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Author Correction: Nuclear Translocation of Glutaminase GLS2 in Human Cancer Cells Associates with Proliferation Arrest and Differentiation

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Correction to: *Scientific Reports* https://doi.org/10.1038/s41598-020-58264-4, published online 10 February 2020

This Article contains errors.

In the Results section under subheading 'Posttranslational modification of human GLS2 protein',

"With regard to posttranslational modifications, LC-MS/MS analysis identified the chymotryptic peptide – KEKKCFPKGVDMMAAL - being modified with acetylhypusine in the fourth lysine residue (K-336 of the whole GLS2 amino acid sequence) (Fig. 6-A)."

should read:

"With regard to posttranslational modifications, LC-MS/MS analysis identified the chymotryptic peptide – KEKKCFPKGVDMMAAL - being modified with acetylhypusine in the fourth amino acid residue (K-332 of the whole GLS2 amino acid sequence) (Fig. 6-A)."

In the last paragraph of the Discussion section,

"The hypusine-modified lysine in the GAB primary structure (K-336) is located in an unfolded segment of the protein, a short turn of 9 residues connecting two alpha helices in a sequence highly enriched in polar amino acids (KKCFPKGVD), which strongly suggest that this hypusinated lysine is exposed to the external medium."

should read:

"The hypusine-modified lysine in the GAB primary structure (K-332) is located in an unfolded segment of the protein, a short turn of 9 residues connecting two alpha helices in a sequence highly enriched in polar amino acids (KKCFPKGVD), which strongly suggest that this hypusinated lysine is exposed to the external medium."

In the Methods section the subheading 'LC-MS/MS analysis using Orbitrap Q-Exactive HF'

should read:

'LC-MS/MS analysis using a Thermo Orbitrap Velos'

Under the same subheading,

"Mass spectrometry was performed on a hybrid linear trap quadrupole Orbitrap Q-Exactive HF spectrometer (ThermoFisher Scientific, Waltham, MA) using the Xcalibur version 2.1.0 coupled to an Agilent 1200 HPLC nanoflow system via a nanoelectrospray ion source using liquid junction (Proxeon, Odense, Denmark)."

should read:

"Mass spectrometry was performed on a Thermo LTQ-Orbitrap Velos spectrometer (ThermoFisher Scientific, Waltham, MA) using the Xcalibur version 2.1.0 coupled to an Agilent 1200 HPLC nanoflow system via a nanoelectrospray ion source using liquid junction (Proxeon, Odense, Denmark)."

Finally, the Data Availability statement is incomplete.

"The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request. All data generated or analysed during this study are included in this published article [and its supplementary information files]."

should read:

"The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD021033. The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request. All data generated or analysed during this study are included in this published article [and its supplementary information files]."