Sven Rahmann

List of Publications by Year
in descending order

113	7,044	126907	76900
papers	citations	33	74
		h-index	g-index

144	144	144	13990
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	1.6	188
2	Detecting high-scoring local alignments in pangenome graphs. Bioinformatics, 2021, 37, 2266-2274.	4.1	6
3	Proteomic and bioinformatic profiling of neutrophils in CLL reveals functional defects that predispose to bacterial infections. Blood Advances, 2021, 5, 1259-1272.	5.2	6
4	GAMIBHEAR: whole-genome haplotype reconstruction from Genome Architecture Mapping data. Bioinformatics, 2021, 37, 3128-3135.	4.1	1
5	Fast lightweight accurate xenograft sorting. Algorithms for Molecular Biology, 2021, 16, 2.	1.2	9
6	Sustainable data analysis with Snakemake. F1000Research, 2021, 10, 33.	1.6	642
7	Rapid T-cell receptor interaction grouping with ting. Bioinformatics, 2021, 37, 3444-3448.	4.1	1
8	Osteosarcopenia, an Asymmetrical Overlap of Two Connected Syndromes: Data from the OsteoSys Study. Nutrients, 2021, 13, 3786.	4.1	7
9	Meiotic recombination in the offspring of Microbotryum hybrids and its impact on pathogenicity. BMC Evolutionary Biology, 2020, 20, 123.	3.2	2
10	Machine learning reveals a PD-L1â€"independent prediction of response to immunotherapy of non-small cell lung cancer by gene expression context. European Journal of Cancer, 2020, 140, 76-85.	2.8	30
11	A germ cellâ€specific ageing pattern in otherwise healthy men. Aging Cell, 2020, 19, e13242.	6.7	27
12	Epitope similarity cannot explain the pre-formed T cell immunity towards structural SARS-CoV-2 proteins. Scientific Reports, 2020, 10, 18995.	3.3	15
13	wg-blimp: an end-to-end analysis pipeline for whole genome bisulfite sequencing data. BMC Bioinformatics, 2020, 21, 169.	2.6	26
14	CDKN2A deletion in supratentorial ependymoma with RELA alteration indicates a dismal prognosis: a retrospective analysis of the HIT ependymoma trial cohort. Acta Neuropathologica, 2020, 140, 405-407.	7.7	30
15	Cost-optimal assignment of elements in genome-scale multi-way bucketed Cuckoo hash tables. , 2020, , 186-198.		4
16	Interaction-Specific Changes in the Transcriptome of Polynucleobacter asymbioticus Caused by Varying Protistan Communities. Frontiers in Microbiology, 2019, 10, 1498.	3.5	5
17	Genome-Wide Analysis of the Nucleosome Landscape in Individuals with Coffin-Siris Syndrome. Cytogenetic and Genome Research, 2019, 159, 1-11.	1.1	5
18	The Role of Pre-existing Cross-Reactive Central Memory CD4 T-Cells in Vaccination With Previously Unseen Influenza Strains. Frontiers in Immunology, 2019, 10, 593.	4.8	27

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19	Machine learning-based predictors for immune checkpoint inhibitor therapy of non-small-cell lung cancer. Annals of Oncology, 2019, 30, 655-657.	1.2	18
20	Improved risk-stratification for posterior fossa ependymoma of childhood considering clinical, histological and genetic features â€" a retrospective analysis of the HIT ependymoma trial cohort. Acta Neuropathologica Communications, 2019, 7, 181.	5.2	21
21	Impact of RAS mutation subtype on clinical outcomeâ€"a cross-entity comparison of patients with advanced non-small cell lung cancer and colorectal cancer. Oncogene, 2019, 38, 2953-2966.	5.9	38
22	Silver stress differentially affects growth of phototrophic and heterotrophic chrysomonad flagellate populations. Environmental Pollution, 2019, 244, 314-322.	7.5	6
23	Protein Complex Similarity Based on Weisfeiler-Lehman Labeling. Lecture Notes in Computer Science, 2019, , 308-322.	1.3	1
24	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	6.5	207
25	Cancer evolution, mutations, and clonal selection in relapse neuroblastoma. Cell and Tissue Research, 2018, 372, 263-268.	2.9	21
26	Evolution of heterotrophy in chrysophytes as reflected by comparative transcriptomics. FEMS Microbiology Ecology, 2018, 94, .	2.7	40
27	Modeling and simulating networks of interdependent protein interactions. Integrative Biology (United Kingdom), 2018, 10, 290-305.	1.3	7
28	Locus-Specific DNA Methylation Analysis by Targeted Deep Bisulfite Sequencing. Methods in Molecular Biology, 2018, 1767, 351-366.	0.9	28
29	<scp>ddrage</scp>: A data set generator to evaluate ddRADseq analysis software. Molecular Ecology Resources, 2018, 18, 681-690.	4.8	7
30	A mechanistic classification of clinical phenotypes in neuroblastoma. Science, 2018, 362, 1165-1170.	12.6	213
31	Circulating microRNA biomarkers for metastatic disease in neuroblastoma patients. JCI Insight, 2018, 3, .	5.0	28
32	A detailed comparison of analysis processes for MCC-IMS data in disease classificationâ€"Automated methods can replace manual peak annotations. PLoS ONE, 2017, 12, e0184321.	2.5	7
33	A hybrid parameter estimation algorithm for beta mixtures and applications to methylation state classification. Algorithms for Molecular Biology, 2017, 12, 21.	1.2	19
34	Regions of common inter-individual DNA methylation differences in human monocytes: genetic basis and potential function. Epigenetics and Chromatin, 2017, 10, 37.	3.9	20
35	TaxMapper: an analysis tool, reference database and workflow for metatranscriptome analysis of eukaryotic microorganisms. BMC Genomics, 2017, 18, 787.	2.8	8
36	Quantitative Proteomics Reveals Ecophysiological Effects of Light and Silver Stress on the Mixotrophic Protist Poterioochromonas malhamensis. PLoS ONE, 2017, 12, e0168183.	2.5	8

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37	Comprehensive transcriptome analysis provides new insights into nutritional strategies and phylogenetic relationships of chrysophytes. PeerJ, 2017, 5, e2832.	2.0	38
38	Modeling and Simulating Constrained Protein Interaction Networks. Genomics and Computational Biology, 2017, 4, 100049.	0.7	1
39	SimLoRD: Simulation of Long Read Data. Bioinformatics, 2016, 32, 2704-2706.	4.1	81
40	A Hybrid Parameter Estimation Algorithm for Beta Mixtures and Applications to Methylation State Classification. Lecture Notes in Computer Science, 2016, , 307-319.	1.3	1
41	Recurrent alterations of *TNFAIP3* (A20) in T-cell large granular lymphocytic leukemia. International Journal of Cancer, 2016, 138, 121-124.	5.1	36
42	Epigenetic dynamics of monocyte-to-macrophage differentiation. Epigenetics and Chromatin, 2016, 9, 33.	3.9	73
43	Trade‐off between taxon diversity and functional diversity in European lake ecosystems. Molecular Ecology, 2016, 25, 5876-5888.	3.9	24
44	Human TLR 8 senses UR / URR motifs in bacterial and mitochondrial RNA. EMBO Reports, 2015, 16, 1656-1663.	4.5	110
45	An online peak extraction algorithm for ion mobility spectrometry data. Algorithms for Molecular Biology, 2015, 10, 17.	1.2	7
46	N6-Adenosine Methylation in MiRNAs. PLoS ONE, 2015, 10, e0118438.	2.5	115
47	Mutational dynamics between primary and relapse neuroblastomas. Nature Genetics, 2015, 47, 872-877.	21.4	253
48	Supratentorial ependymomas of childhood carry C11orf95–RELA fusions leading to pathological activation of the NF-κB signaling pathway. Acta Neuropathologica, 2014, 127, 609-611.	7.7	103
49	A modular computational framework for automated peak extraction from ion mobility spectra. BMC Bioinformatics, 2014, 15, 25.	2.6	16
50	Effects of Silver Nitrate and Silver Nanoparticles on a Planktonic Community: General Trends after Short-Term Exposure. PLoS ONE, 2014, 9, e95340.	2.5	65
51	Massively parallel read mapping on GPUs with the *q*-group index and PEANUT. PeerJ, 2014, 2, e606.	2.0	3
52	An Online Peak Extraction Algorithm for Ion Mobility Spectrometry Data. Lecture Notes in Computer Science, 2014, , 232-246.	1.3	1
53	Oto-facial syndrome and esophageal atresia, intellectual disability and zygomatic anomalies - expanding the phenotypes associated with EFTUD2 mutations. Orphanet Journal of Rare Diseases, 2013, 8, 110.	2.7	56
54	Exome sequencing identifies recurrent somatic mutations in EIF1AX and SF3B1 in uveal melanoma with disomy 3. Nature Genetics, 2013, 45, 933-936.	21.4	436

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55	Identifying transcriptional miRNA biomarkers by integrating high-throughput sequencing and real-time PCR data. Methods, 2013, 59, 154-163.	3.8	10
56	A comprehensive molecular study on Coffinâ€"Siris and Nicolaidesâ€"Baraitser syndromes identifies a broad molecular and clinical spectrum converging on altered chromatin remodeling. Human Molecular Genetics, 2013, 22, 5121-5135.	2.9	190
57	Nextâ€generation RNA sequencing reveals differential expression of MYCN target genes and suggests the mTOR pathway as a promising therapy target in *MYCNâ€*amplified neuroblastoma. International Journal of Cancer, 2013, 132, E106-15.	5.1	26
58	Peak Detection Method Evaluation for Ion Mobility Spectrometry by Using Machine Learning Approaches. Metabolites, 2013, 3, 277-293.	2.9	24
59	Snakemakeâ€"a scalable bioinformatics workflow engine. Bioinformatics, 2012, 28, 2520-2522.	4.1	2,041
60	Efficiently mining protein interaction dependencies from large text corpora. Integrative Biology (United Kingdom), 2012, 4, 805.	1.3	8
61	Probabilistic Arithmetic Automata and Their Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1737-1750.	3.0	11
62	Extension and Robustness of Transitivity Clustering for Proteinâ€"Protein Interaction Network Analysis. Internet Mathematics, 2011, 7, 255-273.	0.7	8
63	An Algorithm to Compute the Character Access Count Distribution for Pattern Matching Algorithms. Algorithms, 2011, 4, 285-306.	2.1	3
64	Accurate statistics for local sequence alignment with position-dependent scoring by rare-event sampling. BMC Bioinformatics, 2011, 12, 47.	2.6	8
65	Efficient Online Transcription Factor Binding Site Adjustment by Integrating Transitive Graph Projection with MoRAine 2.0. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	1
66	Structural Identifiability in Low-Rank Matrix Factorization. Algorithmica, 2010, 56, 313-332.	1.3	4
67	Differentiation of chronic obstructive pulmonary disease (COPD) including lung cancer from healthy control group by breath analysis using ion mobility spectrometry. International Journal for Ion Mobility Spectrometry, 2010, 13, 131-139.	1.4	59
68	High-throughput microarray technology in diagnostics of enterobacteria based on genome-wide probe selection and regression analysis. BMC Genomics, 2010, 11, 591.	2.8	11
69	Partitioning biological data with transitivity clustering. Nature Methods, 2010, 7, 419-420.	19.0	84
70	Exact ILP solutions for phylogenetic minimum flip problems. , 2010, , .		39
71	Deep sequencing reveals differential expression of microRNAs in favorable versus unfavorable neuroblastoma. Nucleic Acids Research, 2010, 38, 5919-5928.	14.5	183
72	Speeding Up Exact Motif Discovery by Bounding the Expected Clump Size. Lecture Notes in Computer Science, 2010, , 337-349.	1.3	2

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73	Efficient exact motif discovery. Bioinformatics, 2009, 25, i356-i364.	4.1	48
74	Detecting species-site dependencies in large multiple sequence alignments. Nucleic Acids Research, 2009, 37, 5959-5968.	14.5	12
75	Modeling evolutionary fitness for DNA motif discovery. , 2009, , .		2
76	Massive parallel bisulfite sequencing of CG-rich DNA fragments reveals that methylation of many X-chromosomal CpG islands in female blood DNA is incomplete. Human Molecular Genetics, 2009, 18, 1439-1448.	2.9	37
77	Reliable transfer of transcriptional gene regulatory networks between taxonomically related organisms. BMC Systems Biology, 2009, 3, 8.	3.0	28
78	Modelling cross-hybridization on phylogenetic DNA microarrays increases the detection power of closely related species. Molecular Ecology Resources, 2009, 9, 83-93.	4.8	24
79	Algorithms for subsequence combinatorics. Theoretical Computer Science, 2008, 409, 394-404.	0.9	53
80	Compound Poisson Approximation of the Number of Occurrences of a Position Frequency Matrix (PFM) on Both Strands. Journal of Computational Biology, 2008, 15, 547-564.	1.6	14
81	BETTER GENECHIP MICROARRAY LAYOUTS BY COMBINING PROBE PLACEMENT AND EMBEDDING. Journal of Bioinformatics and Computational Biology, 2008, 06, 623-641.	0.8	0
82	Natural similarity measures between position frequency matrices with an application to clustering. Bioinformatics, 2008, 24, 350-357.	4.1	47
83	Towards the integrated analysis, visualization and reconstruction of microbial gene regulatory networks. Briefings in Bioinformatics, 2008, 10, 75-83.	6.5	21
84	MoRAine - A web server for fast computational transcription factor binding motif re-annotation. Journal of Integrative Bioinformatics, 2008, 5, .	1.5	5
85	Probabilistic Arithmetic Automata and Their Application to Pattern Matching Statistics. , 2008, , 95-106.		15
86	Structural Identifiability in Low-Rank Matrix Factorization. Lecture Notes in Computer Science, 2008, , 140-148.	1.3	1
87	MoRAine--a web server for fast computational transcription factor binding motif re-annotation. Journal of Integrative Bioinformatics, 2008, 5, .	1.5	6
88	Algorithms for Oligonucleotide Microarray Layout. , 2007, , 277-301.		0
89	CoryneRegNet 3.0—An interactive systems biology platform for the analysis of gene regulatory networks in corynebacteria and Escherichia coli. Journal of Biotechnology, 2007, 129, 279-289.	3.8	32
90	IMS2 â€" An integrated medical software system for early lung cancer detection using ion mobility spectrometry data of human breath. Journal of Integrative Bioinformatics, 2007, 4, 186-197.	1.5	20

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91	Integer linear programming approaches for non-unique probe selection. Discrete Applied Mathematics, 2007, 155, 840-856.	0.9	22
92	CoryneCenter â€" An online resource for the integrated analysis of corynebacterial genome and transcriptome data. BMC Systems Biology, 2007, 1, 55.	3.0	11
93	Large scale clustering of protein sequences with FORCE -A layout based heuristic for weighted cluster editing. BMC Bioinformatics, 2007, 8, 396.	2.6	56
94	EXACT AND HEURISTIC ALGORITHMS FOR WEIGHTED CLUSTER EDITING. , 2007, , .		43
95	Deep metazoan phylogeny. In Silico Biology, 2007, 7, 151-4.	0.9	5
96	Exact and heuristic algorithms for weighted cluster editing. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2007, 6, 391-401.	0.4	13
97	CoryneRegNet 2: An Integrative Bioinformatics Approach for Reconstruction and Comparison of Transcriptional Regulatory Networks in Prokaryotes. Journal of Integrative Bioinformatics, 2006, 3, 1-13.	1.5	11
98	CoryneRegNet: An ontology-based data warehouse of corynebacterial transcription factors and regulatory networks. BMC Genomics, 2006, 7, 24.	2.8	52
99	Decoding non-unique oligonucleotide hybridization experiments of targets related by a phylogenetic tree. Bioinformatics, 2006, 22, e424-e430.	4.1	8
100	T-Reg Comparator: an analysis tool for the comparison of position weight matrices. Nucleic Acids Research, 2005, 33, W438-W441.	14.5	42
101	HMM Logos for visualization of protein families. BMC Bioinformatics, 2004, 5, 7.	2.6	195
102	Accurate and robust phylogeny estimation based on profile distances: a study of the Chlorophyceae (Chlorophyta). BMC Evolutionary Biology, 2004, 4, 20.	3.2	43
103	Mean and variance of the Gibbs free energy of oligonucleotides in the nearest neighbor model under varying conditions. Bioinformatics, 2004, 20, 2928-2933.	4.1	5
104	Combinatorics of periods in strings. Journal of Combinatorial Theory - Series A, 2003, 104, 95-113.	0.8	17
105	On the Power of Profiles for Transcription Factor Binding Site Detection. Statistical Applications in Genetics and Molecular Biology, 2003, 2, Article7.	0.6	80
106	Dynamic Programming Algorithms for Two Statistical Problems in Computational Biology. Lecture Notes in Computer Science, 2003, , 151-164.	1.3	15
107	Fast Large Scale Oligonucleotide Selection Using the Longest Common Factor Approach. Journal of Bioinformatics and Computational Biology, 2003, 01, 343-361.	0.8	37
108	The shortest common supersequence problem in a microarray production setting. Bioinformatics, 2003, 19, ii156-ii161.	4.1	29

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109	On the Distribution of the Number of Missing Words in Random Texts. Combinatorics Probability and Computing, 2003, 12, .	1.3	13
110	Fast and sensitive probe selection for DNA chips using jumps in matching statistics. Proceedings, 2003, 2, 57-64.	0.1	4
111	Rapid large-scale oligonucleotide selection for microarrays. Proceedings, 2002, 1, 54-63.	0.1	5
112	Non-symmetric score matrices and the detection of homologous transmembrane proteins. Bioinformatics, 2001, 17, S182-S189.	4.1	63
113	Functional and phylogenetic analysis of the core transcriptome of Ochromonadales. Metabarcoding and Metagenomics, 0, 1, e19862.	0.0	1