Namrata D Udeshi

List of Publications by Year
in descending order

64 papers	11,755 citations	76326 40 h-index	114465 63 g-index
74 all docs	74 docs citations	74 times ranked	15979 citing authors

#	Article	IF	Citations
1	Lenalidomide Causes Selective Degradation of IKZF1 and IKZF3 in Multiple Myeloma Cells. Science, 2014, 343, 301-305.	12.6	1,371
2	Efficient proximity labeling in living cells and organisms with TurboID. Nature Biotechnology, 2018, 36, 880-887.	17.5	1,103
3	Proteomic Mapping of Mitochondria in Living Cells via Spatially Restricted Enzymatic Tagging. Science, 2013, 339, 1328-1331.	12.6	1,023
4	Lenalidomide induces ubiquitination and degradation of CK1Î± in del(5q) MDS. Nature, 2015, 523, 183-188.	27.8	648
5	EMRE Is an Essential Component of the Mitochondrial Calcium Uniporter Complex. Science, 2013, 342, 1379-1382.	12.6	537
6	Integrated proteomic analysis of post-translational modifications by serial enrichment. Nature Methods, 2013, 10, 634-637.	19.0	534
7	Proteomic Mapping of the Human Mitochondrial Intermembrane Space in Live Cells via Ratiometric APEX Tagging. Molecular Cell, 2014, 55, 332-341.	9.7	414
8	Spatially resolved proteomic mapping in living cells with the engineered peroxidase APEX2. Nature Protocols, 2016, 11, 456-475.	12.0	411
9	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatographyâ€"mass spectrometry. Nature Protocols, 2018, 13, 1632-1661.	12.0	377
10	Proteomic Analysis of Unbounded Cellular Compartments: Synaptic Clefts. Cell, 2016, 166, 1295-1307.e21.	28.9	324
11	Refined Preparation and Use of Anti-diglycine Remnant (K-Îµ-GG) Antibody Enables Routine Quantification of 10,000s of Ubiquitination Sites in Single Proteomics Experiments. Molecular and Cellular Proteomics, 2013, 12, 825-831.	3.8	279
12	Proteomic mapping of cytosol-facing outer mitochondrial and ER membranes in living human cells by proximity biotinylation. ELife, 2017, 6, .	6.0	276
13	O-GlcNAc Regulates FoxO Activation in Response to Glucose. Journal of Biological Chemistry, 2008, 283, 16283-16292.	3.4	265
14	Extensive Crosstalk Between O-GlcNAcylation and Phosphorylation Regulates Cytokinesis. Science Signaling, 2010, 3, ra2.	3.6	262
15	Large-scale identification of ubiquitination sites by mass spectrometry. Nature Protocols, 2013, 8, 1950-1960.	12.0	256
16	Enrichment and Site Mapping of O-Linked N-Acetylglucosamine by a Combination of Chemical/Enzymatic Tagging, Photochemical Cleavage, and Electron Transfer Dissociation Mass Spectrometry. Molecular and Cellular Proteomics, 2010, 9, 153-160.	3.8	234
17	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. Cancer Cell, 2019, 36, 369-384.e13.	16.8	224
18	Ubiquitylome analysis identifies dysregulation of effector substrates in SPOP-mutant prostate cancer. Science, 2014, 346, 85-89.	12.6	200

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19	Split-TurboID enables contact-dependent proximity labeling in cells. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12143-12154.	7.1	179
20	Proximity labeling in mammalian cells with TurboID and split-TurboID. Nature Protocols, 2020, 15, 3971-3999.	12.0	171
21	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	28.9	170
22	A PGC-1Î±-O-GlcNAc Transferase Complex Regulates FoxO Transcription Factor Activity in Response to Glucose. Journal of Biological Chemistry, 2009, 284, 5148-5157.	3.4	168
23	iTRAQ Labeling is Superior to mTRAQ for Quantitative Global Proteomics and Phosphoproteomics. Molecular and Cellular Proteomics, 2012, 11, M111.014423.	3.8	159
24	Deep, Quantitative Coverage of the Lysine Acetylome Using Novel Anti-acetyl-lysine Antibodies and an Optimized Proteomic Workflow. Molecular and Cellular Proteomics, 2015, 14, 2429-2440.	3.8	147
25	Opposing effects of cancer-type-specific SPOP mutants on BET protein degradation and sensitivity to BET inhibitors. Nature Medicine, 2017, 23, 1046-1054.	30.7	145
26	Proteomic mapping in live Drosophila tissues using an engineered ascorbate peroxidase. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12093-12098.	7.1	143
27	Methods for Quantification of in vivo Changes in Protein Ubiquitination following Proteasome and Deubiquitinase Inhibition. Molecular and Cellular Proteomics, 2012, 11, 148-159.	3.8	140
28	Probing the lithium-response pathway in hiPSCs implicates the phosphoregulatory set-point for a cytoskeletal modulator in bipolar pathogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4462-E4471.	7.1	129
29	Cell-Surface Proteomic Profiling in the Fly Brain Uncovers Wiring Regulators. Cell, 2020, 180, 373-386.e15.	28.9	118
30	Antibodies to biotin enable large-scale detection of biotinylation sites on proteins. Nature Methods, 2017, 14, 1167-1170.	19.0	114
31	Homo-PROTACs for the Chemical Knockdown of Cereblon. ACS Chemical Biology, 2018, 13, 2771-2782.	3.4	114
32	Proximity Biotinylation as a Method for Mapping Proteins Associated with mtDNA in Living Cells. Cell Chemical Biology, 2017, 24, 404-414.	5.2	102
33	In Situ Peroxidase Labeling and Mass-Spectrometry Connects Alpha-Synuclein Directly to Endocytic Trafficking and mRNA Metabolism in Neurons. Cell Systems, 2017, 4, 242-250.e4.	6.2	91
34	Methods for analyzing peptides and proteins on a chromatographic timescale by electron-transfer dissociation mass spectrometry. Nature Protocols, 2008, 3, 1709-1717.	12.0	83
35	Rapid and deep-scale ubiquitylation profiling for biology and translational research. Nature Communications, 2020, 11, 359.	12.8	75
36	An Unbiased Approach To Identify Endogenous Substrates of â€œHistoneâ€•Deacetylase 8. ACS Chemical Biology, 2014, 9, 2210-2216.	3.4	72

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37	Quantitative Assessment of Chromatin Immunoprecipitation Grade Antibodies Directed against Histone Modifications Reveals Patterns of Co-occurring Marks on Histone Protein Molecules. Molecular and Cellular Proteomics, 2012, 11, 128-137.	3.8	71
38	Crbn I391V is sufficient to confer in vivo sensitivity to thalidomide and its derivatives in mice. Blood, 2018, 132, 1535-1544.	1.4	71
39	The C9orf72-interacting protein Smcr8 is a negative regulator of autoimmunity and lysosomal exocytosis. Genes and Development, 2018, 32, 929-943.	5.9	65
40	Proteomics of protein trafficking by in vivo tissue-specific labeling. Nature Communications, 2021, 12, 2382.	12.8	51
41	Analysis of proteins and peptides on a chromatographic timescale by electronâ€transfer dissociation MS. FEBS Journal, 2007, 274, 6269-6276.	4.7	35
42	Multi-Omics Analysis Identifies MGA as a Negative Regulator of the MYC Pathway in Lung Adenocarcinoma. Molecular Cancer Research, 2020, 18, 574-584.	3.4	33
43	Lso2 is a conserved ribosome-bound protein required for translational recovery in yeast. PLoS Biology, 2018, 16, e2005903.	5.6	31
44	Steroid resistance in Diamond Blackfan anemia associates with p57Kip2 dysregulation in erythroid progenitors. Journal of Clinical Investigation, 2020, 130, 2097-2110.	8.2	29
45	Quantitative-Proteomic Comparison of Alpha and Beta Cells to Uncover Novel Targets for Lineage Reprogramming. PLoS ONE, 2014, 9, e95194.	2.5	27
46	O-GlcNAcylation of the Plum pox virus capsid protein catalyzed by SECRET AGENT: characterization of O-GlcNAc sites by electron transfer dissociation mass spectrometry. Amino Acids, 2011, 40, 869-876.	2.7	26
47	Dual functions of SPOP and ERG dictate androgen therapy responses in prostate cancer. Nature Communications, 2021, 12, 734.	12.8	26
48	Identification and Origin of N-Linked Î²-<scp>d</scp>-N-Acetylglucosamine Monosaccharide Modifications on Arabidopsis Proteins Â Â. Plant Physiology, 2012, 161, 455-464.	4.8	25
49	Avadomide Induces Degradation of ZMYM2 Fusion Oncoproteins in Hematologic Malignancies. Blood Cancer Discovery, 2021, 2, 250-265.	5.0	19
50	Lenalidomide Induces Ubiquitination and Degradation of CSNK1A1 in MDS with Del(5q). Blood, 2014, 124, 4-4.	1.4	19
51	Evaluation of Advanced Precursor Determination for Tandem Mass Tag (TMT)-Based Quantitative Proteomics across Instrument Platforms. Journal of Proteome Research, 2019, 18, 542-547.	3.7	18
52	CBL mutations drive PI3K/AKT signaling via increased interaction with LYN and PIK3R1. Blood, 2021, 137, 2209-2220.	1.4	18
53	RNF43 G659fs is an oncogenic colorectal cancer mutation and sensitizes tumor cells to PI3K/mTOR inhibition. Nature Communications, 2022, 13, .	12.8	18
54	An engineered transcriptional reporter of protein localization identifies regulators of mitochondrial and ER membrane protein trafficking in high-throughput CRISPRi screens. ELife, 2021, 10, .	6.0	17

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55	Degradation of GSPT1 causes TP53-independent cell death in leukemia while sparing normal hematopoietic stem cells. Journal of Clinical Investigation, 2022, 132, .	8.2	17
56	Phosphorylation coexists with Oâ€GlcNAcylation in a plant virus protein and influences viral infection. Molecular Plant Pathology, 2018, 19, 1427-1443.	4.2	16
57	Automating UbiFast for High-throughput and Multiplexed Ubiquitin Enrichment. Molecular and Cellular Proteomics, 2021, 20, 100154.	3.8	12
58	Discovery of suppressors of CRMP2 phosphorylation reveals compounds that mimic the behavioral effects of lithium on amphetamine-induced hyperlocomotion. Translational Psychiatry, 2020, 10, 76.	4.8	10
59	Lysine trimethylation regulates 78-kDa glucose-regulated protein proteostasis during endoplasmic reticulum stress. Journal of Biological Chemistry, 2017, 292, 18878-18885.	3.4	9
60	Regulation of purine metabolism connects KCTD13 to a metabolic disorder with autistic features. IScience, 2021, 24, 101935.	4.1	7
61	Oncogenic Mechanisms of CBL E3 Ubiquitin Ligase Mutations in Myeloid Malignancies. Blood, 2019, 134, 563-563.	1.4	1
62	Inhibition of the CRBN-DDB1-CUL4-ROC1 E3 Ubiquitin Ligase Mediates the Anti-Proliferative and Immunomodulatory Properties of Lenalidomide. Blood, 2012, 120, 919-919.	1.4	1
63	In Situ Peroxidase Labeling and Mass Spectrometry of Alpha-Synuclein in Rat Cortical Neurons. Methods in Molecular Biology, 2019, 1948, 235-246.	0.9	0
64	Pomalidomide-Based Homo-Protacs for the Chemical Knockdown of Cereblon. Blood, 2018, 132, 260-260.	1.4	0