Anthony J Cesnik

List of Publications by Year
in descending order

23 papers	864 citations	623699 14 h-index	610883 24 g-index
31 all docs	31 docs citations	31 times ranked	1286 citing authors

#	Article	IF	Citations
1	Spatiotemporal dissection of the cell cycle with single-cell proteogenomics. Nature, 2021, 590, 649-654.	27.8	104
2	Proteogenomics: Integrating Next-Generation Sequencing and Mass Spectrometry to Characterize Human Proteomic Variation. Annual Review of Analytical Chemistry, 2016, 9, 521-545.	5.4	91
3	Mapping the nucleolar proteome reveals a spatiotemporal organization related to intrinsic protein disorder. Molecular Systems Biology, 2020, 16, e9469.	7.2	91
4	Analysis of the Human Protein Atlas Image Classification competition. Nature Methods, 2019, 16, 1254-1261.	19.0	88
5	The Blood Proteoform Atlas: A reference map of proteoforms in human hematopoietic cells. Science, 2022, 375, 411-418.	12.6	64
6	HyPR-MS for Multiplexed Discovery of MALAT1, NEAT1, and NORAD lncRNA Protein Interactomes. Journal of Proteome Research, 2018, 17, 3022-3038.	3.7	49
7	Elucidating Proteoform Families from Proteoform Intact-Mass and Lysine-Count Measurements. Journal of Proteome Research, 2016, 15, 1213-1221.	3.7	43
8	Proteoform Suite: Software for Constructing, Quantifying, and Visualizing Proteoform Families. Journal of Proteome Research, 2018, 17, 568-578.	3.7	40
9	ProForma: A Standard Proteoform Notation. Journal of Proteome Research, 2018, 17, 1321-1325.	3.7	35
10	Elucidating *Escherichia coli* Proteoform Families Using Intact-Mass Proteomics and a Global PTM Discovery Database. Journal of Proteome Research, 2017, 16, 4156-4165.	3.7	32
11	Human Proteomic Variation Revealed by Combining RNA-Seq Proteogenomics and Global Post-Translational Modification (G-PTM) Search Strategy. Journal of Proteome Research, 2016, 15, 800-808.	3.7	29
12	Expanding Proteoform Identifications in Top-Down Proteomic Analyses by Constructing Proteoform Families. Analytical Chemistry, 2018, 90, 1325-1333.	6.5	27
13	Spritz: A Proteogenomic Database Engine. Journal of Proteome Research, 2021, 20, 1826-1834.	3.7	24
14	Identification and Quantification of Murine Mitochondrial Proteoforms Using an Integrated Top-Down and Intact-Mass Strategy. Journal of Proteome Research, 2018, 17, 3526-3536.	3.7	23
15	Proteomics in non-human primates: utilizing RNA-Seq data to improve protein identification by mass spectrometry in vervet monkeys. BMC Genomics, 2017, 18, 877.	2.8	17
16	Comprehensive in vivo identification of the c-Myc mRNA protein interactome using HyPR-MS. Rna, 2019, 25, 1337-1352.	3.5	15
17	Electrochemical Synthesis of Binary and Ternary Niobium-Containing Oxide Electrodes Using the *p*-Benzoquinone/Hydroquinone Redox Couple. Langmuir, 2015, 31, 9502-9510.	3.5	14
18	Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. Journal of Proteome Research, 2022, 21, 1189-1195.	3.7	14

#	Article	IF	Citations
19	HyCCAPP as a tool to characterize promoter DNA-protein interactions in Saccharomyces cerevisiae. Genomics, 2016, 107, 267-273.	2.9	12
20	Illuminating Non-genetic Cellular Heterogeneity with Imaging-Based Spatial Proteomics. Trends in Cancer, 2021, 7, 278-282.	7.4	12
21	Comprehensive Detection of Single Amino Acid Variants and Evaluation of Their Deleterious Potential in a PANC-1 Cell Line. Journal of Proteome Research, 2020, 19, 1635-1646.	3.7	11
22	Long Noncoding RNAs AC009014.3 and Newly Discovered XPLAID Differentiate Aggressive and Indolent Prostate Cancers. Translational Oncology, 2018, 11, 808-814.	3.7	7
23	MetaNetwork Enhances Biological Insights from Quantitative Proteomics Differences by Combining Clustering and Enrichment Analyses. Journal of Proteome Research, 2022, 21, 410-419.	3.7	2