

# Namrata D Udeshi

## List of Publications by Year in descending order

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Version: 2024-02-01

64  
papers

11,755  
citations

76294

40  
h-index

114418

63  
g-index

74  
all docs

74  
docs citations

74  
times ranked

15979  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNF43 G659fs is an oncogenic colorectal cancer mutation and sensitizes tumor cells to PI3K/mTOR inhibition. <i>Nature Communications</i> , 2022, 13, .	5.8	18
2	Degradation of GSPT1 causes TP53-independent cell death in leukemia while sparing normal hematopoietic stem cells. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	17
3	Regulation of purine metabolism connects KCTD13 to a metabolic disorder with autistic features. <i>IScience</i> , 2021, 24, 101935.	1.9	7
4	Dual functions of SPOP and ERG dictate androgen therapy responses in prostate cancer. <i>Nature Communications</i> , 2021, 12, 734.	5.8	26
5	Avadomide Induces Degradation of ZMYM2 Fusion Oncoproteins in Hematologic Malignancies. <i>Blood Cancer Discovery</i> , 2021, 2, 250-265.	2.6	19
6	<i>CBL</i> mutations drive PI3K/AKT signaling via increased interaction with LYN and PIK3R1. <i>Blood</i> , 2021, 137, 2209-2220.	0.6	18
7	Proteomics of protein trafficking by in vivo tissue-specific labeling. <i>Nature Communications</i> , 2021, 12, 2382.	5.8	51
8	An engineered transcriptional reporter of protein localization identifies regulators of mitochondrial and ER membrane protein trafficking in high-throughput CRISPRi screens. <i>ELife</i> , 2021, 10, .	2.8	17
9	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	13.5	170
10	Automating UbiFast for High-throughput and Multiplexed Ubiquitin Enrichment. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100154.	2.5	12
11	Multi-Omics Analysis Identifies MGA as a Negative Regulator of the MYC Pathway in Lung Adenocarcinoma. <i>Molecular Cancer Research</i> , 2020, 18, 574-584.	1.5	33
12	Proximity labeling in mammalian cells with TurboID and split-TurboID. <i>Nature Protocols</i> , 2020, 15, 3971-3999.	5.5	171
13	Split-TurboID enables contact-dependent proximity labeling in cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12143-12154.	3.3	179
14	Rapid and deep-scale ubiquitylation profiling for biology and translational research. <i>Nature Communications</i> , 2020, 11, 359.	5.8	75
15	Cell-Surface Proteomic Profiling in the Fly Brain Uncovers Wiring Regulators. <i>Cell</i> , 2020, 180, 373-386.e15.	13.5	118
16	Discovery of suppressors of CRMP2 phosphorylation reveals compounds that mimic the behavioral effects of lithium on amphetamine-induced hyperlocomotion. <i>Translational Psychiatry</i> , 2020, 10, 76.	2.4	10
17	Steroid resistance in Diamond Blackfan anemia associates with p57Kip2 dysregulation in erythroid progenitors. <i>Journal of Clinical Investigation</i> , 2020, 130, 2097-2110.	3.9	29
18	Evaluation of Advanced Precursor Determination for Tandem Mass Tag (TMT)-Based Quantitative Proteomics across Instrument Platforms. <i>Journal of Proteome Research</i> , 2019, 18, 542-547.	1.8	18

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19	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. <i>Cancer Cell</i> , 2019, 36, 369-384.e13.	7.7	224
20	In Situ Peroxidase Labeling and Mass Spectrometry of Alpha-Synuclein in Rat Cortical Neurons. <i>Methods in Molecular Biology</i> , 2019, 1948, 235-246.	0.4	0
21	Oncogenic Mechanisms of CBL E3 Ubiquitin Ligase Mutations in Myeloid Malignancies. <i>Blood</i> , 2019, 134, 563-563.	0.6	1
22	Phosphorylation coexists with O-GlcNAcylation in a plant virus protein and influences viral infection. <i>Molecular Plant Pathology</i> , 2018, 19, 1427-1443.	2.0	16
23	Lso2 is a conserved ribosome-bound protein required for translational recovery in yeast. <i>PLoS Biology</i> , 2018, 16, e2005903.	2.6	31
24	The C9orf72-interacting protein Smcr8 is a negative regulator of autoimmunity and lysosomal exocytosis. <i>Genes and Development</i> , 2018, 32, 929-943.	2.7	65
25	Crbn I391V is sufficient to confer in vivo sensitivity to thalidomide and its derivatives in mice. <i>Blood</i> , 2018, 132, 1535-1544.	0.6	71
26	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatography-mass spectrometry. <i>Nature Protocols</i> , 2018, 13, 1632-1661.	5.5	377
27	Homo-PROTACs for the Chemical Knockdown of Cereblon. <i>ACS Chemical Biology</i> , 2018, 13, 2771-2782.	1.6	114
28	Efficient proximity labeling in living cells and organisms with TurboID. <i>Nature Biotechnology</i> , 2018, 36, 880-887.	9.4	1,103
29	Pomalidomide-Based Homo-Protacs for the Chemical Knockdown of Cereblon. <i>Blood</i> , 2018, 132, 260-260.	0.6	0
30	In Situ Peroxidase Labeling and Mass-Spectrometry Connects Alpha-Synuclein Directly to Endocytic Trafficking and mRNA Metabolism in Neurons. <i>Cell Systems</i> , 2017, 4, 242-250.e4.	2.9	91
31	Proximity Biotinylation as a Method for Mapping Proteins Associated with mtDNA in Living Cells. <i>Cell Chemical Biology</i> , 2017, 24, 404-414.	2.5	102
32	Probing the lithium-response pathway in hiPSCs implicates the phosphoregulatory set-point for a cytoskeletal modulator in bipolar pathogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4462-E4471.	3.3	129
33	Antibodies to biotin enable large-scale detection of biotinylation sites on proteins. <i>Nature Methods</i> , 2017, 14, 1167-1170.	9.0	114
34	Lysine trimethylation regulates 78-kDa glucose-regulated protein proteostasis during endoplasmic reticulum stress. <i>Journal of Biological Chemistry</i> , 2017, 292, 18878-18885.	1.6	9
35	Opposing effects of cancer-type-specific SPOP mutants on BET protein degradation and sensitivity to BET inhibitors. <i>Nature Medicine</i> , 2017, 23, 1046-1054.	15.2	145
36	Proteomic mapping of cytosol-facing outer mitochondrial and ER membranes in living human cells by proximity biotinylation. <i>ELife</i> , 2017, 6, .	2.8	276

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37	Proteomic Analysis of Unbounded Cellular Compartments: Synaptic Clefts. <i>Cell</i> , 2016, 166, 1295-1307.e21.	13.5	324
38	Spatially resolved proteomic mapping in living cells with the engineered peroxidase APEX2. <i>Nature Protocols</i> , 2016, 11, 456-475.	5.5	411
39	Lenalidomide induces ubiquitination and degradation of CK1 $\alpha$ in del(5q) MDS. <i>Nature</i> , 2015, 523, 183-188.	13.7	648
40	Deep, Quantitative Coverage of the Lysine Acetylome Using Novel Anti-acetyl-lysine Antibodies and an Optimized Proteomic Workflow. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2429-2440.	2.5	147
41	Proteomic mapping in live <i>Drosophila</i> tissues using an engineered ascorbate peroxidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12093-12098.	3.3	143
42	Quantitative-Proteomic Comparison of Alpha and Beta Cells to Uncover Novel Targets for Lineage Reprogramming. <i>PLoS ONE</i> , 2014, 9, e95194.	1.1	27
43	Lenalidomide Causes Selective Degradation of IKZF1 and IKZF3 in Multiple Myeloma Cells. <i>Science</i> , 2014, 343, 301-305.	6.0	1,371
44	An Unbiased Approach To Identify Endogenous Substrates of Histone Deacetylase 8. <i>ACS Chemical Biology</i> , 2014, 9, 2210-2216.	1.6	72
45	Ubiquitylome analysis identifies dysregulation of effector substrates in SPOP-mutant prostate cancer. <i>Science</i> , 2014, 346, 85-89.	6.0	200
46	Proteomic Mapping of the Human Mitochondrial Intermembrane Space in Live Cells via Ratiometric APEX Tagging. <i>Molecular Cell</i> , 2014, 55, 332-341.	4.5	414
47	Lenalidomide Induces Ubiquitination and Degradation of CSNK1A1 in MDS with Del(5q). <i>Blood</i> , 2014, 124, 4-4.	0.6	19
48	Refined Preparation and Use of Anti-diglycine Remnant (K $\mu$ -GG) Antibody Enables Routine Quantification of 10,000s of Ubiquitination Sites in Single Proteomics Experiments. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 825-831.	2.5	279
49	EMRE Is an Essential Component of the Mitochondrial Calcium Uniporter Complex. <i>Science</i> , 2013, 342, 1379-1382.	6.0	537
50	Large-scale identification of ubiquitination sites by mass spectrometry. <i>Nature Protocols</i> , 2013, 8, 1950-1960.	5.5	256
51	Proteomic Mapping of Mitochondria in Living Cells via Spatially Restricted Enzymatic Tagging. <i>Science</i> , 2013, 339, 1328-1331.	6.0	1,023
52	Integrated proteomic analysis of post-translational modifications by serial enrichment. <i>Nature Methods</i> , 2013, 10, 634-637.	9.0	534
53	Identification and Origin of N-Linked $\beta$ -N-Acetylglucosamine Monosaccharide Modifications on Arabidopsis Proteins. <i>Plant Physiology</i> , 2012, 161, 455-464.	2.3	25
54	Quantitative Assessment of Chromatin Immunoprecipitation Grade Antibodies Directed against Histone Modifications Reveals Patterns of Co-occurring Marks on Histone Protein Molecules. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 128-137.	2.5	71

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55	iTRAQ Labeling is Superior to mTRAQ for Quantitative Global Proteomics and Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014423.	2.5	159
56	Methods for Quantification of in vivo Changes in Protein Ubiquitination following Proteasome and Deubiquitinase Inhibition. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 148-159.	2.5	140
57	Inhibition of the CRBN-DDB1-CUL4-ROC1 E3 Ubiquitin Ligase Mediates the Anti-Proliferative and Immunomodulatory Properties of Lenalidomide. <i>Blood</i> , 2012, 120, 919-919.	0.6	1
58	O-GlcNAcylation of the Plum pox virus capsid protein catalyzed by SECRET AGENT: characterization of O-GlcNAc sites by electron transfer dissociation mass spectrometry. <i>Amino Acids</i> , 2011, 40, 869-876.	1.2	26
59	Enrichment and Site Mapping of O-Linked N-Acetylglucosamine by a Combination of Chemical/Enzymatic Tagging, Photochemical Cleavage, and Electron Transfer Dissociation Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 153-160.	2.5	234
60	Extensive Crosstalk Between O-GlcNAcylation and Phosphorylation Regulates Cytokinesis. <i>Science Signaling</i> , 2010, 3, ra2.	1.6	262
61	A PGC-1 $\beta$ -O-GlcNAc Transferase Complex Regulates FoxO Transcription Factor Activity in Response to Glucose. <i>Journal of Biological Chemistry</i> , 2009, 284, 5148-5157.	1.6	168
62	Methods for analyzing peptides and proteins on a chromatographic timescale by electron-transfer dissociation mass spectrometry. <i>Nature Protocols</i> , 2008, 3, 1709-1717.	5.5	83
63	O-GlcNAc Regulates FoxO Activation in Response to Glucose. <i>Journal of Biological Chemistry</i> , 2008, 283, 16283-16292.	1.6	265
64	Analysis of proteins and peptides on a chromatographic timescale by electron-transfer dissociation MS. <i>FEBS Journal</i> , 2007, 274, 6269-6276.	2.2	35