

Confirmed identification of an HLA-A*02:01+ KRAS G12V+ *cis*-spliced peptide produced by proteasomes

Correspondence to: michele.mishto@kcl.ac.uk, jliepe@mpibpc.mpg.de.

Table S1	MS scans reanalyzed in Beer's matters arising
Table S2	Orbitraps' MS2 spectra assigned to the KRAS _{5-6/8-14} G12V <i>cis</i> -spliced peptide and the KRAS ₅₋₁₃ G12V non-spliced peptide.
Table S3	List of samples that were measured through four different mass spectrometers before and after the MS RAW files provided in our original paper [1] and in the present study
Figure S1	KRAS _{5-6/8-14} G12V <i>cis</i> -spliced and KRAS ₅₋₁₃ G12V non-spliced peptides' MS ion chromatograms of <i>in vitro</i> digestion kinetics measured through Q Exactive HF Orbitrap
Figure S2	KRAS _{5-6/8-14} G12V <i>cis</i> -spliced and KRAS ₅₋₁₃ G12V non-spliced peptides' MS ion chromatograms of <i>in vitro</i> digestion kinetics measured through Q Exactive Orbitrap

Table S1. MS scans reanalyzed in Beer's matters arising. Here, the details of the three MS scans (11558, 11683, 11389) - discussed in Beer's matters arising [2], and generated for our original study [1] – are reported. The file is accessible in the journal's website.

Table S2. Orbitraps' MS2 spectra assigned to the KRAS_{5-6/8-14} G12V *cis*-spliced peptide and the KRAS₅₋₁₃ G12V non-spliced peptide. Information about the MS2 spectra generated by Exploris 480 Orbitrap, Q Exactive HF and Fusion Lumos Orbitraps and assigned to the KRAS_{5-6/8-14} G12V *cis*-spliced peptide and the KRAS₅₋₁₃ G12V non-spliced peptide by our pipeline. The file is accessible in the journal's website.

Table S3. List of samples that were measured through four different mass spectrometers before and after the MS RAW files provided in our original paper [1]. List of samples that were measured through: (i) the Q Exactive Orbitrap and Fusion Lumos Orbitrap before and after the MS Raw files published in the PRIDE repository (PXD015580) associated to our original study [1]; (ii) the Exploris 480 and Q Exactive HF Orbitraps before and after the MS Raw files published in the PRIDE repository (PDX024528) associated to our rebuttal article. Only samples related to our rebuttal article have been listed. To note, we have never measured the synthetic KRAS_{5-6/8-14} peptide prior *in vitro* digestions. The file is accessible in the journal's website.

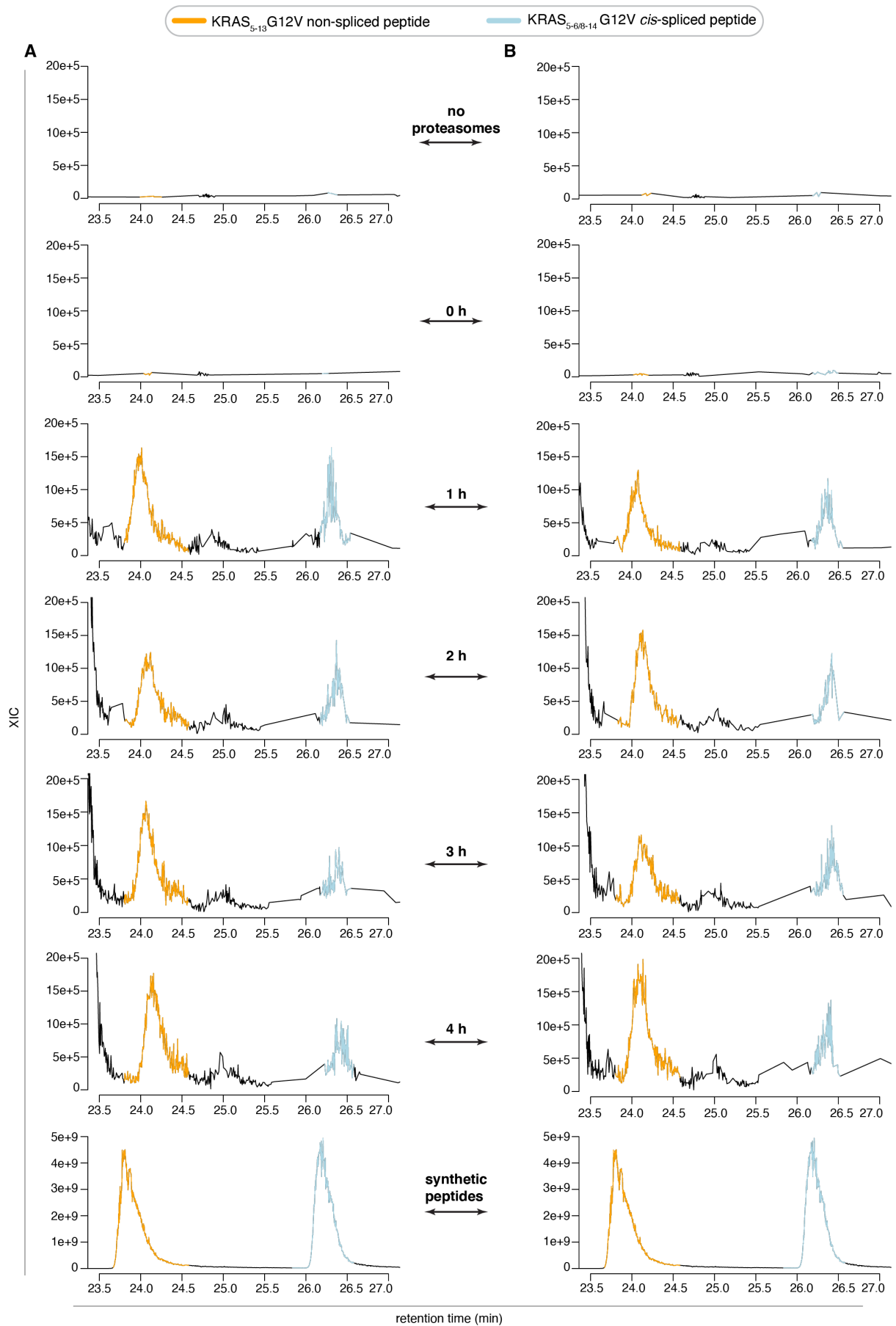


Figure S1. KRAS_{5-6/8-14} G12V *cis*-spliced and KRAS₅₋₁₃ G12V non-spliced peptides' MS ion chromatograms of *in vitro* digestion kinetics measured through Q Exactive HF Orbitrap. (A,B) MS extracted ion chromatograms (for the $m/z = 421.275 - 421.875$) of *in vitro* digestion kinetics (0-4 h) of the synthetic polypeptide KRAS₂₋₃₅ G12V with purified proteasomes named as "MF" (**A**) and "MG" (**B**) series. The peak corresponding to the KRAS_{5-6/8-14} G12V *cis*-spliced and KRAS₅₋₁₃ G12V non-spliced peptides are color labelled. For comparison, the synthetic peptide counterparts are plotted and indicate matching RTs. Samples were measured through Q Exactive HF Orbitrap. Synthetic peptides have been measured after the *in vitro* digestion kinetics (**Table S3**).

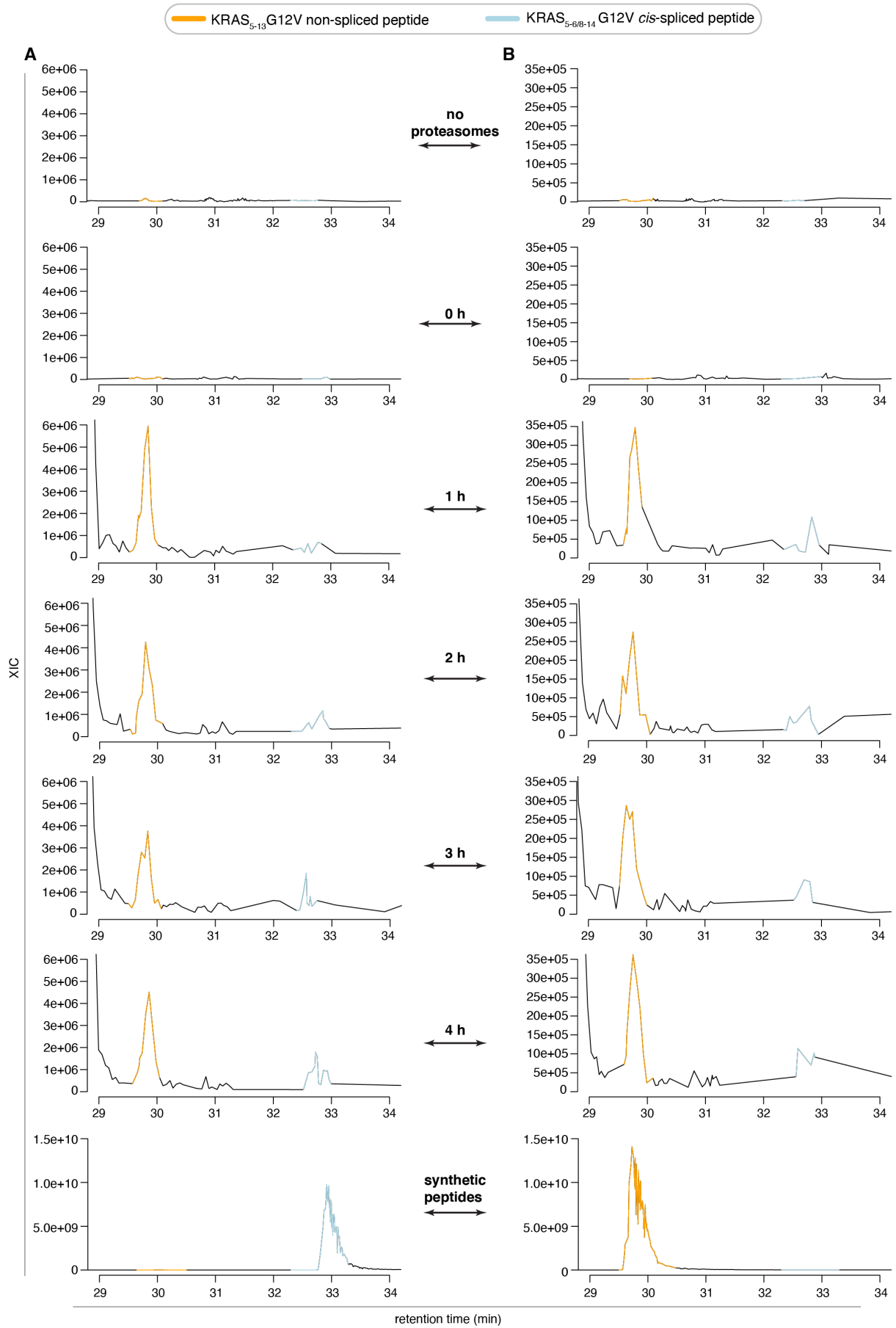


Figure S2. KRAS_{5-6/8-14} G12V *cis*-spliced and KRAS₅₋₁₃ G12V non-spliced peptides' MS ion chromatograms of *in vitro* digestion kinetics measured through Q Exactive Orbitrap. (A,B) MS extracted ion chromatograms (for the m/z = 421.275 – 421.875) of *in vitro* digestion kinetics (0-4 h) of the synthetic polypeptide KRAS₂₋₃₅ G12V with purified proteasomes named as “MF” (A) and “MG” (B) series. The peak corresponding to the KRAS_{5-6/8-14} G12V *cis*-spliced and KRAS₅₋₁₃ G12V non-spliced peptides are color labelled. For comparison, the synthetic peptide counterparts (measured singularly as in opposite to Fig. 4) are plotted and indicate matching RTs. Samples were measured through Q Exactive Orbitrap and the same method as in the original study [1]. Synthetic peptides have been measured after the *in vitro* digestion kinetics (Table S3).

Reference

- [1] M. Mishto, A. Mansurkhodzhaev, G. Ying, A. Bitra, R.A. Cordfunke, S. Henze, D. Paul, J. Sidney, H. Urlaub, J. Neefjes, A. Sette, D.M. Zajonc, and J. Liepe, An in silico-in vitro Pipeline Identifying an HLA-A(*02:01(+)) KRAS G12V(+) Spliced Epitope Candidate for a Broad Tumor-Immune Response in Cancer Patients. *Front Immunol* 10 (2019) 2572.
- [2] I. Beer, Commentary: An in silico-in vitro Pipeline Identifying an HLA-A*02:01+ KRAS G12V+ Spliced Epitope Candidate for a Broad Tumor-Immune Response in Cancer Patients. *Front Immunol* (2021).