Sascha Ott

List of Publications by Year
in descending order

53 papers	4,736 citations	136950 32 h-index	182427 51 g-index
62 all docs	62 docs citations	62 times ranked	9093 citing authors

#	Article	IF	Citations
1	High-Resolution Temporal Profiling of Transcripts during *Arabidopsis* Leaf Senescence Reveals a Distinct Chronology of Processes and Regulation Â Â. Plant Cell, 2011, 23, 873-894.	6.6	776
2	Bringing numerous methods for expression and promoter analysis to a public cloud computing service. Bioinformatics, 2018, 34, 884-886.	4.1	573
3	*Arabidopsis* Defense against *Botrytis cinerea*: Chronology and Regulation Deciphered by High-Resolution Temporal Transcriptomic Analysis Â Â. Plant Cell, 2012, 24, 3530-3557.	6.6	337
4	A local regulatory network around three NAC transcription factors in stress responses and senescence in Arabidopsis leaves. Plant Journal, 2013, 75, 26-39.	5.7	202
5	Wellington: a novel method for the accurate identification of digital genomic footprints from DNase-seq data. Nucleic Acids Research, 2013, 41, e201-e201.	14.5	196
6	Clearance of senescent decidual cells by uterine natural killer cells in cycling human endometrium. ELife, 2017, 6, .	6.0	193
7	Loss of Endometrial Plasticity in Recurrent Pregnancy Loss. Stem Cells, 2016, 34, 346-356.	3.2	168
8	Recurrent pregnancy loss is associated with a pro-senescent decidual response during the peri-implantation window. Communications Biology, 2020, 3, 37.	4.4	158
9	Transcriptional Dynamics Driving MAMP-Triggered Immunity and Pathogen Effector-Mediated Immunosuppression in Arabidopsis Leaves Following Infection with *Pseudomonas syringae* pv tomato DC3000. Plant Cell, 2015, 27, 3038-3064.	6.6	148
10	Circadian control of abscisic acid biosynthesis and signalling pathways revealed by genome‑wide analysis of LHY binding targets. New Phytologist, 2018, 220, 893-907.	7.3	140
11	Arabidopsis HEAT SHOCK TRANSCRIPTION FACTORA1b overexpression enhances water productivity, resistance to drought, and infection. Journal of Experimental Botany, 2013, 64, 3467-3481.	4.8	137
12	Single-Cell Transcriptomics: A High-Resolution Avenue for Plant Functional Genomics. Trends in Plant Science, 2020, 25, 186-197.	8.8	128
13	Identification of a Dynamic Core Transcriptional Network in t(8;21) AML that Regulates Differentiation Block and Self-Renewal. Cell Reports, 2014, 8, 1974-1988.	6.4	106
14	Inducible chromatin priming is associated with the establishment of immunological memory in T cells. EMBO Journal, 2016, 35, 515-535.	7.8	92
15	Time-Series Transcriptomics Reveals That *AGAMOUS-LIKE22* Affects Primary Metabolism and Developmental Processes in Drought-Stressed Arabidopsis. Plant Cell, 2016, 28, 345-366.	6.6	92
16	Peptide–MHC Class I Tetramers Can Fail To Detect Relevant Functional T Cell Clonotypes and Underestimate Antigen-Reactive T Cell Populations. Journal of Immunology, 2018, 200, 2263-2279.	0.8	87
17	Characterisation of pathogen-specific regions and novel effector candidates in Fusarium oxysporum f. sp. cepae. Scientific Reports, 2018, 8, 13530.	3.3	77
18	MEME-LaB: motif analysis in clusters. Bioinformatics, 2013, 29, 1696-1697.	4.1	71

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19	Multiplex PCR and Next Generation Sequencing for the Non-Invasive Detection of Bladder Cancer. PLoS ONE, 2016, 11, e0149756.	2.5	66
20	Conserved Noncoding Sequences Highlight Shared Components of Regulatory Networks in Dicotyledonous Plants. Plant Cell, 2012, 24, 3949-3965.	6.6	64
21	Chronic FLT3-ITD Signaling in Acute Myeloid Leukemia Is Connected to a Specific Chromatin Signature. Cell Reports, 2015, 12, 821-836.	6.4	63
22	Regulation of Cell Type-Specific Immunity Networks in Arabidopsis Roots. Plant Cell, 2020, 32, 2742-2762.	6.6	59
23	Low Vitamin B12 in Pregnancy Is Associated With Adipose-Derived Circulating miRs Targeting PPARÎ³ and Insulin Resistance. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 4200-4209.	3.6	56
24	Nodal cis-regulatory elements reveal epiblast and primitive endoderm heterogeneity in the peri-implantation mouse embryo. Developmental Biology, 2011, 349, 350-362.	2.0	54
25	PD-1+ Polyfunctional T Cells Dominate the Periphery after Tumor-Infiltrating Lymphocyte Therapy for Cancer. Clinical Cancer Research, 2017, 23, 5779-5788.	7.0	53
26	Integration of Kinase and Calcium Signaling at the Level of Chromatin Underlies Inducible Gene Activation in T Cells. Journal of Immunology, 2017, 199, 2652-2667.	0.8	51
27	Wellington-bootstrap: differential DNase-seq footprinting identifies cell-type determining transcription factors. BMC Genomics, 2015, 16, 1000.	2.8	49
28	Targeted deep sequencing of urothelial bladder cancers and associated urinary <scp>DNA</scp>: a 23â€gene panel with utility for nonâ€invasive diagnosis and risk stratification. BJU International, 2019, 124, 532-544.	2.5	47
29	A Novel Nodal Enhancer Dependent on Pluripotency Factors and Smad2/3 Signaling Conditions a Regulatory Switch During Epiblast Maturation. PLoS Biology, 2014, 12, e1001890.	5.6	41
30	Success after failure: the role of endometrial stem cells in recurrent miscarriage. Reproduction, 2016, 152, R159-R166.	2.6	38
31	Wigwams: identifying gene modules co-regulated across multiple biological conditions. Bioinformatics, 2014, 30, 962-970.	4.1	36
32	The immune landscape of SARS-CoV-2-associated Multisystem Inflammatory Syndrome in Children (MIS-C) from acute disease to recovery. IScience, 2021, 24, 103215.	4.1	35
33	Evolutionarily Conserved Regulatory Motifs in the Promoter of the Arabidopsis Clock Gene LATE ELONGATED HYPOCOTYL Â Â. Plant Cell, 2009, 21, 2606-2623.	6.6	34
34	Analysis of chromatin accessibility in decidualizing human endometrial stromal cells. FASEB Journal, 2018, 32, 2467-2477.	0.5	32
35	Characterization of Highly Proliferative Decidual Precursor Cells During the Window of Implantation in Human Endometrium. Stem Cells, 2021, 39, 1067-1080.	3.2	30
36	Extracting Fluorescent Reporter Time Courses of Cell Lineages from High-Throughput Microscopy at Low Temporal Resolution. PLoS ONE, 2011, 6, e27886.	2.5	29

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37	Evolutionary analysis of regulatory sequences (EARS) in plants. Plant Journal, 2010, 64, no-no.	5.7	28
38	Loss of Endometrial Sodium Glucose Cotransporter SGLT1 is Detrimental to Embryo Survival and Fetal Growth in Pregnancy. Scientific Reports, 2017, 7, 12612.	3.3	27
39	Regulation of Resource Partitioning Coordinates Nitrogen and Rhizobia Responses and Autoregulation of Nodulation in Medicago truncatula. Molecular Plant, 2019, 12, 833-846.	8.3	23
40	Macrophage and Neutrophil Interactions in the Pancreatic Tumor Microenvironment Drive the Pathogenesis of Pancreatic Cancer. Cancers, 2022, 14, 194.	3.7	23
41	Artifacts in the data of Hu et al.. Nature Genetics, 2016, 48, 2-3.	21.4	18
42	Impact of Sustained Transforming Growth Factor-β Receptor Inhibition on Chromatin Accessibility and Gene Expression in Cultured Human Endometrial MSC. Frontiers in Cell and Developmental Biology, 2020, 8, 567610.	3.7	15
43	Highly Sensitive and Specific Detection of Bladder Cancer via Targeted Ultra-deep Sequencing of Urinary DNA. European Urology Oncology, 2023, 6, 67-75.	5.4	12
44	Non-Coding Mutations in Urothelial Bladder Cancer: Biological and Clinical Relevance and Potential Utility as Biomarkers. Bladder Cancer, 2019, 5, 263-272.	0.4	10
45	EndoTime: non-categorical timing estimates for luteal endometrium. Human Reproduction, 2022, 37, 747-761.	0.9	10
46	Plant circadian clock control of *Medicago truncatula* nodulation via regulation of nodule cysteine-rich peptides. Journal of Experimental Botany, 2022, 73, 2142-2156.	4.8	9
47	An alignment-free model for comparison of regulatory sequences. Bioinformatics, 2010, 26, 2391-2397.	4.1	8
48	Analysis of 5' gene regions reveals extraordinary conservation of novel non-coding sequences in a wide range of animals. BMC Evolutionary Biology, 2015, 15, 227.	3.2	7
49	Transcriptional programs: Modelling higher order structure in transcriptional control. BMC Bioinformatics, 2009, 10, 218.	2.6	3
50	On the complexity of deriving position specific score matrices from positive and negative sequences. Discrete Applied Mathematics, 2007, 155, 676-685.	0.9	1
51	Conserved *Cis*-Regulatory Modules Control Robustness in *Msx1* Expression at Single-Cell Resolution. Genome Biology and Evolution, 2015, 7, 2762-2778.	2.5	0
52	Biochemical and phenotypic characterisation of the Mycobacterium smegmatis transporter UspABC. Cell Surface, 2021, 7, 100052.	3.0	0
53	Identification of a Dynamic Core Transcriptional Network in t(8;21) AML Regulating Differentiation Block and Self-Renewal. Blood, 2014, 124, 1061-1061.	1.4	0