Erratum to: The Special Issue on “Computational Molecular Medicine”, edited by Rachel Karchin and Melissa S. Cline

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Erratum to: Hum Genet (2014) 133:1199–1215
DOI 10.1007/s00439-014-1476-7,
Hum Genet (2014) 133:1331–1341
DOI 10.1007/s00439-014-1479-4,
Hum Genet (2015) 134:3–11
DOI 10.1007/s00439-014-1482-9

The following three articles are part of the special issue on “Computational Molecular Medicine”, but have accidentally already been published in previous issues. Furthermore, the special topic title “Computational Molecular Medicine” was missed to include in those articles.

Missing heritability of common diseases and treatments outside the protein-coding exome

Wolfgang Sadée · Katherine Hartmann · Michał Seweryn · Maciej Pietrzak · Samuel K. Handelman · Grzegorz A. Rempala
[10.1007/s00439-014-1476-7](https://doi.org/10.1007/s00439-014-1476-7) (Volume 133, Issue 10)

Using familial information for variant filtering in high-throughput sequencing studies

Melanie Bahlo · Rick Tankard · Vesna Lukic · Karen L. Oliver · Katherine R. Smith
[10.1007/s00439-014-1479-4](https://doi.org/10.1007/s00439-014-1479-4) (Volume 133, Issue 11)

Using drug response data to identify molecular effectors, and molecular “omic” data to identify candidate drugs in cancer

William C. Reinhold · Sudhir Varma · Vinodh N. Rajapakse · Augustin Luna · Fabricio Garmus Sousa · Kurt W. Kohn · Yves G. Pommier

[10.1007/s00439-014-1482-9](https://doi.org/10.1007/s00439-014-1482-9) (Volume 134, Issue 1)

The online version of the original articles can be found under doi: [10.1007/s00439-014-1476-7](https://doi.org/10.1007/s00439-014-1476-7), [10.1007/s00439-014-1479-4](https://doi.org/10.1007/s00439-014-1479-4) and [10.1007/s00439-014-1482-9](https://doi.org/10.1007/s00439-014-1482-9).

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