

Retraction

IMMUNOLOGY

Retraction for “The antibody zalutumumab inhibits epidermal growth factor receptor signaling by limiting intra- and inter-molecular flexibility,” by Jeroen J. Lammerts van Bueren, Wim K. Bleeker, Annika Brännström, Anne von Euler, Magnus Jansson, Matthias Peipp, Tanja Schneider-Merck, Thomas Valerius, Jan G. J. van de Winkel, and Paul W. H. I. Parren, which appeared in issue 16, April 22, 2008, of *Proc Natl Acad Sci USA* (105:6109–6114; first published April 21, 2008; 10.1073/pnas.0709477105).

The undersigned authors wish to note the following: “In our study we employed Protein Tomography (PT), an electron tomography method commercialized by Sidec AB, for structural analysis of proteins. Following our publication, doubts were raised with respect to the validity of Sidec PT, and we therefore conducted an extensive validation study with Sidec AB to determine the fidelity of PT for structural analysis of therapeutic antibodies and antibody–antigen complexes in solution. In two independent double blind experiments, PT was found to be highly unreliable in distinguishing structural features of the molecules and complexes studied. First, approximately 90% of the identified protein density maps could not be interpreted due to complex morphology or low quality. Second, among the remaining objects, a high number of the protein images observed did not match with sample composition resulting in misinterpretation of sample identities. These disappointing results led us to reanalyze our previously acquired PT data in situ using a weighted back-projection reconstruction method with IMOD (1) rather than COMET (2), which also indicated our previous analysis to be unreliable. With the current PT methods, we were thus not able to validate tomograms neither obtained from vitrified proteins in solution nor aldehyde-fixed, stained cells. Therefore the undersigned authors no longer feel confident of the PT data presented in Figs. 3, 4, 5, and S4 of our study. The authors stand behind the supporting biochemical data provided in the manuscript and believe the proposed model to be plausible, the validity of which, however, should be addressed with other methods. We found it important to notify our colleagues of the specific technical flaws in our publication and apologize for any inconvenience caused. We hereby retract this manuscript.”

Jeroen J. Lammerts van Bueren
Wim K. Bleeker
Annika Brännström
Magnus Jansson
Matthias Peipp
Tanja Schneider-Merck
Thomas Valerius
Jan G. J. van de Winkel
Paul W. H. I. Parren

1. Kremer JR, Mastronarde DN, McIntosh JR (1996) Computer visualization of three-dimensional image data using IMOD. *J Struct Biol* 116:71–76.
2. Skoglund U, Ofverstedt LG, Burnett RM, Bricogne G (1996) Maximum-entropy three-dimensional reconstruction with deconvolution of the contrast transfer function: a test application with adenovirus. *J Struct Biol* 117:173–188.

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