-specific tyrosine kinase receptor musk; PDBTitle: crystal structure of the musk tyrosine kinase: insights2 into receptor autoregulation |
| 21 | d1lufa_ | Alignment | not modelled | 100.0 | 38 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 22 | d1sm2a_ | Alignment | not modelled | 100.0 | 100 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 23 | c2pvfA_ | Alignment | not modelled | 100.0 | 35 | PDB header: transferase Chain: A: PDB Molecule: fibroblast growth factor receptor 2; PDBTitle: crystal structure of tyrosine phosphorylated activated fgf receptor 22 (fgfr2) kinase domain in complex with atp analog and substrate3 peptide |
| 24 | c2vwiC_ | Alignment | not modelled | 100.0 | 28 | PDB header: transferase Chain: C: PDB Molecule: serine/threonine-protein kinase osr1; PDBTitle: structure of the osr1 kinase, a hypertension drug target |
| 25 | c3ckxA_ | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase 24; PDBTitle: crystal structure of sterile 20-like kinase 3 (mst3, stk24)2 in complex with staurosporine |
| 26 | c3dpkA_ | Alignment | not modelled | 100.0 | 34 | PDB header: transferase Chain: A: PDB Molecule: macrophage colony-stimulating factor 1 receptor; PDBTitle: cfms tyrosine kinase in complex with a pyridopyrimidinone2 inhibitor |
| 27 | d1fmka3 | Alignment | not modelled | 100.0 | 42 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 28 | c1ym7C_ | Alignment | not modelled | 100.0 | 17 | PDB header: transferase Chain: C: PDB Molecule: beta-adrenergic receptor kinase 1; PDBTitle: g protein-coupled receptor kinase 2 (grk2) |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 29 | c2psqA | Alignment | not modelled | 100.0 | 37 | PDB header: transferase Chain: A: PDB Molecule: fibroblast growth factor receptor 2; PDBTitle: crystal structure of unphosphorylated unactivated wild type2 fgf receptor 2 (fgfr2) kinase domain |
| 30 | d2psqa1 | Alignment | not modelled | 100.0 | 37 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 31 | c1koaA | Alignment | not modelled | 100.0 | 23 | PDB header: kinase Chain: A: PDB Molecule: twitchin; PDBTitle: twitchin kinase fragment (c.elegans), autoregulated protein2 kinase and immunoglobulin domains |
| 32 | d3bu3a1 | Alignment | not modelled | 100.0 | 36 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 33 | c3c4yA | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: A: PDB Molecule: rhodopsin kinase; PDBTitle: crystal structure of apo form of g protein coupled receptor kinase 12 at 7.51a |
| 34 | d2j4za1 | Alignment | not modelled | 100.0 | 26 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 35 | c3qa8A | Alignment | not modelled | 100.0 | 22 | PDB header: immune system, signaling protein Chain: A: PDB Molecule: imgc80376 protein; PDBTitle: crystal structure of inhibitor of kappa b kinase beta |
| 36 | c2c30A | Alignment | not modelled | 100.0 | 26 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase pak 6; PDBTitle: crystal structure of the human p21-activated kinase 6 |
| 37 | c3plsA | Alignment | not modelled | 100.0 | 34 | PDB header: transferase Chain: A: PDB Molecule: macrophage-stimulating protein receptor; PDBTitle: ron in complex with ligand amp-pnp |
| 38 | d1t46a | Alignment | not modelled | 100.0 | 34 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 39 | c3lxkA | Alignment | not modelled | 100.0 | 33 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase jak3; PDBTitle: structural and thermodynamic characterization of the tyk2 and jak32 kinase domains in complex with cp-690550 and cmp-6 |
| 40 | c3sxaA | Alignment | not modelled | 100.0 | 57 | PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: cytoplasmic tyrosine-protein kinase bmx; PDBTitle: crystal structure of bmx non-receptor tyrosine kinase complex with2 dasatinib |
| 41 | c3q5iA | Alignment | not modelled | 100.0 | 24 | PDB header: transferase Chain: A: PDB Molecule: protein kinase; PDBTitle: crystal structure of pbanka_031420 |
| 42 | d1p4oa | Alignment | not modelled | 100.0 | 35 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 43 | c3soaA | Alignment | not modelled | 100.0 | 21 | PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: calcium/calmodulin-dependent protein kinase type ii subunit PDBTitle: full-length human camkii |
| 44 | d1mp8a | Alignment | not modelled | 100.0 | 36 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 45 | d1jpaa | Alignment | not modelled | 100.0 | 39 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 46 | c3lvpD | Alignment | not modelled | 100.0 | 37 | PDB header: transferase Chain: D: PDB Molecule: insulin-like growth factor 1 receptor; PDBTitle: crystal structure of bisphosphorylated igf1-r kinase domain (2p) in2 complex with a bis-azaindole inhibitor |
| 47 | c3l9pA | Alignment | not modelled | 100.0 | 38 | PDB header: transferase Chain: A: PDB Molecule: anaplastic lymphoma kinase; PDBTitle: crystal structure of the anaplastic lymphoma kinase catalytic domain |
| 48 | d1fgka | Alignment | not modelled | 100.0 | 33 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 49 | c3eygA | Alignment | not modelled | 100.0 | 31 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase; PDBTitle: crystal structures of jak1 and jak2 inhibitor complexes |
| 50 | c1yvjA | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase jak3; PDBTitle: crystal structure of the jak3 kinase domain in complex with2 a staurosporine analogue |
| 51 | c2bujA | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase 16; PDBTitle: crystal structure of the human serine-threonine kinase 162 in complex with staurosporine |
| 52 | c3fupB | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: B: PDB Molecule: tyrosine-protein kinase jak2; PDBTitle: crystal structures of jak1 and jak2 inhibitor complexes |
| 53 | d1mqba | Alignment | not modelled | 100.0 | 41 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 54 | d1uwha | Alignment | not modelled | 100.0 | 29 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 55 | c2w1iB | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: B: PDB Molecule: jak2; PDBTitle: structure determination of aurora kinase in complex |

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|----|-------------------------|-----------|--------------|-------|----|--|
| | | | | | | with2 inhibitor |
| 56 | c3cc6A_ | Alignment | not modelled | 100.0 | 36 | PDB header: transferase Chain: A: PDB Molecule: protein tyrosine kinase 2 beta; PDBTitle: crystal structure of kinase domain of protein tyrosine kinase 2 beta2 (ptk2b) |
| 57 | c2a1aB_ | Alignment | not modelled | 100.0 | 23 | PDB header: protein synthesis/transferase Chain: B: PDB Molecule: interferon-induced, double-stranded rna-activated protein PDBTitle: pkr kinase domain-eif2alpha complex |
| 58 | d1yhwa1 | Alignment | not modelled | 100.0 | 26 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 59 | c2wtkC_ | Alignment | not modelled | 100.0 | 19 | PDB header: transferase/metal-binding protein Chain: C: PDB Molecule: serine/threonine-protein kinase 11; PDBTitle: structure of the heterotrimeric Ikb1-stradalpha-mo25alpha2 complex |
| 60 | d1xbba_ | Alignment | not modelled | 100.0 | 39 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 61 | c3d4qA_ | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: A: PDB Molecule: b-raf proto-oncogene serine/threonine-protein kinase; PDBTitle: pyrazole-based inhibitors of b-raf kinase |
| 62 | c3lijA_ | Alignment | not modelled | 100.0 | 25 | PDB header: transferase Chain: A: PDB Molecule: calcium/calmodulin dependent protein kinase with PDBTitle: crystal structure of full length cpdpk3 (cgd5_820) in2 complex with ca2+ and amppnp |
| 63 | c3v5qB_ | Alignment | not modelled | 100.0 | 35 | PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: nt-3 growth factor receptor; PDBTitle: discovery of a selective trk inhibitor with efficacy in rodent cancer2 tumor models |
| 64 | c3fbvL_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase, hydrolase Chain: L: PDB Molecule: serine/threonine-protein kinase/endoribonuclease ire1; PDBTitle: crystal structure of the oligomer formed by the kinase-ribonuclease2 domain of ire1 |
| 65 | c3d9vA_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of rock i bound to h-1152p a di-2 methylated variant of fasudil |
| 66 | c2bmcD_ | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: D: PDB Molecule: serine threonine-protein kinase 6; PDBTitle: aurora-2 t287d t288d complexed with pha-680632 |
| 67 | d1phka_ | Alignment | not modelled | 100.0 | 24 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 68 | c2j51A_ | Alignment | not modelled | 100.0 | 24 | PDB header: transferase Chain: A: PDB Molecule: ste20-like serine/threonine-protein kinase; PDBTitle: crystal structure of human ste20-like kinase bound to 5-2 amino-3-((4-(aminosulfonyl)phenyl)amino)-n-(2,6-3 difluorophenyl)-1h-1,2,4-triazole-1-carbothioamide |
| 69 | c2clqA_ | Alignment | not modelled | 100.0 | 26 | PDB header: transferase Chain: A: PDB Molecule: mitogen-activated protein kinase kinase kinase 5; PDBTitle: structure of mitogen-activated protein kinase kinase kinase2 5 |
| 70 | d2jfla1 | Alignment | not modelled | 100.0 | 25 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 71 | c3dfaA_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: calcium-dependent protein kinase cgd3_920; PDBTitle: crystal structure of kinase domain of calcium-dependent protein kinase2 cgd3_920 from cryptosporidium parvum |
| 72 | d1fvra_ | Alignment | not modelled | 100.0 | 41 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 73 | c2y7jB_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: B: PDB Molecule: phosphorylase b kinase gamma catalytic chain, PDBTitle: structure of human phosphorylase kinase, gamma 2 |
| 74 | c3p23B_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase, transferase Chain: B: PDB Molecule: serine/threonine-protein kinase/endoribonuclease ire1; PDBTitle: crystal structure of the human kinase and rnase domains in complex2 with adp |
| 75 | c2qobA_ | Alignment | not modelled | 100.0 | 37 | PDB header: transferase Chain: A: PDB Molecule: ephrin receptor; PDBTitle: human epha3 kinase domain, base structure |
| 76 | c3lxnA_ | Alignment | not modelled | 100.0 | 29 | PDB header: transferase Chain: A: PDB Molecule: non-receptor tyrosine-protein kinase tyk2; PDBTitle: structural and thermodynamic characterization of the tyk2 and jak32 kinase domains in complex with cp-690550 and cmp-6 |
| 77 | c3k54A_ | Alignment | not modelled | 100.0 | 58 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase btk; PDBTitle: structures of human bruton's tyrosine kinase in active and inactive2 conformations suggests a mechanism of activation for tec family3 kinases. |
| 78 | c2vd5A_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: dmpk protein; PDBTitle: structure of human myotonic dystrophy protein kinase in2 complex with the bisindoylmaleide inhibitor bim viii |
| | | | | | | PDB header: transferase Chain: D: PDB Molecule: calcium/calmodulin-dependent protein |

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|-----|-------------------------|-----------|---|-------|----|---|
| 79 | c2qg5D_ | Alignment | not modelled | 100.0 | 24 | kinase; PDBTitle: cryptosporidium parvum calcium dependent protein kinase cgd7_1840 |
| 80 | d1rjba_ | Alignment | not modelled | 100.0 | 38 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 81 | d1xkka_ | Alignment | not modelled | 100.0 | 35 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 82 | c1xkka_ | Alignment | not modelled | 100.0 | 35 | PDB header: transferase Chain: A: PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr kinase domain complexed with a quinazoline inhibitor-2 gw572016 |
| 83 | c2wqmA_ | Alignment | not modelled | 100.0 | 24 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase nek7; PDBTitle: structure of apo human nek7 |
| 84 | c2a27B_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: B: PDB Molecule: death-associated protein kinase 2; PDBTitle: human drp-1 kinase, w305s s308a d40 mutant, crystal form with 82 monomers in the asymmetric unit |
| 85 | d1ckia_ | Alignment | not modelled | 100.0 | 18 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 86 | c3o96A_ | Alignment |  | 100.0 | 25 | PDB header: transferase Chain: A: PDB Molecule: rac-alpha serine/threonine-protein kinase; PDBTitle: crystal structure of human akt1 with an allosteric inhibitor |
| 87 | c3comB_ | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase 4; PDBTitle: crystal structure of mst1 kinase |
| 88 | c3hztA_ | Alignment | not modelled | 100.0 | 25 | PDB header: transferase Chain: A: PDB Molecule: calcium-dependent protein kinase 3; PDBTitle: crystal structure of toxoplasma gondii cdpk3, tgme49_105860 |
| 89 | d1jksa_ | Alignment | not modelled | 100.0 | 23 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 90 | c2cgvA_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase chk1; PDBTitle: identification of chemically diverse chk1 inhibitors by2 receptor-based virtual screening |
| 91 | c3p86B_ | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase ctr1; PDBTitle: crystal structure of ctr1 kinase domain mutant d676n in complex with2 staurosporine |
| 92 | c2chlA_ | Alignment | not modelled | 100.0 | 18 | PDB header: transferase Chain: A: PDB Molecule: casein kinase i isoform gamma-3; PDBTitle: structure of casein kinase 1 gamma 3 |
| 93 | c1mruB_ | Alignment | not modelled | 100.0 | 24 | PDB header: transferase Chain: B: PDB Molecule: probable serine/threonine-protein kinase pknb; PDBTitle: intracellular ser/thr protein kinase domain of2 mycobacterium tuberculosis pknb. |
| 94 | c1xjdA_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: protein kinase c, theta type; PDBTitle: crystal structure of pkc-theta complexed with staurosporine2 at 2a resolution |
| 95 | d1xjda_ | Alignment | not modelled | 100.0 | 22 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 96 | c2bdwB_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: B: PDB Molecule: hypothetical protein k11e8.1d; PDBTitle: crystal structure of the auto-inhibited kinase domain of2 calcium/calmodulin activated kinase ii |
| 97 | d1koba_ | Alignment | not modelled | 100.0 | 21 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 98 | c2pziA_ | Alignment | not modelled | 100.0 | 16 | PDB header: transferase Chain: A: PDB Molecule: probable serine/threonine-protein kinase pknq; PDBTitle: crystal structure of protein kinase pknq from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017 |
| 99 | c2x4fA_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: myosin light chain kinase family member 4; PDBTitle: the crystal structure of the human myosin light chain2 kinase loc340156. |
| 100 | d1byga_ | Alignment | not modelled | 100.0 | 45 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 101 | d1nvra_ | Alignment | not modelled | 100.0 | 21 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 102 | d1o6ya_ | Alignment | not modelled | 100.0 | 24 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 103 | c2wtkB_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase/metal-binding protein Chain: B: PDB Molecule: ste20-related kinase adapter protein alpha; PDBTitle: structure of the heterotrimeric lkb1-stradalpha- |

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|-----|-------------------------|-----------|--------------|-------|----|--|
| | | | | | | mo25alpha2 complex |
| 104 | c2zv2A_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: calcium/calmodulin-dependent protein kinase kinase 2; PDBTitle: crystal structure of human calcium/calmodulin-dependent protein kinase2 kinase 2, beta, camkk2 kinase domain in complex with sto-609 |
| 105 | c2ya9A_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: death-associated protein kinase 2; PDBTitle: crystal structure of the autoinhibited form of mouse dapk2 |
| 106 | d1koa2 | Alignment | not modelled | 100.0 | 23 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 107 | c3brbB_ | Alignment | not modelled | 100.0 | 40 | PDB header: transferase Chain: B: PDB Molecule: proto-oncogene tyrosine-protein kinase mer; PDBTitle: crystal structure of catalytic domain of the proto-oncogene tyrosine-2 protein kinase mer in complex with adp |
| 108 | c2r5tA_ | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase sgk1; PDBTitle: crystal structure of inactive serum and glucocorticoid-2 regulated kinase 1 in complex with amp-pnp |
| 109 | c1kobB_ | Alignment | not modelled | 100.0 | 21 | PDB header: kinase Chain: B: PDB Molecule: twitchin; PDBTitle: twitchin kinase fragment (aplysia), autoregulated protein2 kinase domain |
| 110 | d1tkia_ | Alignment | not modelled | 100.0 | 19 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 111 | c2c47D_ | Alignment | not modelled | 100.0 | 18 | PDB header: transferase Chain: D: PDB Molecule: casein kinase 1 gamma 2 isoform; PDBTitle: structure of casein kinase 1 gamma 2 |
| 112 | c2vz6A_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: calcium calmodulin dependent protein kinase type ii alpha PDBTitle: structure of human calcium calmodulin dependent protein2 kinase type ii alpha (camk2a) in complex with indirubin3 e804 |
| 113 | d1uu3a_ | Alignment | not modelled | 100.0 | 22 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 114 | d1o6la_ | Alignment | not modelled | 100.0 | 23 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 115 | c2r7bA_ | Alignment | not modelled | 100.0 | 22 | PDB header: signaling protein, transferase Chain: A: PDB Molecule: phosphoinositide-dependent protein kinase 1; PDBTitle: crystal structure of the phosphoinositide-dependent kinase-2 1 (pdk-1)catalytic domain bound to a dibenzonaphthridine3 inhibitor |
| 116 | c2qluA_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: activin receptor type iib; PDBTitle: crystal structure of activin receptor type ii kinase domain2 from human |
| 117 | c2qofA_ | Alignment | not modelled | 100.0 | 38 | PDB header: transferase Chain: A: PDB Molecule: ephrin receptor; PDBTitle: human epha3 kinase and juxtamembrane region, y596f mutant |
| 118 | c3dtcA_ | Alignment | not modelled | 100.0 | 33 | PDB header: transferase Chain: A: PDB Molecule: mitogen-activated protein kinase kinase kinase 9; PDBTitle: crystal structure of mixed-lineage kinase mlk1 complexed2 with compound 16 |
| 119 | c1zrzA_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: protein kinase c, iota; PDBTitle: crystal structure of the catalytic domain of atypical2 protein kinase c-iota |
| 120 | c3is5E_ | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: E: PDB Molecule: calcium-dependent protein kinase; PDBTitle: crystal structure of cdpk kinase domain from toxoplasma gondii, 2 tgme49_018720 |