

Annie Moradian

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

5,545
citations

218677

26
h-index

223800

46
g-index

51
all docs

51
docs citations

51
times ranked

13140
citing authors

#	ARTICLE	IF	CITATIONS
1	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , 2012, 486, 395-399.	27.8	1,778
2	The Xist lncRNA interacts directly with SHARP to silence transcription through HDAC3. <i>Nature</i> , 2015, 521, 232-236.	27.8	946
3	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , 2019, 177, 1600-1618.e17.	28.9	701
4	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. <i>Blood</i> , 2011, 117, 2451-2459.	1.4	556
5	The top-down, middle-down, and bottom-up mass spectrometry approaches for characterization of histone variants and their post-translational modifications. <i>Proteomics</i> , 2014, 14, 489-497.	2.2	122
6	Composition and Regulation of the Cellular Repertoire of SCF Ubiquitin Ligases. <i>Cell</i> , 2017, 171, 1326-1339.e14.	28.9	118
7	Cell-specific proteomic analysis in <i>Caenorhabditis elegans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2705-2710.	7.1	99
8	Interaction of Cyclin-Dependent Kinase 12/CrkRS with Cyclin K1 Is Required for the Phosphorylation of the C-Terminal Domain of RNA Polymerase II. <i>Molecular and Cellular Biology</i> , 2012, 32, 4691-4704.	2.3	93
9	Systematic approach for dissecting the molecular mechanisms of transcriptional regulation in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4796-E4805.	7.1	81
10	The methanol-induced conformational transitions of β^2 -lactoglobulin, cytochrome c, and ubiquitin at low pH: A study by electrospray ionization mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 317-328.	2.8	66
11	Identification of Mechanism-Based Inactivation in P450-Catalyzed Cyclopropanation Facilitates Engineering of Improved Enzymes. <i>Journal of the American Chemical Society</i> , 2016, 138, 12527-12533.	13.7	58
12	LONP1 and mtHSP70 cooperate to promote mitochondrial protein folding. <i>Nature Communications</i> , 2021, 12, 265.	12.8	58
13	PIKES Analysis Reveals Response to Degradation and Key Regulatory Mechanisms of the CRL4 Network. <i>Molecular Cell</i> , 2020, 77, 1092-1106.e9.	9.7	56
14	Interrogating marine virus-host interactions and elemental transfer with BONCAT and nanoSIMS-based methods. <i>Environmental Microbiology</i> , 2018, 20, 671-692.	3.8	53
15	SutA is a bacterial transcription factor expressed during slow growth in <i>Pseudomonas aeruginosa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E597-605.	7.1	52
16	The <i>Drosophila</i> effector caspase Dcp-1 regulates mitochondrial dynamics and autophagic flux via SesB. <i>Journal of Cell Biology</i> , 2014, 205, 477-492.	5.2	43
17	A <i>Trichomonas vaginalis</i> Rhomboid Protease and Its Substrate Modulate Parasite Attachment and Cytolysis of Host Cells. <i>PLoS Pathogens</i> , 2015, 11, e1005294.	4.7	43
18	Bioorthogonal Noncanonical Amino Acid Tagging (BONCAT) Enables Time-Resolved Analysis of Protein Synthesis in Native Plant Tissue. <i>Plant Physiology</i> , 2017, 173, 1543-1553.	4.8	43

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19	The Mammalian Proteins MMS19, MIP18, and ANT2 Are Involved in Cytoplasmic Iron-Sulfur Cluster Protein Assembly. <i>Journal of Biological Chemistry</i> , 2012, 287, 43351-43358.	3.4	39
20	BUD13 Promotes a Type I Interferon Response by Countering Intron Retention in Irf7. <i>Molecular Cell</i> , 2019, 73, 803-814.e6.	9.7	39
21	Robust cullin-RING ligase function is established by a multiplicity of poly-ubiquitylation pathways. <i>ELife</i> , 2019, 8, .	6.0	36
22	Data-Independent Acquisition for the Orbitrap Q Exactive HF: A Tutorial. <i>Journal of Proteome Research</i> , 2019, 18, 803-813.	3.7	35
23	Mutations in CIC and IDH1 cooperatively regulate 2-hydroxyglutarate levels and cell clonogenicity. <i>Oncotarget</i> , 2014, 5, 7960-7979.	1.8	35
24	Cytosolic protein interactions of the schizophrenia susceptibility gene dysbindin. <i>Journal of Neurochemistry</i> , 2010, 113, 1491-1503.	3.9	33
25	Tyramide signal amplification mass spectrometry (TSA-MS) ratio identifies nuclear speckle proteins. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	33
26	Deciphering the regulatory genome of Escherichia coli, one hundred promoters at a time. <i>ELife</i> , 2020, 9, .	6.0	31
27	Stable Isotope Analysis of Intact Oxanions Using Electrospray Quadrupole-Orbitrap Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 3077-3085.	6.5	30
28	WNK1 is an assembly factor for the human ER membrane protein complex. <i>Molecular Cell</i> , 2021, 81, 2693-2704.e12.	9.7	29
29	Scanning the isotopic structure of molecules by tandem mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2018, 434, 276-286.	1.5	28
30	High Resolution Parallel Reaction Monitoring with Electron Transfer Dissociation for Middle-Down Proteomics. <i>Analytical Chemistry</i> , 2015, 87, 8360-8366.	6.5	26
31	Nitric Oxide Modulates Endonuclease III Redox Activity by a 800 mV Negative Shift upon [Fe ₄ S ₄] Cluster Nitrosylation. <i>Journal of the American Chemical Society</i> , 2018, 140, 11800-11810.	13.7	24
32	Mass selective axial ion ejection from linear quadrupoles with added octopole fields. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 270-280.	2.8	22
33	Standardized Workflow for Precise Mid- and High-Throughput Proteomics of Blood Biofluids. <i>Clinical Chemistry</i> , 2022, 68, 450-460.	3.2	22
34	Quantitative mass spectrometry reveals changes in SNAP-25 isoforms in schizophrenia. <i>Schizophrenia Research</i> , 2016, 177, 44-51.	2.0	17
35	Vectored antibody gene delivery mediates long-term contraception. <i>Current Biology</i> , 2015, 25, R820-R822.	3.9	14
36	Hsp83 loss suppresses proteasomal activity resulting in an upregulation of caspase-dependent compensatory autophagy. <i>Autophagy</i> , 2017, 13, 1573-1589.	9.1	12

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37	The dormancy-specific regulator, SutA, is intrinsically disordered and modulates transcription initiation in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2019, 112, 992-1009.	2.5	11
38	The SNAP25 Interactome in Ventromedial Caudate in Schizophrenia Includes the Mitochondrial Protein ARF1. <i>Neuroscience</i> , 2019, 420, 97-111.	2.3	10
39	JNK-associated Leucine Zipper Protein Functions as a Docking Platform for Polo-like Kinase 1 and Regulation of the Associating Transcription Factor Forkhead Box Protein K1. <i>Journal of Biological Chemistry</i> , 2015, 290, 29617-29628.	3.4	9
40	A Novel <i>Trichomonas vaginalis</i> Surface Protein Modulates Parasite Attachment via Protein:Host Cell Proteoglycan Interaction. <i>MBio</i> , 2021, 12, .	4.1	9
41	Molecular and structural characterization of the SH3 domain of AHI-1 in regulation of cellular resistance of BCR-ABL+ chronic myeloid leukemia cells to tyrosine kinase inhibitors. <i>Proteomics</i> , 2012, 12, 2094-2106.	2.2	8
42	Two distinct sites of client protein interaction with the chaperone cpSRP43. <i>Journal of Biological Chemistry</i> , 2018, 293, 8861-8873.	3.4	8
43	Collision cross sections of gas phase DNA ions. <i>International Journal of Mass Spectrometry</i> , 2002, 219, 161-170.	1.5	7
44	A Targeted MRM Approach for Tempo-Spatial Proteomics Analyses. <i>Methods in Molecular Biology</i> , 2016, 1394, 75-85.	0.9	4
45	Nano volume fractionation strategy for dilute-and-shoot injections in off-line loss-less proteomic workflows for extensive protein identifications of ultra-low sample amounts. <i>Journal of Chromatography A</i> , 2020, 1609, 460507.	3.7	4
46	High resolution data-independent acquisition with electron transfer dissociation mass spectrometry: Multiplexed analysis of post-translationally modified proteins. <i>International Journal of Mass Spectrometry</i> , 2015, 390, 155-162.	1.5	2
47	Molecular and Structural Characterization of the SH3 Domain of AHI-1 in Regulation of Cellular Resistance of BCR-ABL+ Chronic Myeloid Leukemia Cells to Tyrosine Kinase Inhibitors. <i>Blood</i> , 2011, 118, 966-966.	1.4	0