CORRIGENDA

*J. A. E. Määttä, T. T. Airenne, H. R. Nordlund, J. Jänis, T. A. Paldanius, P. Vainiotalo, M. S. Johnson, M. S. Kulomaa, V. P. Hytönen**

Rational Modification of Ligand-Binding Preference of Avidin by Circular Permutation and Mutagenesis

ChemBioChem **2008**, *9*, 1124–1135

DOI 10.1002/cbic.200700671

An error has been found in the interpretation of the mass spectroscopy data in this paper. On p. 1125, the section under the heading "Mass spectrometry" should read: Electrospray ionization Fourier transform ion cyclotron resonance (ESI FT-ICR) mass spectrometry was used to confirm the amino acid sequences and proper folding of the proteins (mass spectra not presented). For some unknown reason, dcAvd2 was the only protein that could not be identified by this method. A possible reason could be the fragmentation of the protein, which can also be seen in the SDS-PAGE analysis (Figure 1 A). The most abundant isotopic masses were determined to be $14\,685.52 \pm 0.07$ Da for Avd(N118M), $14\,285.24 \pm 0.01$ Da for cpAvd4$\rightarrow$3, and $14\,302.18 \pm 0.03$ Da for cpAvd4$\rightarrow$3(N118M). The theoretical masses of Avd(N118M), cpAvd4$\rightarrow$3, and cpAvd4$\rightarrow$3(N118M) calculated from the sequence-derived elemental compositions were 14 685.50, 14 285.19, and 14 302.19 Da, respectively. Therefore, mass spectrometric analysis confirmed the isolated proteins to be in excellent agreement with the protein design and DNA sequencing. This also implies that there are no post-translational modifications in the isolated proteins.[26] When the disulfide bridges were reduced, the most abundant isotopic masses of the proteins increased by 2 Da, as expected; this indicates proper folding of the polypeptides.

 © 2008 Wiley-VCH Verlag GmbH & Co. KGaA, Weinheim