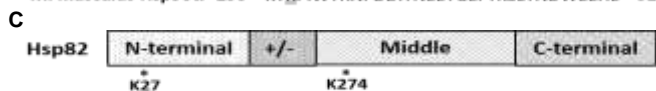


A

<i>H. sapiens</i> Hsp90α	18-	ETFAFQAEIAQLMSLIINTFY <u>SN</u> <u>K</u> EIFLRELIS	-50
<i>G. gallus</i> Hsp90β	13-	ETFAFQAEIAQLMSLIINTFY <u>SN</u> <u>K</u> EIFLRELIS	-45
<i>S. cerevisiae</i> Hsp82	4-	ETFEFQAEITQLMSLIINTV <u>YS</u> <u>N</u> <u>K</u> EIFLRELIS	-36
<i>S. cerevisiae</i> Hsc82	4-	ETFEFQAEITQLMSLIINTV <u>YS</u> <u>N</u> <u>K</u> EIFLRELIS	-36
<i>G. gallus</i> Hsp90α	17-	ETFAFQAEIAQLMSLIINTFY <u>SN</u> <u>K</u> EIFLRELIS	-49
<i>H. sapiens</i> Hsp90β	13-	ETFAFQAEIAQLMSLIINTFY <u>SN</u> <u>K</u> EIFLRELIS	-45
<i>M. musculus</i> Hsp90β	13-	ETFAFQAEIAQLMSLIINTFY <u>SN</u> <u>K</u> EIFLRELIS	-45
<i>M. musculus</i> Hsp90α	18-	ETFAFQAEIAQLMSLIINTFY <u>SN</u> <u>K</u> EIFLRELIS	-50

B

<i>H. sapiens</i> Hsp90α	292-	KT <u>K</u> PIWTRNPDDITNEEYGEFYKSLTNDWEDHL	-324
<i>G. gallus</i> Hsp90β	288-	KT <u>K</u> PIWTRNPDDITQEEYGEFYKSLTNDWEDHL	-321
<i>S. cerevisiae</i> Hsp82	272-	KT <u>K</u> PLWTRNPSDITQEEYNAFYK <u>S</u> ISNDWEDPL	-304
<i>S. cerevisiae</i> Hsc82	268-	KT <u>K</u> PLWTRNPSDITQEEYNAFYK <u>S</u> ISNDWEDPL	-300
<i>G. gallus</i> Hsp90α	288-	KT <u>K</u> PIWTRNPDDITNEEYGEFYKSLTNDWEDHL	-320
<i>H. sapiens</i> Hsp90β	284-	KT <u>K</u> PIWTRNPDDITQEEYGEFYKSLTNDWEDHL	-316
<i>M. musculus</i> Hsp90β	284-	KT <u>K</u> PIWTRNPDDITQEEYGEFYKSLTNDWEDHL	-316
<i>M. musculus</i> Hsp90α	293-	KT <u>K</u> PIWTRNPDDITNEEYGEFYKSLTNDWEEHL	-325



Supporting information Figure S1: (A) & (B) Multiple sequence alignment of Hsp90 isoforms (alpha and beta) from *Homo sapiens*, *Gallus gallus* *Saccharomyces cerevisiae* and *Mus musculus* showed that both the K27 and K274 residues (shown in bold and underlined) are conserved across the eukaryotes. (C) Schematic representation of Hsp82 domain structure illustrates the position of K27 in the N-terminal domain and K274 in the middle domain; (+/-) denotes the charged-linker region.