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Author Correction: Improved prediction of protein-protein interactions using AlphaFold2

Patrick Bryant , Gabriele Pozzati  & Arne Elofsson 

Correction to: *Nature Communications* <https://doi.org/10.1038/s41467-022-28865-w>, published online 10 March 2022.

The original version of this article contained an error in the Methods section, which incorrectly read:

‘This score is created by fitting a sigmoidal curve (Fig. 2c) using “curve_fit” from SciPy v.1.4.1⁵⁶, to the DockQ scores using the average interface pLDDT multiplied with the logarithm of the number of interface contacts, with the following sigmoidal equation:

$$\text{pDockQ} = \frac{L}{1 + e^{-k(x-x_0)}} + b \quad (7)$$

where

x = average interface pLDDT · log(number of interface contacts) (8) and we obtain $L = 0.958$, $x_0 = 160.11$, $k = 1$ and $b = 0.001$.

The correct version states ‘ $L = 0.724$, $x_0 = 152.611$, $k = 0.052$ and $b = 0.018$ ’ in place of ‘ $L = 0.958$, $x_0 = 160.11$, $k = 1$ and $b = 0.001$.’

This has been corrected in both the PDF and HTML versions of the article.

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