

# Marcel H Schulz

## List of Publications by Year in descending order

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Version: 2024-02-01

89  
papers

8,576  
citations

201674

27  
h-index

54911

84  
g-index

110  
all docs

110  
docs citations

110  
times ranked

19734  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. <i>Bioinformatics</i> , 2009, 25, 2865-2871.	4.1	1,811
2	Oases: robust <i>de novo</i> RNA-seq assembly across the dynamic range of expression levels. <i>Bioinformatics</i> , 2012, 28, 1086-1092.	4.1	1,351
3	A Global View of Gene Activity and Alternative Splicing by Deep Sequencing of the Human Transcriptome. <i>Science</i> , 2008, 321, 956-960.	12.6	1,164
4	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013, 10, 1177-1184.	19.0	679
5	Clinical Diagnostics in Human Genetics with Semantic Similarity Searches in Ontologies. <i>American Journal of Human Genetics</i> , 2009, 85, 457-464.	6.2	444
6	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
7	Identification of transcription factor binding sites using ATAC-seq. <i>Genome Biology</i> , 2019, 20, 45.	8.8	346
8	Epigenomic Profiling of Human CD4+ T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. <i>Immunity</i> , 2016, 45, 1148-1161.	14.3	174
9	Single cell sequencing reveals endothelial plasticity with transient mesenchymal activation after myocardial infarction. <i>Nature Communications</i> , 2021, 12, 681.	12.8	158
10	Prediction of alternative isoforms from exon expression levels in RNA-Seq experiments. <i>Nucleic Acids Research</i> , 2010, 38, e112-e112.	14.5	134
11	Mapping translocation breakpoints by next-generation sequencing. <i>Genome Research</i> , 2008, 18, 1143-1149.	5.5	118
12	DREM 2.0: Improved reconstruction of dynamic regulatory networks from time-series expression data. <i>BMC Systems Biology</i> , 2012, 6, 104.	3.0	118
13	Combining transcription factor binding affinities with open-chromatin data for accurate gene expression prediction. <i>Nucleic Acids Research</i> , 2017, 45, 54-66.	14.5	112
14	Detecting genomic indel variants with exact breakpoints in single- and paired-end sequencing data using SplazerS. <i>Bioinformatics</i> , 2012, 28, 619-627.	4.1	95
15	Probabilistic error correction for RNA sequencing. <i>Nucleic Acids Research</i> , 2013, 41, e109-e109.	14.5	68
16	The lncRNA Locus Handsdown Regulates Cardiac Gene Programs and Is Essential for Early Mouse Development. <i>Developmental Cell</i> , 2019, 50, 644-657.e8.	7.0	66
17	Analysis of Cell Type-Specific Effects of MicroRNA-92a Provides Novel Insights Into Target Regulation and Mechanism of Action. <i>Circulation</i> , 2018, 138, 2545-2558.	1.6	61
18	Reconstructing dynamic microRNA-regulated interaction networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15686-15691.	7.1	59

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19	Fiona: a parallel and automatic strategy for read error correction. <i>Bioinformatics</i> , 2014, 30, i356-i363.	4.1	59
20	Bayesian ontology querying for accurate and noise-tolerant semantic searches. <i>Bioinformatics</i> , 2012, 28, 2502-2508.	4.1	55
21	SRSF7 maintains its homeostasis through the expression of Split-ORFs and nuclear body assembly. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 260-273.	8.2	51
22	Large-scale inference of competing endogenous RNA networks with sparse partial correlation. <i>Bioinformatics</i> , 2019, 35, i596-i604.	4.1	50
23	The long non-coding RNA H19 suppresses carcinogenesis and chemoresistance in hepatocellular carcinoma. <i>Cell Stress</i> , 2017, 1, 37-54.	3.2	50
24	Estimation of pairwise sequence similarity of mammalian enhancers with word neighbourhood counts. <i>Bioinformatics</i> , 2012, 28, 656-663.	4.1	45
25	Dysregulation of cholesterol homeostasis in human lung cancer tissue and tumour-associated macrophages. <i>EBioMedicine</i> , 2021, 72, 103578.	6.1	43
26	DECOD: fast and accurate discriminative DNA motif finding. <i>Bioinformatics</i> , 2011, 27, 2361-2367.	4.1	38
27	TEPIC 2 – an extended framework for transcription factor binding prediction and integrative epigenomic analysis. <i>Bioinformatics</i> , 2019, 35, 1608-1609.	4.1	34
28	Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. <i>Nucleic Acids Research</i> , 2019, 47, 10580-10596.	14.5	31
29	More than the ‘Killer Trait’ Infection with the Bacterial Endosymbiont <i>Caedibacter taeniospiralis</i> Causes Transcriptomic Modulation in <i>Paramecium</i> Host. <i>Genome Biology and Evolution</i> , 2018, 10, 646-656.	2.5	30
30	Hepatocellular Carcinoma and Nuclear Paraspeckles: Induction in Chemoresistance and Prediction for Poor Survival. <i>Cellular Physiology and Biochemistry</i> , 2019, 52, 787-801.	1.6	29
31	A hierarchical regulatory network analysis of the vitamin D induced transcriptome reveals novel regulators and complete VDR dependency in monocytes. <i>Scientific Reports</i> , 2021, 11, 6518.	3.3	28
32	EpiRegio: analysis and retrieval of regulatory elements linked to genes. <i>Nucleic Acids Research</i> , 2020, 48, W193-W199.	14.5	26
33	Informed k-mer selection for de novo transcriptome assembly. <i>Bioinformatics</i> , 2016, 32, 1670-1677.	4.1	25
34	Altered glucocorticoid metabolism represents a feature of macrophage aging. <i>Aging Cell</i> , 2020, 19, e13156.	6.7	24
35	Integrative analysis of genomic, functional and protein interaction data predicts long-range enhancer-target gene interactions. <i>Nucleic Acids Research</i> , 2011, 39, 2492-2502.	14.5	22
36	RegulatorTrail: a web service for the identification of key transcriptional regulators. <i>Nucleic Acids Research</i> , 2017, 45, W146-W153.	14.5	21

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37	Exogenous RNAi mechanisms contribute to transcriptome adaptation by phased siRNA clusters in <i>Paramecium</i> . <i>Nucleic Acids Research</i> , 2019, 47, 8036-8049.	14.5	21
38	Integrative prediction of gene expression with chromatin accessibility and conformation data. <i>Epigenetics and Chromatin</i> , 2020, 13, 4.	3.9	21
39	The mRNA-binding Protein TTP/ZFP36 in Hepatocarcinogenesis and Hepatocellular Carcinoma. <i>Cancers</i> , 2019, 11, 1754.	3.7	20
40	The generalised k-Truncated Suffix Tree for time-and space-efficient searches in multiple DNA or protein sequences. <i>International Journal of Bioinformatics Research and Applications</i> , 2008, 4, 81.	0.2	19
41	Phenotypic Plasticity of Fibroblasts during Mammary Carcinoma Development. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4438.	4.1	19
42	Epigenetic regulation of serotype expression antagonizes transcriptome dynamics in <i>Paramecium tetraurelia</i> . <i>DNA Research</i> , 2015, 22, 293-305.	3.4	18
43	Two sets of RNAi components are required for heterochromatin formation in trans triggered by truncated transgenes. <i>Nucleic Acids Research</i> , 2016, 44, 5908-5923.	14.5	17
44	Comparative analysis of common alignment tools for single-cell RNA sequencing. <i>GigaScience</i> , 2022, 11, .	6.4	17
45	Temporal enhancer profiling of parallel lineages identifies AHR and GLIS1 as regulators of mesenchymal multipotency. <i>Nucleic Acids Research</i> , 2019, 47, 1141-1163.	14.5	16
46	A short ultraconserved sequence drives transcription from an alternate FBN1 promoter. <i>International Journal of Biochemistry and Cell Biology</i> , 2008, 40, 638-650.	2.8	15
47	Exact score distribution computation for ontological similarity searches. <i>BMC Bioinformatics</i> , 2011, 12, 441.	2.6	15
48	Fostering accessible online education using Galaxy as an e-learning platform. <i>PLoS Computational Biology</i> , 2021, 17, e1008923.	3.2	15
49	Fast and Adaptive Variable Order Markov Chain Construction. <i>Lecture Notes in Computer Science</i> , 2008, , 306-317.	1.3	15
50	SPONGEdb: a pan-cancer resource for competing endogenous RNA interactions. <i>NAR Cancer</i> , 2021, 3, zcaa042.	3.1	14
51	Machine learning for deciphering cell heterogeneity and gene regulation. <i>Nature Computational Science</i> , 2021, 1, 183-191.	8.0	14
52	Integrative analysis of epigenetics data identifies gene-specific regulatory elements. <i>Nucleic Acids Research</i> , 2021, 49, 10397-10418.	14.5	14
53	JAMI: fast computation of conditional mutual information for ceRNA network analysis. <i>Bioinformatics</i> , 2018, 34, 3050-3051.	4.1	13
54	Deletion of NoxO1 limits atherosclerosis development in female mice. <i>Redox Biology</i> , 2020, 37, 101713.	9.0	13

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55	Short ultraconserved promoter regions delineate a class of preferentially expressed alternatively spliced transcripts. <i>Genomics</i> , 2009, 94, 308-316.	2.9	11
56	On the problem of confounders in modeling gene expression. <i>Bioinformatics</i> , 2019, 35, 711-719.	4.1	11
57	Prediction of single-cell gene expression for transcription factor analysis. <i>GigaScience</i> , 2020, 9, .	6.4	11
58	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. <i>BMC Genomics</i> , 2011, 12, 624.	2.8	10
59	De novo ChIP-seq analysis. <i>Genome Biology</i> , 2015, 16, 205.	8.8	10
60	An ontology-based method for assessing batch effect adjustment approaches in heterogeneous datasets. <i>Bioinformatics</i> , 2018, 34, i908-i916.	4.1	10
61	Transgenic expression of the RNA binding protein IMP2 stabilizes miRNA targets in murine microsteatosis. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 3099-3108.	3.8	10
62	A general concept for consistent documentation of computational analyses. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav050.	3.0	9
63	Improving in-silico normalization using read weights. <i>Scientific Reports</i> , 2019, 9, 5133.	3.3	9
64	<i>In silico</i> read normalization using set multi-cover optimization. <i>Bioinformatics</i> , 2018, 34, 3273-3280.	4.1	8
65	Yeast Viral Killer Toxin K1 Induces Specific Host Cell Adaptions via Intrinsic Selection Pressure. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	8
66	Predicting transcription factor binding using ensemble random forest models. <i>F1000Research</i> , 2018, 7, 1603.	1.6	8
67	Automated analysis of small RNA datasets with RAPID. <i>PeerJ</i> , 2019, 7, e6710.	2.0	8
68	Nuclear receptor activation shapes spatial genome organization essential for gene expression control: lessons learned from the vitamin D receptor. <i>Nucleic Acids Research</i> , 2022, 50, 3745-3763.	14.5	8
69	Environmental Temperature Controls Accumulation of Transacting siRNAs Involved in Heterochromatin Formation. <i>Genes</i> , 2018, 9, 117.	2.4	7
70	Transcriptomics of a KDELR1 knockout cell line reveals modulated cell adhesion properties. <i>Scientific Reports</i> , 2019, 9, 10611.	3.3	7
71	Machine learning based disease prediction from genotype data. <i>Biological Chemistry</i> , 2021, 402, 871-885.	2.5	7
72	Broad domains of histone marks in the highly compact <i>Paramecium</i> macronuclear genome. <i>Genome Research</i> , 2022, 32, 710-725.	5.5	7

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73	Integrative analysis of single-cell expression data reveals distinct regulatory states in bidirectional promoters. <i>Epigenetics and Chromatin</i> , 2018, 11, 66.	3.9	6
74	Efficient String Mining under Constraints Via the Deferred Frequency Index. <i>Lecture Notes in Computer Science</i> , 2008, , 374-388.	1.3	6
75	Fast detection of differential chromatin domains with SCIDDO. <i>Bioinformatics</i> , 2021, 37, 1198-1205.	4.1	6
76	Transcriptome Kinetics of <i>Saccharomyces cerevisiae</i> in Response to Viral Killer Toxin K1. <i>Frontiers in Microbiology</i> , 2019, 10, 1102.	3.5	5
77	Two Piwis with Ago-like functions silence somatic genes at the chromatin level. <i>RNA Biology</i> , 2021, 18, 757-769.	3.1	5
78	Feeding exogenous dsRNA interferes with endogenous sRNA accumulation in <i>Paramecium</i> . <i>DNA Research</i> , 2020, 27, .	3.4	4
79	Exact Score Distribution Computation for Similarity Searches in Ontologies. <i>Lecture Notes in Computer Science</i> , 2009, , 298-309.	1.3	3
80	Energy efficient convolutional neural networks for arrhythmia detection. <i>Array</i> , 2022, 13, 100127.	4.0	2
81	Letting the data speak for themselves: a fully Bayesian approach to transcriptome assembly. <i>Genome Biology</i> , 2014, 15, 498.	8.8	1
82	Improved linking of motifs to their TFs using domain information. <i>Bioinformatics</i> , 2019, 36, 1655-1662.	4.1	1
83	Computational prediction of CRISPR-impaired non-coding regulatory regions. <i>Biological Chemistry</i> , 2021, 402, 973-982.	2.5	1
84	Bioinformatics in theory and application“ highlights of the 36th German Conference on Bioinformatics. <i>Biological Chemistry</i> , 2021, 402, 869-870.	2.5	1
85	DNA-Seq Error Correction Based on Substring Indices. , 2017, , 147-166.		0
86	Probabilistic Models for Error Correction of Nonuniform Sequencing Data. , 2017, , 131-145.		0
87	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. <i>Journal of Computational Biology</i> , 2020, 27, 330-341.	1.6	0
88	CpG content-dependent associations between transcription factors and histone modifications. <i>PLoS ONE</i> , 2021, 16, e0249985.	2.5	0
89	Chromatyping: Reconstructing Nucleosome Profiles from NOMe Sequencing Data. <i>Lecture Notes in Computer Science</i> , 2018, , 21-36.	1.3	0