

Supplementary Table 1

LVIYDVSYSR

LVLYDVSYSR

PG**Q**APVLVLYDDSDRPSG**I**PER

GP**A**GAPVLVLYDDSDRPSG**L**PER

PGQAP**LLV**VYYNNDRPSWIPER

PGQAP**VLV**IYYDNDRPSWIPER

PGQAPVLVYYDDSDRPS**SG**I^{PER}

GPQAPVLVYYDDSDRPE**EK**PER

AS**Q**SISTSLNWYQQK

AS**G**ASLSTSNWYQQK

VTITCQASQ**G**ITK

VTITCQASQGA**I**SK

SL**V**YAASSLQTGVPSK

SL**I**YGASTLQSGVPSK

VL**I**YDASNLATGVPLR

VL**L**YDASNLATGVPLR

Supplementary Table 1 Comparison of a sample of CDR tryptic peptide sequences translated from DNA sequence (top) and sequences obtained by mass spectrometry and the PEAKS software (bottom). I and L, SGI and EK, Q and AG, IT and AIS all have the same nominal mass the software was not able to distinguish and are highlighted by bold/underline.