



Correction: The molecular identity of the TLQP-21 peptide receptor

Bhavani S. Sahu¹ · Megin E. Nguyen^{2,3} · Pedro Rodriguez² · Jean Pierre Pallais² · Vinayak Ghosh¹ · Maria Razzoli² · Yuk Y. Sham^{2,3} · Stephen R. Salton⁴ · Alessandro Bartolomucci²

Accepted: 2 February 2023 / Published online: 20 February 2023
© The Author(s) 2023

Correction to: Cellular and Molecular Life Sciences
(2021) 78:7133–7144
<https://doi.org/10.1007/s00018-021-03944-1>

In this article the legend for Fig. 2 was inadvertently processed incorrectly; the Fig. 2 caption should have appeared as shown below.

Figure 2 Structure and sequence of C3aR1, gC1qR and HSPA8. **A** Left to right: 3-dimensional structures of human C3aR1 (NP_001313406.1, homology model [4]), C1qR (PDB: 6SZW [81]), and structure binding domain of HSPA8 (PDB: 4PO2 [80]). Structures are shown as ribbon representation and colored by chain. **B** Multiple sequence alignment of human and mouse sequences of C3aR1, C1qR, and HSPA8. Alignment performed with MUSCLE in Schrödinger Multiple Sequence Viewer (Maestro, Schrödinger, LLC, New York, NY, 2020) with 10.0 opening gap and 0.20 extending gap penalties and manually inspected. Only sequence regions within 10 residues of

C3aR1 key binding site residues are shown for simplicity. Grey rectangles indicate extension of sequences not shown. Black outline indicates C3aR1 residues that form salt bridge interactions with TLQP-21 pharmacophore

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

The original article can be found online at <https://doi.org/10.1007/s00018-021-03944-1>.

✉ Alessandro Bartolomucci
abartolo@umn.edu

¹ National Brain Research Centre, NH-8, Manesar, Gurugram, Haryana 122052, India

² Department of Integrative Biology and Physiology, University of Minnesota, 2231 6th St. SE, Minneapolis, MN 55455, USA

³ Bioinformatics and Computational Biology Program, University of Minnesota, Minneapolis, USA

⁴ Departments of Neuroscience and Geriatrics and Palliative Medicine, Friedman Brain Institute, Icahn School of Medicine at Mount Sinai, One Gustave L. Levy Place, New York, NY 10029, USA