

Sven Rahmann

List of Publications by Year in descending order

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Version: 2024-02-01

113
papers

7,044
citations

126907

33
h-index

76900

74
g-index

144
all docs

144
docs citations

144
times ranked

13990
citing authors

#	ARTICLE	IF	CITATIONS
1	Snakemake—a scalable bioinformatics workflow engine. <i>Bioinformatics</i> , 2012, 28, 2520-2522.	4.1	2,041
2	Sustainable data analysis with Snakemake. <i>F1000Research</i> , 2021, 10, 33.	1.6	642
3	Exome sequencing identifies recurrent somatic mutations in EIF1AX and SF3B1 in uveal melanoma with disomy 3. <i>Nature Genetics</i> , 2013, 45, 933-936.	21.4	436
4	Mutational dynamics between primary and relapse neuroblastomas. <i>Nature Genetics</i> , 2015, 47, 872-877.	21.4	253
5	A mechanistic classification of clinical phenotypes in neuroblastoma. <i>Science</i> , 2018, 362, 1165-1170.	12.6	213
6	Computational pan-genomics: status, promises and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw089.	6.5	207
7	HMM Logos for visualization of protein families. <i>BMC Bioinformatics</i> , 2004, 5, 7.	2.6	195
8	A comprehensive molecular study on Coffin—Siris and Nicolaides—Baraitser syndromes identifies a broad molecular and clinical spectrum converging on altered chromatin remodeling. <i>Human Molecular Genetics</i> , 2013, 22, 5121-5135.	2.9	190
9	Sustainable data analysis with Snakemake. <i>F1000Research</i> , 2021, 10, 33.	1.6	188
10	Deep sequencing reveals differential expression of microRNAs in favorable versus unfavorable neuroblastoma. <i>Nucleic Acids Research</i> , 2010, 38, 5919-5928.	14.5	183
11	N6-Adenosine Methylation in MiRNAs. <i>PLoS ONE</i> , 2015, 10, e0118438.	2.5	115
12	Human <sc>TLR</sc> 8 senses <sc>UR</sc> / <sc>URR</sc> motifs in bacterial and mitochondrial <sc>RNA</sc>. <i>EMBO Reports</i> , 2015, 16, 1656-1663.	4.5	110
13	Supratentorial ependymomas of childhood carry C11orf95—RELA fusions leading to pathological activation of the NF- κ B signaling pathway. <i>Acta Neuropathologica</i> , 2014, 127, 609-611.	7.7	103
14	Partitioning biological data with transitivity clustering. <i>Nature Methods</i> , 2010, 7, 419-420.	19.0	84
15	SimLoRD: Simulation of Long Read Data. <i>Bioinformatics</i> , 2016, 32, 2704-2706.	4.1	81
16	On the Power of Profiles for Transcription Factor Binding Site Detection. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2003, 2, Article7.	0.6	80
17	Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016, 9, 33.	3.9	73
18	Effects of Silver Nitrate and Silver Nanoparticles on a Planktonic Community: General Trends after Short-Term Exposure. <i>PLoS ONE</i> , 2014, 9, e95340.	2.5	65

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19	Non-symmetric score matrices and the detection of homologous transmembrane proteins. <i>Bioinformatics</i> , 2001, 17, S182-S189.	4.1	63
20	Differentiation of chronic obstructive pulmonary disease (COPD) including lung cancer from healthy control group by breath analysis using ion mobility spectrometry. <i>International Journal for Ion Mobility Spectrometry</i> , 2010, 13, 131-139.	1.4	59
21	Large scale clustering of protein sequences with FORCE -A layout based heuristic for weighted cluster editing. <i>BMC Bioinformatics</i> , 2007, 8, 396.	2.6	56
22	Oto-facial syndrome and esophageal atresia, intellectual disability and zygomatic anomalies - expanding the phenotypes associated with EFTUD2 mutations. <i>Orphanet Journal of Rare Diseases</i> , 2013, 8, 110.	2.7	56
23	Algorithms for subsequence combinatorics. <i>Theoretical Computer Science</i> , 2008, 409, 394-404.	0.9	53
24	CoryneRegNet: An ontology-based data warehouse of corynebacterial transcription factors and regulatory networks. <i>BMC Genomics</i> , 2006, 7, 24.	2.8	52
25	Efficient exact motif discovery. <i>Bioinformatics</i> , 2009, 25, i356-i364.	4.1	48
26	Natural similarity measures between position frequency matrices with an application to clustering. <i>Bioinformatics</i> , 2008, 24, 350-357.	4.1	47
27	Accurate and robust phylogeny estimation based on profile distances: a study of the Chlorophyceae (Chlorophyta). <i>BMC Evolutionary Biology</i> , 2004, 4, 20.	3.2	43
28	EXACT AND HEURISTIC ALGORITHMS FOR WEIGHTED CLUSTER EDITING. , 2007, , .		43
29	T-Reg Comparator: an analysis tool for the comparison of position weight matrices. <i>Nucleic Acids Research</i> , 2005, 33, W438-W441.	14.5	42
30	Evolution of heterotrophy in chrysophytes as reflected by comparative transcriptomics. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	40
31	Exact ILP solutions for phylogenetic minimum flip problems. , 2010, , .		39
32	Impact of RAS mutation subtype on clinical outcome—a cross-entity comparison of patients with advanced non-small cell lung cancer and colorectal cancer. <i>Oncogene</i> , 2019, 38, 2953-2966.	5.9	38
33	Comprehensive transcriptome analysis provides new insights into nutritional strategies and phylogenetic relationships of chrysophytes. <i>PeerJ</i> , 2017, 5, e2832.	2.0	38
34	Fast Large Scale Oligonucleotide Selection Using the Longest Common Factor Approach. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 343-361.	0.8	37
35	Massive parallel bisulfite sequencing of CG-rich DNA fragments reveals that methylation of many X-chromosomal CpG islands in female blood DNA is incomplete. <i>Human Molecular Genetics</i> , 2009, 18, 1439-1448.	2.9	37
36	Recurrent alterations of <i>TNFAIP3</i> (A20) in T-cell large granular lymphocytic leukemia. <i>International Journal of Cancer</i> , 2016, 138, 121-124.	5.1	36

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37	CoryneRegNet 3.0 – An interactive systems biology platform for the analysis of gene regulatory networks in corynebacteria and Escherichia coli. <i>Journal of Biotechnology</i> , 2007, 129, 279-289.	3.8	32
38	Machine learning reveals a PD-L1 – independent prediction of response to immunotherapy of non-small cell lung cancer by gene expression context. <i>European Journal of Cancer</i> , 2020, 140, 76-85.	2.8	30
39	CDKN2A deletion in supratentorial ependymoma with RELA alteration indicates a dismal prognosis: a retrospective analysis of the HIT ependymoma trial cohort. <i>Acta Neuropathologica</i> , 2020, 140, 405-407.	7.7	30
40	The shortest common supersequence problem in a microarray production setting. <i>Bioinformatics</i> , 2003, 19, ii156-ii161.	4.1	29
41	Reliable transfer of transcriptional gene regulatory networks between taxonomically related organisms. <i>BMC Systems Biology</i> , 2009, 3, 8.	3.0	28
42	Locus-Specific DNA Methylation Analysis by Targeted Deep Bisulfite Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1767, 351-366.	0.9	28
43	Circulating microRNA biomarkers for metastatic disease in neuroblastoma patients. <i>JCI Insight</i> , 2018, 3, .	5.0	28
44	The Role of Pre-existing Cross-Reactive Central Memory CD4 T-Cells in Vaccination With Previously Unseen Influenza Strains. <i>Frontiers in Immunology</i> , 2019, 10, 593.	4.8	27
45	A germ cell – specific ageing pattern in otherwise healthy men. <i>Aging Cell</i> , 2020, 19, e13242.	6.7	27
46	Next – generation RNA sequencing reveals differential expression of MYCN target genes and suggests the mTOR pathway as a promising therapy target in MYCN – amplified neuroblastoma. <i>International Journal of Cancer</i> , 2013, 132, E106-15.	5.1	26
47	wg-blimp: an end-to-end analysis pipeline for whole genome bisulfite sequencing data. <i>BMC Bioinformatics</i> , 2020, 21, 169.	2.6	26
48	Modelling cross – hybridization on phylogenetic DNA microarrays increases the detection power of closely related species. <i>Molecular Ecology Resources</i> , 2009, 9, 83-93.	4.8	24
49	Peak Detection Method Evaluation for Ion Mobility Spectrometry by Using Machine Learning Approaches. <i>Metabolites</i> , 2013, 3, 277-293.	2.9	24
50	Trade – off between taxon diversity and functional diversity in European lake ecosystems. <i>Molecular Ecology</i> , 2016, 25, 5876-5888.	3.9	24
51	Integer linear programming approaches for non-unique probe selection. <i>Discrete Applied Mathematics</i> , 2007, 155, 840-856.	0.9	22
52	Towards the integrated analysis, visualization and reconstruction of microbial gene regulatory networks. <i>Briefings in Bioinformatics</i> , 2008, 10, 75-83.	6.5	21
53	Cancer evolution, mutations, and clonal selection in relapse neuroblastoma. <i>Cell and Tissue Research</i> , 2018, 372, 263-268.	2.9	21
54	Improved risk-stratification for posterior fossa ependymoma of childhood considering clinical, histological and genetic features – a retrospective analysis of the HIT ependymoma trial cohort. <i>Acta Neuropathologica Communications</i> , 2019, 7, 181.	5.2	21

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55	IMS2 – An integrated medical software system for early lung cancer detection using ion mobility spectrometry data of human breath. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 186-197.	1.5	20
56	Regions of common inter-individual DNA methylation differences in human monocytes: genetic basis and potential function. <i>Epigenetics and Chromatin</i> , 2017, 10, 37.	3.9	20
57	A hybrid parameter estimation algorithm for beta mixtures and applications to methylation state classification. <i>Algorithms for Molecular Biology</i> , 2017, 12, 21.	1.2	19
58	Machine learning-based predictors for immune checkpoint inhibitor therapy of non-small-cell lung cancer. <i>Annals of Oncology</i> , 2019, 30, 655-657.	1.2	18
59	Combinatorics of periods in strings. <i>Journal of Combinatorial Theory - Series A</i> , 2003, 104, 95-113.	0.8	17
60	A modular computational framework for automated peak extraction from ion mobility spectra. <i>BMC Bioinformatics</i> , 2014, 15, 25.	2.6	16
61	Dynamic Programming Algorithms for Two Statistical Problems in Computational Biology. <i>Lecture Notes in Computer Science</i> , 2003, , 151-164.	1.3	15
62	Epitope similarity cannot explain the pre-formed T cell immunity towards structural SARS-CoV-2 proteins. <i>Scientific Reports</i> , 2020, 10, 18995.	3.3	15
63	Probabilistic Arithmetic Automata and Their Application to Pattern Matching Statistics. , 2008, , 95-106.		15
64	Compound Poisson Approximation of the Number of Occurrences of a Position Frequency Matrix (PFM) on Both Strands. <i>Journal of Computational Biology</i> , 2008, 15, 547-564.	1.6	14
65	On the Distribution of the Number of Missing Words in Random Texts. <i>Combinatorics Probability and Computing</i> , 2003, 12, .	1.3	13
66	Exact and heuristic algorithms for weighted cluster editing. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2007, 6, 391-401.	0.4	13
67	Detecting species-site dependencies in large multiple sequence alignments. <i>Nucleic Acids Research</i> , 2009, 37, 5959-5968.	14.5	12
68	CoryneRegNet 2: An Integrative Bioinformatics Approach for Reconstruction and Comparison of Transcriptional Regulatory Networks in Prokaryotes. <i>Journal of Integrative Bioinformatics</i> , 2006, 3, 1-13.	1.5	11
69	CoryneCenter – An online resource for the integrated analysis of corynebacterial genome and transcriptome data. <i>BMC Systems Biology</i> , 2007, 1, 55.	3.0	11
70	High-throughput microarray technology in diagnostics of enterobacteria based on genome-wide probe selection and regression analysis. <i>BMC Genomics</i> , 2010, 11, 591.	2.8	11
71	Probabilistic Arithmetic Automata and Their Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1737-1750.	3.0	11
72	Identifying transcriptional miRNA biomarkers by integrating high-throughput sequencing and real-time PCR data. <i>Methods</i> , 2013, 59, 154-163.	3.8	10

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73	Fast lightweight accurate xenograft sorting. <i>Algorithms for Molecular Biology</i> , 2021, 16, 2.	1.2	9
74	Decoding non-unique oligonucleotide hybridization experiments of targets related by a phylogenetic tree. <i>Bioinformatics</i> , 2006, 22, e424-e430.	4.1	8
75	Extension and Robustness of Transitivity Clustering for Protein-Protein Interaction Network Analysis. <i>Internet Mathematics</i> , 2011, 7, 255-273.	0.7	8
76	Accurate statistics for local sequence alignment with position-dependent scoring by rare-event sampling. <i>BMC Bioinformatics</i> , 2011, 12, 47.	2.6	8
77	Efficiently mining protein interaction dependencies from large text corpora. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 805.	1.3	8
78	TaxMapper: an analysis tool, reference database and workflow for metatranscriptome analysis of eukaryotic microorganisms. <i>BMC Genomics</i> , 2017, 18, 787.	2.8	8
79	Quantitative Proteomics Reveals Ecophysiological Effects of Light and Silver Stress on the Mixotrophic Protist <i>Poteroiochromonas malhamensis</i> . <i>PLoS ONE</i> , 2017, 12, e0168183.	2.5	8
80	An online peak extraction algorithm for ion mobility spectrometry data. <i>Algorithms for Molecular Biology</i> , 2015, 10, 17.	1.2	7
81	A detailed comparison of analysis processes for MCC-IMS data in disease classification—Automated methods can replace manual peak annotations. <i>PLoS ONE</i> , 2017, 12, e0184321.	2.5	7
82	Modeling and simulating networks of interdependent protein interactions. <i>Integrative Biology (United Kingdom)</i> , 2018, 10, 290-305.	1.3	7
83	<scp>ddrage</scp>: A data set generator to evaluate ddRADseq analysis software. <i>Molecular Ecology Resources</i> , 2018, 18, 681-690.	4.8	7
84	Osteosarcopenia, an Asymmetrical Overlap of Two Connected Syndromes: Data from the OsteoSys Study. <i>Nutrients</i> , 2021, 13, 3786.	4.1	7
85	Silver stress differentially affects growth of phototrophic and heterotrophic chrysoomonad flagellate populations. <i>Environmental Pollution</i> , 2019, 244, 314-322.	7.5	6
86	Detecting high-scoring local alignments in pangenome graphs. <i>Bioinformatics</i> , 2021, 37, 2266-2274.	4.1	6
87	Proteomic and bioinformatic profiling of neutrophils in CLL reveals functional defects that predispose to bacterial infections. <i>Blood Advances</i> , 2021, 5, 1259-1272.	5.2	6
88	MoRAine—a web server for fast computational transcription factor binding motif re-annotation. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.5	6
89	Mean and variance of the Gibbs free energy of oligonucleotides in the nearest neighbor model under varying conditions. <i>Bioinformatics</i> , 2004, 20, 2928-2933.	4.1	5
90	MoRAine - A web server for fast computational transcription factor binding motif re-annotation. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.5	5

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91	Interaction-Specific Changes in the Transcriptome of Polynucleobacter asymbioticus Caused by Varying Protistan Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 1498.	3.5	5
92	Genome-Wide Analysis of the Nucleosome Landscape in Individuals with Coffin-Siris Syndrome. <i>Cytogenetic and Genome Research</i> , 2019, 159, 1-11.	1.1	5
93	Rapid large-scale oligonucleotide selection for microarrays. <i>Proceedings</i> , 2002, 1, 54-63.	0.1	5
94	Deep metazoan phylogeny. <i>In Silico Biology</i> , 2007, 7, 151-4.	0.9	5
95	Structural Identifiability in Low-Rank Matrix Factorization. <i>Algorithmica</i> , 2010, 56, 313-332.	1.3	4
96	Cost-optimal assignment of elements in genome-scale multi-way bucketed Cuckoo hash tables. , 2020, , 186-198.		4
97	Fast and sensitive probe selection for DNA chips using jumps in matching statistics. <i>Proceedings</i> , 2003, 2, 57-64.	0.1	4
98	An Algorithm to Compute the Character Access Count Distribution for Pattern Matching Algorithms. <i>Algorithms</i> , 2011, 4, 285-306.	2.1	3
99	Massively parallel read mapping on GPUs with the <i>i>q</i>-group index and PEANUT. <i>PeerJ</i>, 2014, 2, e606.</i>	2.0	3
100	Modeling evolutionary fitness for DNA motif discovery. , 2009, , .		2
101	Meiotic recombination in the offspring of <i>Microbotryum</i> hybrids and its impact on pathogenicity. <i>BMC Evolutionary Biology</i> , 2020, 20, 123.	3.2	2
102	Speeding Up Exact Motif Discovery by Bounding the Expected Clump Size. <i>Lecture Notes in Computer Science</i> , 2010, , 337-349.	1.3	2
103	Efficient Online Transcription Factor Binding Site Adjustment by Integrating Transitive Graph Projection with MoRAine 2.0. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	1
104	A Hybrid Parameter Estimation Algorithm for Beta Mixtures and Applications to Methylation State Classification. <i>Lecture Notes in Computer Science</i> , 2016, , 307-319.	1.3	1
105	GAMIBHEAR: whole-genome haplotype reconstruction from Genome Architecture Mapping data. <i>Bioinformatics</i> , 2021, 37, 3128-3135.	4.1	1
106	Rapid T-cell receptor interaction grouping with ting. <i>Bioinformatics</i> , 2021, 37, 3444-3448.	4.1	1
107	Structural Identifiability in Low-Rank Matrix Factorization. <i>Lecture Notes in Computer Science</i> , 2008, , 140-148.	1.3	1
108	Functional and phylogenetic analysis of the core transcriptome of Ochromonadales. <i>Metabarcoding and Metagenomics</i> , 0, 1, e19862.	0.0	1

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109	An Online Peak Extraction Algorithm for Ion Mobility Spectrometry Data. Lecture Notes in Computer Science, 2014, , 232-246.	1.3	1
110	Modeling and Simulating Constrained Protein Interaction Networks. Genomics and Computational Biology, 2017, 4, 100049.	0.7	1
111	Protein Complex Similarity Based on Weisfeiler-Lehman Labeling. Lecture Notes in Computer Science, 2019, , 308-322.	1.3	1
112	Algorithms for Oligonucleotide Microarray Layout. , 2007, , 277-301.		0
113	BETTER GENECHIP MICROARRAY LAYOUTS BY COMBINING PROBE PLACEMENT AND EMBEDDING. Journal of Bioinformatics and Computational Biology, 2008, 06, 623-641.	0.8	0