



Publisher Correction: Predicting functional consequences of mutations using molecular interaction network features

Kivilcim Ozturk^{1,2} · Hannah Carter^{1,2,3}

Published online: 24 September 2022
© The Author(s) 2022

Publisher Correction:

Human Genetics (2021) 141:1195–1210

<https://doi.org/10.1007/s00439-021-02329-5>

Publisher's Note: Predicting functional consequences of mutations using molecular interaction network features.

The Publisher regrets that the article by Ozturk, K., Carter, H. (Ozturk and Carter 2022) which is part of this Special Issue: Computational Interpretation of Human Genetic Variation, was published in an earlier issue 141(6):1195–1210.

We would like to express our thanks to the Guest Editors, Prof. Yana Bromberg and Prof. Predrag Radivojac, for their dedication and work assembling this collection of reviews and research for Human Genetics.

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/>.

Reference

Ozturk K, Carter H (2022) Predicting functional consequences of mutations using molecular interaction network features. Hum Genet 141:1195–1210. <https://doi.org/10.1007/s00439-021-02329-5>

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/s00439-021-02329-5>.

✉ Hannah Carter
hkcarter@health.ucsd.edu

¹ Division of Medical Genetics, Department of Medicine, University of California San Diego, La Jolla, CA, USA

² Bioinformatics and Systems Biology Program, University of California San Diego, La Jolla, CA, USA

³ Moores Cancer Center, University of California San Diego, La Jolla, CA, USA