Manfred Claassen

List of Publications by Year
in descending order

46 papers	4,116 citations	279701 23 h-index	206029 48 g-index
58 all docs	58 docs citations	58 times ranked	8111 citing authors

#	Article	IF	Citations
1	Deterministic scRNA-seq captures variation in intestinal crypt and organoid composition. Nature Methods, 2022, 19, 323-330.	9.0	33
2	Immunological Predictors of Dimethyl Fumarate–Induced Lymphopenia. Annals of Neurology, 2022, 91, 676-681.	2.8	8
3	Novel Blood Vascular Endothelial Subtype-Specific Markers in Human Skin Unearthed by Single-Cell Transcriptomic Profiling. Cells, 2022, 11, 1111.	1.8	6
4	psupertime: supervised pseudotime analysis for time-series single-cell RNA-seq data. Bioinformatics, 2022, 38, i290-i298.	1.8	10
5	Visualizing hierarchies in scRNA-seq data using a density tree-biased autoencoder. Bioinformatics, 2022, 38, i316-i324.	1.8	2
6	Privacy-preserving federated neural network learning for disease-associated cell classification. Patterns, 2022, 3, 100487.	3.1	8
7	Identification of ALP+/CD73+ defining markers for enhanced osteogenic potential in human adipose-derived mesenchymal stromal cells by mass cytometry. Stem Cell Research and Therapy, 2021, 12, 7.	2.4	8
8	NASH limits anti-tumour surveillance in immunotherapy-treated HCC. Nature, 2021, 592, 450-456.	13.7	649
9	Latent representation learning in biology and translational medicine. Patterns, 2021, 2, 100198.	3.1	17
10	Negative allosteric modulators of metabotropic glutamate receptor 3 target the stem-like phenotype of glioblastoma. Molecular Therapy - Oncolytics, 2021, 20, 166-174.	2.0	2
11	Mixture-of-Experts Variational Autoencoder for clustering and generating from similarity-based representations on single cell data. PLoS Computational Biology, 2021, 17, e1009086.	1.5	15
12	Distinct immunological signatures discriminate severe COVID-19 from non-SARS-CoV-2-driven critical pneumonia. Immunity, 2021, 54, 1578-1593.e5.	6.6	75
13	Targeting extracellular and juxtamembrane FGFR2 mutations in chemotherapy-refractory cholangiocarcinoma. Npj Precision Oncology, 2021, 5, 80.	2.3	10
14	A weakly supervised deep learning approach for label-free imaging flow-cytometry-based blood diagnostics. Cell Reports Methods, 2021, 1, 100094.	1.4	17
15	Dynamic distribution decomposition for single-cell snapshot time series identifies subpopulations and trajectories during iPSC reprogramming. PLoS Computational Biology, 2020, 16, e1007491.	1.5	4
16	Landscape of Exhausted Virus-Specific CD8ÂT Cells in Chronic LCMV Infection. Cell Reports, 2020, 32, 108078.	2.9	45
17	Exhausted CD8+ T cells exhibit low and strongly inhibited TCR signaling during chronic LCMV infection. Nature Communications, 2020, 11, 4454.	5.8	32
18	Structure-function relationships of HDL in diabetes and coronary heart disease. JCI Insight, 2020, 5, .	2.3	62

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19	GM-CSF and CXCR4 define a T helper cell signature in multiple sclerosis. Nature Medicine, 2019, 25, 1290-1300.	15.2	140
20	Tree–ensemble analysis assesses presence of multifurcations in single cell data. Molecular Systems Biology, 2019, 15, e8552.	3.2	2
21	TGF-Î² induces oncofetal fibronectin, which in turn modulates TGF-Î² superfamily signaling in endothelial cells. Journal of Cell Science, 2018, 131, .	1.2	27
22	Similarities and Differences of Blood N-Glycoproteins in Five Solid Carcinomas at Localized Clinical Stage Analyzed by SWATH-MS. Cell Reports, 2018, 23, 2819-2831.e5.	2.9	36
23	The dynamics of root cap sloughing in Arabidopsis is regulated by peptide signalling. Nature Plants, 2018, 4, 596-604.	4.7	62
24	Automated Gleason grading of prostate cancer tissue microarrays via deep learning. Scientific Reports, 2018, 8, 12054.	1.6	278
25	Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability. Science, 2017, 355, .	6.0	313
26	Nontargeted Metabolomics Reveals the Multilevel Response to Antibiotic Perturbations. Cell Reports, 2017, 19, 1214-1228.	2.9	139
27	Sensitive detection of rare disease-associated cell subsets via representation learning. Nature Communications, 2017, 8, 14825.	5.8	125
28	Metabolic network segmentation: A probabilistic graphical modeling approach to identify the sites and sequential order of metabolic regulation from non-targeted metabolomics data. PLoS Computational Biology, 2017, 13, e1005577.	1.5	10
29	Sparse Regression Based Structure Learning of Stochastic Reaction Networks from Single Cell Snapshot Time Series. PLoS Computational Biology, 2016, 12, e1005234.	1.5	16
30	Analysis of Cell Lineage Trees by Exact Bayesian Inference Identifies Negative Autoregulation of Nanog in Mouse Embryonic Stem Cells. Cell Systems, 2016, 3, 480-490.e13.	2.9	30
31	Epitope-Tagged Autotransporters as Single-Cell Reporters for Gene Expression by a Salmonella Typhimurium wbaP Mutant. PLoS ONE, 2016, 11, e0154828.	1.1	5
32	Computational and experimental single cell biology techniques for the definition of cell type heterogeneity, interplay and intracellular dynamics. Current Opinion in Biotechnology, 2015, 34, 9-15.	3.3	29
33	The Mtb Proteome Library: A Resource of Assays to Quantify the Complete Proteome of Mycobacterium tuberculosis. Cell Host and Microbe, 2013, 13, 602-612.	5.1	165
34	Shooting Movies of Signaling Network Dynamics with Multiparametric Cytometry. Current Topics in Microbiology and Immunology, 2013, 377, 177-189.	0.7	3
35	Inference and Validation of Protein Identifications. Molecular and Cellular Proteomics, 2012, 11, 1097-1104.	2.5	27
36	False discovery rate estimation for cross-linked peptides identified by mass spectrometry. Nature Methods, 2012, 9, 901-903.	9.0	273

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37	Generic Comparison of Protein Inference Engines. Molecular and Cellular Proteomics, 2012, 11, O110.007088.	2.5	20
38	Estimation of Absolute Protein Quantities of Unlabeled Samples by Selected Reaction Monitoring Mass Spectrometry. Molecular and Cellular Proteomics, 2012, 11, M111.013987.	2.5	117
39	Absolute quantification of microbial proteomes at different states by directed mass spectrometry. Molecular Systems Biology, 2011, 7, 510.	3.2	91
40	Comprehensive proteomics. Current Opinion in Biotechnology, 2011, 22, 3-8.	3.3	79
41	Proteome Coverage Prediction for Integrated Proteomics Datasets. Journal of Computational Biology, 2011, 18, 283-293.	0.8	8
42	The quantitative proteome of a human cell line. Molecular Systems Biology, 2011, 7, 549.	3.2	691
43	Proteome Coverage Prediction for Integrated Proteomics Datasets. Lecture Notes in Computer Science, 2010, , 96-109.	1.0	2
44	Proteome coverage prediction with infinite Markov models. Bioinformatics, 2009, 25, i154-i160.	1.8	15
45	Directed mass spectrometry: towards hypothesis-driven proteomics. Current Opinion in Chemical Biology, 2009, 13, 510-517.	2.8	90
46	Protein Identification False Discovery Rates for Very Large Proteomics Data Sets Generated by Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2009, 8, 2405-2417.	2.5	282