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Independent-atom-model pixel counting method calculations for ion collisions from biomolecules[1] TOM KIRCHNER, MARKO HORBATSCH, York University, HANS JURGEN LUDDE, Frankfurt Institute for Advanced Studies (FIAS) — The recently introduced independent-atom-model pixel counting method (IAM-PCM) [1,2] is used to calculate net capture and net ionization cross sections for ion-biomolecule collisions in the 10 keV to 10 MeV impact energy range. Taking advantage of the flexibility of the method we have studied a large class of target systems including nucleobases, amino acids, and nucleotides. Results are compared with experimental data and previous theoretical calculations where available. At low to intermediate energies, where experimental data are sparse, the IAM-PCM cross sections are in marked disagreement with previous perturbative and classical calculations. For the case of net ionization it is shown that they follow a scaling relation and can be parametrized in terms of a simple analytical formula. [1] H.J. Lüdde *et al.*, Eur. Phys. J. D **70**, 82 (2016). [2] H.J. Lüdde *et al.*, Eur. Phys. J. B **91**, 99 (2018).

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