Simon Anders

List of Publications by Year in Descending Order

67 papers	**55,919** citations	**31** h-index	**87** g-index
87 ext. papers	**84,371** ext. citations	**13.4** avg, IF	**8.67** L-index

#	Paper	IF	Citations
67	Analysing high-throughput sequencing data in Python with HTSeq 2.0.. *Bioinformatics*, **2022**,	7.2	14
66	Endothelial GATA4 controls liver fibrosis and regeneration by preventing a pathogenic switch in angiocrine signaling. *Journal of Hepatology*, **2021**, 74, 380-393	13.4	29
65	Colorimetric RT-LAMP and LAMP-sequencing forDetecting SARS-CoV-2 RNA in Clinical Samples. *Bio-protocol*, **2021**, 11, e3964	0.9	0
64	Effectiveness and cost-effectiveness of four different strategies for SARS-CoV-2 surveillance in the general population (CoV-Surv Study): a structured summary of a study protocol for a cluster-randomised, two-factorial controlled trial. *Trials*, **2021**, 22, 39	2.8	12
63	Neurofilament light and heterogeneity of disease progression in amyotrophic lateral sclerosis: development and validation of a prediction model to improve interventional trials. *Translational Neurodegeneration*, **2021**, 10, 31	10.3	2
62	Effectiveness and cost-effectiveness of four different strategies for SARS-CoV-2 surveillance in the general population (CoV-Surv Study): study protocol for a two-factorial randomized controlled multi-arm trial with cluster sampling. *Trials*, **2021**, 22, 656	2.8	1
61	High throughput screening of novel AAV capsids identifies variants for transduction of adult NSCs within the subventricular zone. *Molecular Therapy - Methods and Clinical Development*, **2021**, 23, 33-50	6.4	6
60	DEqMS: A Method for Accurate Variance Estimation in Differential Protein Expression Analysis. *Molecular and Cellular Proteomics*, **2020**, 19, 1047-1057	7.6	31
59	Building an international consortium for tracking coronavirus health status. *Nature Medicine*, **2020**, 26, 1161-1165	50.5	16
58	Exploring dimension-reduced embeddings with Sleepwalk. *Genome Research*, **2020**, 30, 749-756	9.7	2
57	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. *Nature Cell Biology*, **2020**, 22, 896-906	23.4	30
56	Proteogenomic Subtyping of Chronic Lymphocytic Leukemia Identifies a Novel Poor Outcome Subgroup with a Distinct Drug Response Profile. *Blood*, **2020**, 136, 10-11	2.2	
55	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. *Nature Communications*, **2020**, 11, 5783	17.4	8
54	Transcriptome and translatome co-evolution in mammals. *Nature*, **2020**, 588, 642-647	50.4	26
53	A colorimetric RT-LAMP assay and LAMP-sequencing for detecting SARS-CoV-2 RNA in clinical samples. *Science Translational Medicine*, **2020**, 12,	17.5	278
52	SARS-CoV-2 RNA Extraction Using Magnetic Beads for Rapid Large-Scale Testing by RT-qPCR and RT-LAMP. *Viruses*, **2020**, 12,	6.2	39
51	EpiSmokEr: a robust classifier to determine smoking status from DNA methylation data. *Epigenomics*, **2019**, 11, 1469-1486	4.4	35

#	Reference	IF	Citations
50	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins. *Molecular and Cellular Proteomics*, **2019**, 18, 2506-2515	7.6	34
49	Gene expression across mammalian organ development. *Nature*, **2019**, 571, 505-509	50.4	179
48	Alanine Tails Signal Proteolysis in Bacterial Ribosome-Associated Quality Control. *Cell*, **2019**, 178, 76-90.e22	36.2	39
47	Focused multidimensional scaling: interactive visualization for exploration of high-dimensional data. *BMC Bioinformatics*, **2019**, 20, 221	3.6	3
46	Quiescence Modulates Stem Cell Maintenance and Regenerative Capacity in the Aging Brain. *Cell*, **2019**, 176, 1407-1419.e14	56.2	128
45	A Framework for Multi-Omic Prediction of Treatment Response to Biologic Therapy for Psoriasis. *Journal of Investigative Dermatology*, **2019**, 139, 100-107	4.3	18
44	Spatial aspects of oncogenic signalling determine the response to combination therapy in slice explants from Kras-driven lung tumours. *Journal of Pathology*, **2018**, 245, 101-113	9.4	8
43	Drug-perturbation-based stratification of blood cancer. *Journal of Clinical Investigation*, **2018**, 128, 427-445	15.9	72
42	Gene set enrichment analysis of the bronchial epithelium implicates contribution of cell cycle and tissue repair processes in equine asthma. *Scientific Reports*, **2018**, 8, 16408	4.9	7
41	Impaired response of the bronchial epithelium to inflammation characterizes severe equine asthma. *BMC Genomics*, **2017**, 18, 708	4.5	23
40	Identification and Clinical Exploration of Individualized Targeted Therapeutic Approaches in Acute Myeloid Leukemia Patients By Integrating Drug Response and Deep Molecular Profiles. *Blood*, **2017**, 130, 854-854	2.2	1
39	JNJ872 inhibits influenza A virus replication without altering cellular antiviral responses. *Antiviral Research*, **2016**, 133, 23-31	10.8	34
38	Multi-Omics Studies towards Novel Modulators of Influenza A Virus-Host Interaction. *Viruses*, **2016**, 8,	6.2	14
37	Activation of Tryptophan and Phenylalanine Catabolism in the Remission Phase of Allergic Contact Dermatitis: A Pilot Study. *International Archives of Allergy and Immunology*, **2016**, 170, 262-268	3.7	3
36	HTSeq--a Python framework to work with high-throughput sequencing data. *Bioinformatics*, **2015**, 31, 166-9	7.2	10519
35	Improved binding site assignment by high-resolution mapping of RNA-protein interactions using iCLIP. *Nature Communications*, **2015**, 6, 7921	17.4	23
34	FourCSeq: analysis of 4C sequencing data. *Bioinformatics*, **2015**, 31, 3085-91	7.2	74
33	Single-cell polyadenylation site mapping reveals 3' isoform choice variability. *Molecular Systems Biology*, **2015**, 11, 812	12.2	40

32	RNA-Seq workflow: gene-level exploratory analysis and differential expression. *F1000Research*, **2015**, 4, 1070	3.6	181
31	Orchestrating high-throughput genomic analysis with Bioconductor. *Nature Methods*, **2015**, 12, 115-21	21.6	1949
30	Subgroups of T-Cell Prolymphocytic Leukemia (T-PLL) Discovered By High-Throughput Ex Vivo Drug Testing and Genetic Profiling. *Blood*, **2015**, 126, 315-315	2.2	
29	An evaluation of high-throughput approaches to QTL mapping in Saccharomyces cerevisiae. *Genetics*, **2014**, 196, 853-65	4	56
28	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biology*, **2014**, 15, 550	18.3	28138
27	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. *Nature Protocols*, **2013**, 8, 1765-86	18.8	788
26	Accounting for technical noise in single-cell RNA-seq experiments. *Nature Methods*, **2013**, 10, 1093-5	21.6	659
25	Drift and conservation of differential exon usage across tissues in primate species. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 15377-82	11.5	73
24	Direct competition between hnRNP C and U2AF65 protects the transcriptome from the exonization of Alu elements. *Cell*, **2013**, 152, 453-66	56.2	285
23	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. *Nucleic Acids Research*, **2013**, 41, e65	20.1	81
22	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. *Nucleic Acids Research*, **2013**, 41, 6370-6370	20.1	12
21	Detecting differential usage of exons from RNA-Seq data. *Nature Precedings*, **2012**,		11
20	Detecting differential usage of exons from RNA-Seq data. *Nature Precedings*, **2012**,		8
19	Detecting differential usage of exons from RNA-seq data. *Genome Research*, **2012**, 22, 2008-17	9.7	882
18	Relating CNVs to transcriptome data at fine resolution: assessment of the effect of variant size, type, and overlap with functional regions. *Genome Research*, **2011**, 21, 2004-13	9.7	80
17	Differential expression analysis for sequence count data. *Genome Biology*, **2010**, 11, R106	18.3	9952
16	Genome-wide analysis of mRNA decay patterns during early Drosophila development. *Genome Biology*, **2010**, 11, R93	18.3	92
15	ShortRead: a bioconductor package for input, quality assessment and exploration of high-throughput sequence data. *Bioinformatics*, **2009**, 25, 2607-8	7.2	355

LIST OF PUBLICATIONS

14	Visualization of genomic data with the Hilbert curve. *Bioinformatics*, **2009**, 25, 1231-5	7.2	47
13	A variational method based on weighted graph states. *New Journal of Physics*, **2007**, 9, 361-361	2.9	12
12	Fast simulation of stabilizer circuits using a graph-state representation. *Physical Review A*, **2006**, 73,	2.6	60
11	Quantum communication cost of preparing multipartite entanglement. *Physical Review A*, **2006**, 73,	2.6	10
10	RNA-Seq workflow: gene-level exploratory analysis and differential expression. *F1000Research*,4, 1070	3.6	28
9	Exploring dimension-reduced embeddings with Sleepwalk		1
8	HTSeq - A Python framework to work with high-throughput sequencing data		227
7	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2		151
6	Screening for SARS-CoV-2 infections with colorimetric RT-LAMP and LAMP sequencing		14
5	Computational analysis of ligand dose range thermal proteome profiles		1
4	SARS-CoV-2 RNA extraction using magnetic beads for rapid large-scale testing by RT-qPCR and RT-LAMP		4
3	Single cell 3'UTR analysis identifies changes in alternative polyadenylation throughout neuronal differentiation and in autism		3
2	Non-parametric analysis of thermal proteome profiles reveals novel drug-binding proteins		2
1	proDA: Probabilistic Dropout Analysis for Identifying Differentially Abundant Proteins in Label-Free Mass Spectrometry		4