

CORRECTION

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# Correction to: *Neisseria lactamica* Y92–1009 complete genome sequence

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## Correction

After publication of the original article [1] it was identified that an incorrect version of the manuscript has been published. This was caused by a technical error which led to a discrepancy between the editorially-accepted version of the manuscript, and the published version.

A list of Corrections is included below:

- 1) The following abbreviations have been corrected throughout the article:  
*Nla* changed to *N. lactamica*  
*Nme* changed to *N. meningitidis*  
*N.go* changed to *N. gonorrhoeae*  
*Nci* changed to *N. cinerea*
- 2) Table 1: 'Term' and 'Evidence code' columns of the first 7 rows have been updated to the following:

Domain Bacteria	TAS [37]
Phylum <i>Proteobacteria</i>	TAS [38]
Class <i>Betaproteobacteria</i>	TAS [39, 40]
Order <i>Neisseriales</i>	TAS [39, 41]
Family - <i>Neisseriaceae</i>	TAS [42]
Genus <i>Neisseria</i>	TAS [42]
Species <i>Neisseria lactamica</i>	TAS [42, 43]

- 3) Table 2: Missing/blank term for MIGS 13 has been changed to read "Strain is not publicly available".
- 4) 2nd paragraph under heading "Insights from the genome sequence": Sentence containing "... approximately a third (33.5%) of all open reading frames (ORFs) in this genome..." has been shortened to "approximately a third (33.5%) of all ORFs in this genome..."
- 5) 3rd paragraph under heading "Insights from the genome sequence": Bracketed abbreviation '(DUS)' has been removed.
- 6) 3rd paragraph under heading "Insights from the genome sequence": Bracketed abbreviation '(CREEs)' has been removed
- 7) Bracketed link for PHAST '(http://phast.wishartlab.com/index.html)' changed to reference 35.
- 8) Reference 14 initially missing from article, has now been added and correctly referenced
- 9) Reference 33 was removed, as it was a duplicate of reference 30.
- 10) References 36–40 removed, and replaced with updated reference list (36–46):

36. Field D, Garrity G, Gray T, Morrison N, Selengut J, Sterk P, et al. The minimum information about a genome sequence (MIGS) specification. *Nat Biotechnol.* 2008;26:541–7.

37. Woese CR, Kandler O, Wheelis ML. Towards a natural system of organisms: proposal for the domains *Archaea*, *Bacteria*, and *Eucarya*. *Proc Natl Acad Sci.* 1990;87:4576–9. <https://doi.org/10.1073/pnas.87.12.4576>.

38. Garrity GM, Holt JG. The Road Map to the Manual. In: *Bergey's Manual® of Systematic Bacteriology*. 2001. p. 119–66. [https://doi.org/10.1007/978-0-387-21609-6\\_15](https://doi.org/10.1007/978-0-387-21609-6_15).

39. Euzéby. J. List of new names and new combinations previously effectively, but not validly, published. *Int J Syst Evol Microbiol.* 2006;56:1–6.

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40. Garrity GM, Bell JA, Lilburn T. Class II. *Betaproteobacteria* class. Nov. In: Bergey's Manual® of Systematic Bacteriology. 2005. p. 575–922. [https://doi.org/10.1007/0-387-29298-5\\_2](https://doi.org/10.1007/0-387-29298-5_2).

41. Tønjum T. *Neisseriales* ord. Nov. In: Bergey's Manual of Systematics of Archaea and Bacteria. John Wiley & Sons, Ltd.; 2015. <https://doi.org/10.1002/9781118960608.obm00079>.

42. SKERMAN VBD, MCGOWAN V, SNEATH PHA. Approved Lists of Bacterial Names. *Int J Syst Evol Microbiol.* 1980;30:225–420.

43. Hollis DG, Wiggins GL, Weaver RE. *Neisseria lactamica* sp. n., a lactose-fermenting species resembling *Neisseria meningitidis*. *Appl Microbiol.* 1969;17:71–7.

44. Aho EL, Keating a M, McGillivray SM. A comparative analysis of pilin genes from pathogenic and nonpathogenic *Neisseria* species. *Microb Pathog.* 2000;28:81–8.

45. Lennette, Edwin H. *Manual of Clinical Microbiology*. 4th edition. Washington DC: American Society for Microbiology; 1985.

46. *Neisseria* MLST website. <https://pubmlst.org/neisseria/>. Accessed 2 Feb 2017.

The Publisher apologises for this error.

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#### Reference

1. Pandey AK, Cleary DW, Laver JR, Maiden MCJ, Didelot X, Gorringer A, Read RC. *Neisseria lactamica* Y92–1009 complete genome sequence. *Stand Genomic Sci.* 2017;12:41. <https://doi.org/10.1186/s40793-017-0250-6>.