

# Chanchal Kumar

## List of Publications by Year in descending order

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Version: 2024-02-01

27  
papers

12,021  
citations

257450

24  
h-index

477307

29  
g-index

30  
all docs

30  
docs citations

30  
times ranked

17948  
citing authors

#	ARTICLE	IF	CITATIONS
1	Artificial intelligence for proteomics and biomarker discovery. <i>Cell Systems</i> , 2021, 12, 759-770.	6.2	106
2	Metabolomic Profile in HFpEF vs HFrEF Patients. <i>Journal of Cardiac Failure</i> , 2020, 26, 1050-1059.	1.7	46
3	Integration of whole-body [18F]FDG PET/MRI with non-targeted metabolomics can provide new insights on tissue-specific insulin resistance in type 2 diabetes. <i>Scientific Reports</i> , 2020, 10, 8343.	3.3	5
4	A Multi-Omics Approach to Liver Diseases: Integration of Single Nuclei Transcriptomics with Proteomics and HiCap Bulk Data in Human Liver. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 180-194.	2.0	26
5	A Physiology-Based Model of Bile Acid Distribution and Metabolism Under Healthy and Pathologic Conditions in Human Beings. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 10, 149-170.	4.5	30
6	rs953413 Regulates Polyunsaturated Fatty Acid Metabolism by Modulating ELOVL2 Expression. <i>IScience</i> , 2020, 23, 100808.	4.1	19
7	Intra- and inter-individual metabolic profiling highlights carnitine and lysophosphatidylcholine pathways as key molecular defects in type 2 diabetes. <i>Scientific Reports</i> , 2019, 9, 9653.	3.3	32
8	Liver macrophages regulate systemic metabolism through non-inflammatory factors. <i>Nature Metabolism</i> , 2019, 1, 445-459.	11.9	72
9	Combination of Chemical Genetics and Phosphoproteomics for Kinase Signaling Analysis Enables Confident Identification of Cellular Downstream Targets. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.012351.	3.8	50
10	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3.	3.6	1,319
11	Quantitative Analysis of Kinase-Proximal Signaling in Lipopolysaccharide-Induced Innate Immune Response. <i>Journal of Proteome Research</i> , 2010, 9, 2539-2549.	3.7	31
12	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) Applied to Quantitative Proteomics of <i>Bacillus subtilis</i> . <i>Journal of Proteome Research</i> , 2010, 9, 3638-3646.	3.7	108
13	Quantitative proteomic analysis of single pancreatic islets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18902-18907.	7.1	199
14	Comparative Proteomic Phenotyping of Cell Lines and Primary Cells to Assess Preservation of Cell Type-specific Functions. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 443-450.	3.8	426
15	Bioinformatics analysis of mass spectrometry-based proteomics data sets. <i>FEBS Letters</i> , 2009, 583, 1703-1712.	2.8	147
16	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. <i>Science</i> , 2009, 325, 834-840.	12.6	3,883
17	Proteome Differences between Brown and White Fat Mitochondria Reveal Specialized Metabolic Functions. <i>Cell Metabolism</i> , 2009, 10, 324-335.	16.2	205
18	Integrated Analysis of the Cerebrospinal Fluid Peptidome and Proteome. <i>Journal of Proteome Research</i> , 2008, 7, 386-399.	3.7	162

#	ARTICLE	IF	CITATIONS
19	Combined Use of RNAi and Quantitative Proteomics to Study Gene Function in Drosophila. <i>Molecular Cell</i> , 2008, 31, 762-772.	9.7	93
20	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) and Proteome Quantitation of Mouse Embryonic Stem Cells to a Depth of 5,111 Proteins. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 672-683.	3.8	261
21	Phosphoproteome Analysis of <i>E. coli</i> Reveals Evolutionary Conservation of Bacterial Ser/Thr/Tyr Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 299-307.	3.8	385
22	MAPU: Max-Planck Unified database of organellar, cellular, tissue and body fluid proteomes. <i>Nucleic Acids Research</i> , 2007, 35, D771-D779.	14.5	69
23	In-depth Analysis of the Adipocyte Proteome by Mass Spectrometry and Bioinformatics. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1257-1273.	3.8	101
24	The Serine/Threonine/Tyrosine Phosphoproteome of the Model Bacterium <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 697-707.	3.8	359
25	Analysis of the Mouse Liver Proteome Using Advanced Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 2963-2972.	3.7	83
26	The human urinary proteome contains more than 1500 proteins, including a large proportion of membrane proteins. <i>Genome Biology</i> , 2006, 7, R80.	9.6	598
27	Global, In Vivo, and Site-Specific Phosphorylation Dynamics in Signaling Networks. <i>Cell</i> , 2006, 127, 635-648.	28.9	3,201