Knut Hj Reinert

List of Publications by Year
in descending order

123 papers	27,215 citations	61984 43 h-index	22832 112 g-index
138 all docs	138 docs citations	138 times ranked	29367 citing authors

#	Article	IF	Citations
1	LaRA 2: parallel and vectorized program for sequenceâ€"structure alignment of RNA sequences. BMC Bioinformatics, 2022, 23, 18.	2.6	3
2	Co-Design for Energy Efficient and Fast Genomic Search. , 2022, , .		2
3	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	6.5	110
4	RLM: fast and simplified extraction of read-level methylation metrics from bisulfite sequencing data. Bioinformatics, 2021, 37, 3934-3935.	4.1	5
5	Profiling of Sub-Lethal in Vitro Effects of Multi-Walled Carbon Nanotubes Reveals Changes in Chemokines and Chemokine Receptors. Nanomaterials, 2021, 11, 883.	4.1	6
6	Raptor: A fast and space-efficient pre-filter for querying very large collections of nucleotide sequences. IScience, 2021, 24, 102782.	4.1	7
7	PriSeT. , 2021, , .		1
8	Testing assembly strategies of Francisella tularensis genomes to infer an evolutionary conservation analysis of genomic structures. BMC Genomics, 2021, 22, 822.	2.8	2
9	ganon: precise metagenomics classification against large and up-to-date sets of reference sequences. Bioinformatics, 2020, 36, i12-i20.	4.1	39
10	Concentration and chemical form of dietary zinc shape the porcine colon microbiome, its functional capacity and antibiotic resistance gene repertoire. ISME Journal, 2020, 14, 2783-2793.	9.8	37
11	GenMap: ultra-fast computation of genome mappability. Bioinformatics, 2020, 36, 3687-3692.	4.1	107
12	Ranbow: A fast and accurate method for polyploid haplotype reconstruction. PLoS Computational Biology, 2020, 16, e1007843.	3.2	23
13	Rapid and Culture Free Identification of Francisella in Hare Carcasses by High-Resolution Tandem Mass Spectrometry Proteotyping. Frontiers in Microbiology, 2020, 11, 636.	3.5	8
14	EPIFANY: A Method for Efficient High-Confidence Protein Inference. Journal of Proteome Research, 2020, 19, 1060-1072.	3.7	20
15	VARSCOT: variant-aware detection and scoring enables sensitive and personalized off-target detection for CRISPR-Cas9. BMC Biotechnology, 2019, 19, 40.	3.3	9
16	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	6.5	207
17	Formula Feeding Predisposes Neonatal Piglets to Clostridium difficile Gut Infection. Journal of Infectious Diseases, 2018, 217, 1442-1452.	4.0	18
18	Generic accelerated sequence alignment in SeqAn using vectorization and multi-threading. Bioinformatics, 2018, 34, 3437-3445.	4.1	30

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19	DREAM-Yara: an exact read mapper for very large databases with short update time. Bioinformatics, 2018, 34, i766-i772.	4.1	29
20	Flexbar 3.0 â€“ SIMD and multicore parallelization. Bioinformatics, 2017, 33, 2941-2942.	4.1	150
21	OpenMS â€“ A platform for reproducible analysis of mass spectrometry data. Journal of Biotechnology, 2017, 261, 142-148.	3.8	85
22	Development and optimisation of a generic micro LC-ESI-MS method for the qualitative and quantitative determination of 30-mer toxic gliadin peptides in wheat flour for food analysis. Analytical and Bioanalytical Chemistry, 2017, 409, 989-997.	3.7	6
23	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. Journal of Proteomics, 2017, 150, 170-182.	2.4	56
24	EPR-Dictionaries: A Practical and Fast Data Structure for Constant Time Searches in Unidirectional and Bidirectional FM Indices. Lecture Notes in Computer Science, 2017, , 190-206.	1.3	11
25	The SeqAn C++ template library for efficient sequence analysis: A resource for programmers. Journal of Biotechnology, 2017, 261, 157-168.	3.8	90
26	SLIMM: species level identification of microorganisms from metagenomes. PeerJ, 2017, 5, e3138.	2.0	29
27	Alternate-locus aware variant calling in whole genome sequencing. Genome Medicine, 2016, 8, 130.	8.2	16
28	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. Nature Methods, 2016, 13, 741-748.	19.0	537
29	Highâ€performance liquid chromatography with electrospray ionization ion mobility spectrometry: Characterization, data management, and applications. Journal of Separation Science, 2016, 39, 4756-4764.	2.5	9
30	From the desktop to the grid: scalable bioinformatics via workflow conversion. BMC Bioinformatics, 2016, 17, 127.	2.6	12
31	CIDANE: comprehensive isoform discovery and abundance estimation. Genome Biology, 2016, 17, 16.	8.8	45
32	IMSEQâ€”a fast and error aware approach to immunogenetic sequence analysis. Bioinformatics, 2015, 31, 2963-2971.	4.1	98
33	Evaluation of drug-induced neurotoxicity based on metabolomics, proteomics and electrical activity measurements in complementary CNS in vitro models. Toxicology in Vitro, 2015, 30, 138-165.	2.4	75
34	Methods for the detection and assembly of novel sequence in high-throughput sequencing data. Bioinformatics, 2015, 31, 1904-1912.	4.1	18
35	Workflows for automated downstream data analysis and visualization in largeâ€scale computational mass spectrometry. Proteomics, 2015, 15, 1443-1447.	2.2	32
36	Alignment of Next-Generation Sequencing Reads. Annual Review of Genomics and Human Genetics, 2015, 16, 133-151.	6.2	91

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37	LocalAli: an evolutionary-based local alignment approach to identify functionally conserved modules in multiple networks. Bioinformatics, 2015, 31, 363-372.	4.1	32
38	Lambda: the local aligner for massive biological data. Bioinformatics, 2014, 30, i349-i355.	4.1	60
39	Fiona: a parallel and automatic strategy for read error correction. Bioinformatics, 2014, 30, i356-i363.	4.1	59
40	NetCoffee: a fast and accurate global alignment approach to identify functionally conserved proteins in multiple networks. Bioinformatics, 2014, 30, 540-548.	4.1	56
41	Ultrahigh-performance liquid chromatography-ultraviolet absorbance detection-high-resolution-mass spectrometry combined with automated data processing for studying the kinetics of oxidative thermal degradation of thyroxine in the solid state. Journal of Chromatography A, 2014, 1371, 196-203.	3.7	6
42	Journaled string treeâ€"a scalable data structure for analyzing thousands of similar genomes on your laptop. Bioinformatics, 2014, 30, 3499-3505.	4.1	32
43	Gustaf: Detecting and correctly classifying SVs in the NGS twilight zone. Bioinformatics, 2014, 30, 3484-3490.	4.1	46
44	Genome alignment with graph data structures: a comparison. BMC Bioinformatics, 2014, 15, 99.	2.6	32
45	Rapid and Comprehensive Impurity Profiling of Synthetic Thyroxine by Ultrahigh-Performance Liquid Chromatographyâ€"High-Resolution Mass Spectrometry. Analytical Chemistry, 2013, 85, 3309-3317.	6.5	17
46	Optimal precursor ion selection for LC-MALDI MS/MS. BMC Bioinformatics, 2013, 14, 56.	2.6	5
47	The Duplication-Loss Small Phylogeny Problem: From Cherries to Trees. Journal of Computational Biology, 2013, 20, 643-659.	1.6	7
48	Tools for Label-free Peptide Quantification. Molecular and Cellular Proteomics, 2013, 12, 549-556.	3.8	198
49	Predict-IV project overview (EU grant 202222): non animal-based toxicity profiling by integrating toxico dynamics and biokinetics. Toxicology Letters, 2013, 221, S7.	0.8	2
50	Investigation of Reaction Mechanisms of Drug Degradation in the Solid State: A Kinetic Study Implementing Ultrahigh-Performance Liquid Chromatography and High-Resolution Mass Spectrometry for Thermally Stressed Thyroxine. Analytical Chemistry, 2013, 85, 2385-2390.	6.5	11
51	Messages from the chairs. , 2013, , .		0
52	Scalable string similarity search/join with approximate seeds and multiple backtracking. , 2013, , .		5
53	Fast and accurate read mapping with approximate seeds and multiple backtracking. Nucleic Acids Research, 2013, 41, e78-e78.	14.5	77
54	Detecting genomic indel variants with exact breakpoints in single- and paired-end sequencing data using SplazerS. Bioinformatics, 2012, 28, 619-627.	4.1	95

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55	Antilopeâ€"A Lagrangian Relaxation Approach to the de novo Peptide Sequencing Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 385-394.	3.0	12
56	RazerS 3: Faster, fully sensitive read mapping. Bioinformatics, 2012, 28, 2592-2599.	4.1	128
57	PPINGUIN: Peptide Profiling Guided Identification of Proteins improves quantitation of iTRAQ ratios. BMC Bioinformatics, 2012, 13, 34.	2.6	4
58	Inferring Proteolytic Processes from Mass Spectrometry Time Series Data Using Degradation Graphs. PLoS ONE, 2012, 7, e40656.	2.5	2
59	TOPPAS: A Graphical Workflow Editor for the Analysis of High-Throughput Proteomics Data. Journal of Proteome Research, 2012, 11, 3914-3920.	3.7	50
60	Hidden Breakpoints in Genome Alignments. Lecture Notes in Computer Science, 2012, , 391-403.	1.3	0
61	OpenMS and TOPP: Open Source Software for LC-MS Data Analysis. Methods in Molecular Biology, 2011, 696, 353-367.	0.9	68
62	Bioinformatics for Qualitative and Quantitative Proteomics. Methods in Molecular Biology, 2011, 719, 331-349.	0.9	4
63	MSSimulator: Simulation of Mass Spectrometry Data. Journal of Proteome Research, 2011, 10, 2922-2929.	3.7	42
64	Biomarker Discovery and Redundancy Reduction towards Classification using a Multi-factorial MALDI-TOF MS T2DM Mouse Model Dataset. BMC Bioinformatics, 2011, 12, 140.	2.6	5
65	A novel and well-defined benchmarking method for second generation read mapping. BMC Bioinformatics, 2011, 12, 210.	2.6	63
66	STELLAR: fast and exact local alignments. BMC Bioinformatics, 2011, 12, S15.	2.6	28
67	MicroRazerS: rapid alignment of small RNA reads. Bioinformatics, 2010, 26, 123-124.	4.1	37
68	Integration Preferences of Wildtype AAV-2 for Consensus Rep-Binding Sites at Numerous Loci in the Human Genome. PLoS Pathogens, 2010, 6, e1000985.	4.7	72
69	Optimal Decharging and Clustering of Charge Ladders Generated in ESIâˆ'MS. Journal of Proteome Research, 2010, 9, 2688-2695.	3.7	7
70	OpenMS and TOPP: Open Source Software for LC-MS Data Analysis. Methods in Molecular Biology, 2010, 604, 201-211.	0.9	27
71	Practical Multiple Sequence Alignment. , 2010, , 21-43.		0
72	Fast Structural Alignment of Biomolecules Using a Hash Table, N-Grams and String Descriptors. Algorithms, 2009, 2, 692-709.	2.1	23

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73	Approaching clinical proteomics: current state and future fields of application in fluid proteomics. Clinical Chemistry and Laboratory Medicine, 2009, 47, 724-44.	2.3	112
74	RazerSâ€"fast read mapping with sensitivity control. Genome Research, 2009, 19, 1646-1654.	5.5	125
75	A consistency-based consensus algorithm for de novo and reference-guided sequence assembly of short reads. Bioinformatics, 2009, 25, 1118-1124.	4.1	30
76	Approaching clinical proteomics: Current state and future fields of application in cellular proteomics. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2009, 75A, 816-832.	1.5	52
77	Statistical quality assessment and outlier detection for liquid chromatography-mass spectrometry experiments. BioData Mining, 2009, 2, 4.	4.0	23
78	An Iterative Strategy for Precursor Ion Selection for LC-MS/MS Based Shotgun Proteomics. Journal of Proteome Research, 2009, 8, 3239-3251.	3.7	18
79	Integer Linear Programming in Computational Biology. Lecture Notes in Computer Science, 2009, , 199-218.	1.3	5
80	SeqAn An efficient, generic C++ library for sequence analysis. BMC Bioinformatics, 2008, 9, 11.	2.6	287
81	OpenMS â€" An open-source software framework for mass spectrometry. BMC Bioinformatics, 2008, 9, 163.	2.6	556
82	LC-MSsim â€" a simulation software for liquid chromatography mass spectrometry data. BMC Bioinformatics, 2008, 9, 423.	2.6	42
83	Robust consensus computation. BMC Bioinformatics, 2008, 9, .	2.6	3
84	Segment-based multiple sequence alignment. Bioinformatics, 2008, 24, i187-i192.	4.1	44
85	Computational Quantification of Peptides from LC-MS Data. Journal of Computational Biology, 2008, 15, 685-704.	1.6	12
86	Fast and Adaptive Variable Order Markov Chain Construction. Lecture Notes in Computer Science, 2008, , 306-317.	1.3	15
87	A geometric approach for the alignment of liquid chromatographyâ€"mass spectrometry data. Bioinformatics, 2007, 23, i273-i281.	4.1	78
88	A Fast and Accurate Algorithm for the Quantification of Peptides from Mass Spectrometry Data. Lecture Notes in Computer Science, 2007, , 473-487.	1.3	9
89	Integer linear programming approaches for non-unique probe selection. Discrete Applied Mathematics, 2007, 155, 840-856.	0.9	22
90	Accurate multiple sequence-structure alignment of RNA sequences using combinatorial optimization. BMC Bioinformatics, 2007, 8, 271.	2.6	74

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91	TOPP--the OpenMS proteomics pipeline. Bioinformatics, 2007, 23, e191-e197.	4.1	249
92	Analytical model of peptide mass cluster centres with applications. Proteome Science, 2006, 4, 18.	1.7	25
93	Absolute Myoglobin Quantitation in Serum by Combining Two-Dimensional Liquid Chromatographyâ^'Electrospray Ionization Mass Spectrometry and Novel Data Analysis Algorithms. Journal of Proteome Research, 2006, 5, 414-421.	3.7	77
94	A branch-and-cut algorithm for multiple sequence alignment. Mathematical Programming, 2006, 105, 387-425.	2.4	16
95	High-accuracy peak picking of proteomics data using wavelet techniques. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 243-54.	0.7	22
96	HIGH-ACCURACY PEAK PICKING OF PROTEOMICS DATA USING WAVELET TECHNIQUES. , 2005, , .		33
97	Calibration of mass spectrometric peptide mass fingerprint data without specific external or internal calibrants. BMC Bioinformatics, 2005, 6, 203.	2.6	21
98	Transformation and other factors of the peptide mass spectrometry pairwise peak-list comparison process. BMC Bioinformatics, 2005, 6, 285.	2.6	17
99	Fast and Accurate Structural RNA Alignment by Progressive Lagrangian Optimization. Lecture Notes in Computer Science, 2005, , 217-228.	1.3	4
100	Multiple Structural RNA Alignment with Lagrangian Relaxation. Lecture Notes in Computer Science, 2005, , 303-314.	1.3	5
101	Algorithms for the Automated Absolute Quantification of Diagnostic Markers in Complex Proteomics Samples. Lecture Notes in Computer Science, 2005, , 151-162.	1.3	4
102	Differenzielle Proteomanalyse â€“ Experimentelle Methoden, algorithmische Herausforderungen (Differential Analysis in Proteomics: Experimental Methods, Algorithmic Challenges). IT - Information Technology, 2004, 46, 31-38.	0.9	0
103	Whole-genome shotgun assembly and comparison of human genome assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1916-1921.	7.1	164
104	Optimal robust non-unique probe selection using Integer Linear Programming. Bioinformatics, 2004, 20, i186-i193.	4.1	75
105	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. Science, 2002, 296, 1661-1671.	12.6	344
106	The greedy path-merging algorithm for contig scaffolding. Journal of the ACM, 2002, 49, 603-615.	2.2	77
107	Multiple sequence alignment with arbitrary gap costs: Computing an optimal solution using polyhedral combinatorics. Bioinformatics, 2002, 18, S4-S16.	4.1	22
108	Segment Match Refinement and Applications. Lecture Notes in Computer Science, 2002, , 126-139.	1.3	7

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109	Recent Segmental Duplications in the Human Genome. Science, 2002, 297, 1003-1007.	12.6	1,238
110	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	12.6	12,623
111	Design of a compartmentalized shotgun assembler for the human genome. Bioinformatics, 2001, 17, S132-S139.	4.1	56
112	The greedy path-merging algorithm for sequence assembly. , 2001, , .		12
113	Comparing Assemblies Using Fragments and Mate-Pairs. Lecture Notes in Computer Science, 2001, , 294-306.	1.3	16
114	A polyhedral approach to sequence alignment problems. Discrete Applied Mathematics, 2000, 104, 143-186.	0.9	48
115	The Genome Sequence of Drosophila melanogaster. Science, 2000, 287, 2185-2195.	12.6	5,566
116	An iterative method for faster sum-of-pairs multiple sequence alignment. Bioinformatics, 2000, 16, 808-814.	4.1	54
117	A Whole-Genome Assembly of Drosophila. Science, 2000, 287, 2196-2204.	12.6	1,449
118	The Practical Use of the A* Algorithm for Exact Multiple Sequence Alignment. Journal of Computational Biology, 2000, 7, 655-671.	1.6	25
119	An exact solution for the segment-to-segment multiple sequence alignment problem. Bioinformatics, 1999, 15, 203-210.	4.1	35
120	A polyhedral approach to RNA sequence structure alignment. , 1998, , .		13
121	A Polyhedral Approach to RNA Sequence Structure Alignment. Journal of Computational Biology, 1998, 5, 517-530.	1.6	48
122	Visualization challenges for a new cyber-pharmaceutical computing paradigm. , 0, , .		5
123	Bioinformatics Support for Genome-Sequencing Projects. , 0, , 25-55.		0