

Jeremy C Clair

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7409911/publications.pdf>

Version: 2024-02-01

40
papers

2,117
citations

304743

22
h-index

276875

41
g-index

46
all docs

46
docs citations

46
times ranked

2958
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic Analysis of Human Lung Development. American Journal of Respiratory and Critical Care Medicine, 2022, 205, 208-218.	5.6	9
2	A census of the lung: CellCards from LungMAP. Developmental Cell, 2022, 57, 112-145.e2.	7.0	67
3	A microphysiological model of human trophoblast invasion during implantation. Nature Communications, 2022, 13, 1252.	12.8	37
4	Three-dimensional feature matching improves coverage for single-cell proteomics based on ion mobility filtering. Cell Systems, 2022, 13, 426-434.e4.	6.2	49
5	The <i>Campylobacter jejuni</i> CiaD effector co-opts the host cell protein IQGAP1 to promote cell entry. Nature Communications, 2021, 12, 1339.	12.8	10
6	Proteomic Profiling of the Substantia Nigra to Identify Determinants of Lewy Body Pathology and Dopaminergic Neuronal Loss. Journal of Proteome Research, 2021, 20, 2266-2282.	3.7	10
7	Repetitive diacetyl vapor exposure promotes ubiquitin proteasome stress and precedes bronchiolitis obliterans pathology. Archives of Toxicology, 2021, 95, 2469-2483.	4.2	8
8	Interpreting the lipidome: bioinformatic approaches to embrace the complexity. Metabolomics, 2021, 17, 55.	3.0	7
9	Accumulation of Succinyl Coenzyme A Perturbs the Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Succinylome and Is Associated with Increased Susceptibility to Beta-Lactam Antibiotics. MBio, 2021, 12, e0053021.	4.1	16
10	High-throughput and high-efficiency sample preparation for single-cell proteomics using a nested nanowell chip. Nature Communications, 2021, 12, 6246.	12.8	76
11	A <i>Histoplasma capsulatum</i> Lipid Metabolic Map Identifies Antifungal Targets. MBio, 2021, 12, e0297221.	4.1	6
12	A porcine ligated loop model reveals new insight into the host immune response against <i>Campylobacter jejuni</i> . Gut Microbes, 2020, 12, 1814121.	9.8	7
13	The spore coat is essential for <i>Bacillus subtilis</i> spore resistance to pulsed light, and pulsed light treatment eliminates some spore coat proteins. International Journal of Food Microbiology, 2020, 323, 108592.	4.7	13
14	Amylases in the Human Vagina. MSphere, 2020, 5, .	2.9	30
15	Integration of transcriptomic and proteomic data identifies biological functions in cell populations from human infant lung. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2019, 317, L347-L360.	2.9	28
16	High-Throughput Single Cell Proteomics Enabled by Multiplex Isobaric Labeling in a Nanodroplet Sample Preparation Platform. Analytical Chemistry, 2019, 91, 13119-13127.	6.5	156
17	A multiomics focusing towards the molecular networks of lung development. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2019, 317, L554-L555.	2.9	1
18	Multi-omics Signature of <i>Candida auris</i> , an Emerging and Multidrug-Resistant Pathogen. MSystems, 2019, 4, .	3.8	65

#	ARTICLE	IF	CITATIONS
19	Campylobacter jejuni Demonstrates Conserved Proteomic and Transcriptomic Responses When Co-cultured With Human INT 407 and Caco-2 Epithelial Cells. <i>Frontiers in Microbiology</i> , 2019, 10, 755.	3.5	19
20	Lipid Mini-On: mining and ontology tool for enrichment analysis of lipidomic data. <i>Bioinformatics</i> , 2019, 35, 4507-4508.	4.1	38
21	Stochastic Variation in Expression of the Tricarboxylic Acid Cycle Produces Persister Cells. <i>MBio</i> , 2019, 10, .	4.1	84
22	Individual Variability of Protein Expression in Human Tissues. <i>Journal of Proteome Research</i> , 2018, 17, 3914-3922.	3.7	15
23	Cell type-resolved human lung lipidome reveals cellular cooperation in lung function. <i>Scientific Reports</i> , 2018, 8, 13455.	3.3	31
24	Proteomic Analysis of Single Mammalian Cells Enabled by Microfluidic Nanodroplet Sample Preparation and Ultrasensitive NanoLC-MS. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 12370-12374.	13.8	186
25	Time-resolved proteome profiling of normal lung development. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2018, 315, L11-L24.	2.9	25
26	Proteomic Analysis of Single Mammalian Cells Enabled by Microfluidic Nanodroplet Sample Preparation and Ultrasensitive NanoLC-MS. <i>Angewandte Chemie</i> , 2018, 130, 12550-12554.	2.0	31
27	Redeploying β -Lactam Antibiotics as a Novel Antivirulence Strategy for the Treatment of Methicillin-Resistant <i>Staphylococcus aureus</i> Infections. <i>Journal of Infectious Diseases</i> , 2017, 215, 80-87.	4.0	28
28	Quantitative Proteomic Analysis of Mass Limited Tissue Samples for Spatially Resolved Tissue Profiling. <i>Methods in Molecular Biology</i> , 2017, 1788, 269-277.	0.9	4
29	The food-borne pathogen <i>Campylobacter jejuni</i> responds to the bile salt deoxycholate with countermeasures to reactive oxygen species. <i>Scientific Reports</i> , 2017, 7, 15455.	3.3	27
30	Lipidomics reveals dramatic lipid compositional changes in the maturing postnatal lung. <i>Scientific Reports</i> , 2017, 7, 40555.	3.3	67
31	Alveolar injury and regeneration following deletion of ABCA3. <i>JCI Insight</i> , 2017, 2, .	5.0	37
32	EMC3 coordinates surfactant protein and lipid homeostasis required for respiration. <i>Journal of Clinical Investigation</i> , 2017, 127, 4314-4325.	8.2	48
33	Inactivation by Pulsed Light of <i>Bacillus subtilis</i> Spores with Impaired Protection Factors. <i>Photochemistry and Photobiology</i> , 2016, 92, 301-307.	2.5	12
34	Spatially-Resolved Proteomics: Rapid Quantitative Analysis of Laser Capture Microdissected Alveolar Tissue Samples. <i>Scientific Reports</i> , 2016, 6, 39223.	3.3	69
35	Persister formation in <i>Staphylococcus aureus</i> is associated with ATP depletion. <i>Nature Microbiology</i> , 2016, 1, .	13.3	508
36	Proteomic Evidences for Rex Regulation of Metabolism in Toxin-Producing <i>Bacillus cereus</i> ATCC 14579. <i>PLoS ONE</i> , 2014, 9, e107354.	2.5	21

#	ARTICLE	IF	CITATIONS
37	OhrRA functions as a redox-responsive system controlling toxinogenesis in <i>Bacillus cereus</i> . <i>Journal of Proteomics</i> , 2013, 94, 527-539.	2.4	26
38	Restricting Fermentative Potential by Proteome Remodeling. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013102.	3.8	44
39	Exoproteomics: exploring the world around biological systems. <i>Expert Review of Proteomics</i> , 2012, 9, 561-575.	3.0	80
40	Expanding the Known Repertoire of Virulence Factors Produced by <i>Bacillus cereus</i> through Early Secretome Profiling in Three Redox Conditions. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1486-1498.	3.8	105