

# Navdeep Jaitly

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11761149/publications.pdf>

Version: 2024-02-01

29  
papers

10,397  
citations

304368

22  
h-index

580395

25  
g-index

30  
all docs

30  
docs citations

30  
times ranked

11737  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNN-T Models Fail to Generalize to Out-of-Domain Audio: Causes and Solutions. , 2021, , .		11
2	Deep Learning for Automated Occlusion Edge Detection in RGB-D Frames. Journal of Signal Processing Systems, 2017, 88, 205-217.	1.4	25
3	MultiAlign: a multiple LC-MS analysis tool for targeted omics analysis. BMC Bioinformatics, 2013, 14, 49.	1.2	24
4	Hybrid speech recognition with Deep Bidirectional LSTM. , 2013, , .		1,021
5	Deep Neural Networks for Acoustic Modeling in Speech Recognition: The Shared Views of Four Research Groups. IEEE Signal Processing Magazine, 2012, 29, 82-97.	4.6	7,242
6	Learning a better representation of speech soundwaves using restricted boltzmann machines. , 2011, , .		127
7	A Bayesian method for 3D macromolecular structure inference using class average images from single particle electron microscopy. Bioinformatics, 2010, 26, 2406-2415.	1.8	20
8	Novel Ser/Thr Protein Phosphatase 5 (PP5) Regulated Targets during DNA Damage Identified by Proteomics Analysis. Journal of Proteome Research, 2010, 9, 945-953.	1.8	18
9	Identification of a Putative Protein Profile Associated with Tamoxifen Therapy Resistance in Breast Cancer. Molecular and Cellular Proteomics, 2009, 8, 1278-1294.	2.5	94
10	Decon2LS: An open-source software package for automated processing and visualization of high resolution mass spectrometry data. BMC Bioinformatics, 2009, 10, 87.	1.2	190
11	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an 18O-Labeled "Universal" Reference Sample. Journal of Proteome Research, 2009, 8, 290-299.	1.8	59
12	An Architecture for Real Time Data Acquisition and Online Signal Processing for High Throughput Tandem Mass Spectrometry. , 2009, , .		1
13	Global Systems-Level Analysis of Hfq and SmpB Deletion Mutants in Salmonella: Implications for Virulence and Global Protein Translation. PLoS ONE, 2009, 4, e4809.	1.1	109
14	Application of the accurate mass and time tag approach in studies of the human blood lipidome. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2008, 871, 243-252.	1.2	36
15	Elimination of Systematic Mass Measurement Errors in Liquid Chromatography~Mass Spectrometry Based Proteomics Using Regression Models and a Priori Partial Knowledge of the Sample Content. Analytical Chemistry, 2008, 80, 693-706.	3.2	38
16	Characterization of Strategies for Obtaining Confident Identifications in Bottom-Up Proteomics Measurements Using Hybrid FTMS Instruments. Analytical Chemistry, 2008, 80, 8514-8525.	3.2	24
17	The Influence of Sample Preparation and Replicate Analyses on HeLa Cell Phosphoproteome Coverage. Journal of Proteome Research, 2008, 7, 2215-2221.	1.8	31
18	DANTE: a statistical tool for quantitative analysis of -omics data. Bioinformatics, 2008, 24, 1556-1558.	1.8	397

#	ARTICLE	IF	CITATIONS
19	DeconMSn: a software tool for accurate parent ion monoisotopic mass determination for tandem mass spectra. <i>Bioinformatics</i> , 2008, 24, 1021-1023.	1.8	143
20	Proteomic Profiling of Intact Proteins Using WAX-RPLC 2-D Separations and FTICR Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 602-610.	1.8	81
21	VIPER: an advanced software package to support high-throughput LC-MS peptide identification. <i>Bioinformatics</i> , 2007, 23, 2021-2023.	1.8	194
22	Spatial mapping of protein abundances in the mouse brain by voxelation integrated with high-throughput liquid chromatography-mass spectrometry. <i>Genome Research</i> , 2007, 17, 328-336.	2.4	62
23	Applying a Targeted Label-Free Approach Using LC-MS AMT Tags to Evaluate Changes in Protein Phosphorylation Following Phosphatase Inhibition. <i>Journal of Proteome Research</i> , 2007, 6, 4489-4497.	1.8	22
24	Capillary LC Coupled with High-Mass Measurement Accuracy Mass Spectrometry for Metabolic Profiling. <i>Analytical Chemistry</i> , 2007, 79, 6081-6093.	3.2	47
25	Accurate Mass Measurements in Proteomics. <i>Chemical Reviews</i> , 2007, 107, 3621-3653.	23.0	102
26	Robust Algorithm for Alignment of Liquid Chromatography-Mass Spectrometry Analyses in an Accurate Mass and Time Tag Data Analysis Pipeline. <i>Analytical Chemistry</i> , 2006, 78, 7397-7409.	3.2	155
27	Mass Measurement Accuracy in Analyses of Highly Complex Mixtures Based Upon Multidimensional Recalibration. <i>Analytical Chemistry</i> , 2006, 78, 8374-8385.	3.2	32
28	Proteomic approaches to bacterial differentiation. <i>Journal of Microbiological Methods</i> , 2006, 67, 473-486.	0.7	23
29	PRISM: A data management system for high-throughput proteomics. <i>Proteomics</i> , 2006, 6, 1783-1790.	1.3	69