































# Phyre2

|               |                              |
|---------------|------------------------------|
| Email         | l.a.kelley@imperial.ac.uk    |
| Description   | Q64434                       |
| Date          | Wed Jul 10 14:13:37 BST 2013 |
| Unique Job ID | 0445f14aec1f9bd              |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c2fo0A_</a> | <br>Alignment   |    | 100.0      | 37     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase abl1 (1b isoform);<br><b>PDBTitle:</b> organization of the sh3-sh2 unit in active and inactive forms of the2 c-abl tyrosine kinase                              |
| 2  | <a href="#">c1y57A_</a> | <br>Alignment   |    | 100.0      | 42     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase src;<br><b>PDBTitle:</b> structure of unphosphorylated c-src in complex with an inhibitor   |
| 3  | <a href="#">c1op1A_</a> | <br>Alignment   |    | 100.0      | 38     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase; <b>PDBTitle:</b> structural basis for the auto-inhibition of c-abl tyrosine2 kinase  |
| 4  | <a href="#">c2h8hA_</a> | <br>Alignment   |   | 100.0      | 42     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase src;<br><b>PDBTitle:</b> src kinase in complex with a quinazoline inhibitor   |
| 5  | <a href="#">c1k9aB_</a> | <br>Alignment |  | 100.0      | 38     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> carboxyl-terminal src kinase;<br><b>PDBTitle:</b> crystal structure analysis of full-length carboxyl-terminal2 src kinase at 2.5 a resolution  |
| 6  | <a href="#">c2c0iA_</a> | <br>Alignment |  | 100.0      | 44     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase hck;<br><b>PDBTitle:</b> src family kinase hck with bound inhibitor a-420983   |
| 7  | <a href="#">c2ozoA_</a> | <br>Alignment |  | 100.0      | 32     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase zap-70;<br><b>PDBTitle:</b> autoinhibited intact human zap-70  |
| 8  | <a href="#">c4fi2A_</a> | <br>Alignment |  | 100.0      | 35     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase syk;<br><b>PDBTitle:</b> structural and biophysical characterization of the syk activation2 switch   |
| 9  | <a href="#">c3cblA_</a> | <br>Alignment |  | 100.0      | 39     | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase fes/fps;<br><b>PDBTitle:</b> crystal structure of human feline sarcoma viral oncogene homologue (v-2 fes) in complex with staurosporine and a consensus peptide |
| 10 | <a href="#">c2j0kB_</a> | <br>Alignment |  | 100.0      | 38     | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> focal adhesion kinase 1;<br><b>PDBTitle:</b> crystal structure of a fragment of focal adhesion kinase2 containing the ferm and kinase domains.   |
| 11 | <a href="#">d1qcfa3</a> | <br>Alignment |  | 100.0      | 45     | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |

|    |                         |           |   |       |    |   |
|----|-------------------------|-----------|---|-------|----|---|
| 12 | <a href="#">d1opja_</a> | Alignment |    | 100.0 | 42 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit  |
| 13 | <a href="#">d1qpca_</a> | Alignment |    | 100.0 | 44 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit  |
| 14 | <a href="#">c3zzwA_</a> | Alignment |    | 100.0 | 34 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase transmembrane receptor ror2;<br><b>PDBTitle:</b> crystal structure of the kinase domain of ror2   |
| 15 | <a href="#">c4im2A_</a> | Alignment |    | 100.0 | 26 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase tbk1;<br><b>PDBTitle:</b> structure of tank-binding kinase 1  |
| 16 | <a href="#">d1lufa_</a> | Alignment |    | 100.0 | 36 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit  |
| 17 | <a href="#">c1lufA_</a> | Alignment |    | 100.0 | 36 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> muscle-specific tyrosine kinase receptor musk;<br><b>PDBTitle:</b> crystal structure of the musk tyrosine kinase: insights2 into receptor autoregulation  |
| 18 | <a href="#">c2ivsA_</a> | Alignment |   | 100.0 | 39 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase receptor<br><b>PDBTitle:</b> crystal structure of non-phosphorylated ret tyrosine kinase2 domain   |
| 19 | <a href="#">d1u59a_</a> | Alignment |  | 100.0 | 33 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit  |
| 20 | <a href="#">d1k2pa_</a> | Alignment |  | 100.0 | 39 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit  |
| 21 | <a href="#">c3g0eA_</a> | Alignment | not modelled  | 100.0 | 40 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mast/stem cell growth factor receptor;<br><b>PDBTitle:</b> kit kinase domain in complex with sunitinib  |
| 22 | <a href="#">c2pvfA_</a> | Alignment | not modelled  | 100.0 | 44 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fibroblast growth factor receptor 2;<br><b>PDBTitle:</b> crystal structure of tyrosine phosphorylated activated fgf receptor 22 (fgfr2) kinase domain in complex with atp analog and substrate3 peptide |
| 23 | <a href="#">c3nyoB_</a> | Alignment | not modelled  | 100.0 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> g protein-coupled receptor kinase 6;<br><b>PDBTitle:</b> crystal structure of g protein-coupled receptor kinase 6 in complex2 with amp  |
| 24 | <a href="#">c3qa8H_</a> | Alignment | not modelled  | 100.0 | 24 | <b>PDB header:</b> immune system, signaling protein<br><b>Chain:</b> H: <b>PDB Molecule:</b> mgc80376 protein;<br><b>PDBTitle:</b> crystal structure of inhibitor of kappa b kinase beta  |
| 25 | <a href="#">c3dpkA_</a> | Alignment | not modelled  | 100.0 | 44 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> macrophage colony-stimulating factor 1 receptor;<br><b>PDBTitle:</b> cfms tyrosine kinase in complex with a pyridopyrimidinone2 inhibitor   |
| 26 | <a href="#">c3pfqA_</a> | Alignment | not modelled  | 100.0 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c beta type;<br><b>PDBTitle:</b> crystal structure and allosteric activation of protein kinase c beta2 ii  |
| 27 | <a href="#">c2vwiC_</a> | Alignment | not modelled  | 100.0 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> serine/threonine-protein kinase osr1;<br><b>PDBTitle:</b> structure of the osr1 kinase, a hypertension drug target  |
| 28 | <a href="#">c2acxB_</a> | Alignment | not modelled  | 100.0 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> g protein-coupled receptor kinase 6;<br><b>PDBTitle:</b> crystal structure of g protein coupled receptor kinase 6   |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
|    |                         |           |              |       |    | bound to2 amppnp   |
| 29 | <a href="#">d3bu3a1</a> | Alignment | not modelled | 100.0 | 37 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 30 | <a href="#">c3c4yA</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> rhodopsin kinase;<br><b>PDBTitle:</b> crystal structure of apo form of g protein coupled receptor kinase 12 at 7.51a   |
| 31 | <a href="#">c2psqA</a>  | Alignment | not modelled | 100.0 | 46 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fibroblast growth factor receptor 2;<br><b>PDBTitle:</b> crystal structure of unphosphorylated unactivated wild type2 fgf receptor 2 (fgfr2) kinase domain               |
| 32 | <a href="#">d2psqa1</a> | Alignment | not modelled | 100.0 | 46 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 33 | <a href="#">c3c4wB</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> rhodopsin kinase;<br><b>PDBTitle:</b> crystal structure of g protein coupled receptor kinase 1 bound to atp2 and magnesium chloride at 2.7a                              |
| 34 | <a href="#">c4aojA</a>  | Alignment | not modelled | 100.0 | 38 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> high affinity nerve growth factor receptor;<br><b>PDBTitle:</b> human trka in complex with the inhibitor az-23   |
| 35 | <a href="#">c2c30A</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 6;<br><b>PDBTitle:</b> crystal structure of the human p21-activated kinase 6   |
| 36 | <a href="#">d1fmka3</a> | Alignment | not modelled | 100.0 | 49 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 37 | <a href="#">c3ckxA</a>  | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase 24;<br><b>PDBTitle:</b> crystal structure of sterile 20-like kinase 3 (mst3, stk24)2 in complex with staurosporine                       |
| 38 | <a href="#">c1koaA</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> kinase<br><b>Chain:</b> A: <b>PDB Molecule:</b> twitchin;<br><b>PDBTitle:</b> twitchin kinase fragment (c.elegans), autoregulated protein2 kinase and immunoglobulin domains  |
| 39 | <a href="#">c3lxkA</a>  | Alignment | not modelled | 100.0 | 34 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase jak3;<br><b>PDBTitle:</b> structural and thermodynamic characterization of the tyk2 and jak32 kinase domains in complex with cp-690550 and cmp-6 |
| 40 | <a href="#">c3qa8A</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> immune system, signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> imgc80376 protein;<br><b>PDBTitle:</b> crystal structure of inhibitor of kappa b kinase beta  |
| 41 | <a href="#">d2j4za1</a> | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 42 | <a href="#">d1t46a</a>  | Alignment | not modelled | 100.0 | 39 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 43 | <a href="#">c1ym7C</a>  | Alignment | not modelled | 100.0 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> C: <b>PDB Molecule:</b> beta-adrenergic receptor kinase 1;<br><b>PDBTitle:</b> g protein-coupled receptor kinase 2 (grk2)  |
| 44 | <a href="#">c3soaA</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> calcium/calmodulin-dependent protein kinase type ii subunit<br><b>PDBTitle:</b> full-length human camkii   |
| 45 | <a href="#">d1fgka</a>  | Alignment | not modelled | 100.0 | 44 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 46 | <a href="#">c3kulB</a>  | Alignment | not modelled | 100.0 | 39 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 8;<br><b>PDBTitle:</b> kinase domain of human ephrin type-a receptor 8 (epha8)  |
| 47 | <a href="#">c4fijA</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 4;<br><b>PDBTitle:</b> catalytic domain of human pak4  |
| 48 | <a href="#">d1jpaa</a>  | Alignment | not modelled | 100.0 | 38 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 49 | <a href="#">c3plsA</a>  | Alignment | not modelled | 100.0 | 36 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> macrophage-stimulating protein receptor;<br><b>PDBTitle:</b> ron in complex with ligand amp-pnp  |
| 50 | <a href="#">c3l9pA</a>  | Alignment | not modelled | 100.0 | 39 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> anaplastic lymphoma kinase;<br><b>PDBTitle:</b> crystal structure of the anaplastic lymphoma kinase catalytic domain   |
| 51 | <a href="#">d1p4oa</a>  | Alignment | not modelled | 100.0 | 36 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 52 | <a href="#">d1sm2a</a>  | Alignment | not modelled | 100.0 | 39 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 53 | <a href="#">c4ebwA</a>  | Alignment | not modelled | 100.0 | 38 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> focal adhesion kinase 1;<br><b>PDBTitle:</b> structure of focal adhesion kinase catalytic domain in complex with2 novel allosteric inhibitor       |
| 54 | <a href="#">c3q5iA</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase;<br><b>PDBTitle:</b> crystal structure of pbanka_031420   |
| 55 | <a href="#">c3lvpD</a>  | Alignment | not modelled | 100.0 | 38 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> insulin-like growth factor 1 receptor;   |

|    |                         |           |              |       |    |  |
|----|-------------------------|-----------|--------------|-------|----|--|
| 55 | <a href="#">c3vvpB_</a> | Alignment | not modelled | 100.0 | 36 | <b>PDBTitle:</b> crystal structure of bisphosphorylated igf1-r kinase domain (2p) in2 complex with a bis-azaindole inhibitor   |
| 56 | <a href="#">d1mp8a_</a> | Alignment | not modelled | 100.0 | 37 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 57 | <a href="#">c4dn5A_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 14;<br><b>PDBTitle:</b> crystal structure of nf-kb-inducing kinase (nik)  |
| 58 | <a href="#">d1yhwa1</a> | Alignment | not modelled | 100.0 | 21 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 59 | <a href="#">c3tkuB_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase mrck beta;<br><b>PDBTitle:</b> mrck beta in complex with fasudil   |
| 60 | <a href="#">c2bujA_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase 16;<br><b>PDBTitle:</b> crystal structure of the human serine-threonine kinase 162 in complex with staurosporine   |
| 61 | <a href="#">c4fieB_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 4;<br><b>PDBTitle:</b> full-length human pak4  |
| 62 | <a href="#">c3sxaA_</a> | Alignment | not modelled | 100.0 | 41 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic tyrosine-protein kinase bmx;<br><b>PDBTitle:</b> crystal structure of bmx non-receptor tyrosine kinase complex with2 dasatinib   |
| 63 | <a href="#">c3fupB_</a> | Alignment | not modelled | 100.0 | 35 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine-protein kinase jak2;<br><b>PDBTitle:</b> crystal structures of jak1 and jak2 inhibitor complexes  |
| 64 | <a href="#">c3cc6A_</a> | Alignment | not modelled | 100.0 | 38 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein tyrosine kinase 2 beta;<br><b>PDBTitle:</b> crystal structure of kinase domain of protein tyrosine kinase 2 beta2 (ptk2b)  |
| 65 | <a href="#">d1mqba_</a> | Alignment | not modelled | 100.0 | 40 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 66 | <a href="#">d1xbba_</a> | Alignment | not modelled | 100.0 | 37 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 67 | <a href="#">c1yvjA_</a> | Alignment | not modelled | 100.0 | 34 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase jak3;<br><b>PDBTitle:</b> crystal structure of the jak3 kinase domain in complex with2 a staurosporine analogue  |
| 68 | <a href="#">c3v5qB_</a> | Alignment | not modelled | 100.0 | 35 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> B: <b>PDB Molecule:</b> int-3 growth factor receptor;<br><b>PDBTitle:</b> discovery of a selective trk inhibitor with efficacy in rodent cancer2 tumor models  |
| 69 | <a href="#">c2jamB_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> calcium/calmodulin-dependent protein kinase type<br><b>PDBTitle:</b> crystal structure of human calmodulin-dependent protein2 kinase i g   |
| 70 | <a href="#">c2w1iB_</a> | Alignment | not modelled | 100.0 | 35 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> jak2;<br><b>PDBTitle:</b> structure determination of aurora kinase in complex with2 inhibitor  |
| 71 | <a href="#">c3eygA_</a> | Alignment | not modelled | 100.0 | 34 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase;<br><b>PDBTitle:</b> crystal structures of jak1 and jak2 inhibitor complexes   |
| 72 | <a href="#">c2a1aB_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> protein synthesis/transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> interferon-induced, double-stranded rna-activated protein<br><b>PDBTitle:</b> pkr kinase domain-eif2alpha complex  |
| 73 | <a href="#">c2j51A_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ste20-like serine/threonine-protein kinase;<br><b>PDBTitle:</b> 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 |
| 74 | <a href="#">d1uwha_</a> | Alignment | not modelled | 100.0 | 34 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 75 | <a href="#">c3vw6B_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> B: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 5;<br><b>PDBTitle:</b> crystal structure of human apoptosis signal-regulating kinase 1 (ask1)2 with imidazopyridine inhibitor                             |
| 76 | <a href="#">d1rjba_</a> | Alignment | not modelled | 100.0 | 42 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 77 | <a href="#">c3lijA_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> calcium/calmodulin dependent protein kinase with<br><b>PDBTitle:</b> crystal structure of full length cpdpk3 (cgd5_820) in2 complex with ca2+ and amppnp   |
| 78 | <a href="#">c3d4qA_</a> | Alignment | not modelled | 100.0 | 34 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> b-raf proto-oncogene serine/threonine-protein kinase;<br><b>PDBTitle:</b> pyrazole-based inhibitors of b-raf kinase  |
| 79 | <a href="#">c3lxnA_</a> | Alignment | not modelled | 100.0 | 34 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> non-receptor tyrosine-protein kinase tyk2;<br><b>PDBTitle:</b> structural and thermodynamic characterization of the tyk2 and jak32 kinase domains in complex with cp-690550 and cmp-6  |
| 80 | <a href="#">c2wtkC_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> transferase/metal-binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> serine/threonine-protein kinase 11;<br><b>PDBTitle:</b> structure of the heterotrimeric lkb1-stradaalpha-  |

|     |                         |           |              |       |    |   |
|-----|-------------------------|-----------|--------------|-------|----|---|
|     |                         |           |              |       |    | mo25alpha2 complex  |
| 81  | <a href="#">c2clqA</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase 5;<br><b>PDBTitle:</b> structure of mitogen-activated protein kinase kinase2 5  |
| 82  | <a href="#">c2bmcD</a>  | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> serine threonine-protein kinase 6;<br><b>PDBTitle:</b> aurora-2 t287d t288d complexed with pha-680632   |
| 83  | <a href="#">d1phka</a>  | Alignment | not modelled | 100.0 | 22 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit  |
| 84  | <a href="#">d2ifia1</a> | Alignment | not modelled | 100.0 | 23 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit  |
| 85  | <a href="#">c2qg5D</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> D: <b>PDB Molecule:</b> calcium/calmodulin-dependent protein kinase;<br><b>PDBTitle:</b> cryptosporidium parvum calcium dependent protein kinase cgd7_1840  |
| 86  | <a href="#">d1fvra</a>  | Alignment | not modelled | 100.0 | 38 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit  |
| 87  | <a href="#">c4eutA</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase tbk1;<br><b>PDBTitle:</b> structure of bx-795 complexed with unphosphorylated human tbk1 kinase-2 uld domain                              |
| 88  | <a href="#">d1byga</a>  | Alignment | not modelled | 100.0 | 46 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit  |
| 89  | <a href="#">c2qobA</a>  | Alignment | not modelled | 100.0 | 38 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ephrin receptor;<br><b>PDBTitle:</b> human epha3 kinase domain, base structure  |
| 90  | <a href="#">c3fbvL</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> transferase, hydrolase<br><b>Chain:</b> L: <b>PDB Molecule:</b> serine/threonine-protein kinase/endoribonuclease ire1;<br><b>PDBTitle:</b> crystal structure of the oligomer formed by the kinase-ribonuclease2 domain of ire1                       |
| 91  | <a href="#">c3dfaA</a>  | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> calcium-dependent protein kinase cgd3_920;<br><b>PDBTitle:</b> crystal structure of kinase domain of calcium-dependent protein kinase2 cgd3_920 from cryptosporidium parvum                     |
| 92  | <a href="#">c1xkka</a>  | Alignment | not modelled | 100.0 | 36 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> epidermal growth factor receptor;<br><b>PDBTitle:</b> egfr kinase domain complexed with a quinazoline inhibitor-2 gw572016  |
| 93  | <a href="#">d1xkka</a>  | Alignment | not modelled | 100.0 | 36 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit  |
| 94  | <a href="#">c2y7jB</a>  | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphorylase b kinase gamma catalytic chain,<br><b>PDBTitle:</b> structure of human phosphorylase kinase, gamma 2  |
| 95  | <a href="#">c3d9vA</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> rho-associated protein kinase 1;<br><b>PDBTitle:</b> crystal structure of rock i bound to h-1152p a di-2 methylated variant of fasudil  |
| 96  | <a href="#">c3p86B</a>  | Alignment | not modelled | 100.0 | 36 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase ctr1;<br><b>PDBTitle:</b> crystal structure of ctr1 kinase domain mutant d676n in complex with2 staurosporine   |
| 97  | <a href="#">c3hztA</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> calcium-dependent protein kinase 3;<br><b>PDBTitle:</b> crystal structure of toxoplasma gondii cdpk3, tgme49_105860   |
| 98  | <a href="#">c3zosA</a>  | Alignment | not modelled | 100.0 | 34 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> epithelial discoidin domain-containing receptor 1;<br><b>PDBTitle:</b> structure of the ddr1 kinase domain in complex with ponatinib  |
| 99  | <a href="#">c2wqmA</a>  | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase nek7;<br><b>PDBTitle:</b> structure of apo human nek7   |
| 100 | <a href="#">c3k54A</a>  | Alignment | not modelled | 100.0 | 40 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase btk;<br><b>PDBTitle:</b> structures of human bruton's tyrosine kinase in active and inactive2 conformations suggests a mechanism of activation for tec family3 kinases. |
| 101 | <a href="#">d1koba</a>  | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit  |
| 102 | <a href="#">c2cgvA</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase chk1;<br><b>PDBTitle:</b> identification of chemically diverse chk1 inhibitors by2 receptor-based virtual screening   |
| 103 | <a href="#">c4e1zA</a>  | Alignment | not modelled | 100.0 | 33 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> non-receptor tyrosine-protein kinase tyk2;<br><b>PDBTitle:</b> structure of mouse tyk-2 complexed to a 3-aminoindazole inhibitor  |
| 104 | <a href="#">c3p23B</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> hydrolase, transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase/endoribonuclease ire1;<br><b>PDBTitle:</b> crystal structure of the human kinase and rnase domains in complex2 with adp                              |
| 105 | <a href="#">c4hzcA</a>  | Alignment | not modelled | 100.0 | 41 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> activated cdc42 kinase 1;   |

|     |                         |           |              |       |    |  |
|-----|-------------------------|-----------|--------------|-------|----|--|
| 105 | <a href="#">c4n2aA_</a> | Alignment | not modelled | 100.0 | 41 | <b>PDBTitle:</b> crystal structure of ack1 kinase domain with c-terminal sh3 domain  |
| 106 | <a href="#">d1jksa_</a> | Alignment | not modelled | 100.0 | 25 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 107 | <a href="#">c2a27B_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> death-associated protein kinase 2;<br><b>PDBTitle:</b> human drp-1 kinase, w305s s308a d40 mutant, crystal form with 82 monomers in the asymmetric unit  |
| 108 | <a href="#">d1xjda_</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 109 | <a href="#">c1xjdA_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c, theta type;<br><b>PDBTitle:</b> crystal structure of pkc-theta complexed with staurosporine2 at 2a resolution  |
| 110 | <a href="#">d1ckia_</a> | Alignment | not modelled | 100.0 | 18 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 111 | <a href="#">c2x4fA_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> myosin light chain kinase family member 4;<br><b>PDBTitle:</b> the crystal structure of the human myosin light chain2 kinase loc340156.  |
| 112 | <a href="#">d1o6ya_</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 113 | <a href="#">c1mruB_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable serine/threonine-protein kinase pknb;<br><b>PDBTitle:</b> intracellular ser/thr protein kinase domain of2 mycobacterium tuberculosis pknb.  |
| 114 | <a href="#">c3comB_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase 4;<br><b>PDBTitle:</b> crystal structure of mst1 kinase  |
| 115 | <a href="#">c2bdwB_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein k11e8.1d;<br><b>PDBTitle:</b> crystal structure of the auto-inhibited kinase domain of2 calcium/calmodulin activated kinase ii  |
| 116 | <a href="#">d1nvra_</a> | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> Protein kinase-like (PK-like)<br><b>Superfamily:</b> Protein kinase-like (PK-like)<br><b>Family:</b> Protein kinases, catalytic subunit   |
| 117 | <a href="#">c2r5tA_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase sgk1;<br><b>PDBTitle:</b> crystal structure of inactive serum and glucocorticoid-2 regulated kinase 1 in complex with amp-pnp  |
| 118 | <a href="#">c2zv2A_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> calcium/calmodulin-dependent protein kinase kinase 2;<br><b>PDBTitle:</b> crystal structure of human calcium/calmodulin-dependent protein kinase2 kinase 2, beta, camkk2 kinase domain in complex with sto-609 |
| 119 | <a href="#">c4fvrA_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase jak2;<br><b>PDBTitle:</b> crystal structure of the jak2 pseudokinase domain mutant v617f (mg-2 atp-bound form)   |
| 120 | <a href="#">c4eqmE_</a> | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> E: <b>PDB Molecule:</b> protein kinase;<br><b>PDBTitle:</b> structural analysis of staphylococcus aureus serine/threonine kinase2 pknb   |