Abstract Submitted
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Ion-biomolecule collisions studied within the independent atom model including geometric screening corrections[1] H.J. LÜDDE, A. ACHENBACH, T. KALKBRENNER, H.C. JANKOWIAK, Goethe University Frankfurt, T. KIRCHNER, York University — A recently introduced model to account for geometric screening corrections in an independent-atom-model description of ion-molecule collisions [1] is applied to proton collisions from amino acids and DNA and RNA nucleobases. 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. We present net capture and net ionization cross sections over wide ranges of impact energy and analyze the strength of the screening effect by comparing the PCM results with Bragg additivity rule cross sections and with experimental data where available. [1] H.J. Lüdde et al, J. Phys. Conf. Ser. 635, 032076 (2015)

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