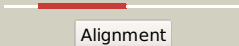









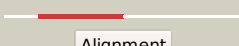

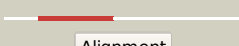











Phyre2

| | |
|---------------|------------------------------|
| Email | I.a.kelley@imperial.ac.uk |
| Description | Q4JIM5 |
| Date | Tue Jul 30 13:05:37 BST 2013 |
| Unique Job ID | d13a926718a654c3 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c2fo0A_ |  Alignment |  | 100.0 | 89 | 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 | c1op1A_ |  Alignment |  | 100.0 | 90 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase; PDBTitle: structural basis for the auto-inhibition of c-abl tyrosine2 kinase |
| 3 | c1y57A_ |  Alignment |  | 100.0 | 44 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase src; PDBTitle: structure of unphosphorylated c-src in complex with an inhibitor |
| 4 | c2h8hA_ |  Alignment |  | 100.0 | 44 | 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 | 40 | 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 | c2c01A_ |  Alignment |  | 100.0 | 43 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase hck; PDBTitle: src family kinase hck with bound inhibitor a-420983 |
| 7 | c4fi2A_ |  Alignment |  | 100.0 | 40 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase syk; PDBTitle: structural and biophysical characterization of the syk activation2 switch |
| 8 | c2ozoA_ |  Alignment |  | 100.0 | 36 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase zap-70; PDBTitle: autoinhibited intact human zap-70 |
| 9 | c3cblA_ |  Alignment |  | 100.0 | 40 | 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 |
| 10 | c2j0kB_ |  Alignment |  | 100.0 | 41 | 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. |
| 11 | d1opja_ |  Alignment |  | 100.0 | 89 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c3nyoB_ | Alignment | | 100.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: g protein-coupled receptor kinase 6; PDBTitle: crystal structure of g protein-coupled receptor kinase 6 in complex2 with amp |
| 13 | c4im2A_ | Alignment | | 100.0 | 22 | PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: serine/threonine-protein kinase tbk1; PDBTitle: structure of tank-binding kinase 1 |
| 14 | c3qa8H_ | Alignment | | 100.0 | 24 | PDB header: immune system, signaling protein Chain: H: PDB Molecule: mgc80376 protein; PDBTitle: crystal structure of inhibitor of kappa b kinase beta |
| 15 | c3pfqA_ | Alignment | | 100.0 | 25 | PDB header: transferase Chain: A: PDB Molecule: protein kinase c beta type; PDBTitle: crystal structure and allosteric activation of protein kinase c beta2 ii |
| 16 | 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 |
| 17 | d1qcfa3 | Alignment | | 100.0 | 46 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 18 | c3qa8A_ | Alignment | | 100.0 | 25 | PDB header: immune system, signaling protein Chain: A: PDB Molecule: mgc80376 protein; PDBTitle: crystal structure of inhibitor of kappa b kinase beta |
| 19 | c3c4wB_ | Alignment | | 100.0 | 20 | PDB header: transferase Chain: B: PDB Molecule: rhodopsin kinase; PDBTitle: crystal structure of g protein coupled receptor kinase 1 bound to atp2 and magnesium chloride at 2.7a |
| 20 | c1ym7C_ | Alignment | | 100.0 | 19 | PDB header: transferase Chain: C: PDB Molecule: beta-adrenergic receptor kinase 1; PDBTitle: g protein-coupled receptor kinase 2 (grk2) |
| 21 | 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 |
| 22 | c3zzwA_ | Alignment | not modelled | 100.0 | 35 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase transmembrane receptor ror2; PDBTitle: crystal structure of the kinase domain of ror2 |
| 23 | d1qpca_ | Alignment | not modelled | 100.0 | 47 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 24 | c2vwiC_ | Alignment | not modelled | 100.0 | 25 | PDB header: transferase Chain: C: PDB Molecule: serine/threonine-protein kinase osr1; PDBTitle: structure of the osr1 kinase, a hypertension drug target |
| 25 | c1koaA_ | Alignment | not modelled | 100.0 | 18 | PDB header: kinase Chain: A: PDB Molecule: twitchin; PDBTitle: twitchin kinase fragment (c.elegans), autoregulated protein2 kinase and immunoglobulin domains |
| 26 | c3ckxA_ | Alignment | not modelled | 100.0 | 25 | 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 |
| 27 | c3tkuB_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: serine/threonine-protein kinase mrck beta; PDBTitle: mrck beta in complex with fasudil |
| 28 | c2ivsA_ | Alignment | not modelled | 100.0 | 42 | PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase receptor PDBTitle: crystal structure of non-phosphorylated ret tyrosine kinase2 domain |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 29 | c3g0eA | Alignment | not modelled | 100.0 | 39 | PDB header: transferase Chain: A: PDB Molecule: mast/stem cell growth factor receptor; PDBTitle: kit kinase domain in complex with sunitinib |
| 30 | c1lufA | Alignment | not modelled | 100.0 | 42 | 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 |
| 31 | d1lufa | Alignment | not modelled | 100.0 | 42 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 32 | c3soaA | Alignment | not modelled | 100.0 | 22 | PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: calcium/calmodulin-dependent protein kinase type ii subunit PDBTitle: full-length human camkii |
| 33 | c2pvfA | Alignment | not modelled | 100.0 | 42 | 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 |
| 34 | d2j4za1 | Alignment | not modelled | 100.0 | 25 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 35 | c2c30A | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase pak 6; PDBTitle: crystal structure of the human p21-activated kinase 6 |
| 36 | d1k2pa | Alignment | not modelled | 100.0 | 46 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 37 | c3q5iA | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: A: PDB Molecule: protein kinase; PDBTitle: crystal structure of pbanka_031420 |
| 38 | c3dpkA | Alignment | not modelled | 100.0 | 40 | PDB header: transferase Chain: A: PDB Molecule: macrophage colony-stimulating factor 1 receptor; PDBTitle: cfms tyrosine kinase in complex with a pyridopyrimidinone2 inhibitor |
| 39 | d1u59a | Alignment | not modelled | 100.0 | 39 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 40 | c2psqA | Alignment | not modelled | 100.0 | 42 | 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 |
| 41 | d2psqa1 | Alignment | not modelled | 100.0 | 42 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 42 | c4fijA | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase pak 4; PDBTitle: catalytic domain of human pak4 |
| 43 | d3bu3a1 | Alignment | not modelled | 100.0 | 42 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 44 | c4dn5A | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: A: PDB Molecule: mitogen-activated protein kinase kinase kinase 14; PDBTitle: crystal structure of nf-kb-inducing kinase (nik) |
| 45 | c4aojA | Alignment | not modelled | 100.0 | 39 | PDB header: transferase Chain: A: PDB Molecule: high affinity nerve growth factor receptor; PDBTitle: human trka in complex with the inhibitor az-23 |
| 46 | d1t46a | Alignment | not modelled | 100.0 | 38 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 47 | d1fmka3 | Alignment | not modelled | 100.0 | 49 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 48 | c3kulB | Alignment | not modelled | 100.0 | 40 | PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 8; PDBTitle: kinase domain of human ephrin type-a receptor 8 (epha8) |
| 49 | c4fieB | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase pak 4; PDBTitle: full-length human pak4 |
| 50 | c3lxA | Alignment | not modelled | 100.0 | 38 | 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 |
| 51 | c3d9vA | Alignment | not modelled | 100.0 | 24 | 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 |
| 52 | c2jamB | Alignment | not modelled | 100.0 | 25 | PDB header: transferase Chain: B: PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: crystal structure of human calmodulin-dependent protein2 kinase i g |
| 53 | c3lijA | Alignment | not modelled | 100.0 | 27 | PDB header: transferase Chain: A: PDB Molecule: calcium/calmodulin dependent protein kinase with PDBTitle: crystal structure of full length cpdck3 (cgd5_820) in2 complex with ca2+ and amppnp |
| 54 | c3l9nA | Alignment | not modelled | 100.0 | 40 | PDB header: transferase Chain: A: PDB Molecule: anaplastic lymphoma kinase; |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 54 | c39pA | Alignment | not modelled | 100.0 | 40 | PDBTitle: crystal structure of the anaplastic lymphoma kinase catalytic domain PDB header: transferase/transferase inhibitor |
| 55 | c4eutA | Alignment | not modelled | 100.0 | 21 | Chain: A: PDB Molecule: serine/threonine-protein kinase tbk1; PDBTitle: structure of bx-795 complexed with unphosphorylated human tbk1 kinase-2 uld domain |
| 56 | c2wtkC | Alignment | not modelled | 100.0 | 24 | PDB header: transferase/metal-binding protein Chain: C: PDB Molecule: serine/threonine-protein kinase 11; PDBTitle: structure of the heterotrimeric lkb1-stradalpha-mo25alpha2 complex |
| 57 | d1yhwa1 | Alignment | not modelled | 100.0 | 25 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 58 | d1p4oa | Alignment | not modelled | 100.0 | 42 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 59 | c3plsA | Alignment | not modelled | 100.0 | 38 | PDB header: transferase Chain: A: PDB Molecule: macrophage-stimulating protein receptor; PDBTitle: ron in complex with ligand amp-prp |
| 60 | c4ebwA | Alignment | not modelled | 100.0 | 41 | PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: focal adhesion kinase 1; PDBTitle: structure of focal adhesion kinase catalytic domain in complex with2 novel allosteric inhibitor |
| 61 | c2a1aB | Alignment | not modelled | 100.0 | 21 | PDB header: protein synthesis/transferase Chain: B: PDB Molecule: interferon-induced, double-stranded rna-activated protein PDBTitle: pkr kinase domain-eif2alpha complex |
| 62 | d1fgka | Alignment | not modelled | 100.0 | 40 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 63 | c2pziA | Alignment | not modelled | 100.0 | 20 | PDB header: transferase Chain: A: PDB Molecule: probable serine/threonine-protein kinase pkng; PDBTitle: crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothioephene ax20017 |
| 64 | c3lvpD | Alignment | not modelled | 100.0 | 44 | 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 |
| 65 | d1phka | Alignment | not modelled | 100.0 | 23 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 66 | c2bmcD | Alignment | not modelled | 100.0 | 25 | PDB header: transferase Chain: D: PDB Molecule: serine threonine-protein kinase 6; PDBTitle: aurora-2 t287d t288d complexed with pha-680632 |
| 67 | c3vw6B | Alignment | not modelled | 100.0 | 27 | PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: mitogen-activated protein kinase kinase kinase 5; PDBTitle: crystal structure of human apoptosis signal-regulating kinase 1 (ask1)2 with imidazopyridine inhibitor |
| 68 | c2bujA | Alignment | not modelled | 100.0 | 21 | 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 |
| 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 | d1sm2a | Alignment | not modelled | 100.0 | 43 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 71 | c1yvjA | Alignment | not modelled | 100.0 | 37 | 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 |
| 72 | d1jpaA | Alignment | not modelled | 100.0 | 37 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 73 | d1mp8a | Alignment | not modelled | 100.0 | 40 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 74 | c2vd5A | Alignment | not modelled | 100.0 | 23 | 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 |
| 75 | c2qg5D | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: D: PDB Molecule: calcium/calmodulin-dependent protein kinase; PDBTitle: cryptosporidium parvum calcium dependent protein kinase cgd7_1840 |
| 76 | d1xbba | Alignment | not modelled | 100.0 | 43 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 77 | c2j51A | Alignment | not modelled | 100.0 | 25 | 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 |
| 78 | c2y7jB | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: B: PDB Molecule: phosphorylase b kinase gamma catalytic chain, PDBTitle: structure of human phosphorylase kinase, gamma 2 |
| | | | | | | PDB header: transferase, hydrolase Chain: L: PDB Molecule: serine/threonine-protein |

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|-----|-------------------------|-----------|--------------|-------|----|--|
| 79 | c3fbvL_ | Alignment | not modelled | 100.0 | 23 | kinase/endoribonuclease ire1; PDBTitle: crystal structure of the oligomer formed by the kinase-ribonuclease2 domain of ire1 |
| 80 | c3dfaA_ | Alignment | not modelled | 100.0 | 26 | 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 |
| 81 | 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 |
| 82 | c3sxaA_ | Alignment | not modelled | 100.0 | 42 | 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 |
| 83 | c3eygA_ | Alignment | not modelled | 100.0 | 34 | PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase; PDBTitle: crystal structures of jak1 and jak2 inhibitor complexes |
| 84 | d1rjba_ | Alignment | not modelled | 100.0 | 43 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 85 | d1ksa_ | Alignment | not modelled | 100.0 | 24 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 86 | c3fupB_ | Alignment | not modelled | 100.0 | 35 | PDB header: transferase Chain: B: PDB Molecule: tyrosine-protein kinase jak2; PDBTitle: crystal structures of jak1 and jak2 inhibitor complexes |
| 87 | d2ifla1 | Alignment | not modelled | 100.0 | 26 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 88 | c3cc6A_ | Alignment | not modelled | 100.0 | 41 | 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) |
| 89 | d1uwha_ | Alignment | not modelled | 100.0 | 33 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 90 | c3hztA_ | Alignment | not modelled | 100.0 | 28 | PDB header: transferase Chain: A: PDB Molecule: calcium-dependent protein kinase 3; PDBTitle: crystal structure of toxoplasma gondii cdpk3, tgme49_105860 |
| 91 | c3d4qA_ | Alignment | not modelled | 100.0 | 32 | PDB header: transferase Chain: A: PDB Molecule: b-raf proto-oncogene serine/threonine-protein kinase; PDBTitle: pyrazole-based inhibitors of b-raf kinase |
| 92 | c2bdwB_ | Alignment | not modelled | 100.0 | 24 | 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 |
| 93 | d1xjda_ | Alignment | not modelled | 100.0 | 25 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 94 | c1xjda_ | Alignment | not modelled | 100.0 | 25 | 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 | c3v5qB_ | Alignment | not modelled | 100.0 | 38 | 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 |
| 96 | d1fvra_ | Alignment | not modelled | 100.0 | 43 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 97 | d1mqba_ | Alignment | not modelled | 100.0 | 39 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 98 | c3comB_ | Alignment | not modelled | 100.0 | 26 | PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase 4; PDBTitle: crystal structure of mst1 kinase |
| 99 | c3p23B_ | Alignment | not modelled | 100.0 | 23 | 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 |
| 100 | c2zv2A_ | Alignment | not modelled | 100.0 | 24 | 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 |
| 101 | c2wtkB_ | Alignment | not modelled | 100.0 | 20 | PDB header: transferase/metal-binding protein Chain: B: PDB Molecule: ste20-related kinase adapter protein alpha; PDBTitle: structure of the heterotrimeric lkb1-stradalpha-mo25alpha2 complex |
| 102 | c2w1iB_ | Alignment | not modelled | 100.0 | 35 | PDB header: transferase Chain: B: PDB Molecule: jak2; PDBTitle: structure determination of aurora kinase in complex with2 inhibitor |
| 103 | c2cgvA_ | Alignment | not modelled | 100.0 | 24 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase chk1; PDBTitle: identification of chemically diverse chk1 inhibitors by2 receptor-based virtual screening |
| | | | | | | PDB header: transferase Chain: B: PDB Molecule: probable serine/threonine-protein kinase |

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|-----|-------------------------|-----------|--------------|-------|----|--|
| 104 | c1mruB_ | Alignment | not modelled | 100.0 | 24 | pknb; PDBTitle: intracellular ser/thr protein kinase domain of2 mycobacterium tuberculosis pknb. |
| 105 | c2ya9A_ | Alignment | not modelled | 100.0 | 21 | PDB header: transferase Chain: A: PDB Molecule: death-associated protein kinase 2; PDBTitle: crystal structure of the autoinhibited form of mouse dapk2 |
| 106 | d1koba_ | Alignment | not modelled | 100.0 | 18 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 107 | d1o6ya_ | Alignment | not modelled | 100.0 | 24 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 108 | d1nvra_ | Alignment | not modelled | 100.0 | 24 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 109 | c2x4fA_ | Alignment | not modelled | 100.0 | 22 | 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. |
| 110 | d1o6la_ | Alignment | not modelled | 100.0 | 25 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 111 | d1ckia_ | Alignment | not modelled | 100.0 | 20 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 112 | c2wqmA_ | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase nek7; PDBTitle: structure of apo human nek7 |
| 113 | d1xkka_ | Alignment | not modelled | 100.0 | 40 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 114 | c1xkka_ | Alignment | not modelled | 100.0 | 40 | PDB header: transferase Chain: A: PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr kinase domain complexed with a quinazoline inhibitor-2 gw572016 |
| 115 | d1koa2 | Alignment | not modelled | 100.0 | 19 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 116 | c2chlA_ | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: casein kinase i isoform gamma-3; PDBTitle: structure of casein kinase 1 gamma 3 |
| 117 | c4eqmE_ | Alignment | not modelled | 100.0 | 22 | PDB header: transferase Chain: E: PDB Molecule: protein kinase; PDBTitle: structural analysis of staphylococcus aureus serine/threonine kinase2 pknb |
| 118 | c2qobA_ | Alignment | not modelled | 100.0 | 39 | PDB header: transferase Chain: A: PDB Molecule: ephrin receptor; PDBTitle: human epha3 kinase domain, base structure |
| 119 | d1tkia_ | Alignment | not modelled | 100.0 | 17 | Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit |
| 120 | c2vz6A_ | Alignment | not modelled | 100.0 | 24 | 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 |