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Publisher Correction: Mass & secondary structure propensity of amino acids explain their mutability and evolutionary replacements

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Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-017-08041-7>, published online 10 August 2017

The original version of this Article contained a typographical error in the Abstract.

“Asn ↔ Asp, PTMhe ↔ Tyr, Lys ↔ Arg, Gln ↔ Glu, Ile ↔ Val, Met → Leu”

now reads:

“Asn ↔ Asp, Phe ↔ Tyr, Lys ↔ Arg, Gln ↔ Glu, Ile ↔ Val, Met → Leu”

Additionally, there was an error in the Results and Discussion section, under the subheading ‘Mass over the frequency at the most probable conformation correlates with mutability’.

“the correlation with force-field derived appears in green; and the correlation with the genetic code based matrix is plotted in purple.”

now reads:

“the correlation with force-field derived appears in purple; and the correlation with the genetic code based matrix is plotted in green.”

These errors have now been corrected in the HTML and PDF versions of the Article.



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