Update Notice: Immunopeptidomics Workflow for Isolation and LC-MS/MS Analysis of MHC Class I-Bound Peptides Under Hypoxic Conditions

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Following the publication of our article, "Immunopeptidomics Workflow for Isolation and LC-MS/MS Analysis of MHC Class I-Bound Peptides Under Hypoxic Conditions" (Estephan et al., 2025; doi: 10.21769/BioProtoc.5505), it has been brought to our attention that the legend for Figure 1 requires a citation to the primary research article from which the western blot in Figure 1A was adapted.
The legend for Figure 1 has been updated to include a citation to the original publication. The updated legend also clarifies the cell lines presented in the figure by removing the specific cell line name from the legend title. The corrected legend is provided below.

Updated Figure 1 legend:
Figure 1. Overview of immunopeptidomics data analysis for cells exposed to normoxia or hypoxia for 24 h. (A) Representative western blot of HT29 cells exposed to hypoxic conditions ($<0.1\%$ O_2) for the indicated time points. (B) Total number of major histocompatibility complex (MHC) I peptides present on HCT116 cells in normoxia and hypoxia ($<0.1\%$ O_2). (C) Unique number of MHC I peptides in normoxia vs. hypoxia after 24 h. (D) Allele binding distribution of MHC I peptides. (E) Length frequency distribution of MHC I peptides. (F) Seqlogo comparison of MHC binding motifs in normoxia and hypoxia for three different MHC I subtypes. Peptides were assessed using NetMHCPan 4.1. Data represent mean ± SEM from three biological replicates. Statistical significance was determined using an unpaired Student's t-test. Adapted from Estephan et al. [28].