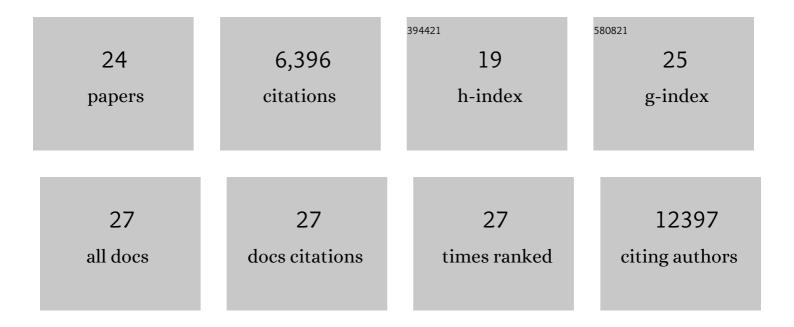
Brian K Erickson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2945739/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Multiplexed proteomics of autophagy-deficient murine macrophages reveals enhanced antimicrobial immunity via the oxidative stress response. ELife, 2021, 10, .	6.0	10
2	Full-Featured, Real-Time Database Searching Platform Enables Fast and Accurate Multiplexed Quantitative Proteomics. Journal of Proteome Research, 2020, 19, 2026-2034.	3.7	171
3	Quantitative Proteomics of the Cancer Cell Line Encyclopedia. Cell, 2020, 180, 387-402.e16.	28.9	596
4	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
5	Active Instrument Engagement Combined with a Real-Time Database Search for Improved Performance of Sample Multiplexing Workflows. Journal of Proteome Research, 2019, 18, 1299-1306.	3.7	109
6	TomahaqCompanion: 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
7	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
8	Architecture of the human interactome defines protein communities and disease networks. Nature, 2017, 545, 505-509.	27.8	1,190
9	UCP1 deficiency causes brown fat respiratory chain depletion and sensitizes mitochondria to calcium overload-induced dysfunction. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7981-7986.	7.1	136
10	A Strategy to Combine Sample Multiplexing with Targeted Proteomics Assays for High-Throughput Protein Signature Characterization. Molecular Cell, 2017, 65, 361-370.	9.7	118
11	Identification and quantification of protein S-nitrosation by nitrite in the mouse heart during ischemia. Journal of Biological Chemistry, 2017, 292, 14486-14495.	3.4	34
12	Mitochondrial ROS regulate thermogenic energy expenditure and sulfenylation of UCP1. Nature, 2016, 532, 112-116.	27.8	341
13	Evaluating Multiplexed Quantitative Phosphopeptide Analysis on a Hybrid Quadrupole Mass Filter/Linear Ion Trap/Orbitrap Mass Spectrometer. Analytical Chemistry, 2015, 87, 1241-1249.	6.5	146
14	The BioPlex Network: A Systematic Exploration of the Human Interactome. Cell, 2015, 162, 425-440.	28.9	1,241
15	A Creatine-Driven Substrate Cycle Enhances Energy Expenditure and Thermogenesis in Beige Fat. Cell, 2015, 163, 643-655.	28.9	575
16	The Nuclear Proteome of a Vertebrate. Current Biology, 2015, 25, 2663-2671.	3.9	117
17	Generation of Multiple Reporter Ions from a Single Isobaric Reagent Increases Multiplexing Capacity for Quantitative Proteomics. Analytical Chemistry, 2015, 87, 9855-9863.	6.5	42
18	MultiNotch MS3 Enables Accurate, Sensitive, and Multiplexed Detection of Differential Expression across Cancer Cell Line Proteomes. Analytical Chemistry, 2014, 86, 7150-7158.	6.5	1,130

BRIAN K ERICKSON

#	Article	IF	CITATIONS
19	Effects of Diet on Resource Utilization by a Model Human Gut Microbiota Containing Bacteroides cellulosilyticus WH2, a Symbiont with an Extensive Glycobiome. PLoS Biology, 2013, 11, e1001637.	5.6	244
20	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
21	Strategies for Metagenomic-Guided Whole-Community Proteomics of Complex Microbial Environments. PLoS ONE, 2011, 6, e27173.	2.5	58
22	Posttranslational modification and sequence variation of redox-active proteins correlate with biofilm life cycle in natural microbial communities. ISME Journal, 2010, 4, 1398-1409.	9.8	26
23	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
24	Experimental Approach for Deep Proteome Measurements from Small-Scale Microbial Biomass Samples. Analytical Chemistry, 2008, 80, 9517-9525.	6.5	30