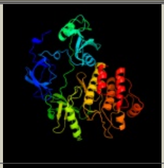
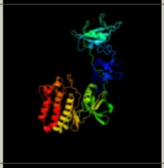
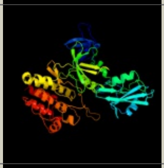
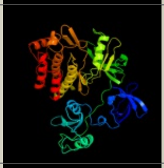
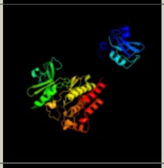
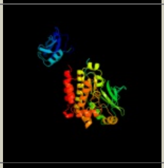
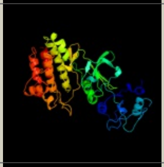
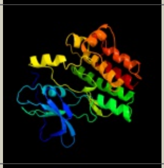
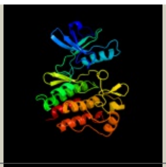
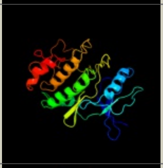
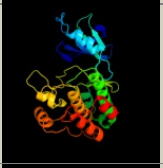
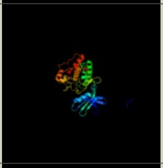
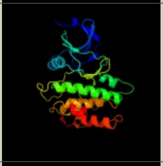
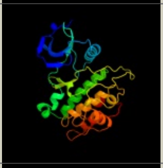
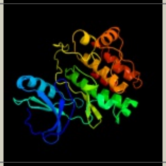
Email	l.a.kelley@imperial.ac.uk
Description	P08630
Date	Wed Feb 13 11:12:46 GMT 2013
Unique Job ID	e56f2dad7a05dda1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fo0A_	Alignment		100.0	41	**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	42	**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	41	**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	43	**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	41	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase hck; **PDBTitle:** src family kinase hck with bound inhibitor a-420983
7	c4fl2A_	Alignment		100.0	33	**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	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase zap-70; **PDBTitle:** autoinhibited intact human zap-70
9	c3cblA_	Alignment		100.0	38	**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	37	**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	d1qcfa3	Alignment		100.0	45	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit

12	d1opja_	Alignment		100.0	46	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
13	c3qa8H_	Alignment		100.0	25	**PDB header:**immune system, signaling protein **Chain:** H: **PDB Molecule:**mgc80376 protein; **PDBTitle:** crystal structure of inhibitor of kappa b kinase beta
14	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
15	c3pfqA_	Alignment		100.0	24	**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	c3nyoB_	Alignment		100.0	23	**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
17	d1qpca_	Alignment		100.0	44	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
18	c2acxB_	Alignment		100.0	23	**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
19	d1k2pa_	Alignment		100.0	57	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
20	c3c4wB_	Alignment		100.0	21	**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
21	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)
22	c2ivsA_	Alignment	not modelled	100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase receptor **PDBTitle:** crystal structure of non-phosphorylated ret tyrosine kinase2 domain
23	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
24	c3c4yA_	Alignment	not modelled	100.0	22	**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
25	d1u59a_	Alignment	not modelled	100.0	39	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
26	c3g0eA_	Alignment	not modelled	100.0	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mast/stem cell growth factor receptor; **PDBTitle:** kit kinase domain in complex with sunitinib
27	c3qa8A_	Alignment	not modelled	100.0	24	**PDB header:**immune system, signaling protein **Chain:** A: **PDB Molecule:**mgc80376 protein; **PDBTitle:** crystal structure of inhibitor of kappa b kinase beta
28	d1lufa_	Alignment	not modelled	100.0	39	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
						PDB header:transferase

29	c1lufA_	Alignment	not modelled	100.0	39	**Chain:** A: **PDB Molecule:**muscle-specific tyrosine kinase receptor musk; **PDBTitle:** crystal structure of the musk tyrosine kinase: insights2 into receptor autoregulation
30	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
31	c1koaA_	Alignment	not modelled	100.0	25	**PDB header:**kinase **Chain:** A: **PDB Molecule:**twitchin; **PDBTitle:** twitchin kinase fragment (c.elegans), autoregulated protein2 kinase and immunoglobulin domains
32	c2pvfA_	Alignment	not modelled	100.0	37	**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
33	d2j4za1	Alignment	not modelled	100.0	25	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
34	c3tkuB_	Alignment	not modelled	100.0	21	**PDB header:**transferase/transferase inhibitor **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase mrck beta; **PDBTitle:** mrck beta in complex with fasudil
35	c3dpkA_	Alignment	not modelled	100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrophage colony-stimulating factor 1 receptor; **PDBTitle:** cfms tyrosine kinase in complex with a pyridopyrimidinone2 inhibitor
36	c2psqA_	Alignment	not modelled	100.0	38	**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
37	d2psqa1	Alignment	not modelled	100.0	38	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
38	d3bu3a1	Alignment	not modelled	100.0	37	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
39	c2c30A_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase pak 6; **PDBTitle:** crystal structure of the human p21-activated kinase 6
40	d1fmka3	Alignment	not modelled	100.0	49	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
41	c3soaA_	Alignment	not modelled	100.0	23	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**calcium/calmodulin-dependent protein kinase type ii subunit **PDBTitle:** full-length human camkii
42	c3q5iA_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase; **PDBTitle:** crystal structure of pbanka_031420
43	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)
44	c4aojA_	Alignment	not modelled	100.0	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**high affinity nerve growth factor receptor; **PDBTitle:** human trka in complex with the inhibitor az-23
45	c3kulB_	Alignment	not modelled	100.0	39	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 8; **PDBTitle:** kinase domain of human ephrin type-a receptor 8 (epha8)
46	c4fijA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase pak 4; **PDBTitle:** catalytic domain of human pak4
47	d1sm2a_	Alignment	not modelled	100.0	54	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
48	d1t46a_	Alignment	not modelled	100.0	35	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
49	c3lxkA_	Alignment	not modelled	100.0	36	**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
50	c3plsA_	Alignment	not modelled	100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrophage-stimulating protein receptor; **PDBTitle:** ron in complex with ligand amp-pnp
51	c3sxrA_	Alignment	not modelled	100.0	55	**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
52	d1p4oa_	Alignment	not modelled	100.0	33	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
53	c2jamB_	Alignment	not modelled	100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calcium/calmodulin-dependent protein kinase type **PDBTitle:** crystal structure of human calmodulin-dependent protein2 kinase i g
54	c4fieB_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak 4;

						PDBTitle: full-length human pak4
55	c2a1aB_	Alignment	not modelled	100.0	25	**PDB header:**protein synthesis/transferase **Chain:** B: **PDB Molecule:**interferon-induced, double-stranded rna-activated protein **PDBTitle:** pkr kinase domain-eif2alpha complex
56	c4ebwA_	Alignment	not modelled	100.0	38	**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
57	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
58	c2bujA_	Alignment	not modelled	100.0	18	**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
59	c3lvpD_	Alignment	not modelled	100.0	35	**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
60	c3d9vA_	Alignment	not modelled	100.0	21	**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
61	d1yhwa1	Alignment	not modelled	100.0	22	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
62	d1mp8a_	Alignment	not modelled	100.0	37	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
63	c3fbvL_	Alignment	not modelled	100.0	26	**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
64	c3lijA_	Alignment	not modelled	100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calcium/calmodulin dependent protein kinase with **PDBTitle:** crystal structure of full length cpcdpk3 (cgd5_820) in2 complex with ca2+ and amppnp
65	d1fgka_	Alignment	not modelled	100.0	36	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
66	c4eutA_	Alignment	not modelled	100.0	25	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase tbk1; **PDBTitle:** structure of bx-795 complexed with unphosphorylated human tbk1 kinase-2 uld domain
67	c2clqA_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mitogen-activated protein kinase kinase kinase 5; **PDBTitle:** structure of mitogen-activated protein kinase kinase kinase2 5
68	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
69	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
70	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
71	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
72	d1phka_	Alignment	not modelled	100.0	22	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
73	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
74	d1uwha_	Alignment	not modelled	100.0	34	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
75	d1jpaa_	Alignment	not modelled	100.0	37	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
76	c1yvjA_	Alignment	not modelled	100.0	35	**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
77	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
78	c3cc6A_	Alignment	not modelled	100.0	39	**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)
79	c2y7iB_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphorylase b kinase gamma catalytic

79	c2y7jB_	Alignment	not modelled	100.0	20	chain, **PDBTitle:** structure of human phosphorylase kinase, gamma 2
80	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
81	d1xbba_	Alignment	not modelled	100.0	38	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
82	d2jfla1	Alignment	not modelled	100.0	26	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
83	c3dfaA_	Alignment	not modelled	100.0	24	**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
84	c3d4qA_	Alignment	not modelled	100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**b-raf proto-oncogene serine/threonine-protein kinase; **PDBTitle:** pyrazole-based inhibitors of b-raf kinase
85	c2vd5A_	Alignment	not modelled	100.0	22	**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
86	d1mqba_	Alignment	not modelled	100.0	40	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
87	c2qg5D_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**calcium/calmodulin-dependent protein kinase; **PDBTitle:** cryptosporidium parvum calcium dependent protein kinase cgd7_1840
88	c2a27B_	Alignment	not modelled	100.0	21	**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
89	c3p23B_	Alignment	not modelled	100.0	22	**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
90	d1jksa_	Alignment	not modelled	100.0	24	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
91	d1fvra_	Alignment	not modelled	100.0	40	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
92	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
93	c3v5qB_	Alignment	not modelled	100.0	40	**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
94	d1rjba_	Alignment	not modelled	100.0	43	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
95	c3lxnA_	Alignment	not modelled	100.0	34	**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
96	c3comB_	Alignment	not modelled	100.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase 4; **PDBTitle:** crystal structure of mst1 kinase
97	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
98	c2bdwB_	Alignment	not modelled	100.0	25	**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
99	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.
100	c2wqmA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase nek7; **PDBTitle:** structure of apo human nek7
101	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
102	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
103	d1xjda_	Alignment	not modelled	100.0	22	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit

104	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
105	d1koba_	Alignment	not modelled	100.0	23	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
106	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
107	d1nvra_	Alignment	not modelled	100.0	21	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
108	c1xkkA_	Alignment	not modelled	100.0	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** egfr kinase domain complexed with a quinazoline inhibitor-2 gw572016
109	d1xkka_	Alignment	not modelled	100.0	37	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
110	c3k54A_	Alignment	not modelled	100.0	55	**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.
111	c2qobA_	Alignment	not modelled	100.0	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin receptor; **PDBTitle:** human epha3 kinase domain, base structure
112	c4g3dE_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** E: **PDB Molecule:**nf-kappa-beta-inducing kinase; **PDBTitle:** crystal structure of human nf-kappab inducing kinase (nik)
113	d1ckia_	Alignment	not modelled	100.0	20	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
114	d1o6ya_	Alignment	not modelled	100.0	25	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
115	c2pziA_	Alignment	not modelled	100.0	16	**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 tetrahydrobenzothiophene ax20017
116	c2x4fA_	Alignment	not modelled	100.0	21	**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.
117	c3p86B_	Alignment	not modelled	100.0	36	**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
118	d1koaa2	Alignment	not modelled	100.0	24	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
119	c1kobB_	Alignment	not modelled	100.0	23	**PDB header:**kinase **Chain:** B: **PDB Molecule:**twitchin; **PDBTitle:** twitchin kinase fragment (aplysia), autoregulated protein2 kinase domain
120	c4eqmE_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** E: **PDB Molecule:**protein kinase; **PDBTitle:** structural analysis of staphylococcus aureus serine/threonine kinase2 pknb