Supplementary Table 1. Amino acid alignment of known bipartite nuclear localization signals

Protein Name (Source)	***A possible consensus of bipartite NLSs***	***Spacer length***
	K R – $X_{(10-12)}$ –K (K/R) (K/R) or K R – $X_{(10-12)}$ –K (K/R) –X – (K/R) (K/R) (K/R) – $X_{(10–12)}$ – (K/R) K R – $X_{(10-12)}$ – K R R K	
Npl	**K R** *P A A T K K A G Q A* **K K K K** L D	10
NIN2	R K **K R** *K T E E E S P L K D K A* **K K** S K	13
SWI5	**K K** *Y E N V V I K R S P R* **K R** G R P R K	11
Rb	**K R** *S A E G S N P P K P L* **K K** L R	12
PB2	K R **K R** *D S S I L T D S Q T A T* **K R** I R M A	13
CBP80	S **R R** *R H S D E N D G G O P H K* **R R K** T S	13
c-Met	Q **H** *V V I G P S S L I V* **H**	10

Npl, nucleoplasmin; NIN2, Xenopus phosphoprotein NIN2; SWI5, Saccharomyces cerevisiae protein SWI5; Rb, retinoblastoma protein; Pb2, influenza virus polymerase Pb2; CBP80, human cap-binding protein 80; c-Met, human receptor tyrosine kinase protein c-Met.

Ref. Molecular basis for specificity of nuclear import and prediction of nuclear localization. (Biochim Biophys Acta. 2011 Sep; 1813 (9):1562-77.)