Knut Hj Reinert

List of Publications by Year
in descending order

123 papers	27,215 citations	61857 43 h-index	22764 112 g-index
138 all docs	138 docs citations	138 times ranked	29367 citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	6.0	12,623
2	The Genome Sequence of Drosophila melanogaster. Science, 2000, 287, 2185-2195.	6.0	5,566
3	A Whole-Genome Assembly of Drosophila. Science, 2000, 287, 2196-2204.	6.0	1,449
4	Recent Segmental Duplications in the Human Genome. Science, 2002, 297, 1003-1007.	6.0	1,238
5	OpenMS â€" An open-source software framework for mass spectrometry. BMC Bioinformatics, 2008, 9, 163.	1.2	556
6	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. Nature Methods, 2016, 13, 741-748.	9.0	537
7	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. Science, 2002, 296, 1661-1671.	6.0	344
8	SeqAn An efficient, generic C++ library for sequence analysis. BMC Bioinformatics, 2008, 9, 11.	1.2	287
9	TOPP--the OpenMS proteomics pipeline. Bioinformatics, 2007, 23, e191-e197.	1.8	249
10	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	3.2	207
11	Tools for Label-free Peptide Quantification. Molecular and Cellular Proteomics, 2013, 12, 549-556.	2.5	198
12	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.	3.3	164
13	Flexbar 3.0 â€" SIMD and multicore parallelization. Bioinformatics, 2017, 33, 2941-2942.	1.8	150
14	RazerS 3: Faster, fully sensitive read mapping. Bioinformatics, 2012, 28, 2592-2599.	1.8	128
15	RazerSâ€"fast read mapping with sensitivity control. Genome Research, 2009, 19, 1646-1654.	2.4	125
16	Approaching clinical proteomics: current state and future fields of application in fluid proteomics. Clinical Chemistry and Laboratory Medicine, 2009, 47, 724-44.	1.4	112
17	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	3.2	110
18	GenMap: ultra-fast computation of genome mappability. Bioinformatics, 2020, 36, 3687-3692.	1.8	107

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19	IMSEQâ€"a fast and error aware approach to immunogenetic sequence analysis. Bioinformatics, 2015, 31, 2963-2971.	1.8	98
20	Detecting genomic indel variants with exact breakpoints in single- and paired-end sequencing data using SplazerS. Bioinformatics, 2012, 28, 619-627.	1.8	95
21	Alignment of Next-Generation Sequencing Reads. Annual Review of Genomics and Human Genetics, 2015, 16, 133-151.	2.5	91
22	The SeqAn C++ template library for efficient sequence analysis: A resource for programmers. Journal of Biotechnology, 2017, 261, 157-168.	1.9	90
23	OpenMS â€" A platform for reproducible analysis of mass spectrometry data. Journal of Biotechnology, 2017, 261, 142-148.	1.9	85
24	A geometric approach for the alignment of liquid chromatographyâ€"mass spectrometry data. Bioinformatics, 2007, 23, i273-i281.	1.8	78
25	The greedy path-merging algorithm for contig scaffolding. Journal of the ACM, 2002, 49, 603-615.	1.8	77
26	Absolute Myoglobin Quantitation in Serum by Combining Two-Dimensional Liquid Chromatographyâˆ'Electrospray Ionization Mass Spectrometry and Novel Data Analysis Algorithms. Journal of Proteome Research, 2006, 5, 414-421.	1.8	77
27	Fast and accurate read mapping with approximate seeds and multiple backtracking. Nucleic Acids Research, 2013, 41, e78-e78.	6.5	77
28	Optimal robust non-unique probe selection using Integer Linear Programming. Bioinformatics, 2004, 20, i186-i193.	1.8	75
29	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.	1.1	75
30	Accurate multiple sequence-structure alignment of RNA sequences using combinatorial optimization. BMC Bioinformatics, 2007, 8, 271.	1.2	74
31	Integration Preferences of Wildtype AAV-2 for Consensus Rep-Binding Sites at Numerous Loci in the Human Genome. PLoS Pathogens, 2010, 6, e1000985.	2.1	72
32	OpenMS and TOPP: Open Source Software for LC-MS Data Analysis. Methods in Molecular Biology, 2011, 696, 353-367.	0.4	68
33	A novel and well-defined benchmarking method for second generation read mapping. BMC Bioinformatics, 2011, 12, 210.	1.2	63
34	Lambda: the local aligner for massive biological data. Bioinformatics, 2014, 30, i349-i355.	1.8	60
35	Fiona: a parallel and automatic strategy for read error correction. Bioinformatics, 2014, 30, i356-i363.	1.8	59
36	Design of a compartmentalized shotgun assembler for the human genome. Bioinformatics, 2001, 17, S132-S139.	1.8	56

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37	NetCoffee: a fast and accurate global alignment approach to identify functionally conserved proteins in multiple networks. Bioinformatics, 2014, 30, 540-548.	1.8	56
38	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. Journal of Proteomics, 2017, 150, 170-182.	1.2	56
39	An iterative method for faster sum-of-pairs multiple sequence alignment. Bioinformatics, 2000, 16, 808-814.	1.8	54
40	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.	1.1	52
41	TOPPAS: A Graphical Workflow Editor for the Analysis of High-Throughput Proteomics Data. Journal of Proteome Research, 2012, 11, 3914-3920.	1.8	50
42	A Polyhedral Approach to RNA Sequence Structure Alignment. Journal of Computational Biology, 1998, 5, 517-530.	0.8	48
43	A polyhedral approach to sequence alignment problems. Discrete Applied Mathematics, 2000, 104, 143-186.	0.5	48
44	Gustaf: Detecting and correctly classifying SVs in the NGS twilight zone. Bioinformatics, 2014, 30, 3484-3490.	1.8	46
45	CIDANE: comprehensive isoform discovery and abundance estimation. Genome Biology, 2016, 17, 16.	3.8	45
46	Segment-based multiple sequence alignment. Bioinformatics, 2008, 24, i187-i192.	1.8	44
47	LC-MSsim â€" a simulation software for liquid chromatography mass spectrometry data. BMC Bioinformatics, 2008, 9, 423.	1.2	42
48	MSSimulator: Simulation of Mass Spectrometry Data. Journal of Proteome Research, 2011, 10, 2922-2929.	1.8	42
49	ganon: precise metagenomics classification against large and up-to-date sets of reference sequences. Bioinformatics, 2020, 36, i12-i20.	1.8	39
50	MicroRazerS: rapid alignment of small RNA reads. Bioinformatics, 2010, 26, 123-124.	1.8	37
51	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.	4.4	37
52	An exact solution for the segment-to-segment multiple sequence alignment problem. Bioinformatics, 1999, 15, 203-210.	1.8	35
53	HIGH-ACCURACY PEAK PICKING OF PROTEOMICS DATA USING WAVELET TECHNIQUES. , 2005, , .		33
54	Journaled string treeâ€"a scalable data structure for analyzing thousands of similar genomes on your laptop. Bioinformatics, 2014, 30, 3499-3505.	1.8	32

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55	Genome alignment with graph data structures: a comparison. BMC Bioinformatics, 2014, 15, 99.	1.2	32
56	Workflows for automated downstream data analysis and visualization in large‐scale computational mass spectrometry. Proteomics, 2015, 15, 1443-1447.	1.3	32
57	LocalAli: an evolutionary-based local alignment approach to identify functionally *conserved* modules in multiple networks. Bioinformatics, 2015, 31, 363-372.	1.8	32
58	A consistency-based consensus algorithm for *de novo* and reference-guided sequence assembly of short reads. Bioinformatics, 2009, 25, 1118-1124.	1.8	30
59	Generic accelerated sequence alignment in SeqAn using vectorization and multi-threading. Bioinformatics, 2018, 34, 3437-3445.	1.8	30
60	DREAM-Yara: an exact read mapper for very large databases with short update time. Bioinformatics, 2018, 34, i766-i772.	1.8	29
61	SLIMM: species level identification of microorganisms from metagenomes. PeerJ, 2017, 5, e3138.	0.9	29
62	STELLAR: fast and exact local alignments. BMC Bioinformatics, 2011, 12, S15.	1.2	28
63	OpenMS and TOPP: Open Source Software for LC-MS Data Analysis. Methods in Molecular Biology, 2010, 604, 201-211.	0.4	27
64	The Practical Use of the A* Algorithm for Exact Multiple Sequence Alignment. Journal of Computational Biology, 2000, 7, 655-671.	0.8	25
65	Analytical model of peptide mass cluster centres with applications. Proteome Science, 2006, 4, 18.	0.7	25
66	Fast Structural Alignment of Biomolecules Using a Hash Table, N-Grams and String Descriptors. Algorithms, 2009, 2, 692-709.	1.2	23
67	Statistical quality assessment and outlier detection for liquid chromatography-mass spectrometry experiments. BioData Mining, 2009, 2, 4.	2.2	23
68	Ranbow: A fast and accurate method for polyploid haplotype reconstruction. PLoS Computational Biology, 2020, 16, e1007843.	1.5	23
69	Multiple sequence alignment with arbitrary gap costs: Computing an optimal solution using polyhedral combinatorics. Bioinformatics, 2002, 18, S4-S16.	1.8	22
70	Integer linear programming approaches for non-unique probe selection. Discrete Applied Mathematics, 2007, 155, 840-856.	0.5	22
71	High-accuracy peak picking of proteomics data using wavelet techniques. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 243-54.	0.7	22
72	Calibration of mass spectrometric peptide mass fingerprint data without specific external or internal calibrants. BMC Bioinformatics, 2005, 6, 203.	1.2	21

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73	EPIFANY: A Method for Efficient High-Confidence Protein Inference. Journal of Proteome Research, 2020, 19, 1060-1072.	1.8	20
74	An Iterative Strategy for Precursor Ion Selection for LC-MS/MS Based Shotgun Proteomics. Journal of Proteome Research, 2009, 8, 3239-3251.	1.8	18
75	Methods for the detection and assembly of novel sequence in high-throughput sequencing data. Bioinformatics, 2015, 31, 1904-1912.	1.8	18
76	Formula Feeding Predisposes Neonatal Piglets to Clostridium difficile Gut Infection. Journal of Infectious Diseases, 2018, 217, 1442-1452.	1.9	18
77	Transformation and other factors of the peptide mass spectrometry pairwise peak-list comparison process. BMC Bioinformatics, 2005, 6, 285.	1.2	17
78	Rapid and Comprehensive Impurity Profiling of Synthetic Thyroxine by Ultrahigh-Performance Liquid Chromatographyâ€"High-Resolution Mass Spectrometry. Analytical Chemistry, 2013, 85, 3309-3317.	3.2	17
79	A branch-and-cut algorithm for multiple sequence alignment. Mathematical Programming, 2006, 105, 387-425.	1.6	16
80	Alternate-locus aware variant calling in whole genome sequencing. Genome Medicine, 2016, 8, 130.	3.6	16
81	Comparing Assemblies Using Fragments and Mate-Pairs. Lecture Notes in Computer Science, 2001, , 294-306.	1.0	16
82	Fast and Adaptive Variable Order Markov Chain Construction. Lecture Notes in Computer Science, 2008, , 306-317.	1.0	15
83	A polyhedral approach to RNA sequence structure alignment. , 1998, , .		13
84	The greedy path-merging algorithm for sequence assembly. , 2001, , .		12
85	Computational Quantification of Peptides from LC-MS Data. Journal of Computational Biology, 2008, 15, 685-704.	0.8	12
86	Antilopeâ€"A Lagrangian Relaxation Approach to the de novo Peptide Sequencing Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 385-394.	1.9	12
87	From the desktop to the grid: scalable bioinformatics via workflow conversion. BMC Bioinformatics, 2016, 17, 127.	1.2	12
88	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.	3.2	11
89	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.	1.0	11
90	A Fast and Accurate Algorithm for the Quantification of Peptides from Mass Spectrometry Data. Lecture Notes in Computer Science, 2007, , 473-487.	1.0	9

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91	High‑performance liquid chromatography with electrospray ionization ion mobility spectrometry: Characterization, data management, and applications. Journal of Separation Science, 2016, 39, 4756-4764.	1.3	9
92	VARSCOT: variant-aware detection and scoring enables sensitive and personalized off-target detection for CRISPR-Cas9. BMC Biotechnology, 2019, 19, 40.	1.7	9
93	Rapid and Culture Free Identification of Francisella in Hare Carcasses by High-Resolution Tandem Mass Spectrometry Proteotyping. Frontiers in Microbiology, 2020, 11, 636.	1.5	8
94	Segment Match Refinement and Applications. Lecture Notes in Computer Science, 2002, , 126-139.	1.0	7
95	Optimal Decharging and Clustering of Charge Ladders Generated in ESIˆˇMS. Journal of Proteome Research, 2010, 9, 2688-2695.	1.8	7
96	The Duplication-Loss Small Phylogeny Problem: From Cherries to Trees. Journal of Computational Biology, 2013, 20, 643-659.	0.8	7
97	Raptor: A fast and space-efficient pre-filter for querying very large collections of nucleotide sequences. IScience, 2021, 24, 102782.	1.9	7
98	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.	1.8	6
99	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.	1.9	6
100	Profiling of Sub-Lethal in Vitro Effects of Multi-Walled Carbon Nanotubes Reveals Changes in Chemokines and Chemokine Receptors. Nanomaterials, 2021, 11, 883.	1.9	6
101	Visualization challenges for a new cyber-pharmaceutical computing paradigm. , 0, , .		5
102	Biomarker Discovery and Redundancy Reduction towards Classification using a Multi-factorial MALDI-TOF MS T2DM Mouse Model Dataset. BMC Bioinformatics, 2011, 12, 140.	1.2	5
103	Optimal precursor ion selection for LC-MALDI MS/MS. BMC Bioinformatics, 2013, 14, 56.	1.2	5
104	Scalable string similarity search/join with approximate seeds and multiple backtracking. , 2013, , .		5
105	RLM: fast and simplified extraction of read-level methylation metrics from bisulfite sequencing data. Bioinformatics, 2021, 37, 3934-3935.	1.8	5
106	Multiple Structural RNA Alignment with Lagrangian Relaxation. Lecture Notes in Computer Science, 2005, , 303-314.	1.0	5
107	Integer Linear Programming in Computational Biology. Lecture Notes in Computer Science, 2009, , 199-218.	1.0	5
108	Fast and Accurate Structural RNA Alignment by Progressive Lagrangian Optimization. Lecture Notes in Computer Science, 2005, , 217-228.	1.0	4

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109	Bioinformatics for Qualitative and Quantitative Proteomics. Methods in Molecular Biology, 2011, 719, 331-349.	0.4	4
110	PPINGUIN: Peptide Profiling Guided Identification of Proteins improves quantitation of iTRAQ ratios. BMC Bioinformatics, 2012, 13, 34.	1.2	4
111	Algorithms for the Automated Absolute Quantification of Diagnostic Markers in Complex Proteomics Samples. Lecture Notes in Computer Science, 2005, , 151-162.	1.0	4
112	Robust consensus computation. BMC Bioinformatics, 2008, 9, .	1.2	3
113	LaRA 2: parallel and vectorized program for sequence–structure alignment of RNA sequences. BMC Bioinformatics, 2022, 23, 18.	1.2	3
114	Inferring Proteolytic Processes from Mass Spectrometry Time Series Data Using Degradation Graphs. PLoS ONE, 2012, 7, e40656.	1.1	2
115	Predict-IV project overview (EU grant 202222): non animal-based toxicity profiling by integrating toxico dynamics and biokinetics. Toxicology Letters, 2013, 221, S7.	0.4	2
116	Testing assembly strategies of Francisella tularensis genomes to infer an evolutionary conservation analysis of genomic structures. BMC Genomics, 2021, 22, 822.	1.2	2
117	Co-Design for Energy Efficient and Fast Genomic Search. , 2022, , .		2
118	PriSeT. , 2021, , .		1
119	Differenzielle Proteomanalyse â€" Experimentelle Methoden, algorithmische Herausforderungen (Differential Analysis in Proteomics: Experimental Methods, Algorithmic Challenges). IT - Information Technology, 2004, 46, 31-38.	0.6	0
120	Bioinformatics Support for Genome-Sequencing Projects. , 0, , 25-55.		0
121	Messages from the chairs. , 2013, , .		0
122	Practical Multiple Sequence Alignment. , 2010, , 21-43.		0
123	Hidden Breakpoints in Genome Alignments. Lecture Notes in Computer Science, 2012, , 391-403.	1.0	0