

Eric D Merkley

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

1,014
citations

567281

15
h-index

454955

30
g-index

33
all docs

33
docs citations

33
times ranked

1870
citing authors

#	ARTICLE	IF	CITATIONS
1	Distance restraints from crosslinking mass spectrometry: Mining a molecular dynamics simulation database to evaluate lysine–lysine distances. <i>Protein Science</i> , 2014, 23, 747-759.	7.6	243
2	Identification and Characterization of MtoA: A Decaheme c-Type Cytochrome of the Neutrophilic Fe(II)-Oxidizing Bacterium <i>Sideroxydans lithotrophicus</i> ES-1. <i>Frontiers in Microbiology</i> , 2012, 3, 37.	3.5	186
3	Dynameomics: A Comprehensive Database of Protein Dynamics. <i>Structure</i> , 2010, 18, 423-435.	3.3	131
4	The succinated proteome. <i>Mass Spectrometry Reviews</i> , 2014, 33, 98-109.	5.4	66
5	Mutations in Global Regulators Lead to Metabolic Selection during Adaptation to Complex Environments. <i>PLoS Genetics</i> , 2014, 10, e1004872.	3.5	50
6	Applications and challenges of forensic proteomics. <i>Forensic Science International</i> , 2019, 297, 350-363.	2.2	39
7	Temperature dependence of the flexibility of thermophilic and mesophilic flavoenzymes of the nitroreductase fold. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 327-336.	2.1	36
8	Live Cell Chemical Profiling of Temporal Redox Dynamics in a Photoautotrophic Cyanobacterium. <i>ACS Chemical Biology</i> , 2014, 9, 291-300.	3.4	35
9	Cross-linking and mass spectrometry methodologies to facilitate structural biology: finding a path through the maze. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 77-90.	1.2	25
10	Mixed-Isotope Labeling with LC-IMS-MS for Characterization of Protein–Protein Interactions by Chemical Cross-Linking. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 444-449.	2.8	24
11	Flying blind, or just flying under the radar? The underappreciated power of <i>de novo</i> methods of mass spectrometric peptide identification. <i>Protein Science</i> , 2020, 29, 1864-1878.	7.6	23
12	Changes in Protein Expression Across Laboratory and Field Experiments in <i>Geobacter bemidjensis</i> . <i>Journal of Proteome Research</i> , 2015, 14, 1361-1375.	3.7	18
13	Ricin-like proteins from the castor plant do not influence liquid chromatography-mass spectrometry detection of ricin in forensically relevant samples. <i>Toxicon</i> , 2017, 140, 18-31.	1.6	18
14	Investigation of <i>Yersinia pestis</i> Laboratory Adaptation through a Combined Genomics and Proteomics Approach. <i>PLoS ONE</i> , 2015, 10, e0142997.	2.5	17
15	Proteomics Goes to Court: A Statistical Foundation for Forensic Toxin/Organism Identification Using Bottom-Up Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 3075-3085.	3.7	16
16	Defending Our Public Biological Databases as a Global Critical Infrastructure. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 58.	4.1	13
17	Detection and Identification of Heme <i>c</i> -Modified Peptides by Histidine Affinity Chromatography, High-Performance Liquid Chromatography–Mass Spectrometry, and Database Searching. <i>Journal of Proteome Research</i> , 2012, 11, 6147-6158.	3.7	9
18	Probabilistic Limit of Detection for Ricin Identification Using a Shotgun Proteomics Assay. <i>Analytical Chemistry</i> , 2019, 91, 12399-12406.	6.5	8

#	ARTICLE	IF	CITATIONS
19	Conformational Changes below the T _m : Molecular Dynamics Studies of the Thermal Pretransition of Ribonuclease A. <i>Biochemistry</i> , 2008, 47, 880-892.	2.5	7
20	Effects of bacterial inactivation methods on downstream proteomic analysis. <i>Journal of Microbiological Methods</i> , 2015, 112, 3-10.	1.6	7
21	A temperature-dependent conformational change of NADH oxidase from <i>Thermus thermophilus</i> HB8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 546-555.	2.6	6
22	Protein abundances can distinguish between naturally-occurring and laboratory strains of <i>Yersinia pestis</i> , the causative agent of plague. <i>PLoS ONE</i> , 2017, 12, e0183478.	2.5	6
23	Uncovering Hidden Members and Functions of the Soil Microbiome Using <i>De Novo</i> Metaproteomics. <i>Journal of Proteome Research</i> , 2022, 21, 2023-2035.	3.7	6
24	Identification of <i>c</i> -Type Heme-Containing Peptides Using Nonactivated Immobilized Metal Affinity Chromatography Resin Enrichment and Higher-Energy Collisional Dissociation. <i>Analytical Chemistry</i> , 2011, 83, 7260-7268.	6.5	5
25	Constructing a Tandem Mass Spectral Library for Forensic Ricin Identification. <i>Journal of Proteome Research</i> , 2019, 18, 3926-3935.	3.7	5
26	Bayesian Inference for Integrating <i>Yarrowia lipolytica</i> Multiomics Datasets with Metabolic Modeling. <i>ACS Synthetic Biology</i> , 2021, 10, 2968-2981.	3.8	4
27	Uniformly ¹⁵ N-Labeled Recombinant Ricin A-Chain as an Internal Retention Time Standard for Increased Confidence in Forensic Identification of Ricin by Untargeted Nanoflow Liquid Chromatography-Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 13372-13376.	6.5	3
28	Introduction to Forensic Proteomics. <i>ACS Symposium Series</i> , 2019, , 1-8.	0.5	2
29	The Statistical Defensibility of Forensic Proteomics. <i>ACS Symposium Series</i> , 2019, , 203-228.	0.5	1
30	Proteomics for bioforensics. , 2020, , 251-265.		0
31	<i>De novo</i> sequencing and native mass spectrometry revealed hetero-association of dirigent protein homologs and potential interacting proteins in <i>Forsythia</i> — <i>intermedia</i> . <i>Analyst</i> , 2021, 146, 7670-7681.	3.5	0