

# Manfred Claassen

## List of Publications by Year in descending order

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Version: 2024-02-01

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	The quantitative proteome of a human cell line. <i>Molecular Systems Biology</i> , 2011, 7, 549.	3.2	691
2	NASH limits anti-tumour surveillance in immunotherapy-treated HCC. <i>Nature</i> , 2021, 592, 450-456.	13.7	649
3	Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability. <i>Science</i> , 2017, 355, .	6.0	313
4	Protein Identification False Discovery Rates for Very Large Proteomics Data Sets Generated by Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2405-2417.	2.5	282
5	Automated Gleason grading of prostate cancer tissue microarrays via deep learning. <i>Scientific Reports</i> , 2018, 8, 12054.	1.6	278
6	False discovery rate estimation for cross-linked peptides identified by mass spectrometry. <i>Nature Methods</i> , 2012, 9, 901-903.	9.0	273
7	The Mtb Proteome Library: A Resource of Assays to Quantify the Complete Proteome of <i>Mycobacterium tuberculosis</i> . <i>Cell Host and Microbe</i> , 2013, 13, 602-612.	5.1	165
8	GM-CSF and CXCR4 define a T helper cell signature in multiple sclerosis. <i>Nature Medicine</i> , 2019, 25, 1290-1300.	15.2	140
9	Nontargeted Metabolomics Reveals the Multilevel Response to Antibiotic Perturbations. <i>Cell Reports</i> , 2017, 19, 1214-1228.	2.9	139
10	Sensitive detection of rare disease-associated cell subsets via representation learning. <i>Nature Communications</i> , 2017, 8, 14825.	5.8	125
11	Estimation of Absolute Protein Quantities of Unlabeled Samples by Selected Reaction Monitoring Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013987.	2.5	117
12	Absolute quantification of microbial proteomes at different states by directed mass spectrometry. <i>Molecular Systems Biology</i> , 2011, 7, 510.	3.2	91
13	Directed mass spectrometry: towards hypothesis-driven proteomics. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 510-517.	2.8	90
14	Comprehensive proteomics. <i>Current Opinion in Biotechnology</i> , 2011, 22, 3-8.	3.3	79
15	Distinct immunological signatures discriminate severe COVID-19 from non-SARS-CoV-2-driven critical pneumonia. <i>Immunity</i> , 2021, 54, 1578-1593.e5.	6.6	75
16	The dynamics of root cap sloughing in <i>Arabidopsis</i> is regulated by peptide signalling. <i>Nature Plants</i> , 2018, 4, 596-604.	4.7	62
17	Structure-function relationships of HDL in diabetes and coronary heart disease. <i>JCI Insight</i> , 2020, 5, .	2.3	62
18	Landscape of Exhausted Virus-Specific CD8 <sup>+</sup> T Cells in Chronic LCMV Infection. <i>Cell Reports</i> , 2020, 32, 108078.	2.9	45

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19	Similarities and Differences of Blood N-Glycoproteins in Five Solid Carcinomas at Localized Clinical Stage Analyzed by SWATH-MS. <i>Cell Reports</i> , 2018, 23, 2819-2831.e5.	2.9	36
20	Deterministic scRNA-seq captures variation in intestinal crypt and organoid composition. <i>Nature Methods</i> , 2022, 19, 323-330.	9.0	33
21	Exhausted CD8+ T cells exhibit low and strongly inhibited TCR signaling during chronic LCMV infection. <i>Nature Communications</i> , 2020, 11, 4454.	5.8	32
22	Analysis of Cell Lineage Trees by Exact Bayesian Inference Identifies Negative Autoregulation of Nanog in Mouse Embryonic Stem Cells. <i>Cell Systems</i> , 2016, 3, 480-490.e13.	2.9	30
23	Computational and experimental single cell biology techniques for the definition of cell type heterogeneity, interplay and intracellular dynamics. <i>Current Opinion in Biotechnology</i> , 2015, 34, 9-15.	3.3	29
24	Inference and Validation of Protein Identifications. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1097-1104.	2.5	27
25	TGF- $\beta$ 2 induces oncofetal fibronectin, which in turn modulates TGF- $\beta$ 2 superfamily signaling in endothelial cells. <i>Journal of Cell Science</i> , 2018, 131, .	1.2	27
26	Generic Comparison of Protein Inference Engines. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O110.007088.	2.5	20
27	Latent representation learning in biology and translational medicine. <i>Patterns</i> , 2021, 2, 100198.	3.1	17
28	A weakly supervised deep learning approach for label-free imaging flow-cytometry-based blood diagnostics. <i>Cell Reports Methods</i> , 2021, 1, 100094.	1.4	17
29	Sparse Regression Based Structure Learning of Stochastic Reaction Networks from Single Cell Snapshot Time Series. <i>PLoS Computational Biology</i> , 2016, 12, e1005234.	1.5	16
30	Proteome coverage prediction with infinite Markov models. <i>Bioinformatics</i> , 2009, 25, i154-i160.	1.8	15
31	Mixture-of-Experts Variational Autoencoder for clustering and generating from similarity-based representations on single cell data. <i>PLoS Computational Biology</i> , 2021, 17, e1009086.	1.5	15
32	Targeting extracellular and juxtamembrane FGFR2 mutations in chemotherapy-refractory cholangiocarcinoma. <i>Npj Precision Oncology</i> , 2021, 5, 80.	2.3	10
33	Metabolic network segmentation: A probabilistic graphical modeling approach to identify the sites and sequential order of metabolic regulation from non-targeted metabolomics data. <i>PLoS Computational Biology</i> , 2017, 13, e1005577.	1.5	10
34	psupertime: supervised pseudotime analysis for time-series single-cell RNA-seq data. <i>Bioinformatics</i> , 2022, 38, i290-i298.	1.8	10
35	Proteome Coverage Prediction for Integrated Proteomics Datasets. <i>Journal of Computational Biology</i> , 2011, 18, 283-293.	0.8	8
36	Identification of ALP+/CD73+ defining markers for enhanced osteogenic potential in human adipose-derived mesenchymal stromal cells by mass cytometry. <i>Stem Cell Research and Therapy</i> , 2021, 12, 7.	2.4	8

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37	Immunological Predictors of Dimethyl Fumarate-Induced Lymphopenia. <i>Annals of Neurology</i> , 2022, 91, 676-681.	2.8	8
38	Privacy-preserving federated neural network learning for disease-associated cell classification. <i>Patterns</i> , 2022, 3, 100487.	3.1	8
39	Novel Blood Vascular Endothelial Subtype-Specific Markers in Human Skin Unearthed by Single-Cell Transcriptomic Profiling. <i>Cells</i> , 2022, 11, 1111.	1.8	6
40	Epitope-Tagged Autotransporters as Single-Cell Reporters for Gene Expression by a <i>Salmonella</i> Typhimurium wbaP Mutant. <i>PLoS ONE</i> , 2016, 11, e0154828.	1.1	5
41	Dynamic distribution decomposition for single-cell snapshot time series identifies subpopulations and trajectories during iPSC reprogramming. <i>PLoS Computational Biology</i> , 2020, 16, e1007491.	1.5	4
42	Shooting Movies of Signaling Network Dynamics with Multiparametric Cytometry. <i>Current Topics in Microbiology and Immunology</i> , 2013, 377, 177-189.	0.7	3
43	Tree-ensemble analysis assesses presence of multifurcations in single cell data. <i>Molecular Systems Biology</i> , 2019, 15, e8552.	3.2	2
44	Negative allosteric modulators of metabotropic glutamate receptor 3 target the stem-like phenotype of glioblastoma. <i>Molecular Therapy - Oncolytics</i> , 2021, 20, 166-174.	2.0	2
45	Proteome Coverage Prediction for Integrated Proteomics Datasets. <i>Lecture Notes in Computer Science</i> , 2010, , 96-109.	1.0	2
46	Visualizing hierarchies in scRNA-seq data using a density tree-biased autoencoder. <i>Bioinformatics</i> , 2022, 38, i316-i324.	1.8	2