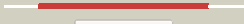



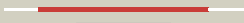





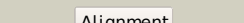

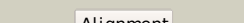

















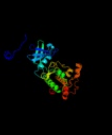


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P41240
Date	Thu Apr 26 09:28:47 BST 2012
Unique Job ID	2b20a759e2d6e186

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1k9aB_</a>	 Alignment		100.0	98	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxyl-terminal src kinase; <b>PDBTitle:</b> crystal structure analysis of full-length carboxyl-terminal2 src kinase at 2.5 a resolution
2	<a href="#">c2fo0A_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase abl1 (1b isoform); <b>PDBTitle:</b> organization of the sh3-sh2 unit in active and inactive forms of the2 c-abl tyrosine kinase
3	<a href="#">c1oplA_</a>	 Alignment		100.0	39	<b>PDB header:</b> transferase <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="#">c1y57A_</a>	 Alignment		100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase src; <b>PDBTitle:</b> structure of unphosphorylated c-src in complex with an inhibitor
5	<a href="#">c2h8hA_</a>	 Alignment		100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase src; <b>PDBTitle:</b> src kinase in complex with a quinazoline inhibitor
6	<a href="#">c2c0iA_</a>	 Alignment		100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase hck; <b>PDBTitle:</b> src family kinase hck with bound inhibitor a-420983
7	<a href="#">c2ozoA_</a>	 Alignment		100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase zap-70; <b>PDBTitle:</b> autoinhibited intact human zap-70
8	<a href="#">c3cblA_</a>	 Alignment		100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase fes/fps; <b>PDBTitle:</b> crystal structure of human feline sarcoma viral oncogene homologue (v-2 fes) in complex with staurosporine and a consensus peptide
9	<a href="#">c2j0kB_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> focal adhesion kinase 1; <b>PDBTitle:</b> crystal structure of a fragment of focal adhesion kinase2 containing the ferm and kinase domains.
10	<a href="#">d1qcfa3</a>	 Alignment		100.0	43	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
11	<a href="#">d1lopa_</a>	 Alignment		100.0	43	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit

12	<a href="#">c3zzwA</a>	Alignment		100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase transmembrane receptor ror2; <b>PDBTitle:</b> crystal structure of the kinase domain of ror2
13	<a href="#">d1qpca</a>	Alignment		100.0	43	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
14	<a href="#">d1lufa</a>	Alignment		100.0	36	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
15	<a href="#">c1lufA</a>	Alignment		100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> muscle-specific tyrosine kinase receptor musk; <b>PDBTitle:</b> crystal structure of the musk tyrosine kinase: insights2 into receptor autoregulation
16	<a href="#">c2ivsA</a>	Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase receptor <b>PDBTitle:</b> crystal structure of non-phosphorylated ret tyrosine kinase2 domain
17	<a href="#">d1u59a</a>	Alignment		100.0	37	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
18	<a href="#">c3g0eA</a>	Alignment		100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mast/stem cell growth factor receptor; <b>PDBTitle:</b> kit kinase domain in complex with sunitinib
19	<a href="#">d1k2pa</a>	Alignment		100.0	43	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
20	<a href="#">c3pfqA</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c beta type; <b>PDBTitle:</b> crystal structure and allosteric activation of protein kinase c beta2 ii
21	<a href="#">c2pvfA</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fibroblast growth factor receptor 2; <b>PDBTitle:</b> crystal structure of tyrosine phosphorylated activated fgf receptor 22 (fgfr2) kinase domain in complex with atp analog and substrate3 peptide
22	<a href="#">c3dpkA</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage colony-stimulating factor 1 receptor; <b>PDBTitle:</b> cfms tyrosine kinase in complex with a pyridopyrimidinone2 inhibitor
23	<a href="#">d3bu3a1</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
24	<a href="#">d2psqa1</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
25	<a href="#">c2psqA</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fibroblast growth factor receptor 2; <b>PDBTitle:</b> crystal structure of unphosphorylated unactivated wild type2 fgf receptor 2 (fgfr2) kinase domain
26	<a href="#">c2acxB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> g protein-coupled receptor kinase 6; <b>PDBTitle:</b> crystal structure of g protein coupled receptor kinase 6 bound to2 amppnp
27	<a href="#">d1fmka3</a>	Alignment	not modelled	100.0	43	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
28	<a href="#">c2vwiC</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> serine/threonine-protein kinase osr1; <b>PDBTitle:</b> structure of the osr1 kinase, a hypertension drug target

29	<a href="#">c3ckxA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase 24; <b>PDBTitle:</b> crystal structure of sterile 20-like kinase 3 (mst3, stk24)2 in complex with staurosporine
30	<a href="#">c3qa8A</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> immune system, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> mgc80376 protein; <b>PDBTitle:</b> crystal structure of inhibitor of kappa b kinase beta
31	<a href="#">d2j4za1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
32	<a href="#">c3lxA</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase jak3; <b>PDBTitle:</b> structural and thermodynamic characterization of the tyk2 and jak32 kinase domains in complex with cp-690550 and cmp-6
33	<a href="#">d1fgka</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
34	<a href="#">d1t46a</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
35	<a href="#">c3c4yA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodopsin kinase; <b>PDBTitle:</b> crystal structure of apo form of g protein coupled receptor kinase 12 at 7.51a
36	<a href="#">c2c30A</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase pak 6; <b>PDBTitle:</b> crystal structure of the human p21-activated kinase 6
37	<a href="#">c1ym7C</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-adrenergic receptor kinase 1; <b>PDBTitle:</b> g protein-coupled receptor kinase 2 (grk2)
38	<a href="#">d1p4oa</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
39	<a href="#">c3plsA</a>	Alignment	not modelled	100.0	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage-stimulating protein receptor; <b>PDBTitle:</b> ron in complex with ligand amp-pnp
40	<a href="#">c1koaA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> kinase <b>Chain:</b> A: <b>PDB Molecule:</b> twitchin; <b>PDBTitle:</b> twitchin kinase fragment (c.elegans), autoregulated protein2 kinase and immunoglobulin domains
41	<a href="#">c3l9pA</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anaplastic lymphoma kinase; <b>PDBTitle:</b> crystal structure of the anaplastic lymphoma kinase catalytic domain
42	<a href="#">d1mp8a</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
43	<a href="#">d1sm2a</a>	Alignment	not modelled	100.0	44	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
44	<a href="#">c3lvpD</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> insulin-like growth factor 1 receptor; <b>PDBTitle:</b> crystal structure of bisphosphorylated igf1-r kinase domain (2p) in2 complex with a bis-azaindole inhibitor
45	<a href="#">d1jpaA</a>	Alignment	not modelled	100.0	40	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
46	<a href="#">c3soaA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> calcium/calmodulin-dependent protein kinase type ii subunit <b>PDBTitle:</b> full-length human camkii
47	<a href="#">c3q5iA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase; <b>PDBTitle:</b> crystal structure of pbanka_031420
48	<a href="#">d1xbba</a>	Alignment	not modelled	100.0	42	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
49	<a href="#">c2bujA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase 16; <b>PDBTitle:</b> crystal structure of the human serine-threonine kinase 162 in complex with staurosporine
50	<a href="#">c3eygA</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase; <b>PDBTitle:</b> crystal structures of jak1 and jak2 inhibitor complexes
51	<a href="#">d1uwha</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
52	<a href="#">c3cc6A</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein tyrosine kinase 2 beta; <b>PDBTitle:</b> crystal structure of kinase domain of protein tyrosine kinase 2 beta2 (ptk2b)
53	<a href="#">d1byga</a>	Alignment	not modelled	100.0	100	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
54	<a href="#">c3fupB</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine-protein kinase jak2; <b>PDBTitle:</b> crystal structures of jak1 and jak2 inhibitor complexes
55	<a href="#">c3v5qB</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> nt-3 growth factor receptor; <b>PDBTitle:</b> discovery of a selective trk inhibitor with efficacy in

					rodent cancer2 tumor models
56	<a href="#">c1yvjA_</a>	Alignment	not modelled	100.0	36 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase jak3; <b>PDBTitle:</b> crystal structure of the jak3 kinase domain in complex with2 staurosporine analogue
57	<a href="#">c2a1aB_</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> protein synthesis/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> interferon-induced, double-stranded rna-activated protein <b>PDBTitle:</b> pkr kinase domain-eif2alpha complex
58	<a href="#">c3d4qA_</a>	Alignment	not modelled	100.0	33 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> b-raf proto-oncogene serine/threonine-protein kinase; <b>PDBTitle:</b> pyrazole-based inhibitors of b-raf kinase
59	<a href="#">c3sxrA_</a>	Alignment	not modelled	100.0	41 <b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic tyrosine-protein kinase bmx; <b>PDBTitle:</b> crystal structure of bmx non-receptor tyrosine kinase complex with2 dasatinib
60	<a href="#">d1yhwa1</a>	Alignment	not modelled	100.0	25 <b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
61	<a href="#">c2w1iB_</a>	Alignment	not modelled	100.0	37 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> jak2; <b>PDBTitle:</b> structure determination of aurora kinase in complex with2 inhibitor
62	<a href="#">d1mqba_</a>	Alignment	not modelled	100.0	39 <b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
63	<a href="#">c3lxaA_</a>	Alignment	not modelled	100.0	39 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> non-receptor tyrosine-protein kinase tyk2; <b>PDBTitle:</b> structural and thermodynamic characterization of the tyk2 and jak32 kinase domains in complex with cp-690550 and cmp-6
64	<a href="#">d1fvra_</a>	Alignment	not modelled	100.0	40 <b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
65	<a href="#">c3lijA_</a>	Alignment	not modelled	100.0	29 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calcium/calmodulin dependent protein kinase with <b>PDBTitle:</b> crystal structure of full length cpcdpk3 (cgd5_820) in2 complex with ca2+ and amppnp
66	<a href="#">c2clqA_</a>	Alignment	not modelled	100.0	26 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 5; <b>PDBTitle:</b> structure of mitogen-activated protein kinase kinase kinase2 5
67	<a href="#">c2bmcD_</a>	Alignment	not modelled	100.0	24 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> serine threonine-protein kinase 6; <b>PDBTitle:</b> aurora-2 t287d t288d complexed with pha-680632
68	<a href="#">d1rjba_</a>	Alignment	not modelled	100.0	44 <b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
69	<a href="#">c2wtkC_</a>	Alignment	not modelled	100.0	27 <b>PDB header:</b> transferase/metal-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> serine/threonine-protein kinase 11; <b>PDBTitle:</b> structure of the heterotrimeric lkb1-stradalpha-mo25alpha2 complex
70	<a href="#">c3p86B_</a>	Alignment	not modelled	100.0	37 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase ctr1; <b>PDBTitle:</b> crystal structure of ctr1 kinase domain mutant d676n in complex with2 staurosporine
71	<a href="#">c2qobA_</a>	Alignment	not modelled	100.0	37 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin receptor; <b>PDBTitle:</b> human epha3 kinase domain, base structure
72	<a href="#">d1phka_</a>	Alignment	not modelled	100.0	22 <b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
73	<a href="#">c1xkka_</a>	Alignment	not modelled	100.0	35 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> egfr kinase domain complexed with a quinazoline inhibitor-2 gw572016
74	<a href="#">d1xkka_</a>	Alignment	not modelled	100.0	35 <b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
75	<a href="#">c3fbvL_</a>	Alignment	not modelled	100.0	25 <b>PDB header:</b> transferase, hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> serine/threonine-protein kinase/endoribonuclease ire1; <b>PDBTitle:</b> crystal structure of the oligomer formed by the kinase-ribonuclease2 domain of ire1
76	<a href="#">d1ckia_</a>	Alignment	not modelled	100.0	20 <b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
77	<a href="#">c3dfaA_</a>	Alignment	not modelled	100.0	26 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-dependent protein kinase cgd3_920; <b>PDBTitle:</b> crystal structure of kinase domain of calcium-dependent protein kinase2 cgd3_920 from cryptosporidium parvum
78	<a href="#">d2jfla1</a>	Alignment	not modelled	100.0	25 <b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
79	<a href="#">c2j51A_</a>	Alignment	not modelled	100.0	26 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ste20-like serine/threonine-protein kinase; <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 <b>PDB header:</b> transferase

80	<a href="#">c3comB_</a>	Alignment	not modelled	100.0	26	<b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase 4; <b>PDBTitle:</b> crystal structure of mst1 kinase
81	<a href="#">c2cgvA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase chk1; <b>PDBTitle:</b> identification of chemically diverse chk1 inhibitors by2 receptor-based virtual screening
82	<a href="#">c3k54A_</a>	Alignment	not modelled	100.0	45	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase btk; <b>PDBTitle:</b> structures of human bruton's tyrosine kinase in active and inactive2 conformations suggests a mechanism of activation for tec family3 kinases.
83	<a href="#">d1o6ya_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
84	<a href="#">c2qg5D_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> calcium/calmodulin-dependent protein kinase; <b>PDBTitle:</b> cryptosporidium parvum calcium dependent protein kinase cgd7_1840
85	<a href="#">c2wqmA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase nek7; <b>PDBTitle:</b> structure of apo human nek7
86	<a href="#">c2y7jB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphorylase b kinase gamma catalytic chain, <b>PDBTitle:</b> structure of human phosphorylase kinase, gamma 2
87	<a href="#">c1mruB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable serine/threonine-protein kinase pknb; <b>PDBTitle:</b> intracellular ser/thr protein kinase domain of2 mycobacterium tuberculosis pknb.
88	<a href="#">c3p23B_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase/endoribonuclease ire1; <b>PDBTitle:</b> crystal structure of the human kinase and rnase domains in complex2 with adp
89	<a href="#">c2a27B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> death-associated protein kinase 2; <b>PDBTitle:</b> human drp-1 kinase, w305s s308a d40 mutant, crystal form with 82 monomers in the asymmetric unit
90	<a href="#">c3d9vA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rho-associated protein kinase 1; <b>PDBTitle:</b> crystal structure of rock i bound to h-1152p a di-2 methylated variant of fasudil
91	<a href="#">c3hztA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-dependent protein kinase 3; <b>PDBTitle:</b> crystal structure of toxoplasma gondii cdpk3, tgme49_105860
92	<a href="#">c3dtcA_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 9; <b>PDBTitle:</b> crystal structure of mixed-lineage kinase mlk1 complexed2 with compound 16
93	<a href="#">d1jksa_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
94	<a href="#">d1xjda_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
95	<a href="#">c1xjda_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c, theta type; <b>PDBTitle:</b> crystal structure of pkc-theta complexed with staurosporine2 at 2a resolution
96	<a href="#">c2bdwB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein k11e8.1d; <b>PDBTitle:</b> crystal structure of the auto-inhibited kinase domain of2 calcium/calmodulin activated kinase ii
97	<a href="#">c3brbB_</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> proto-oncogene tyrosine-protein kinase mer; <b>PDBTitle:</b> crystal structure of catalytic domain of the proto-oncogene tyrosine-2 protein kinase mer in complex with adp
98	<a href="#">c2zv2A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> calcium/calmodulin-dependent protein kinase kinase 2; <b>PDBTitle:</b> crystal structure of human calcium/calmodulin-dependent protein kinase2 kinase 2, beta, camkk2 kinase domain in complex with sto-609
99	<a href="#">c2ya9A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> death-associated protein kinase 2; <b>PDBTitle:</b> crystal structure of the autoinhibited form of mouse dapk2
100	<a href="#">d1nvra_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
101	<a href="#">d1koba_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
102	<a href="#">c2pziA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable serine/threonine-protein kinase pknq; <b>PDBTitle:</b> crystal structure of protein kinase pknq from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
103	<a href="#">c2vd5A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dmpk protein; <b>PDBTitle:</b> structure of human myotonic dystrophy protein kinase in2 complex with the bisindolylmaleide inhibitor bim viii

104	<a href="#">c2r5tA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine-protein kinase sgk1; <b>PDBTitle:</b> crystal structure of inactive serum and glucocorticoid-2 regulated kinase 1 in complex with amp-pnp
105	<a href="#">d1u46a_</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
106	<a href="#">c2wtkB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase/metal-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ste20-related kinase adapter protein alpha; <b>PDBTitle:</b> structure of the heterotrimeric Ikb1-stradalpha-mo25alpha2 complex
107	<a href="#">c2chlA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> casein kinase i isoform gamma-3; <b>PDBTitle:</b> structure of casein kinase 1 gamma 3
108	<a href="#">c2x4fA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> myosin light chain kinase family member 4; <b>PDBTitle:</b> the crystal structure of the human myosin light chain2 kinase loc340156.
109	<a href="#">d1ywna1</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
110	<a href="#">d1uu3a_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
111	<a href="#">c2r7bA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> signaling protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoinositide-dependent protein kinase 1; <b>PDBTitle:</b> crystal structure of the phosphoinositide-dependent kinase-2 1 (pdk-1)catalytic domain bound to a dibenzonaphthyridine3 inhibitor
112	<a href="#">d1koaa2</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
113	<a href="#">c2qluA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> activin receptor type iib; <b>PDBTitle:</b> crystal structure of activin receptor type ii kinase domain2 from human
114	<a href="#">c2vz6A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calcium calmodulin dependent protein kinase type ii alpha <b>PDBTitle:</b> structure of human calcium calmodulin dependent protein2 kinase type ii alpha (camk2a) in complex with indirubin3 e804
115	<a href="#">c2qofA_</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin receptor; <b>PDBTitle:</b> human epha3 kinase and juxtamembrane region, y596f mutant
116	<a href="#">c1kobB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> kinase <b>Chain:</b> B: <b>PDB Molecule:</b> twitchin; <b>PDBTitle:</b> twitchin kinase fragment (aplysia), autoregulated protein2 kinase domain
117	<a href="#">d1o6la_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Protein kinase-like (PK-like) <b>Superfamily:</b> Protein kinase-like (PK-like) <b>Family:</b> Protein kinases, catalytic subunit
118	<a href="#">c2c47D_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> casein kinase 1 gamma 2 isoform; <b>PDBTitle:</b> structure of casein kinase 1 gamma 2
119	<a href="#">c3qd2B_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 2- alpha kinase 3; <b>PDBTitle:</b> crsytal structure of mouse perk kinase domain
120	<a href="#">c2y94A_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-amp-activated protein kinase catalytic subunit alpha-1; <b>PDBTitle:</b> structure of an active form of mammalian ampk