

Jacob M Wozniak

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

1,257
citations

623574

14
h-index

580701

25
g-index

30
all docs

30
docs citations

30
times ranked

2317
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Analysis of T-Cell Spatial Proteomics and the Influence of HIV Expression. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100194.	2.5	2
2	Phosphoproteomic analysis of thrombin- and p38 MAPK-regulated signaling networks in endothelial cells. <i>Journal of Biological Chemistry</i> , 2022, 298, 101801.	1.6	8
3	CLK1 reorganizes the splicing factor U1-70K for early spliceosomal protein assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
4	mTORC2 controls the activity of PKC and Akt by phosphorylating a conserved TOR interaction motif. <i>Science Signaling</i> , 2021, 14, .	1.6	64
5	Disruption of innate defense responses by endoglycosidase HPSE promotes cell survival. <i>JCI Insight</i> , 2021, 6, .	2.3	14
6	Heat shock protein 27 activity is linked to endothelial barrier recovery after proinflammatory GPCR-induced disruption. <i>Science Signaling</i> , 2021, 14, eabc1044.	1.6	23
7	Targeted Protein Acetylation in Cells Using Heterobifunctional Molecules. <i>Journal of the American Chemical Society</i> , 2021, 143, 16700-16708.	6.6	46
8	A combined EM and proteomic analysis places HIV-1 Vpu at the crossroads of retromer and ESCRT complexes: PTPN23 is a Vpu-cofactor. <i>PLoS Pathogens</i> , 2021, 17, e1009409.	2.1	0
9	AssessORF: combining evolutionary conservation and proteomics to assess prokaryotic gene predictions. <i>Bioinformatics</i> , 2020, 36, 1022-1029.	1.8	10
10	Untargeted mass spectrometry-based metabolomics approach unveils molecular changes in raw and processed foods and beverages. <i>Food Chemistry</i> , 2020, 302, 125290.	4.2	52
11	Mortality Risk Profiling of Staphylococcus aureus Bacteremia by Multi-omic Serum Analysis Reveals Early Predictive and Pathogenic Signatures. <i>Cell</i> , 2020, 182, 1311-1327.e14.	13.5	58
12	Exposure of Mycobacterium abscessus to Environmental Stress and Clinically Used Antibiotics Reveals Common Proteome Response among Pathogenic Mycobacteria. <i>Microorganisms</i> , 2020, 8, 698.	1.6	18
13	Molecular dissection of Chagas induced cardiomyopathy reveals central disease associated and druggable signaling pathways. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007980.	1.3	9
14	Phosphoproteomic analysis of protease-activated receptor-1 biased signaling reveals unique modulators of endothelial barrier function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5039-5048.	3.3	25
15	Organ-level protein networks as a reference for the host effects of the microbiome. <i>Genome Research</i> , 2020, 30, 276-286.	2.4	6
16	A Hetero-Multimeric Chitinase-Containing Plasmodium falciparum and Plasmodium gallinaceum Ookinete-Secreted Protein Complex Involved in Mosquito Midgut Invasion. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 615343.	1.8	4
17	Functional and Proteomic Analysis of Streptococcus pyogenes Virulence Upon Loss of Its Native Cas9 Nuclease. <i>Frontiers in Microbiology</i> , 2019, 10, 1967.	1.5	11
18	EGFR is required for Wnt9a-Fzd9b signalling specificity in haematopoietic stem cells. <i>Nature Cell Biology</i> , 2019, 21, 721-730.	4.6	42

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19	Quantitative Multiplex Substrate Profiling of Peptidases by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 968a-981.	2.5	28
20	Quantitative analysis of <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> proteome in response to antibiotics and during exposure to different environmental conditions. <i>Clinical Proteomics</i> , 2019, 16, 39.	1.1	23
21	<i>PTMphinder</i> : an R package for PTM site localization and motif extraction from proteomic datasets. <i>PeerJ</i> , 2019, 7, e7046.	0.9	8
22	Context-Dependent and Disease-Specific Diversity in Protein Interactions within Stress Granules. <i>Cell</i> , 2018, 172, 590-604.e13.	13.5	672
23	Optimization of carbon and energy utilization through differential translational efficiency. <i>Nature Communications</i> , 2018, 9, 4474.	5.8	35
24	Defining Host Responses during Systemic Bacterial Infection through Construction of a Murine Organ Proteome Atlas. <i>Cell Systems</i> , 2018, 6, 579-592.e4.	2.9	23
25	Context-Dependent and Disease-Specific Diversity in Stress Granules Formed from Pre-existing Protein Interactions. <i>FASEB Journal</i> , 2018, 32, 252.3.	0.2	2
26	Quantitative Temporal Viromics of an Inducible HIV-1 Model Yields Insight to Global Host Targets and Phospho-Dynamics Associated with Protein Vpr. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1447-1461.	2.5	60