

## **OPEN** Author Correction: Exploring the **Sequence-based Prediction of Folding Initiation Sites in Proteins**

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This Article contains errors in the Methods section under subheading 'Code availability'.

"The EFoldMine code is available from https://www.dropbox.com/s/eslk4bkpflsgiia/code.zip (note: this is a temporary link, will be replaced when accepted), for academic use only as a stand-alone package with the following dependencies: Python 2.7 including numpy (> = 1.6.1), ScipPy (> = 0.9) and the scikit-learn package (http:// scikit-learn.org/stable/install.html)."

should read:

"The EFoldMine code is available from https://figshare.com/articles/EFoldMine\_code/5649373, for academic use only as a stand-alone package with the following dependencies: Python 2.7 including numpy (> = 1.6.1), ScipPy (> = 0.9) and the scikit-learn package (http://scikit-learn.org/stable/install.html)."

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