In silico modelling of the biodistribution of therapeutic immunoconjugates with thiazolic payload

Targeted therapy of cancer has been introduced in the last years in clinical trials and innovative antibody-drug conjugated products have been approved especially for salvage management of patients with advanced forms of cancer. A mathematical model [1] was used to predict the distribution at systemic level of three series of newly designed therapeutic immunoconjugates with thiazolic payload. Both, the molecular target of cytotoxic payload and the antigenic determinant are macromolecules deeply involved in the initiation of carcinogenesis and proliferation (DNA topoisomerase II-alpha), enzymes overexpressed in cancer cells and involved in removing of physical barriers to cellular invasion (matrix metalloproteinases) and promotion of cell migration and angiogenesis (tenascin C).
The mathematical model estimated the concentration profiles in the tumor environment surrounding individual capillaries, showing how two key-determinants (the maximum enzyme conversion rate and the residual antibody/Fab fragment concentration in plasma and normal tissue) regulates the levels of drug and each of the antibody-drug conjugates series.
Such computations could enhance the accuracy of preclinical screenings, making also possible to tailor the antibody-drug conjugates therapy for individual patients.

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"Synthesis, screening and controlled release of some novel thiazole, bithiazole and thiazolidin-4-one compounds with antioxidant, antiproliferative and antimicrobial activity"

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