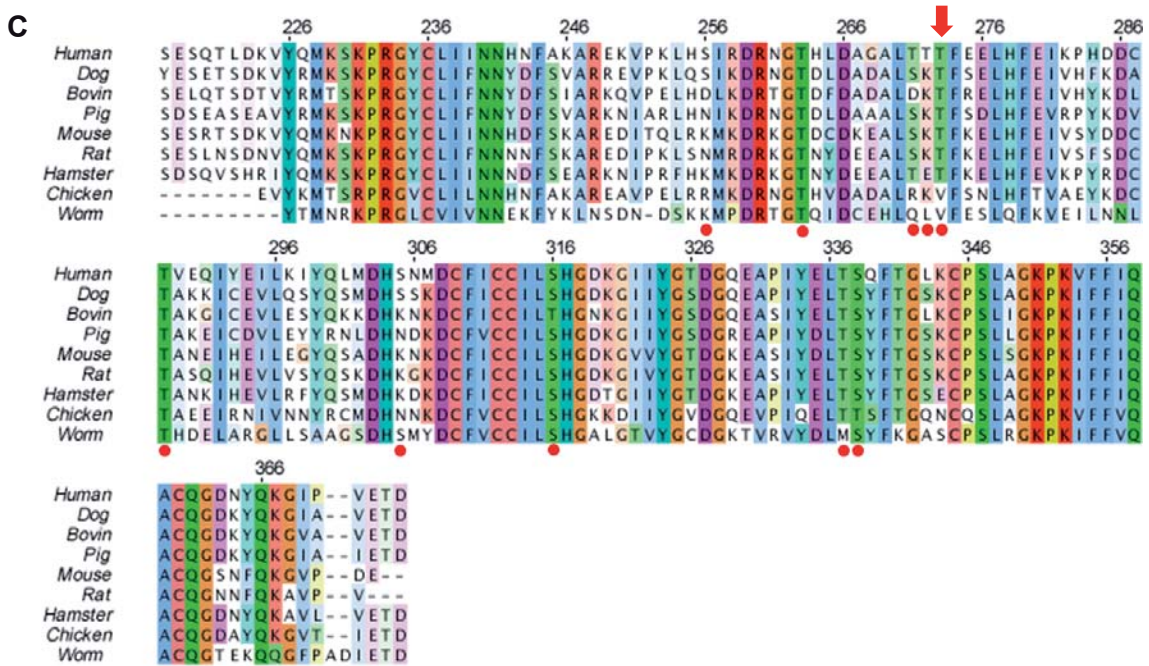


B

Position	-4	-3	-2	-1	0	+1	+2	+3	+4
www.phosphosite.org	F	E	E	F	S	D	D	E	D
Salviet al, 2012	E	E/D	X	E/D	S/T	E/D	E/D	E/D	E/D



D

position	T273
TOP loc p-value	0.76 (CellCycleAllphases)
surrounding sequence	DAGALTTTFEELHFE
matching motifs	CK2 (S/T-X-X-E), NEK6 (L-X-X-S/T)

Supplementary Information, Figure S3. The Plk3 consensus site and phylogenetic alignment of caspase-8-p18.

(A) Schematic representation of the consensus site for Plk3 phosphorylation based on the analysis of 21 input sequences in Plk3 substrates (www.phosphosite.org). (B) Schematic representation of the substrate consensus sequences of Plk3 based on www.phosphosite.org and an analysis of peptide libraries for the identification of Plk3 phosphorylation sites. (C) Phylogenetic alignment of caspase-8-p18 using ClustalW2 among different species (Jalview representation). The conserved threonines/serines that exhibit additional acidic surrounding residues are highlighted by red points. T273 is highlighted by a red arrow. (D) Analysis of caspase-8 phosphorylation shown in PHOSIDA, a posttranslational modification database obtained from a high-resolution MS analysis.