



Correction: Effective *in silico* prediction of new oxazolidinone antibiotics: force field simulations of the antibiotic–ribosome complex supervised by experiment and electronic structure methods

Jörg Grunenberg^{*1} and Giuseppe Licari^{*1,2}

Correction

Open Access

Address:

¹Institut für Organische Chemie, Hagenring 30, TU-Braunschweig,
38106 Braunschweig, Germany and ²Physical Chemistry Department,
Sciences II, University of Geneva, 30, Quai Ernest Ansermet,
CH-1211 Geneva 4, Switzerland

Email:

Jörg Grunenberg^{*} - Joerg.Grunenberg@tu-bs.de; Giuseppe Licari^{*} -
Giuseppe.Licari@unige.ch

^{*} Corresponding author

Beilstein J. Org. Chem. **2016**, *12*, 608–610.

doi:10.3762/bjoc.12.59

Received: 21 March 2016

Accepted: 22 March 2016

Published: 31 March 2016

Associate Editor: P. R. Schreiner

© 2016 Grunenberg and Licari; licensee Beilstein-Institut.

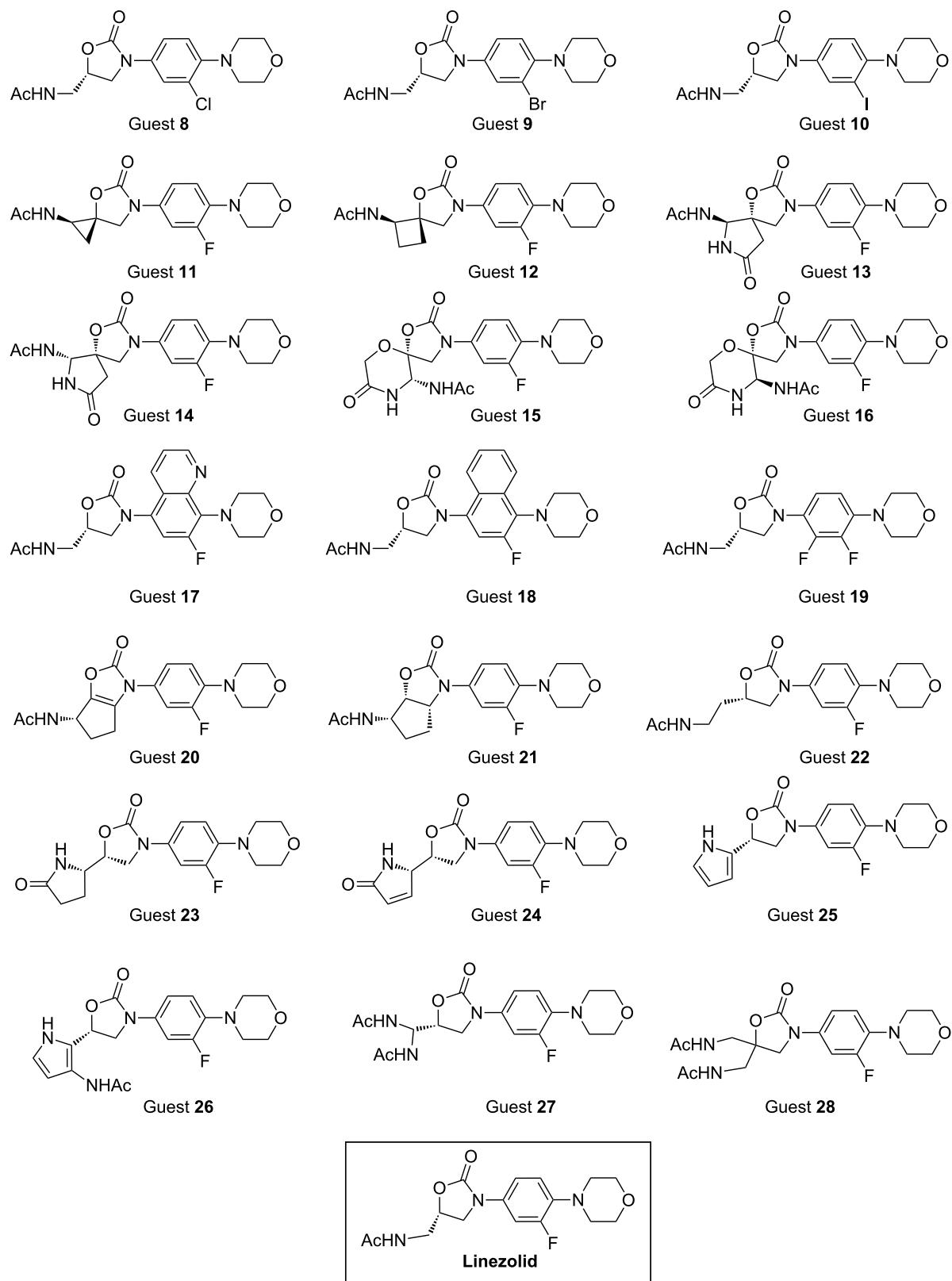
License and terms: see end of document.

Keywords:

compliance constants; computational chemistry; drug design;
molecular recognition; relaxed force constants

This correction refers to *Beilstein J. Org. Chem.* **2016**, *12*, 415–428. doi:10.3762/bjoc.12.45

Our original publication contains an erratic number of predicted antibiotic structures in Scheme 2. With this Erratum we provide the corrected Scheme 2.



Scheme 1: Scheme 2 in the original article: Predicted new linezolid-like candidates.

License and Terms

This is an Open Access article under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

The license is subject to the *Beilstein Journal of Organic Chemistry* terms and conditions:
(<http://www.beilstein-journals.org/bjoc>)

The definitive version of this article is the electronic one which can be found at:
[doi:10.3762/bjoc.12.59](https://doi.org/10.3762/bjoc.12.59)