

# Suruchi Aggarwal

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4273142/publications.pdf>

Version: 2024-02-01

14  
papers

215  
citations

1040056

9  
h-index

1199594

12  
g-index

14  
all docs

14  
docs citations

14  
times ranked

275  
citing authors

#	ARTICLE	IF	CITATIONS
1	Studying Autophagy Using a TMT-Based Quantitative Proteomics Approach. <i>Methods in Molecular Biology</i> , 2022, 2445, 183-203.	0.9	2
2	Posttranslational modifications in systems biology. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 127, 93-126.	2.3	16
3	Big data, integrative omics and network biology. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 127, 127-160.	2.3	21
4	Proteomic landscape of Japanese encephalitis virus-infected fibroblasts. <i>Journal of General Virology</i> , 2021, 102, .	2.9	15
5	Proteome analysis revealed the essential functions of protein phosphatase PP2A in the induction of Th9 cells. <i>Scientific Reports</i> , 2020, 10, 10992.	3.3	6
6	HyperQuant™ A Computational Pipeline for Higher Order Multiplexed Quantitative Proteomics. <i>ACS Omega</i> , 2020, 5, 10857-10867.	3.5	7
7	Post-translational Modification Crosstalk and Hotspots in Sirtuin Interactors Implicated in Cardiovascular Diseases. <i>Frontiers in Genetics</i> , 2020, 11, 356.	2.3	25
8	Quantitative Proteome Analysis of <i>Atg5</i> -Deficient Mouse Embryonic Fibroblasts Reveals the Range of the Autophagy-Modulated Basal Cellular Proteome. <i>MSystems</i> , 2019, 4, .	3.8	9
9	Advances in Higher Order Multiplexing Techniques in Proteomics. <i>Journal of Proteome Research</i> , 2019, 18, 2360-2369.	3.7	22
10	Perturbed Signaling and Role of Posttranslational Modifications in Cancer Drug Resistance. , 2017, , 483-510.		7
11	Emergence of Drug Resistance in Mycobacterium and Other Bacterial Pathogens: The Posttranslational Modification Perspective. , 2017, , 209-231.		2
12	Dataset generated using hyperplexing and click chemistry to monitor temporal dynamics of newly synthesized macrophage secretome post infection by mycobacterial strains. <i>Data in Brief</i> , 2016, 9, 349-354.	1.0	15
13	False Discovery Rate Estimation in Proteomics. <i>Methods in Molecular Biology</i> , 2016, 1362, 119-128.	0.9	45
14	Dissecting the iTRAQ Data Analysis. <i>Methods in Molecular Biology</i> , 2016, 1362, 277-291.	0.9	23