Navdeep Jaitly

List of Publications by Year
in descending order

29 papers	10,397 citations	304602 22 h-index	580701 25 g-index
30 all docs	30 docs citations	30 times ranked	11737 citing authors

#	Article	IF	Citations
1	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
2	Hybrid speech recognition with Deep Bidirectional LSTM. , 2013, , .		1,021
3	DAnTE: a statistical tool for quantitative analysis of -omics data. Bioinformatics, 2008, 24, 1556-1558.	1.8	397
4	VIPER: an advanced software package to support high-throughput LC-MS peptide identification. Bioinformatics, 2007, 23, 2021-2023.	1.8	194
5	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
6	Robust Algorithm for Alignment of Liquid Chromatographyâˆ'Mass Spectrometry Analyses in an Accurate Mass and Time Tag Data Analysis Pipeline. Analytical Chemistry, 2006, 78, 7397-7409.	3.2	155
7	DeconMSn: a software tool for accurate parent ion monoisotopic mass determination for tandem mass spectra. Bioinformatics, 2008, 24, 1021-1023.	1.8	143
8	Learning a better representation of speech soundwaves using restricted boltzmann machines. , 2011, , .		127
9	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
10	Accurate Mass Measurements in Proteomics. Chemical Reviews, 2007, 107, 3621-3653.	23.0	102
11	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
12	Proteomic Profiling of Intact Proteins Using WAX-RPLC 2-D Separations and FTICR Mass Spectrometry. Journal of Proteome Research, 2007, 6, 602-610.	1.8	81
13	PRISM: A data management system for high-throughput proteomics. Proteomics, 2006, 6, 1783-1790.	1.3	69
14	Spatial mapping of protein abundances in the mouse brain by voxelation integrated with high-throughput liquid chromatography-mass spectrometry. Genome Research, 2007, 17, 328-336.	2.4	62
15	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an 18O-Labeled â€œUniversalâ€•Reference Sample. Journal of Proteome Research, 2009, 8, 290-299.	1.8	59
16	Capillary LC Coupled with High-Mass Measurement Accuracy Mass Spectrometry for Metabolic Profiling. Analytical Chemistry, 2007, 79, 6081-6093.	3.2	47
17	Elimination of Systematic Mass Measurement Errors in Liquid Chromatographyâˆ'Mass Spectrometry Based Proteomics Using Regression Models anda PrioriPartial Knowledge of the Sample Content. Analytical Chemistry, 2008, 80, 693-706.	3.2	38
18	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

#	Article	IF	Citations
19	Mass Measurement Accuracy in Analyses of Highly Complex Mixtures Based Upon Multidimensional Recalibration. Analytical Chemistry, 2006, 78, 8374-8385.	3.2	32
20	The Influence of Sample Preparation and Replicate Analyses on HeLa Cell Phosphoproteome Coverage. Journal of Proteome Research, 2008, 7, 2215-2221.	1.8	31
21	Deep Learning for Automated Occlusion Edge Detection in RGB-D Frames. Journal of Signal Processing Systems, 2017, 88, 205-217.	1.4	25
22	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
23	MultiAlign: a multiple LC-MS analysis tool for targeted omics analysis. BMC Bioinformatics, 2013, 14, 49.	1.2	24
24	Proteomic approaches to bacterial differentiation. Journal of Microbiological Methods, 2006, 67, 473-486.	0.7	23
25	Applying a Targeted Label-Free Approach Using LCâˆ'MS AMT Tags to Evaluate Changes in Protein Phosphorylation Following Phosphatase Inhibition. Journal of Proteome Research, 2007, 6, 4489-4497.	1.8	22
26	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
27	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
28	RNN-T Models Fail to Generalize to Out-of-Domain Audio: Causes and Solutions. , 2021, , .		11
29	An Architecture for Real Time Data Acquisition and Online Signal Processing for High Throughput Tandem Mass Spectrometry. , 2009, , .		1