

# Tobias Hahn

## List of Publications by Year in descending order

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Version: 2024-02-01

21  
papers

550  
citations

516710

16  
h-index

713466

21  
g-index

22  
all docs

22  
docs citations

22  
times ranked

294  
citing authors

#	ARTICLE	IF	CITATIONS
1	Modeling the Gibbs–Donnan effect during ultrafiltration and diafiltration processes using the Poisson–Boltzmann theory in combination with a basic Stern model. <i>Journal of Membrane Science</i> , 2022, 648, 120333.	8.2	15
2	Analysis of complex protein elution behavior in preparative ion exchange processes using a colloidal particle adsorption model. <i>Journal of Chromatography A</i> , 2021, 1654, 462439.	3.7	16
3	Protein adsorption on ion exchange adsorbents: A comparison of a stoichiometric and non-stoichiometric modeling approach. <i>Journal of Chromatography A</i> , 2021, 1653, 462397.	3.7	21
4	Adsorption of colloidal proteins in ion-exchange chromatography under consideration of charge regulation. <i>Journal of Chromatography A</i> , 2020, 1611, 460608.	3.7	11
5	Toward in silico CMC: An industrial collaborative approach to model-based process development. <i>Biotechnology and Bioengineering</i> , 2020, 117, 3986-4000.	3.3	26
6	Good modeling practice for industrial chromatography: Mechanistic modeling of ion exchange chromatography of a bispecific antibody. <i>Computers and Chemical Engineering</i> , 2019, 130, 106532.	3.8	42
7	Estimation of adsorption isotherm and mass transfer parameters in protein chromatography using artificial neural networks. <i>Journal of Chromatography A</i> , 2017, 1487, 211-217.	3.7	42
8	Modeling of complex antibody elution behavior under high protein load densities in ion exchange chromatography using an asymmetric activity coefficient. <i>Biotechnology Journal</i> , 2017, 12, 1600336.	3.5	24
9	Root cause investigation of deviations in protein chromatography based on mechanistic models and artificial neural networks. <i>Journal of Chromatography A</i> , 2017, 1515, 146-153.	3.7	27
10	Deconvolution of high-throughput multicomponent isotherms using multivariate data analysis of protein spectra. <i>Engineering in Life Sciences</i> , 2016, 16, 194-201.	3.6	7
11	Application of spectral deconvolution and inverse mechanistic modelling as a tool for root cause investigation in protein chromatography. <i>Journal of Chromatography A</i> , 2016, 1437, 158-167.	3.7	20
12	Water on hydrophobic surfaces: Mechanistic modeling of hydrophobic interaction chromatography. <i>Journal of Chromatography A</i> , 2016, 1465, 71-78.	3.7	27
13	A mechanistic model of ion-exchange chromatography on polymer fiber stationary phases. <i>Journal of Chromatography A</i> , 2016, 1475, 18-30.	3.7	12
14	A versatile noninvasive method for adsorbent quantification in batch and column chromatography based on the ionic capacity. <i>Biotechnology Progress</i> , 2016, 32, 666-677.	2.6	22
15	UV absorption-based inverse modeling of protein chromatography. <i>Engineering in Life Sciences</i> , 2016, 16, 99-106.	3.6	33
16	Calibration-free inverse modeling of ion-exchange chromatography in industrial antibody purification. <i>Engineering in Life Sciences</i> , 2016, 16, 107-113.	3.6	21
17	Modeling and simulation of anion-exchange membrane chromatography for purification of Sf9 insect cell-derived virus-like particles. <i>Journal of Chromatography A</i> , 2016, 1429, 142-154.	3.7	31
18	High-throughput micro-scale cultivations and chromatography modeling: Powerful tools for integrated process development. <i>Biotechnology and Bioengineering</i> , 2015, 112, 2123-2133.	3.3	21

#	ARTICLE	IF	CITATIONS
19	Simulating and Optimizing Preparative Protein Chromatography with ChromX. Journal of Chemical Education, 2015, 92, 1497-1502.	2.3	44
20	Adjoint-based estimation and optimization for column liquid chromatography models. Computers and Chemical Engineering, 2014, 64, 41-54.	3.8	32
21	Model-based integrated optimization and evaluation of a multi-step ion exchange chromatography. Separation and Purification Technology, 2014, 136, 207-222.	7.9	56