A

Residues	Peptide sequence	Modifications	# of PSMs
52-68	NVSSFPDDATSPLQENR	1x phospho [S/T]	99
51-68	RNVSSFPDDATSPLQENR	1x phospho [S/T]	53
52-83	NVSSFPDDATSPLQENRRNNQGTVNWSVDDIVK	1x phospho [S/T]	9
52-68	NVSSFPDDATSPLQENR	2x phospho [S55;S62]	7
51-83	RNVSSFPDDATSPLQENRRNNQGTVNWSVDDIVK	1x phospho [S62]	2
354-366	EATWTMSNITAGR	1x phospho [T358]	1
487-494	ASLSLIEK	1x phospho [S490]	1
1-13	MSTNENANTPAAR	1x oxidation [M1]	3

B

KPNA2 (impα1)...NVSSFPDDAT----SPLQENRNNQG
KPNA1 (impα5)...NVATAEEETEEEVMSDGGFHEAQIS
KPNA3 (impα4)...NVPQEESLED----SDVDADFKAQN
KPNA4 (impα3)...NVPHEDICED----SDIDGDYRVQN
KPNA5 (impα6)...NVYLPRNDESMLE-SPIQDPDISST
KPNA6 (impα7)...NVELINEEAAMFD-SLLMDSYVSST
KPNA7 (impα8)...NITSFCPDTP----SEKTAKGVAVS

Fig. S1. Mitotically phosphorylated peptides of importin α identified by mass spec.

(A) Sequences of the mitosis-specific phosphorylated peptides of importin α1 identified by mass spectrometry and the number of identified peptides (# PSMs).

(B) The CDK1 phosphorylation consensus motif at Ser62 in importin α1 (KPNA2) is poorly conserved between members of the importin α protein family. Alignment of the sequences corresponding to the phosphorylated importin α1 peptide of the seven human protein members of the importin α (karyopherin α/KPNA) protein family. The serine/proline CDK1 consensus motif of KPNA2 (importin α1) highlighted in red, is present in KPNA5 (importin α6) but not in other family members.