



OPEN ACCESS

EDITED AND REVIEWED BY
Annalisa Pastore,
King's College London, United Kingdom

*CORRESPONDENCE
N. V. Petukhova,
✉ petuhovanv@1spbgmu.ru

RECEIVED 25 October 2024
ACCEPTED 11 November 2024
PUBLISHED 28 November 2024

CITATION
Bug DS, Moiseev IS, Porozov YB and
Petukhova NV (2024) Corrigendum: Shedding
light on the *DICER1* mutational spectrum of
uncertain significance in malignant
neoplasms.
Front. Mol. Biosci. 11:1517143.
doi: 10.3389/fmolb.2024.1517143

COPYRIGHT
© 2024 Bug, Moiseev, Porozov and
Petukhova. This is an open-access article
distributed under the terms of the [Creative
Commons Attribution License \(CC BY\)](#). The
use, distribution or reproduction in other
forums is permitted, provided the original
author(s) and the copyright owner(s) are
credited and that the original publication in
this journal is cited, in accordance with
accepted academic practice. No use,
distribution or reproduction is permitted
which does not comply with these terms.

Corrigendum: Shedding light on the *DICER1* mutational spectrum of uncertain significance in malignant neoplasms

D. S. Bug¹, I. S. Moiseev², Yu. B. Porozov^{3,4} and N. V. Petukhova^{1*}

¹Bioinformatics Research Center, Pavlov First Saint Petersburg Medical State University, St. Petersburg, Russia, ²R. M. Gorbacheva Scientific Research Institute of Pediatric Hematology and Transplantation, Pavlov First Saint Petersburg State Medical University, St. Petersburg, Russia, ³St. Petersburg School of Physics, Mathematics, and Computer Science, HSE University, Saint Petersburg, Russia, ⁴Advitam Laboratory, Belgrade, Serbia

KEYWORDS

Dicer1, variant of uncertain significance, variant effect prediction, gene evolution, oncology, molecular dynamics

A Corrigendum on Shedding light on the *DICER1* mutational spectrum of uncertain significance in malignant neoplasms

by Bug DS, Moiseev IS, Porozov YB and Petukhova NV (2024). *Front. Mol. Biosci.* 11:1441180.
doi: 10.3389/fmolb.2024.1441180

In the published article, there was an error in [Figure 7](#) as published. The [Figures 7, 8](#) were mixed up. The corrected [Figure 7](#) and its caption appear below.

In the published article, there was an error in [Figure 8](#) as published. The [Figures 7, 8](#) were mixed up. The corrected [Figure 8](#) and its caption appear below.

The authors apologize for these error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

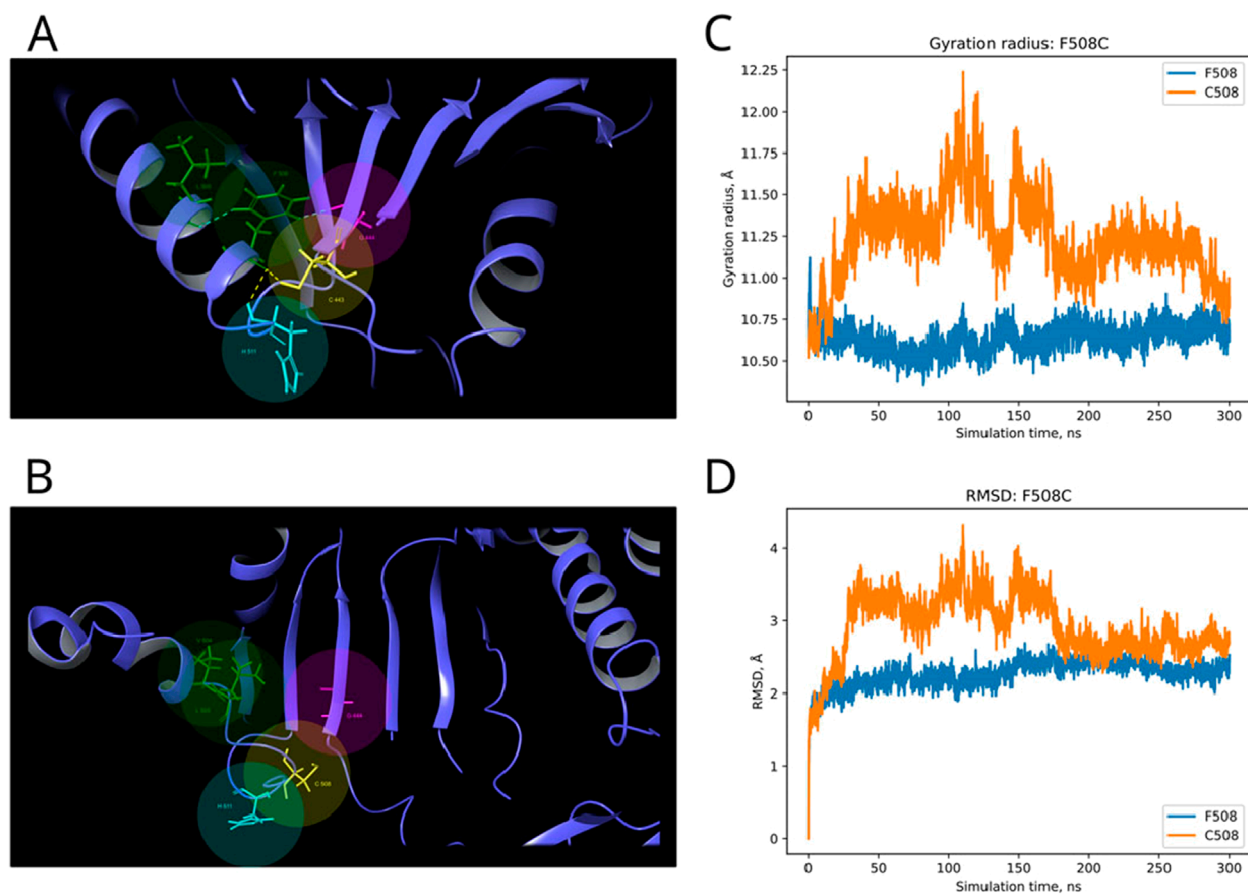


FIGURE 7

Structural alterations of Dicer1 variant F508C. **(A)** Interactions formed by wild-type amino acid F508. **(B)** Interactions formed by mutation C508. Amino acids taking part in bond formation are marked by spheres. H-bonds are indicated by dashed yellow lines, and aromatic H-bonds are indicated by dashed blue lines. Protein secondary structural elements (α -helixes, β -strands, and disordered loops) are shown in blue by cartoon representation. The radius of gyration **(C)** and RMSD **(D)** fluctuations of the 10 Å region around the wild-type amino acid and corresponding mutation through a 300-ns MD simulation.

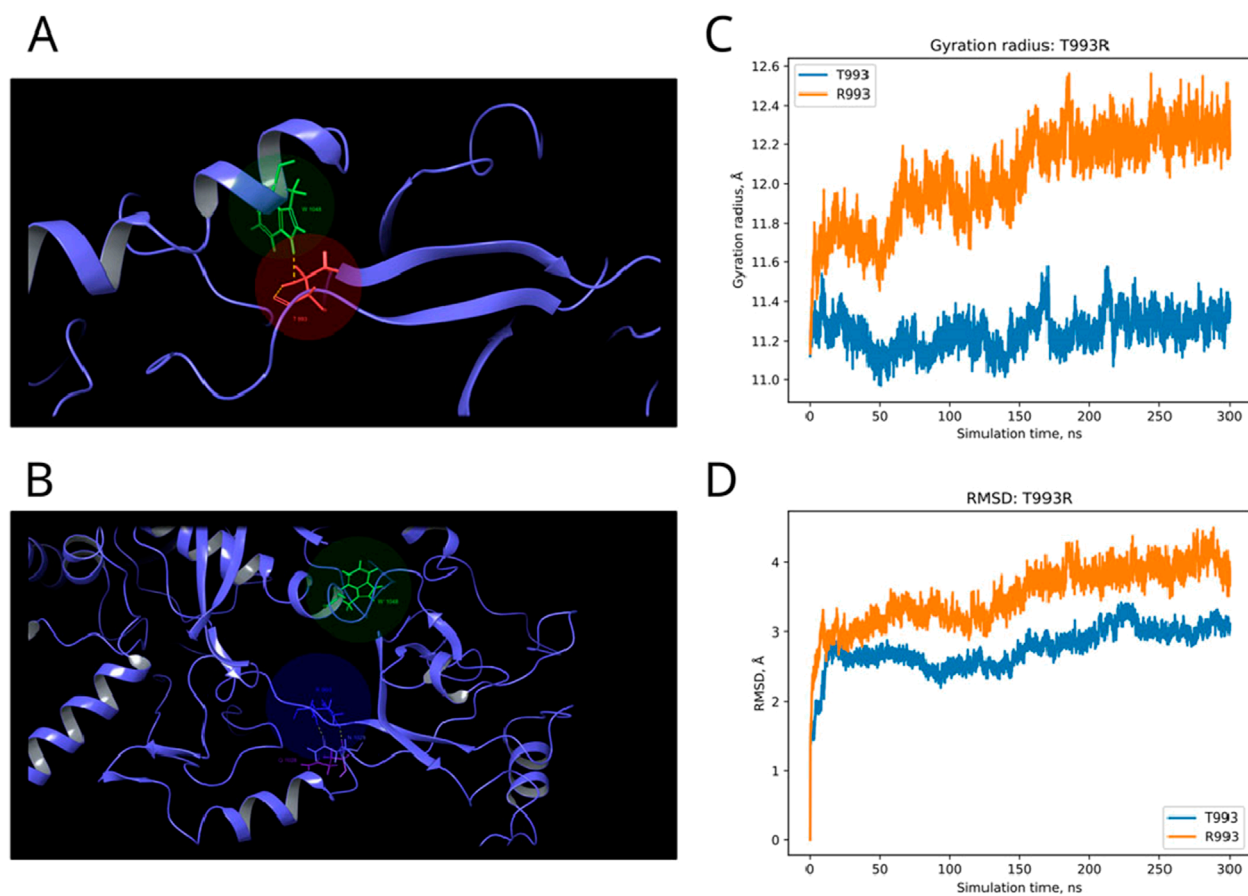


FIGURE 8

Structural alterations of Dicer1 variant T993R. **(A)** Interactions formed by wild-type amino acid T993. **(B)** Interactions formed by mutation R993. Amino acids taking part in bond formation are marked by spheres. H-bonds are indicated by dashed yellow lines, and aromatic H-bonds are indicated by dashed blue lines. Protein secondary structural elements (α -helixes, β -strands, and disordered loops) are shown in blue by cartoon representation. The radius of gyration **(C)** and RMSD **(D)** fluctuations of the 10 Å region around the wild-type amino acid and corresponding mutation through a 300-ns MD simulation.