Abstract Submitted
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An independent atom model description of ion-molecule collisions including geometric screening corrections: application to biomolecules[1] H. J. LÜDDE, A. ACHENBACH, T. KALKBRENNER, H.C. JANKOWIAK, Goethe University Frankfurt, T. KIRCHNER, York University — Recently, we proposed to calculate electron removal cross sections for ion-molecule collisions in an independent atom model that accounts for geometric screening corrections [1]. The correction coefficients are obtained from using a pixel counting method (PCM) for the exact calculation of the effective cross sectional area that emerges when the molecular cross section is pictured as a structure of (overlapping) atomic cross sections. This structure varies with the relative orientation of the molecule with respect to the projectile beam direction and, accordingly, orientation-independent total cross sections are obtained from averaging the pixel count over many orientations. In this contribution, we apply the PCM to proton collisions from amino acids and DNA and RNA nucleobases. The strength of the screening effect is analyzed by comparing the PCM results with Bragg additivity rule cross sections and with experimental data where available. [1] H.J. Lüdde *et al.*, Eur. Phys. J. D **70**, 82 (2016).

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