Steffen MÃ¶ller

List of Publications by Year
in descending order

59 papers	2,775 citations	304743 22 h-index	189892 50 g-index
64 all docs	64 docs citations	64 times ranked	4508 citing authors

#	Article	IF	Citations
1	Evaluation of methods for the prediction of membrane spanning regions. Bioinformatics, 2001, 17, 646-653.	4.1	1,050
2	AFP-Pred: A random forest approach for predicting antifreeze proteins from sequence-derived properties. Journal of Theoretical Biology, 2011, 270, 56-62.	1.7	226
3	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	14.5	113
4	A collection of well characterised integral membrane proteins. Bioinformatics, 2000, 16, 1159-1160.	4.1	92
5	Genome-wide mapping of gene–microbiota interactions in susceptibility to autoimmune skin blistering. Nature Communications, 2013, 4, 2462.	12.8	87
6	Single-cell analyses of aging, inflammation and senescence. Ageing Research Reviews, 2020, 64, 101156.	10.9	85
7	A novel method for automatic functional annotation of proteins. Bioinformatics, 1999, 15, 228-233.	4.1	84
8	Health and Aging: Unifying Concepts, Scores, Biomarkers and Pathways. , 2019, 10, 883.		56
9	Cytoskeletal Rearrangements in Synovial Fibroblasts as a Novel Pathophysiological Determinant of Modeled Rheumatoid Arthritis. PLoS Genetics, 2005, 1, e48.	3.5	49
10	Mitochondrial gene polymorphisms alter hepatic cellular energy metabolism and aggravate diet-induced non-alcoholic steatohepatitis. Molecular Metabolism, 2016, 5, 283-295.	6.5	45
11	Community-driven computational biology with Debian Linux. BMC Bioinformatics, 2010, 11, S5.	2.6	42
12	Community-driven development for computational biology at Sprints, Hackathons and Codefests. BMC Bioinformatics, 2014, 15, S7.	2.6	42
13	EDITtoTrEMBL: a distributed approach to high-quality automated protein sequence annotation. Bioinformatics, 1999, 15, 219-227.	4.1	38
14	Genetic control of psoriasis is relatively distinct from that of metabolic syndrome and coronary artery disease. Experimental Dermatology, 2013, 22, 552-553.	2.9	37
15	Identification of Quantitative Trait Loci in Experimental Epidermolysis Bullosa Acquisita. Journal of Investigative Dermatology, 2012, 132, 1409-1415.	0.7	35
16	Gene-diet interactions associated with complex trait variation in an advanced intercross outbred mouse line. Nature Communications, 2019, 10, 4097.	12.8	35
17	Time course transcriptomics of IFNB1b drug therapy in multiple sclerosis. Autoimmunity, 2010, 43, 172-178.	2.6	34
18	SPRED: A machine learning approach for the identification of classical and non-classical secretory proteins in mammalian genomes. Biochemical and Biophysical Research Communications, 2010, 391, 1306-1311.	2.1	33

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19	Allelic and copy-number variations of FcγRs affect granulocyte function and susceptibility for autoimmune blistering diseases. Journal of Autoimmunity, 2015, 61, 36-44.	6.5	32
20	Liver steatosis is a risk factor for hepatotoxicity in patients with inflammatory bowel disease under immunosuppressive treatment. European Journal of Gastroenterology and Hepatology, 2015, 27, 698-704.	1.6	28
21	Scalable Workflows and Reproducible Data Analysis for Genomics. Methods in Molecular Biology, 2019, 1910, 723-745.	0.9	25
22	SNPtoGO: characterizing SNPs by enriched GO terms. Bioinformatics, 2008, 24, 146-148.	4.1	24
23	Fine Mapping of Collagen-Induced Arthritis Quantitative Trait Loci in an Advanced Intercross Line. Journal of Immunology, 2006, 177, 7042-7049.	0.8	23
24	The retinoid‐related orphan receptor alpha is essential for the end‐stage effector phase of experimental epidermolysis bullosa acquisita. Journal of Pathology, 2015, 237, 111-122.	4.5	23
25	The KOX zinc finger genes: Genome wide mapping of 368 ZNF PAC clones with zinc finger gene clusters predominantly in 23 chromosomal loci are confirmed by human sequences annotated in EnsEMBL. Cytogenetic and Genome Research, 2002, 98, 147-153.	1.1	22
26	Expressionview: visualization of quantitative trait loci and gene-expression data in Ensembl. Genome Biology, 2003, 4, R77.	9.6	21
27	Intergenomic consensus in multifactorial inheritance loci: the case of multiple sclerosis. Genes and Immunity, 2004, 5, 615-620.	4.1	20
28	Definition of a 1.06-Mb Region Linked to Neuroinflammation in Humans, Rats and Mice. Genetics, 2006, 173, 1539-1545.	2.9	20
29	Robust Cross-Platform Workflows: How Technical and Scientific Communities Collaborate to Develop, Test and Share Best Practices for Data Analysis. Data Science and Engineering, 2017, 2, 232-244.	6.4	19
30	Male-specific association between MT-ND4 11719 A/G polymorphism and ulcerative colitis: a mitochondria-wide genetic association study. BMC Gastroenterology, 2016, 16, 118.	2.0	17
31	FocusHeuristics – expression-data-driven network optimization and disease gene prediction. Scientific Reports, 2017, 7, 42638.	3.3	17
32	Gene expression profiling of arthritis using a QTL chip reveals a complex gene regulation of the Cia5 region in mice. Genes and Immunity, 2005, 6, 575-583.	4.1	16
33	xQTL workbench: a scalable web environment for multi-level QTL analysis. Bioinformatics, 2012, 28, 1042-1044.	4.1	16
34	Scoring functions for drug-effect similarity. Briefings in Bioinformatics, 2021, 22, .	6.5	15
35	Integrating ARC grid middleware with Taverna workflows. Bioinformatics, 2008, 24, 1221-1222.	4.1	14
36	Evaluation of methods for the prediction of membrane spanning regions. Bioinformatics, 2002, 18, 218-218.	4.1	12

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37	Cloud-Based High Throughput Virtual Screening in Novel Drug Discovery. Lecture Notes in Computer Science, 2019, , 250-278.	1.3	12
38	Healthspan pathway maps in C. elegans and humans highlight transcription, proliferation/biosynthesis and lipids. Aging, 2020, 12, 12534-12581.	3.1	12
39	Consistent integration of non-reliable heterogeneous information resources applied to the annotation of transmembrane proteins. Computers & Chemistry, 2001, 26, 41-49.	1.2	11
40	Bioinformatics tools and database resources for systems genetics analysis in mice--a short review and an evaluation of future needs. Briefings in Bioinformatics, 2012, 13, 135-142.	6.5	11
41	Combining genetic mapping with genome-wide expression in experimental autoimmune encephalomyelitis highlights a gene network enriched for T cell functions and candidate genes regulating autoimmunity. Human Molecular Genetics, 2013, 22, 4952-4966.	2.9	11
42	Non-linear conversion between genetic and physical chromosomal distances. Bioinformatics, 2004, 20, 1966-1967.	4.1	8
43	Nerve Conduction Velocity Is Regulated by the Inositol Polyphosphate-4-Phosphatase II Gene. American Journal of Pathology, 2014, 184, 2420-2429.	3.8	8
44	Dissecting genetics of cutaneous miRNA in a mouse model of an autoimmune blistering disease. BMC Genomics, 2016, 17, 112.	2.8	8
45	A Family with Atypical Hailey Hailey Disease- Is There More to the Underlying Genetics than ATP2C1?. PLoS ONE, 2015, 10, e0121253.	2.5	8
46	Multiple Sclerosis Therapy Monitoring Based on Gene Expression. Current Pharmaceutical Design, 2006, 12, 3761-79.	1.9	7
47	Quantitative Trait Locus Analysis Implicates CD4+/CD44high Memory T Cells in the Pathogenesis of Murine Autoimmune Pancreatitis. PLoS ONE, 2015, 10, e0136298.	2.5	7
48	Perspectives on automated composition of workflows in the life sciences. F1000Research, 2021, 10, 897.	1.6	7
49	ptRNApred: computational identification and classification of post-transcriptional RNA. Nucleic Acids Research, 2014, 42, e167-e167.	14.5	6
50	Scalable Computing for Evolutionary Genomics. Methods in Molecular Biology, 2012, 856, 529-545.	0.9	5
51	A workflow for the integrative transcriptomic description of molecular pathology and the suggestion of normalizing compounds, exemplified by Parkinson's disease. Scientific Reports, 2018, 8, 7937.	3.3	5
52	Suppression of the TGF-β pathway by a macrolide antibiotic decreases fibrotic responses by ocular fibroblasts *in vitro*. Royal Society Open Science, 2020, 7, 200441.	2.4	5
53	Hardy-Weinberg equilibrium revisited for inferences on genotypes featuring allele and copy-number variations. Scientific Reports, 2015, 5, 9066.	3.3	3
54	Selecting SNPs for association studies based on population frequencies: a novel interactive tool and its application to polygenic diseases. In Silico Biology, 2004, 4, 417-27.	0.9	3

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55	In silico fine-mapping: narrowing disease-associated loci by intergenomics. Bioinformatics, 2005, 21, 1737-1738.	4.1	2
56	High-throughput Molecular Docking Now in Reach for a Wider Biochemical Community. , 2012, , .		2
57	Genetic Control of Spontaneous Arthritis in a Four-Way Advanced Intercross Line. PLoS ONE, 2013, 8, e75611.	2.5	2
58	Collection of soluble variants of membrane proteins for transcriptomics and proteomics. In Silico Biology, 2005, 5, 295-311.	0.9	2
59	Comparative Genomics for the Investigation of Autoimmune Diseases. Current Pharmaceutical Design, 2006, 12, 3707-22.	1.9	1