Marcel H Schulz

List of Publications by Year
in descending order

89 papers	8,576 citations	230014 27 h-index	62345 84 g-index
110 all docs	110 docs citations	110 times ranked	22010 citing authors

#	Article	IF	Citations
1	Comparative analysis of common alignment tools for single-cell RNA sequencing. GigaScience, 2022, 11, .	3.3	17
2	Energy efficient convolutional neural networks for arrhythmia detection. Array, 2022, 13, 100127.	2.5	2
3	Nuclear receptor activation shapes spatial genome organization essential for gene expression control: lessons learned from the vitamin D receptor. Nucleic Acids Research, 2022, 50, 3745-3763.	6.5	8
4	Broad domains of histone marks in the highly compact <i>Paramecium</i> macronuclear genome. Genome Research, 2022, 32, 710-725.	2.4	7
5	SPONGEdb: a pan-cancer resource for competing endogenous RNA interactions. NAR Cancer, 2021, 3, zcaa042.	1.6	14
6	Single cell sequencing reveals endothelial plasticity with transient mesenchymal activation after myocardial infarction. Nature Communications, 2021, 12, 681.	5.8	158
7	A hierarchical regulatory network analysis of the vitamin D induced transcriptome reveals novel regulators and complete VDR dependency in monocytes. Scientific Reports, 2021, 11, 6518.	1.6	28
8	Computational prediction of CRISPR-impaired non-coding regulatory regions. Biological Chemistry, 2021, 402, 973-982.	1.2	1
9	Machine learning for deciphering cell heterogeneity and gene regulation. Nature Computational Science, 2021, 1, 183-191.	3.8	14
10	CpG content-dependent associations between transcription factors and histone modifications. PLoS ONE, 2021, 16, e0249985.	1.1	0
11	Fostering accessible online education using Galaxy as an e-learning platform. PLoS Computational Biology, 2021, 17, e1008923.	1.5	15
12	Bioinformatics in theory and application– highlights of the 36th German Conference on Bioinformatics. Biological Chemistry, 2021, 402, 869-870.	1.2	1
13	Machine learning based disease prediction from genotype data. Biological Chemistry, 2021, 402, 871-885.	1.2	7
14	Integrative analysis of epigenetics data identifies gene-specific regulatory elements. Nucleic Acids Research, 2021, 49, 10397-10418.	6.5	14
15	Dysregulation of cholesterol homeostasis in human lung cancer tissue and tumour-associated macrophages. EBioMedicine, 2021, 72, 103578.	2.7	43
16	Two Piwis with Ago-like functions silence somatic genes at the chromatin level. RNA Biology, 2021, 18, 757-769.	1.5	5
17	Fast detection of differential chromatin domains with SCIDDO. Bioinformatics, 2021, 37, 1198-1205.	1.8	6
18	Prediction of single-cell gene expression for transcription factor analysis. GigaScience, 2020, 9, .	3.3	11

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19	Deletion of NoxO1 limits atherosclerosis development in female mice. Redox Biology, 2020, 37, 101713.	3.9	13
20	Yeast Viral Killer Toxin K1 Induces Specific Host Cell Adaptions via Intrinsic Selection Pressure. Applied and Environmental Microbiology, 2020, 86, .	1.4	8
21	Feeding exogenous dsRNA interferes with endogenous sRNA accumulation in Paramecium. DNA Research, 2020, 27, .	1.5	4
22	EpiRegio: analysis and retrieval of regulatory elements linked to genes. Nucleic Acids Research, 2020, 48, W193-W199.	6.5	26
23	Altered glucocorticoid metabolism represents a feature of macroph–aging. Aging Cell, 2020, 19, e13156.	3.0	24
24	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. Journal of Computational Biology, 2020, 27, 330-341.	0.8	0
25	Integrative prediction of gene expression with chromatin accessibility and conformation data. Epigenetics and Chromatin, 2020, 13, 4.	1.8	21
26	SRSF7 maintains its homeostasis through the expression of Split-ORFs and nuclear body assembly. Nature Structural and Molecular Biology, 2020, 27, 260-273.	3.6	51
27	On the problem of confounders in modeling gene expression. Bioinformatics, 2019, 35, 711-719.	1.8	11
28	The lncRNA Locus Handsdown Regulates Cardiac Gene Programs and Is Essential for Early Mouse Development. Developmental Cell, 2019, 50, 644-657.e8.	3.1	66
29	Large-scale inference of competing endogenous RNA networks with sparse partial correlation. Bioinformatics, 2019, 35, i596-i604.	1.8	50
30	Transcriptomics of a KDELR1 knockout cell line reveals modulated cell adhesion properties. Scientific Reports, 2019, 9, 10611.	1.6	7
31	Exogenous RNAi mechanisms contribute to transcriptome adaptation by phased siRNA clusters in Paramecium. Nucleic Acids Research, 2019, 47, 8036-8049.	6.5	21
32	The mRNA-binding Protein TTP/ZFP36 in Hepatocarcinogenesis and Hepatocellular Carcinoma. Cancers, 2019, 11, 1754.	1.7	20
33	Phenotypic Plasticity of Fibroblasts during Mammary Carcinoma Development. International Journal of Molecular Sciences, 2019, 20, 4438.	1.8	19
34	Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. Nucleic Acids Research, 2019, 47, 10580-10596.	6.5	31
35	Transcriptome Kinetics of Saccharomyces cerevisiae in Response to Viral Killer Toxin K1. Frontiers in Microbiology, 2019, 10, 1102.	1.5	5
36	Identification of transcription factor binding sites using ATAC-seq. Genome Biology, 2019, 20, 45.	3.8	346

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37	Improving in-silico normalization using read weights. Scientific Reports, 2019, 9, 5133.	1.6	9
38	Improved linking of motifs to their TFs using domain information. Bioinformatics, 2019, 36, 1655-1662.	1.8	1
39	Temporal enhancer profiling of parallel lineages identifies AHR and GLIS1 as regulators of mesenchymal multipotency. Nucleic Acids Research, 2019, 47, 1141-1163.	6.5	16
40	TEPIC 2â€"an extended framework for transcription factor binding prediction and integrative epigenomic analysis. Bioinformatics, 2019, 35, 1608-1609.	1.8	34
41	Hepatocellular Carcinoma and Nuclear Paraspeckles: Induction in Chemoresistance and Prediction for Poor Survival. Cellular Physiology and Biochemistry, 2019, 52, 787-801.	1.1	29
42	Automated analysis of small RNA datasets with RAPID. PeerJ, 2019, 7, e6710.	0.9	8
43	JAMI: fast computation of conditional mutual information for ceRNA network analysis. Bioinformatics, 2018, 34, 3050-3051.	1.8	13
44	More than the â€œKiller Traitâ€ Infection with the Bacterial Endosymbiont Caedibacter taeniospiralis Causes Transcriptomic Modulation in Paramecium Host. Genome Biology and Evolution, 2018, 10, 646-656.	1.1	30
45	Integrative analysis of single-cell expression data reveals distinct regulatory states in bidirectional promoters. Epigenetics and Chromatin, 2018, 11, 66.	1.8	6
46	Analysis of Cell Type-Specific Effects of MicroRNA-92a Provides Novel Insights Into Target Regulation and Mechanism of Action. Circulation, 2018, 138, 2545-2558.	1.6	61
47	An ontology-based method for assessing batch effect adjustment approaches in heterogeneous datasets. Bioinformatics, 2018, 34, i908-i916.	1.8	10
48	Environmental Temperature Controls Accumulation of Transacting siRNAs Involved in Heterochromatin Formation. Genes, 2018, 9, 117.	1.0	7
49	Transgenic expression of the RNA binding protein IMP2 stabilizes miRNA targets in murine microsteatosis. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 3099-3108.	1.8	10
50	<i>In silico</i> read normalization using set multi-cover optimization. Bioinformatics, 2018, 34, 3273-3280.	1.8	8
51	Predicting transcription factor binding using ensemble random forest models. F1000Research, 2018, 7, 1603.	0.8	8
52	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. Lecture Notes in Computer Science, 2018, , 21-36.	1.0	0
53	RegulatorTrail: a web service for the identification of key transcriptional regulators. Nucleic Acids Research, 2017, 45, W146-W153.	6.5	21
54	DNA-Seq Error Correction Based on Substring Indices. , 2017, , 147-166.		0

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55	Probabilistic Models for Error Correction of Nonuniform Sequencing Data. , 2017, , 131-145.		0
56	Combining transcription factor binding affinities with open-chromatin data for accurate gene expression prediction. Nucleic Acids Research, 2017, 45, 54-66.	6.5	112
57	The long non-coding RNA H19 suppresses carcinogenesis and chemoresistance in hepatocellular carcinoma. Cell Stress, 2017, 1, 37-54.	1.4	50
58	Epigenomic Profiling of Human CD4+ T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. Immunity, 2016, 45, 1148-1161.	6.6	174
59	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
60	Informed *k*mer selection for *de novo* transcriptome assembly. Bioinformatics, 2016, 32, 1670-1677.	1.8	25
61	Two sets of RNAi components are required for heterochromatin formation *in trans* triggered by truncated transgenes. Nucleic Acids Research, 2016, 44, 5908-5923.	6.5	17
62	A general concept for consistent documentation of computational analyses. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav050.	1.4	9
63	De novo ChIP-seq analysis. Genome Biology, 2015, 16, 205.	3.8	10
64	Epigenetic regulation of serotype expression antagonizes transcriptome dynamics in *Paramecium tetraurelia*. DNA Research, 2015, 22, 293-305.	1.5	18
65	Letting the data speak for themselves: a fully Bayesian approach to transcriptome assembly. Genome Biology, 2014, 15, 498.	3.8	1
66	Fiona: a parallel and automatic strategy for read error correction. Bioinformatics, 2014, 30, i356-i363.	1.8	59
67	Assessment of transcript reconstruction methods for RNA-seq. Nature Methods, 2013, 10, 1177-1184.	9.0	679
68	Probabilistic error correction for RNA sequencing. Nucleic Acids Research, 2013, 41, e109-e109.	6.5	68
69	Reconstructing dynamic microRNA-regulated interaction networks. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15686-15691.	3.3	59
70	Bayesian ontology querying for accurate and noise-tolerant semantic searches. Bioinformatics, 2012, 28, 2502-2508.	1.8	55
71	Detecting genomic indel variants with exact breakpoints in single- and paired-end sequencing data using SplazerS. Bioinformatics, 2012, 28, 619-627.	1.8	95
72	Estimation of pairwise sequence similarity of mammalian enhancers with word neighbourhood counts. Bioinformatics, 2012, 28, 656-663.	1.8	45

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73	*Oases:* robust *de novo* RNA-seq assembly across the dynamic range of expression levels. Bioinformatics, 2012, 28, 1086-1092.	1.8	1,351
74	DREM 2.0: Improved reconstruction of dynamic regulatory networks from time-series expression data. BMC Systems Biology, 2012, 6, 104.	3.0	118
75	DECOD: fast and accurate discriminative DNA motif finding. Bioinformatics, 2011, 27, 2361-2367.	1.8	38
76	Exact score distribution computation for ontological similarity searches. BMC Bioinformatics, 2011, 12, 441.	1.2	15
77	A tandem sequence motif acts as a distance-dependent enhancer in a set of genes involved in translation by binding the proteins NonO and SFPQ. BMC Genomics, 2011, 12, 624.	1.2	10
78	Integrative analysis of genomic, functional and protein interaction data predicts long-range enhancer-target gene interactions. Nucleic Acids Research, 2011, 39, 2492-2502.	6.5	22
79	Prediction of alternative isoforms from exon expression levels in RNA-Seq experiments. Nucleic Acids Research, 2010, 38, e112-e112.	6.5	134
80	Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. Bioinformatics, 2009, 25, 2865-2871.	1.8	1,811
81	Clinical Diagnostics in Human Genetics with Semantic Similarity Searches in Ontologies. American Journal of Human Genetics, 2009, 85, 457-464.	2.6	444
82	Short ultraconserved promoter regions delineate a class of preferentially expressed alternatively spliced transcripts. Genomics, 2009, 94, 308-316.	1.3	11
83	Exact Score Distribution Computation for Similarity Searches in Ontologies. Lecture Notes in Computer Science, 2009, , 298-309.	1.0	3
84	A short ultraconserved sequence drives transcription from an alternate FBN1 promoter. International Journal of Biochemistry and Cell Biology, 2008, 40, 638-650.	1.2	15
85	A Global View of Gene Activity and Alternative Splicing by Deep Sequencing of the Human Transcriptome. Science, 2008, 321, 956-960.	6.0	1,164
86	Mapping translocation breakpoints by next-generation sequencing. Genome Research, 2008, 18, 1143-1149.	2.4	118
87	The generalised k-Truncated Suffix Tree for time-and space-efficient searches in multiple DNA or protein sequences. International Journal of Bioinformatics Research and Applications, 2008, 4, 81.	0.1	19
88	Efficient String Mining under Constraints Via the Deferred Frequency Index. Lecture Notes in Computer Science, 2008, , 374-388.	1.0	6
89	Fast and Adaptive Variable Order Markov Chain Construction. Lecture Notes in Computer Science, 2008, , 306-317.	1.0	15