

Brian K Erickson

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

6,396
citations

394421
19
h-index

580821
25
g-index

27
all docs

27
docs citations

27
times ranked

12397
citing authors

#	ARTICLE	IF	CITATIONS
1	The BioPlex Network: A Systematic Exploration of the Human Interactome. <i>Cell</i> , 2015, 162, 425-440.	28.9	1,241
2	Architecture of the human interactome defines protein communities and disease networks. <i>Nature</i> , 2017, 545, 505-509.	27.8	1,190
3	MultiNotch MS3 Enables Accurate, Sensitive, and Multiplexed Detection of Differential Expression across Cancer Cell Line Proteomes. <i>Analytical Chemistry</i> , 2014, 86, 7150-7158.	6.5	1,130
4	Quantitative Proteomics of the Cancer Cell Line Encyclopedia. <i>Cell</i> , 2020, 180, 387-402.e16.	28.9	596
5	A Creatine-Driven Substrate Cycle Enhances Energy Expenditure and Thermogenesis in Beige Fat. <i>Cell</i> , 2015, 163, 643-655.	28.9	575
6	Mitochondrial ROS regulate thermogenic energy expenditure and sulfenylation of UCP1. <i>Nature</i> , 2016, 532, 112-116.	27.8	341
7	Effects of Diet on Resource Utilization by a Model Human Gut Microbiota Containing <i>Bacteroides cellulosilyticus</i> WH2, a Symbiont with an Extensive Glycobiome. <i>PLoS Biology</i> , 2013, 11, e1001637.	5.6	244
8	Full-Featured, Real-Time Database Searching Platform Enables Fast and Accurate Multiplexed Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 2026-2034.	3.7	171
9	Evaluating Multiplexed Quantitative Phosphopeptide Analysis on a Hybrid Quadrupole Mass Filter/Linear Ion Trap/Orbitrap Mass Spectrometer. <i>Analytical Chemistry</i> , 2015, 87, 1241-1249.	6.5	146
10	UCP1 deficiency causes brown fat respiratory chain depletion and sensitizes mitochondria to calcium overload-induced dysfunction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7981-7986.	7.1	136
11	A Strategy to Combine Sample Multiplexing with Targeted Proteomics Assays for High-Throughput Protein Signature Characterization. <i>Molecular Cell</i> , 2017, 65, 361-370.	9.7	118
12	The Nuclear Proteome of a Vertebrate. <i>Current Biology</i> , 2015, 25, 2663-2671.	3.9	117
13	Active Instrument Engagement Combined with a Real-Time Database Search for Improved Performance of Sample Multiplexing Workflows. <i>Journal of Proteome Research</i> , 2019, 18, 1299-1306.	3.7	109
14	Strategies for Metagenomic-Guided Whole-Community Proteomics of Complex Microbial Environments. <i>PLoS ONE</i> , 2011, 6, e27173.	2.5	58
15	Generation of Multiple Reporter Ions from a Single Isobaric Reagent Increases Multiplexing Capacity for Quantitative Proteomics. <i>Analytical Chemistry</i> , 2015, 87, 9855-9863.	6.5	42
16	Identification and quantification of protein S-nitrosation by nitrite in the mouse heart during ischemia. <i>Journal of Biological Chemistry</i> , 2017, 292, 14486-14495.	3.4	34
17	Experimental Approach for Deep Proteome Measurements from Small-Scale Microbial Biomass Samples. <i>Analytical Chemistry</i> , 2008, 80, 9517-9525.	6.5	30
18	Posttranslational modification and sequence variation of redox-active proteins correlate with biofilm life cycle in natural microbial communities. <i>ISME Journal</i> , 2010, 4, 1398-1409.	9.8	26

#	ARTICLE	IF	CITATIONS
19	Comparison of Proteomic Quantification Approaches for Hepatic Drug Transporters: Multiplexed Global Quantitation Correlates with Targeted Proteomic Quantitation. Drug Metabolism and Disposition, 2018, 46, 692-696.	3.3	25
20	Computational Prediction and Experimental Validation of Signal Peptide Cleavages in the Extracellular Proteome of a Natural Microbial Community. Journal of Proteome Research, 2010, 9, 2148-2159.	3.7	17
21	TomahqCompanion: A Tool for the Creation and Analysis of Isobaric Label Based Multiplexed Targeted Assays. Journal of Proteome Research, 2019, 18, 594-605.	3.7	14
22	Multiplexed proteomics of autophagy-deficient murine macrophages reveals enhanced antimicrobial immunity via the oxidative stress response. ELife, 2021, 10, .	6.0	10
23	Parallel Notched Gas-Phase Enrichment for Improved Proteome Identification and Quantification with Fast Spectral Acquisition Rates. Journal of Proteome Research, 2020, 19, 2750-2757.	3.7	4
24	Metal Affinity Enrichment Increases the Range and Depth of Proteome Identification for Extracellular Microbial Proteins. Journal of Proteome Research, 2012, 11, 861-870.	3.7	1