a GSESGDNVR**S SAGAVRDAGG AFGKREQAEE ERYFRARAKE QLAALKKHHE NEISHH**AKEI ERLQKEIERH KQSIKKLKQS EDDD

b GSDQSENVDR GAGSIREAGG AFGKREQAEE ERYFRAQSRE QLAALKKHHE EEIVHHKKEI ERLQKEIERH KQKIKMLKH- -DDR

c VSDSSDSMDT GAGSIREAGG AFGKREKAEE DRYFREKTKE QLAALRKHHE DEIDHHSKEI ERLQKQIERH KKKIQQLKNN -H--

d **-SEGSTGTPR GSG----SED SFVKRERATE DFFVRQREKE QLRHLK---- EQLEKQRKKI DS**LENKIDSM TK-------- ----

a : *Bos taurus*

b : *Homo sapiens*

c : *Mus musculus*

d : *Saccharomyces cerevisiae*

**S3 Fig. Sequence of inhibitory peptides IF1 from different species**.

The partial sequence from *Bos taurus* written in bold (a) is sufficient for fully preserving the inhibitory effect of IF1 and its high affinity for F1-ATPase [1]. The peptide with the partial sequence from *Saccharomyces cerevisiae* in bold (d) inhibits F0F1 ATPase activity of murine tissue homogenates with the same efficiency as the full peptide (this work). Replacement of the underlined residue (F28) by a tryptophan increased the peptide absorbance at 280 nm and facilitated its purification when overexpressed in *E. coli*. This mutation did not alter its inhibitory properties [2].

1. van Raaij MJ, Orriss GL, Montgomery MG, Runswick MJ, Fearnley IM, Skehel JM, et al. The ATPase inhibitor protein from bovine heart mitochondria: the minimal inhibitory sequence. Biochemistry. 1996;35(49):15618-25. doi: 10.1021/bi960628f. PubMed PMID: 8961923.

2. Andrianaivomananjaona T, Moune-Dimala M, Herga S, David V, Haraux F. How the N-terminal extremity of Saccharomyces cerevisiae IF1 interacts with ATP synthase: a kinetic approach. Biochim Biophys Acta. 2011;1807(2):197-204. PubMed PMID: 20951672.