



Contents lists available at [ScienceDirect](http://www.sciencedirect.com)

Journal of Structural Biology

journal homepage: www.elsevier.com/locate/yjsbi



Corrigendum

Corrigendum to “A dose-rate effect in single-particle electron microscopy” [*J. Struct. Biol.* 161 (2008) 92–100]

James Z. Chen^a, Carsten Sachse^{a,b}, Chen Xu^a, Thorsten Mielke^c,
Christian M.T. Spahn^d, Nikolaus Grigorieff^{a,*}

^aHoward Hughes Medical Institute, Rosenstiel Center—MS029, Brandeis University, 415 South Street, Waltham, MA 02545-9110, USA

^bLeibniz Institut für Altersforschung, Fritz-Lipmann Institut, Beutenbergstrasse 11, 07745 Jena, Germany

^cUltraStrukturNetzwerk, Max Planck Institute for Molecular Genetics, Ihnestrasse 73, 14195 Berlin, Germany

^dInstitut für Medizinische Physik und Biophysik, Charité—Universitätsmedizin Berlin, Ziegelstrasse 5-9, 10117 Berlin, Germany

This research article describes the analysis of electron microscope images of ice-embedded samples, recorded using different imaging protocols. The image analysis was carried out to detect differences in the samples after imaging using different imaging protocols, as well as in the resulting image contrast. The report contains the following incorrect data analysis: Fig. 5a shows an analysis of power spectra calculated from images of tobacco mosaic virus, recorded using a newly developed imaging protocol (LINDA) and a more conventional protocol (HiFlux). The spectra shown in Fig. 5a suggest that peaks due to layer lines originating from the virus extend to higher resolution for LINDA imaging, compared to HiFlux imaging. The peaks in question are indicated by two arrows. The interpretation of these two peaks is incorrect because their positions do not coincide with the expected positions of layer lines originating from the virus (the positions of peaks in both spectra at lower resolution do coincide with the expected layer line positions). The spurious peaks most likely are the result of a limited range of defocus values present in the data. This led to false peaks in the spectrum produced by the contrast transfer function correction (Eq. (1)). The power spectrum analysis was improved and repeated for both the LINDA and HiFlux data sets. The spectra obtained with the new analysis no longer indicate a significant improvement of image contrast when the LINDA protocol is used. Other results presented in the article remain unaffected by this correction.

DOI of original article: [10.1016/j.jsb.2007.09.017](https://doi.org/10.1016/j.jsb.2007.09.017).

* Corresponding author. Fax: +1 781 736 2419.

E-mail address: niko@brandeis.edu (N. Grigorieff).