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Authors: Wojciech Kazimierz Marek, Dominik Sauer, Astrid Dürrauer, Alois Jungbauer, Wojciech Piątkowski, Dorota Antos



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# Prediction tool for loading, isocratic elution, gradient elution and scaling up of ion exchange chromatography of proteins

Wojciech Kazimierz Marek<sup>a,\*</sup>, Dominik Sauer<sup>b</sup>, Astrid Dürauer<sup>b,c</sup>, Alois Jungbauer<sup>b,c</sup>, Wojciech Piątkowski<sup>a</sup>, Dorota Antos<sup>a</sup>

<sup>a</sup>*Department of Chemical and Process Engineering, Powstańców Warszawy Ave. 6, 35-959 Rzeszów, Poland*

<sup>b</sup>*Austrian Centre of Industrial Biotechnology, Muthgasse 11, 1190 Vienna, Austria*

<sup>c</sup>*Department of Biotechnology, University of Natural Resources and Life Sciences Vienna, Muthgasse 18, 1190 Vienna, Austria*

\*Corresponding author; E-mail address: [wmarek@prz.edu.pl](mailto:wmarek@prz.edu.pl) (W.K. Marek), tel.: +48 177432020; fax: +48 178543655

## Highlights

- Mathematical tool for design and scaling up of protein chromatography is suggested
- Moment analysis was used for determining kinetic parameters of mass transfer
- Two model ion-exchange chromatography systems were selected for the study
- The design procedure was successfully verified over a wide space of the operating conditions

## Abstract

An efficient mathematical tool for the design and scaling up of protein chromatography is suggested, in which the model parameters can be determined quickly over a wide operating space without large material investments. The design method is based on mathematical modelling of column dynamics and moment analysis. The accuracy of the dynamic models that are most frequently used for simulations of chromatographic processes is analyzed, and possible errors that can be generated using the moment analysis are indicated. The so-called transport dispersive model was eventually employed for the process simulations. The model was modified to account for the protein dispersion in void volumes of chromatographic systems. The manner of the model calibration was

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