

# Chunaram Choudhary

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7115579/publications.pdf>

Version: 2024-02-01

84  
papers

18,568  
citations

34493

54  
h-index

54771

88  
g-index

92  
all docs

92  
docs citations

92  
times ranked

29964  
citing authors

#	ARTICLE	IF	CITATIONS
1	HDAC6 modulates myofibril stiffness and diastolic function of the heart. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	12
2	Proteome dynamics at broken replication forks reveal a distinct ATM-directed repair response suppressing DNA double-strand break ubiquitination. <i>Molecular Cell</i> , 2021, 81, 1084-1099.e6.	4.5	57
3	SIK2 orchestrates actin-dependent host response upon <i>Salmonella</i> infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2024144118.	3.3	10
4	Enhancers are activated by p300/CBP activity-dependent PIC assembly, RNAPII recruitment, and pause release. <i>Molecular Cell</i> , 2021, 81, 2166-2182.e6.	4.5	94
5	HBO1 is required for the maintenance of leukaemia stem cells. <i>Nature</i> , 2020, 577, 266-270.	13.7	105
6	Equilibrium between nascent and parental MCM proteins protects replicating genomes. <i>Nature</i> , 2020, 587, 297-302.	13.7	65
7	Sequencing of the First Draft of the Human Acetylome. <i>Clinical Chemistry</i> , 2020, 66, 852-853.	1.5	1
8	Histone Acetyltransferase MOF Blocks Acquisition of Quiescence in Ground-State ESCs through Activating Fatty Acid Oxidation. <i>Cell Stem Cell</i> , 2020, 27, 441-458.e10.	5.2	37
9	Analysis and Interpretation of Protein Post-Translational Modification Site Stoichiometry. <i>Trends in Biochemical Sciences</i> , 2019, 44, 943-960.	3.7	55
10	Analysis of human acetylation stoichiometry defines mechanistic constraints on protein regulation. <i>Nature Communications</i> , 2019, 10, 1055.	5.8	129
11	Functions and mechanisms of non-histone protein acetylation. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 156-174.	16.1	717
12	Acetylation of intrinsically disordered regions regulates phase separation. <i>Nature Chemical Biology</i> , 2019, 15, 51-61.	3.9	190
13	DNA Repair Network Analysis Reveals Shieldin as a Key Regulator of NHEJ and PARP Inhibitor Sensitivity. <i>Cell</i> , 2018, 173, 972-988.e23.	13.5	349
14	p38-MK2 signaling axis regulates RNA metabolism after UV-light-induced DNA damage. <i>Nature Communications</i> , 2018, 9, 1017.	5.8	61
15	Deletion of APC7 or APC16 Allows Proliferation of Human Cells without the Spindle Assembly Checkpoint. <i>Cell Reports</i> , 2018, 25, 2317-2328.e5.	2.9	11
16	Time-Resolved Analysis Reveals Rapid Dynamics and Broad Scope of the CBP/p300 Acetylome. <i>Cell</i> , 2018, 174, 231-244.e12.	13.5	313
17	STK3 is a therapeutic target for a subset of acute myeloid leukemias. <i>Oncotarget</i> , 2018, 9, 25458-25473.	0.8	10
18	Accurate Quantification of Site-specific Acetylation Stoichiometry Reveals the Impact of Sirtuin Deacetylase CobB on the <i>E. coli</i> Acetylome. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 759-769.	2.5	80

#	ARTICLE	IF	CITATIONS
19	Discovery of a selective catalytic p300/CBP inhibitor that targets lineage-specific tumours. <i>Nature</i> , 2017, 550, 128-132.	13.7	498
20	Redox-sensitive alteration of replisome architecture safeguards genome integrity. <i>Science</i> , 2017, 358, 797-802.	6.0	127
21	lncRNA Panct1 Maintains Mouse Embryonic Stem Cell Identity by Regulating TOBF1 Recruitment to Oct-Sox Sequences in Early G1. <i>Cell Reports</i> , 2017, 21, 3012-3021.	2.9	35
22	<scp>SPATA</scp> 2 links <scp>CYLD</scp> to the <scp>TNF</scp> receptor signaling complex and modulates the receptor signaling outcomes. <i>EMBO Journal</i> , 2016, 35, 1868-1884.	3.5	129
23	Deubiquitylating enzyme USP9x regulates hippo pathway activity by controlling angiomin protein turnover. <i>Cell Discovery</i> , 2016, 2, 16001.	3.1	34
24	The Spindle Assembly Checkpoint Is Not Essential for Viability of Human Cells with Genetically Lowered APC/C Activity. <i>Cell Reports</i> , 2016, 14, 1829-1840.	2.9	49
25	Mte1 interacts with Mph1 and promotes crossover recombination and telomere maintenance. <i>Genes and Development</i> , 2016, 30, 700-717.	2.7	27
26	A PTIP-PA1 subcomplex promotes transcription for IgH class switching independently from the associated MLL3/MLL4 methyltransferase complex. <i>Genes and Development</i> , 2016, 30, 149-163.	2.7	27
27	Analysis of acetylation stoichiometry suggests that <scp>SIRT</scp> 3 repairs nonenzymatic acetylation lesions. <i>EMBO Journal</i> , 2015, 34, 2620-2632.	3.5	133
28	Systems-wide analysis of <scp>BCR</scp> signalosomes and downstream phosphorylation and ubiquitylation. <i>Molecular Systems Biology</i> , 2015, 11, 810.	3.2	119
29	Systems Analyses Reveal Shared and Diverse Attributes of Oct4 Regulation in Pluripotent Cells. <i>Cell Systems</i> , 2015, 1, 141-151.	2.9	15
30	Ubiquitin-SUMO Circuitry Controls Activated Fanconi Anemia ID Complex Dosage in Response to DNA Damage. <i>Molecular Cell</i> , 2015, 57, 150-164.	4.5	106
31	FBH1 influences DNA replication fork stability and homologous recombination through ubiquitylation of RAD51. <i>Nature Communications</i> , 2015, 6, 5931.	5.8	59
32	Cmr1/WDR76 defines a nuclear genotoxic stress body linking genome integrity and protein quality control. <i>Nature Communications</i> , 2015, 6, 6533.	5.8	80
33	Acetylation site specificities of lysine deacetylase inhibitors in human cells. <i>Nature Biotechnology</i> , 2015, 33, 415-423.	9.4	237
34	Histone H1 couples initiation and amplification of ubiquitin signalling after DNA damage. <i>Nature</i> , 2015, 527, 389-393.	13.7	317
35	Avoiding abundance bias in the functional annotation of posttranslationally modified proteins. <i>Nature Methods</i> , 2015, 12, 1003-1004.	9.0	60
36	Proteome-wide analysis of SUMO2 targets in response to pathological DNA replication stress in human cells. <i>DNA Repair</i> , 2015, 25, 84-96.	1.3	30

#	ARTICLE	IF	CITATIONS
37	Paradoxical resistance of multiple myeloma to proteasome inhibitors by decreased levels of 19S proteasomal subunits. <i>ELife</i> , 2015, 4, e08153.	2.8	84
38	A quantitative 14-3-3 interaction screen connects the nuclear exosome targeting complex to the DNA damage response. <i>Genes and Development</i> , 2014, 28, 1977-1982.	2.7	50
39	Time-resolved dissection of early phosphoproteome and ensuing proteome changes in response to TGF- $\beta$ 2. <i>Science Signaling</i> , 2014, 7, rs5.	1.6	39
40	Acetylation dynamics and stoichiometry in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2014, 10, 716.	3.2	220
41	UBL5 is essential for pre-mRNA splicing and sister chromatid cohesion in human cells. <i>EMBO Reports</i> , 2014, 15, 956-964.	2.0	41
42	The growing landscape of lysine acetylation links metabolism and cell signalling. <i>Nature Reviews Molecular Cell Biology</i> , 2014, 15, 536-550.	16.1	1,153
43	Convergence of Ubiquitylation and Phosphorylation Signaling in Rapamycin-treated Yeast Cells. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1979-1992.	2.5	49
44	Specificity and Commonality of the Phosphoinositide-Binding Proteome Analyzed by Quantitative Mass Spectrometry. <i>Cell Reports</i> , 2014, 6, 578-591.	2.9	75
45	UBL5 is essential for pre-mRNA splicing and sister chromatid cohesion in human cells. <i>EMBO Reports</i> , 2014, 15, 1330-1330.	2.0	1
46	Lysine Succinylation Is a Frequently Occurring Modification in Prokaryotes and Eukaryotes and Extensively Overlaps with Acetylation. <i>Cell Reports</i> , 2013, 4, 842-851.	2.9	619
47	OTULIN Restricts Met1-Linked Ubiquitination to Control Innate Immune Signaling. <i>Molecular Cell</i> , 2013, 50, 818-830.	4.5	209
48	Acetyl-Phosphate Is a Critical Determinant of Lysine Acetylation in <i>E. coli</i> . <i>Molecular Cell</i> , 2013, 51, 265-272.	4.5	407
49	A new cellular stress response that triggers centriolar satellite reorganization and ciliogenesis. <i>EMBO Journal</i> , 2013, 32, 3029-3040.	3.5	115
50	RNF111/Arkadia is a SUMO-targeted ubiquitin ligase that facilitates the DNA damage response. <i>Journal of Cell Biology</i> , 2013, 201, 797-807.	2.3	129
51	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1578-1585.	2.5	244
52	Proteome-wide Analysis of Lysine Acetylation Suggests its Broad Regulatory Scope in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1510-1522.	2.5	255
53	SOCS1 cooperates with FLT3-ITD in the development of myeloproliferative disease by promoting the escape from external cytokine control. <i>Blood</i> , 2012, 120, 1691-1702.	0.6	27
54	Proteomic Analysis of Lysine Acetylation Sites in Rat Tissues Reveals Organ Specificity and Subcellular Patterns. <i>Cell Reports</i> , 2012, 2, 419-431.	2.9	493

#	ARTICLE	IF	CITATIONS
55	DVC1 (C1orf124) is a DNA damage-targeting p97 adaptor that promotes ubiquitin-dependent responses to replication blocks. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1084-1092.	3.6	153
56	Systems-wide analysis of ubiquitylation dynamics reveals a key role for PAF15 ubiquitylation in DNA-damage bypass. <i>Nature Cell Biology</i> , 2012, 14, 1089-1098.	4.6	234
57	Proteomic Investigations Reveal a Role for RNA Processing Factor THRAP3 in the DNA Damage Response. <i>Molecular Cell</i> , 2012, 46, 212-225.	4.5	298
58	Proteomic Investigations of Lysine Acetylation Identify Diverse Substrates of Mitochondrial Deacetylase Sirt3. <i>PLoS ONE</i> , 2012, 7, e50545.	1.1	128
59	Proteome-Wide Mapping of the <i>Drosophila</i> Acetylome Demonstrates a High Degree of Conservation of Lysine Acetylation. <i>Science Signaling</i> , 2011, 4, ra48.	1.6	243
60	Phosphorylation of the Autophagy Receptor Optineurin Restricts <i>Salmonella</i> Growth. <i>Science</i> , 2011, 333, 228-233.	6.0	1,125
61	A phospho-proteomic screen identifies substrates of the checkpoint kinase Chk1. <i>Genome Biology</i> , 2011, 12, R78.	13.9	123
62	A Proteome-wide, Quantitative Survey of In Vivo Ubiquitylation Sites Reveals Widespread Regulatory Roles. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.013284.	2.5	754
63	Decoding signalling networks by mass spectrometry-based proteomics. <i>Nature Reviews Molecular Cell Biology</i> , 2010, 11, 427-439.	16.1	534
64	Predicting post-translational lysine acetylation using support vector machines. <i>Bioinformatics</i> , 2010, 26, 1666-1668.	1.8	61
65	SOCS1 Cooperates with FLT3-ITD In the Development of Myeloproliferative Disease by Promoting the Escape From External Cytokine Control.. <i>Blood</i> , 2010, 116, 1054-1054.	0.6	0
66	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. <i>Science</i> , 2009, 325, 834-840.	6.0	3,883
67	Mislocalized Activation of Oncogenic RTKs Switches Downstream Signaling Outcomes. <i>Molecular Cell</i> , 2009, 36, 326-339.	4.5	278
68	Activation of Wnt signaling in cKit-ITD mediated transformation and imatinib sensitivity in acute myeloid leukemia. <i>International Journal of Hematology</i> , 2008, 88, 174-180.	0.7	11
69	Activation of Wnt signalling in acute myeloid leukemia by induction of Frizzled-4. <i>International Journal of Oncology</i> , 2008, 33, 1215-21.	1.4	18
70	Activation mechanisms of STAT5 by oncogenic Flt3-ITD. <i>Blood</i> , 2007, 110, 370-374.	0.6	170
71	Flt3-dependent transformation by inactivating c-Cbl mutations in AML. <i>Blood</i> , 2007, 110, 1004-1012.	0.6	177
72	Wnt signaling regulates transendothelial migration of monocytes. <i>Journal of Leukocyte Biology</i> , 2006, 79, 1306-1313.	1.5	60

#	ARTICLE	IF	CITATIONS
73	Activation Mechanisms of STAT5 by Oncogenic Flt3-ITD.. Blood, 2006, 108, 1435-1435.	0.6	27
74	Constitutive Activation of Akt by Flt3 Internal Tandem Duplications Is Necessary for Increased Survival, Proliferation, and Myeloid Transformation. Cancer Research, 2005, 65, 9643-9650.	0.4	205
75	Identification of a novel activating mutation (Y842C) within the activation loop of FLT3 in patients with acute myeloid leukemia (AML). Blood, 2005, 105, 335-340.	0.6	97
76	Flt3 tandem duplication mutations cooperate with Wnt signaling in leukemic signal transduction. Blood, 2005, 105, 3699-3706.	0.6	99
77	AML-associated Flt3 kinase domain mutations show signal transduction differences compared with Flt3 ITD mutations. Blood, 2005, 106, 265-273.	0.6	224
78	RGS2 is an important target gene of Flt3-ITD mutations in AML and functions in myeloid differentiation and leukemic transformation. Blood, 2005, 105, 2107-2114.	0.6	70
79	Signal Transduction of Oncogenic Flt3. International Journal of Hematology, 2005, 82, 93-99.	0.7	77
80	Tyrosine Phosphorylation Regulates Maturation of Receptor Tyrosine Kinases. Molecular and Cellular Biology, 2005, 25, 3690-3703.	1.1	135
81	The Cyclin A1-CDK2 Complex Regulates DNA Double-Strand Break Repair. Molecular and Cellular Biology, 2004, 24, 8917-8928.	1.1	106
82	Flt3 Internal Tandem Duplications Cooperate with Wnt Signaling in Leukemic Signal Transduction.. Blood, 2004, 104, 822-822.	0.6	10
83	Constitutive Activation of Akt and mTOR by Flt3 Internal Tandem Duplications Mediates Myeloid Leukemogenesis and Can Be Inhibited by Rapamycin.. Blood, 2004, 104, 2532-2532.	0.6	8
84	Suppression of myeloid transcription factors and induction of STAT response genes by AML-specific Flt3 mutations. Blood, 2003, 101, 3164-3173.	0.6	274