Simon Anders

List of Publications by Year
in descending order

62 papers	101,539 citations	126907 33 h-index	161849 54 g-index
87 all docs	87 docs citations	87 times ranked	140779 citing authors

#	Article	IF	Citations
1	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 2014, 15, 550.	8.8	58,325
2	HTSeqâ€"a Python framework to work with high-throughput sequencing data. Bioinformatics, 2015, 31, 166-169.	4.1	17,270
3	Differential expression analysis for sequence count data. Genome Biology, 2010, 11, R106.	8.8	13,707
4	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	19.0	3,070
5	Detecting differential usage of exons from RNA-seq data. Genome Research, 2012, 22, 2008-2017.	5.5	1,341
6	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. Nature Protocols, 2013, 8, 1765-1786.	12.0	1,124
7	Accounting for technical noise in single-cell RNA-seq experiments. Nature Methods, 2013, 10, 1093-1095.	19.0	929
8	A colorimetric RT-LAMP assay and LAMP-sequencing for detecting SARS-CoV-2 RNA in clinical samples. Science Translational Medicine, 2020, 12, .	12.4	516
9	Gene expression across mammalian organ development. Nature, 2019, 571, 505-509.	27.8	490
10	ShortRead: a bioconductor package for input, quality assessment and exploration of high-throughput sequence data. Bioinformatics, 2009, 25, 2607-2608.	4.1	481
11	Direct Competition between hnRNP C and U2AF65 Protects the Transcriptome from the Exonization of Alu Elements. Cell, 2013, 152, 453-466.	28.9	398
12	Analysing high-throughput sequencing data in Python with HTSeq 2.0. Bioinformatics, 2022, 38, 2943-2945.	4.1	335
13	RNA-Seq workflow: gene-level exploratory analysis and differential expression. F1000Research, 2015, 4, 1070.	1.6	304
14	Quiescence Modulates Stem Cell Maintenance and Regenerative Capacity in the Aging Brain. Cell, 2019, 176, 1407-1419.e14.	28.9	265
15	DEqMS: A Method for Accurate Variance Estimation in Differential Protein Expression Analysis. Molecular and Cellular Proteomics, 2020, 19, 1047-1057.	3.8	127
16	Genome-wide analysis of mRNA decay patterns during early Drosophila development. Genome Biology, 2010, 11, R93.	9.6	124
17	Drug-perturbation-based stratification of blood cancer. Journal of Clinical Investigation, 2017, 128, 427-445.	8.2	124
18	Transcriptome and translatome co-evolution in mammals. Nature, 2020, 588, 642-647.	27.8	122

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19	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, 2004-2013.	5.5	109
20	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, 15377-15382.	7.1	103
21	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. Nucleic Acids Research, 2013, 41, e65-e65.	14.5	98
22	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. Nature Cell Biology, 2020, 22, 896-906.	10.3	93
23	FourCSeq: analysis of 4C sequencing data. Bioinformatics, 2015, 31, 3085-3091.	4.1	91
24	Fast simulation of stabilizer circuits using a graph-state representation. Physical Review A, 2006, 73, .	2.5	87
25	An Evaluation of High-Throughput Approaches to QTL Mapping in <i>Saccharomyces cerevisiae</i>. Genetics, 2014, 196, 853-865.	2.9	86
26	EpiSmokEr: a robust classifier to determine smoking status from DNA methylation data. Epigenomics, 2019, 11, 1469-1486.	2.1	85
27	Alanine Tails Signal Proteolysis in Bacterial Ribosome-Associated Quality Control. Cell, 2019, 178, 76-90.e22.	28.9	81
28	Endothelial GATA4 controls liver fibrosis and regeneration by preventing a pathogenic switch in angiocrine signaling. Journal of Hepatology, 2021, 74, 380-393.	3.7	81
29	SARS-CoV-2 RNA Extraction Using Magnetic Beads for Rapid Large-Scale Testing by RT-qPCR and RT-LAMP. Viruses, 2020, 12, 863.	3.3	79
30	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins*. Molecular and Cellular Proteomics, 2019, 18, 2506-2515.	3.8	75
31	Visualization of genomic data with the Hilbert curve. Bioinformatics, 2009, 25, 1231-1235.	4.1	61
32	RNA-Seq workflow: gene-level exploratory analysis and differential expression. F1000Research, 0, 4, 1070.	1.6	55
33	Single‐cell polyadenylation site mapping reveals 3′ isoform choice variability. Molecular Systems Biology, 2015, 11, 812.	7.2	52
34	JNJ872 inhibits influenza A virus replication without altering cellular antiviral responses. Antiviral Research, 2016, 133, 23-31.	4.1	40
35	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. Nature Communications, 2020, 11, 5783.	12.8	34
36	Improved binding site assignment by high-resolution mapping of RNA–protein interactions using iCLIP. Nature Communications, 2015, 6, 7921.	12.8	32

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37	Impaired response of the bronchial epithelium to inflammation characterizes severe equine asthma. BMC Genomics, 2017, 18, 708.	2.8	32
38	A Framework for Multi-Omic Prediction of Treatment Response to Biologic Therapy for Psoriasis. Journal of Investigative Dermatology, 2019, 139, 100-107.	0.7	30
39	Multi-Omics Studies towards Novel Modulators of Influenza A Virus–Host Interaction. Viruses, 2016, 8, 269.	3.3	23
40	Building an international consortium for tracking coronavirus health status. Nature Medicine, 2020, 26, 1161-1165.	30.7	23
41	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.	1.6	23
42	Detecting differential usage of exons from RNA-Seq data. Nature Precedings, 0, , .	0.1	21
43	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.	4.5	19
44	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.	8.0	18
45	A variational method based on weighted graph states. New Journal of Physics, 2007, 9, 361-361.	2.9	17
46	Detecting differential usage of exons from RNA-Seq data. Nature Precedings, 0, , .	0.1	17
47	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. Nucleic Acids Research, 2013, 41, 6370-6370.	14.5	17
48	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.	4.1	16
49	Quantum communication cost of preparing multipartite entanglement. Physical Review A, 2006, 73, .	2.5	14
50	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.	3.3	14
51	Focused multidimensional scaling: interactive visualization for exploration of high-dimensional data. BMC Bioinformatics, 2019, 20, 221.	2.6	12
52	Exploring dimension-reduced embeddings with Sleepwalk. Genome Research, 2020, 30, 749-756.	5.5	8
53	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.	2.1	7
54	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.	1.6	6

#	Article	IF	Citations
55	Colorimetric RT-LAMP and LAMP-sequencing for Detecting SARS-CoV-2 RNA in Clinical Samples. Bio-protocol, 2021, 11, e3964.	0.4	4
56	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.	1.4	1
57	Abstract LB-305: A computational approach to identify recurrent somatic driver events in noncoding regions in human cancers. , 2015, , .		0
58	Subgroups of T-Cell Prolymphocytic Leukemia (T-PLL) Discovered By High-Throughput Ex Vivo Drug Testing and Genetic Profiling. Blood, 2015, 126, 315-315.	1.4	0
59	Abstract 286: Transcriptomic features predicting drug sensitivity and resistance in acute myeloid leukemia. , 2018, , .		0
60	Abstract 3899: Discovery and clinical implementation of individualized therapies in acute myeloid leukemia based onex vivodrug sensitivity testing and multi-omics profiling. , 2018, , .		0
61	Abstract 458: Precision systems medicine in acute myeloid leukemia: real-time translation of tailored therapeutic opportunities arising from ex-vivo drug sensitivity testing and molecular profiling. , 2019, , .		0
62	Proteogenomic Subtyping of Chronic Lymphocytic Leukemia Identifies a Novel Poor Outcome Subgroup with a Distinct Drug Response Profile. Blood, 2020, 136, 10-11.	1.4	0