

# Steven Cramer

## List of Publications by Year in descending order

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98  
papers

2,976  
citations

172207

29  
h-index

189595

50  
g-index

99  
all docs

99  
docs citations

99  
times ranked

1583  
citing authors

#	ARTICLE	IF	CITATIONS
1	Steric mass-action ion exchange: Displacement profiles and induced salt gradients. <i>AIChE Journal</i> , 1992, 38, 1969-1978.	1.8	495
2	Salting-In and Salting-Out of Hydrophobic Solutes in Aqueous Salt Solutions. <i>Journal of Physical Chemistry B</i> , 2001, 105, 6380-6386.	1.2	163
3	Antibody variable region interactions with Protein A: Implications for the development of generic purification processes. <i>Biotechnology and Bioengineering</i> , 2005, 92, 665-673.	1.7	139
4	Downstream bioprocessing: recent advances and future promise. <i>Current Opinion in Chemical Engineering</i> , 2011, 1, 27-37.	3.8	122
5	Protein Interactions in Hydrophobic Charge Induction Chromatography (HCIC). <i>Biotechnology Progress</i> , 2005, 21, 498-508.	1.3	80
6	On-demand manufacturing of clinical-quality biopharmaceuticals. <i>Nature Biotechnology</i> , 2018, 36, 988-995.	9.4	75
7	Aligned Carbon Nanotube Stationary Phases for Electrochromatographic Chip Separations. <i>Chromatographia</i> , 2009, 69, 473-480.	0.7	72
8	Evaluation of protein adsorption and preferred binding regions in multimodal chromatography using NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16811-16816.	3.3	66
9	Evaluation of selectivity in multimodal anion exchange systems: A priori prediction of protein retention and examination of mobile phase modifier effects. <i>Journal of Chromatography A</i> , 2011, 1218, 7813-7820.	1.8	57
10	Protected amino acids as novel low-molecular-weight displacers in cation-exchange displacement chromatography. <i>Biotechnology and Bioengineering</i> , 1995, 48, 452-460.	1.7	54
11	Optimization of step gradient separations: Consideration of nonlinear adsorption. <i>Biotechnology and Bioengineering</i> , 1995, 47, 355-372.	1.7	52
12	Mobile phase modifier effects in multimodal cation exchange chromatography. <i>Biotechnology and Bioengineering</i> , 2012, 109, 176-186.	1.7	51
13	The effect of geometrical presentation of multimodal cation-exchange ligands on selective recognition of hydrophobic regions on protein surfaces. <i>Journal of Chromatography A</i> , 2015, 1412, 33-42.	1.8	51
14	Investigation of protein binding affinity in multimodal chromatographic systems using a homologous protein library. <i>Journal of Chromatography A</i> , 2010, 1217, 191-198.	1.8	48
15	Kinetic resolution of racemic glycidyl butyrate using a multiphase membrane enzyme reactor: Experiments and model verification. <i>Biotechnology and Bioengineering</i> , 1993, 41, 979-990.	1.7	47
16	Recent Advances in the Theory and Practice of Displacement Chromatography. <i>Separation and Purification Reviews</i> , 1990, 19, 31-91.	0.8	45
17	Selective displacement chromatography of proteins. , 1997, 56, 119-129.		44
18	A Methodology for the Characterization of Ion-Exchange Resins. <i>Separation Science and Technology</i> , 2000, 35, 1719-1742.	1.3	42

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19	ELP-z and ELP-zz capturing scaffolds for the purification of immunoglobulins by affinity precipitation. <i>Journal of Biotechnology</i> , 2013, 163, 10-16.	1.9	42
20	Molecular Simulations of Multimodal Ligand-Protein Binding: Elucidation of Binding Sites and Correlation with Experiments. <i>Journal of Physical Chemistry B</i> , 2011, 115, 13320-13327.	1.2	41
21	Use of MiniColumns for linear isotherm parameter estimation and prediction of benchtop column performance. <i>Journal of Chromatography A</i> , 2015, 1418, 94-102.	1.8	41
22	Investigation into the Molecular and Thermodynamic Basis of Protein Interactions in Multimodal Chromatography Using Functionalized Nanoparticles. <i>Langmuir</i> , 2014, 30, 13205-13216.	1.6	39
23	Defining the property space for chromatographic ligands from a homologous series of mixed-mode ligands. <i>Journal of Chromatography A</i> , 2015, 1407, 58-68.	1.8	39
24	Investigation of Mobile Phase Salt Type Effects on Protein Retention and Selectivity in Cation-Exchange Systems Using Quantitative Structure Retention Relationship Models. <i>Langmuir</i> , 2003, 19, 8443-8454.	1.6	38
25	Prediction of protein retention times in gradient hydrophobic interaction chromatographic systems. <i>Journal of Chromatography A</i> , 2008, 1177, 207-214.	1.8	38
26	Investigation of protein selectivity in multimodal chromatography using <i>in silico</i> designed Fab fragment variants. <i>Biotechnology and Bioengineering</i> , 2015, 112, 2305-2315.	1.7	38
27	Displacement Chromatography of Proteins Under Elevated Flow Rate and Crossing Isotherm Conditions. <i>Biotechnology Progress</i> , 1989, 5, 92-97.	1.3	34
28	Purification of an Antigenic Vaccine Protein by Selective Displacement Chromatography. <i>Biotechnology Progress</i> , 1998, 14, 92-101.	1.3	32
29	Affinity precipitation of a monoclonal antibody from an industrial harvest feedstock using an ELP-stimuli responsive biopolymer. <i>Biotechnology and Bioengineering</i> , 2014, 111, 1595-1603.	1.7	32
30	Domain contributions to antibody retention in multimodal chromatography systems. <i>Journal of Chromatography A</i> , 2018, 1563, 89-98.	1.8	32
31	QSAR models for prediction of chromatographic behavior of homologous Fab variants. <i>Biotechnology and Bioengineering</i> , 2017, 114, 1231-1240.	1.7	31
32	Methods development in multimodal chromatography with mobile phase modifiers using the steric mass action model. <i>Journal of Chromatography A</i> , 2013, 1318, 149-155.	1.8	30
33	Utilization of Lysozyme Charge Ladders to Examine the Effects of Protein Surface Charge Distribution on Binding Affinity in Ion Exchange Systems. <i>Langmuir</i> , 2010, 26, 759-768.	1.6	27
34	Probing multimodal ligand binding regions on ubiquitin using nuclear magnetic resonance, chromatography, and molecular dynamics simulations. <i>Journal of Chromatography A</i> , 2012, 1229, 113-120.	1.8	27
35	Modeling shock layers in ion-exchange displacement chromatography. <i>AIChE Journal</i> , 1999, 45, 27-37.	1.8	26
36	Transient profiles in ion-exchange displacement chromatography. <i>AIChE Journal</i> , 1995, 41, 1676-1686.	1.8	25

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37	Model-based process development for the purification of a modified human growth hormone using multimodal chromatography. <i>Biotechnology Progress</i> , 2014, 30, 1057-1064.	1.3	24
38	Single Molecule Force Spectroscopy and Molecular Dynamics Simulations as a Combined Platform for Probing Protein Face-Specific Binding. <i>Langmuir</i> , 2017, 33, 10851-10860.	1.6	24
39	Purification of Oligonucleotides by High Affinity, Low Molecular Weight Displacers. <i>Biotechnology Progress</i> , 2000, 16, 1064-1070.	1.3	23
40	High-throughput screening for the development of a monoclonal antibody affinity precipitation step using ELP-stimuli responsive biopolymers. <i>Biotechnology and Bioengineering</i> , 2013, 110, 2664-2676.	1.7	23
41	Purification of proteins using peptide-ELP based affinity precipitation. <i>Journal of Biotechnology</i> , 2020, 309, 59-67.	1.9	23
42	Evaluation of selectivity in homologous multimodal chromatographic systems using in silico designed antibody fragment libraries. <i>Journal of Chromatography A</i> , 2015, 1426, 102-109.	1.8	22
43	Protein-Surface Interaction Maps for Ion-Exchange Chromatography. <i>Langmuir</i> , 2011, 27, 3561-3568.	1.6	21
44	Interactions of Multimodal Ligands with Proteins: Insights into Selectivity Using Molecular Dynamics Simulations. <i>Langmuir</i> , 2015, 31, 7512-7523.	1.6	21
45	Predicting Column Performance in Displacement Chromatography from High Throughput Screening Batch Experiments. <i>Separation Science and Technology</i> , 2003, 38, 1499-1517.	1.3	20
46	Effects of Urea on Selectivity and Protein-Ligand Interactions in Multimodal Cation Exchange Chromatography. <i>Langmuir</i> , 2013, 29, 158-167.	1.6	19
47	Understanding operational system differences for transfer of miniaturized chromatography column data using simulations. <i>Journal of Chromatography A</i> , 2017, 1515, 154-163.	1.8	19
48	Application of a Spherical Harmonics Expansion Approach for Calculating Ligand Density Distributions around Proteins. <i>Journal of Physical Chemistry B</i> , 2014, 118, 13066-13076.	1.2	18
49	A molecular modeling based method to predict elution behavior and binding patches of proteins in multimodal chromatography. <i>Journal of Chromatography A</i> , 2017, 1511, 45-58.	1.8	18
50	Mechanistic modeling based process development for monoclonal antibody monomer-aggregate separations in multimodal cation exchange chromatography. <i>Journal of Chromatography A</i> , 2019, 1602, 317-325.	1.8	18
51	The effect of pH on antibody retention in multimodal cation exchange chromatographic systems. <i>Journal of Chromatography A</i> , 2020, 1617, 460838.	1.8	18
52	Investigating the impact of aromatic ring substitutions on selectivity for a multimodal anion exchange prototype library. <i>Journal of Chromatography A</i> , 2018, 1569, 101-109.	1.8	16
53	Immobilized Metal Affinity Chromatography: Displacer Characteristics of Traditional Mobile Phase Modifiers. <i>Biotechnology Progress</i> , 1996, 12, 84-91.	1.3	15
54	An impurity characterization based approach for the rapid development of integrated downstream purification processes. <i>Biotechnology and Bioengineering</i> , 2018, 115, 2048-2060.	1.7	15

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55	A combined screening and in silico strategy for the rapid design of integrated downstream processes for process and product-related impurity removal. <i>Biotechnology and Bioengineering</i> , 2019, 116, 2178-2190.	1.7	15
56	Towards continuous mAb purification: Clearance of host cell proteins from CHO cell culture harvests via flow-through affinity chromatography using peptide-based adsorbents. <i>Biotechnology and Bioengineering</i> , 2022, 119, 1873-1889.	1.7	14
57	Purification of Recombinant Brain Derived Neurotrophic Factor Using Reversed Phase Displacement Chromatography. <i>Biotechnology Progress</i> , 2001, 17, 897-906.	1.3	13
58	Development of an ELP-Z based mAb affinity precipitation process using scaled-down filtration techniques. <i>Journal of Biotechnology</i> , 2014, 192, 11-19.	1.9	13
59	Development of QSAR models for <i>in silico</i> screening of antibody solubility. <i>MAbs</i> , 2022, 14, 2062807.	2.6	13
60	Development of phage biopanning strategies to identify affinity peptide ligands for kappa light chain Fab fragments. <i>Biotechnology Progress</i> , 2019, 35, e2884.	1.3	12
61	Identification of preferred multimodal ligand-binding regions on IgG1 F <sub>C</sub> using nuclear magnetic resonance and molecular dynamics simulations. <i>Biotechnology and Bioengineering</i> , 2021, 118, 809-822.	1.7	12
62	Adaptive immune responses in vaccinated patients with symptomatic SARS-CoV-2 Alpha infection. <i>JCI Insight</i> , 2022, 7, .	2.3	12
63	Investigation of cathepsin D-mAb interactions using a combined experimental and computational tool set. <i>Biotechnology and Bioengineering</i> , 2019, 116, 1684-1697.	1.7	11
64	Design of peptide affinity ligands for S-protein: a comparison of combinatorial and de novo design strategies. <i>Molecular Diversity</i> , 2013, 17, 357-369.	2.1	10
65	IMAC: Nonlinear elution chromatography of proteins. , 1997, 54, 373-390.		9
66	Displacement Chromatography of Proteins using Low Molecular Weight Anionic Displacers. <i>Adsorption</i> , 1998, 4, 373-381.	1.4	9
67	Formation of Ligand Clusters on Multimodal Chromatographic Surfaces. <i>Langmuir</i> , 2019, 35, 16770-16779.	1.6	9
68	Highland games: A benchmarking exercise in predicting biophysical and drug properties of monoclonal antibodies from amino acid sequences. <i>Biotechnology and Bioengineering</i> , 2020, 117, 2100-2115.	1.7	9
69	High Throughput Determination and QSER Modeling of Displacer DC <sub>50</sub> Values for Ion Exchange Systems. <i>Separation Science and Technology</i> , 2006, 41, 3079-3107.	1.3	8
70	Effect of guanidine and arginine on protein-ligand interactions in multimodal cation-exchange chromatography. <i>Biotechnology Progress</i> , 2017, 33, 435-447.	1.3	8
71	Development of a platform process for the production and purification of single-domain antibodies. <i>Biotechnology and Bioengineering</i> , 2021, 118, 3348-3358.	1.7	8
72	Ion Exchange Chromatographic Behavior of a Homologous Cytochrome C Variant Library Obtained by Controlled Succinylation. <i>Separation Science and Technology</i> , 2010, 45, 2144-2152.	1.3	7

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73	Selective displacement chromatography in multimodal cation exchange systems. Journal of Chromatography A, 2011, 1218, 9250-9259.	1.8	7
74	Design of peptide ligands for affinity purification of human growth hormone. Journal of Chemical Technology and Biotechnology, 2019, 94, 2345-2354.	1.6	7
75	A thermodynamic evaluation of antibody-surface interactions in multimodal cation exchange chromatography. Journal of Chromatography A, 2020, 1628, 461479.	1.8	7
76	Understanding the effects of system differences for parameter estimation and scale-up of high throughput chromatographic data. Journal of Chromatography A, 2022, 1661, 462696.	1.8	7
77	Conformational Equilibria of Multimodal Chromatography Ligands in Water and Bound to Protein Surfaces. Journal of Physical Chemistry B, 2019, 123, 4833-4843.	1.2	6
78	Quantifying orthogonality and separability: A method for optimizing resin selection and design. Journal of Chromatography A, 2020, 1628, 461429.	1.8	6
79	Evaluation of guanidine-based multimodal anion exchangers for protein selectivity and orthogonality. Journal of Chromatography A, 2021, 1653, 462398.	1.8	6
80	Probing IgG1 F <sub>C</sub> Multimodal Nanoparticle Interactions: A Combined Nuclear Magnetic Resonance and Molecular Dynamics Simulations Approach. Langmuir, 2021, 37, 12188-12203.	1.6	6
81	EVALUATION OF LOT-TO-LOT CONSISTENCY IN ION EXCHANGE CHROMATOGRAPHY. Journal of Liquid Chromatography and Related Technologies, 1999, 22, 1733-1758.	0.5	5
82	Protein Binding Kinetics in Multimodal Systems: Implications for Protein Separations. Analytical Chemistry, 2018, 90, 2609-2617.	3.2	5
83	Implementation of an experimental and computational tool set to study protein-mAb interactions. Biotechnology Progress, 2019, 35, e2825.	1.3	5
84	Systematic workflow for studying domain contributions of bispecific antibodies to selectivity in multimodal chromatography. Biotechnology and Bioengineering, 2022, 119, 211-225.	1.7	5
85	Evaluation of lentiviral vector stability and development of ion exchange purification processes. Biotechnology Progress, 2022, 38, .	1.3	5
86	Parameters Governing the Formation of Photopolymerized Silica Sol-gel Monoliths in PDMS Microfluidic Chips. Chromatographia, 2013, 76, 993-1002.	0.7	4
87	The Role of Ligand-Ligand Interactions in Multimodal Ligand Conformational Equilibria and Surface Pattern Formation. Langmuir, 2020, 36, 9054-9063.	1.6	4
88	Single-step purification of a small non-mAb biologic by peptide-ELP-based affinity precipitation. Biotechnology and Bioengineering, 2020, 117, 3775-3784.	1.7	4
89	Rapid optimization of processes for the integrated purification of biopharmaceuticals. Biotechnology and Bioengineering, 2021, 118, 3435-3446.	1.7	4
90	Synthesis and characterization of particle loaded sol-gel composite material for microfluidic chip system. Journal of Sol-Gel Science and Technology, 2008, 45, 133-141.	1.1	3

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91	Affinity precipitation of monoclonal antibodies using ELP-Z in the elution without resolubilization mode. <i>Journal of Biotechnology</i> , 2021, 338, 1-4.	1.9	3
92	Ion-Exchange Displacement Chromatography of Proteins. <i>ACS Symposium Series</i> , 1993, , 27-42.	0.5	2
93	Mechanism of sequence-based separation of single-stranded DNA in capillary zone electrophoresis. <i>Electrophoresis</i> , 2020, 41, 705-713.	1.3	2
94	Behavior of Water Near Multimodal Chromatography Ligands and Its Consequences for Modulating Protein-Ligand Interactions. <i>Journal of Physical Chemistry B</i> , 2021, 125, 6112-6120.	1.2	2
95	A framework for calculating orthogonal selectivities in multimodal systems directly from cell culture fluid. <i>Biotechnology and Bioengineering</i> , 2022, 119, 299-314.	1.7	2
96	Prediction of Protein Retention Times in Anion-Exchange Chromatography Systems Using Support Vector Regression. <i>ACS Symposium Series</i> , 2005, , 111-125.	0.5	1
97	Advancing a rapid, high throughput screening platform for optimization of lentivirus production. <i>Biotechnology Journal</i> , 2021, 16, 2000621.	1.8	1
98	Alkyl Based Selective Displacers for Protein Purification in Ion Exchange Chromatography. <i>Chromatographia</i> , 2010, 72, 1025-1034.	0.7	0