Correction to: In Situ Imaging of Virus-Infected Cells by Cryo-Electron Tomography: An Overview

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Correction to:
Chapter 1 in: S. Vijayakrishnan et al. (eds.), *Virus Infected Cells*, Subcellular Biochemistry 106, https://doi.org/10.1007/978-3-031-40086-5_1

The following reference citation **(Li S, 2022)** has been cited on page 4, and the respective reference **(Li S. (2022). Cryo-electron tomography of enveloped viruses. *Trends Biochem Sci*, *47*(2), 173–186. doi:10.1016/j.tibs.2021.08.005)** is included in References list at the end of the chapter.

The following reference citation **(Vankadari et al., 2002)** has been cited on page 15, and the respective reference **(Vankadari N, Shepherd DC, Carter SD, Ghoshal D. (2002). Three-dimensional insights into human enveloped viruses in vitro and in situ. Biochem Soc Trans, 50(1), 95–105. doi:10.1042/BST20210433)** is included in References list at the end of the chapter.

The following figure **(Fig. 1.1)** caption has been updated with the following missing text "**Figure adapted from Li S (2022) under CC BY 4.0.**". The updated figure caption is as follows:

Fig. 1.1 Correlation of structural biology and imaging methods with sample size and resolution. Sample length, resolution, and the extent of nativeness (in vitro or in situ) are the main determinants when choosing structural biology and imaging methods. Sample size and resolution ranges of the most common methods are shown for comparison, highlighting the suitability of cryo-ET for imaging a wide range of molecular and cellular samples including protein assemblies, viruses, and cells. In combination with correlative light-electron microscopy (CLEM) and cryo-focused

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ion beam milling (cryo-FIB), cryo-ET resolves native structures of protein at relatively high resolution as well as provides abundant information on protein–protein, protein–membrane, or protein–nucleic acids interactions in an in situ setting. Figure adapted from Li S (2022) under CC BY 4.0. The various sample types used in this figure were created with Biorender.com

The following figure **(Fig. 1.5)** caption has been updated from the following text **"Figures were made using publicly available atomic coordinates and maps from the protein data bank (PDB) and Electron Microscopy Data Bank (EMDB) using UCSF ChimeraX (Pettersen et al. 2021)" to the following text "Figure was adapted from Vankadari et al. (2002) under CC BY 4.0 using publicly available atomic coordinates and maps from the protein data bank (PDB) and Electron Microscopy Data Bank (EMDB) and UCSF ChimeraX (Pettersen et al., 2021)"**. The updated figure caption is as follows:

Fig. 1.5 Structures of purified enveloped viruses resolved by cryo-ET and STA. A selection of high-resolution structures of representative enveloped purified viruses determined by cryo-ET and STA is shown. (a) Structure of mature HIV-1 capsid (PDB: 3J3Y) colour coded with CA hexamers (brown) and pentamers (blue). (b) Ultrastructure of the SARS-CoV-2 virion (EMD-30430); lipid envelope (grey), S protein (blue), and RNPs (yellow). (c) The STA reconstructed prefusion LASV glycoprotein (GP) trimers (yellow) embedded on the viral envelope (blue) and filled with internal material (grey) segmented from the tomogram. Figure reproduced from Li et al. (2016) under CC BY 4.0. (d) Structure of the helical IAV M1 matrix protein (grey and blue) (EMD-22384). (e) Structure of RVFV prefusion GP pentamers (blue) and hexamers (brown) reprojected on the viral envelope (EMDB-4197). (f) Structure of mature HSV-1 capsid (EMD-5452) denoting the five-fold portal structure (blue) and surrounding hexamers (cyan). Figure was adapted from Vankadari et al. (2002) under CC BY 4.0 using publicly available atomic coordinates and maps from the protein data bank (PDB) and Electron Microscopy Data Bank (EMDB) and UCSF ChimeraX (Pettersen et al., 2021)