

Knut Hj Reinert

List of Publications by Year in Descending Order

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Version: 2024-04-23

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

126
papers

22,453
citations

40
h-index

138
g-index

138
ext. papers

25,232
ext. citations

6.2
avg, IF

5.78
L-index

#	Paper	IF	Citations
126	LaRA 2: parallel and vectorized program for sequence-structure alignment of RNA sequences.. <i>BMC Bioinformatics</i> , 2022 , 23, 18	3.6	0
125	Testing assembly strategies of Francisella tularensis genomes to infer an evolutionary conservation analysis of genomic structures. <i>BMC Genomics</i> , 2021 , 22, 822	4.5	0
124	Raptor: A fast and space-efficient pre-filter for querying very large collections of nucleotide sequences. <i>IScience</i> , 2021 , 24, 102782	6.1	0
123	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021 , 22, 642-663	13.4	56
122	Profiling of Sub-Lethal in Vitro Effects of Multi-Walled Carbon Nanotubes Reveals Changes in Chemokines and Chemokine Receptors. <i>Nanomaterials</i> , 2021 , 11,	5.4	2
121	GenMap: ultra-fast computation of genome mappability. <i>Bioinformatics</i> , 2020 , 36, 3687-3692	7.2	27
120	Ranbow: A fast and accurate method for polyploid haplotype reconstruction. <i>PLoS Computational Biology</i> , 2020 , 16, e1007843	5	11
119	Rapid and Culture Free Identification of in Hare Carcasses by High-Resolution Tandem Mass Spectrometry Proteotyping. <i>Frontiers in Microbiology</i> , 2020 , 11, 636	5.7	2
118	EPIFANY: A Method for Efficient High-Confidence Protein Inference. <i>Journal of Proteome Research</i> , 2020 , 19, 1060-1072	5.6	6
117	ganon: precise metagenomics classification against large and up-to-date sets of reference sequences. <i>Bioinformatics</i> , 2020 , 36, i12-i20	7.2	14
116	Concentration and chemical form of dietary zinc shape the porcine colon microbiome, its functional capacity and antibiotic resistance gene repertoire. <i>ISME Journal</i> , 2020 , 14, 2783-2793	11.9	15
115	VARSCOT: variant-aware detection and scoring enables sensitive and personalized off-target detection for CRISPR-Cas9. <i>BMC Biotechnology</i> , 2019 , 19, 40	3.5	5
114	Formula Feeding Predisposes Neonatal Piglets to Clostridium difficile Gut Infection. <i>Journal of Infectious Diseases</i> , 2018 , 217, 1442-1452	7	14
113	Generic accelerated sequence alignment in SeqAn using vectorization and multi-threading. <i>Bioinformatics</i> , 2018 , 34, 3437-3445	7.2	17
112	Computational pan-genomics: status, promises and challenges. <i>Briefings in Bioinformatics</i> , 2018 , 19, 118-134	13.5	130
111	DREAM-Yara: an exact read mapper for very large databases with short update time. <i>Bioinformatics</i> , 2018 , 34, i766-i772	7.2	16
110	Flexbar 3.0 - SIMD and multicore parallelization. <i>Bioinformatics</i> , 2017 , 33, 2941-2942	7.2	74

109	OpenMS - A platform for reproducible analysis of mass spectrometry data. <i>Journal of Biotechnology</i> , 2017 , 261, 142-148	3.7	61
108	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. <i>Analytical and Bioanalytical Chemistry</i> , 2017 , 409, 989-997	4.4	4
107	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. <i>Journal of Proteomics</i> , 2017 , 150, 170-182	3.9	39
106	SLIMM: species level identification of microorganisms from metagenomes. <i>PeerJ</i> , 2017 , 5, e3138	3.1	20
105	EPR-Dictionaries: A Practical and Fast Data Structure for Constant Time Searches in Unidirectional and Bidirectional FM Indices. <i>Lecture Notes in Computer Science</i> , 2017 , 190-206	0.9	10
104	The SeqAn C++ template library for efficient sequence analysis: A resource for programmers. <i>Journal of Biotechnology</i> , 2017 , 261, 157-168	3.7	49
103	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016 , 13, 741-8	21.6	337
102	High-performance liquid chromatography with electrospray ionization ion mobility spectrometry: Characterization, data management, and applications. <i>Journal of Separation Science</i> , 2016 , 39, 4756-4764	2.4	6
101	From the desktop to the grid: scalable bioinformatics via workflow conversion. <i>BMC Bioinformatics</i> , 2016 , 17, 127	3.6	11
100	CIDANE: comprehensive isoform discovery and abundance estimation. <i>Genome Biology</i> , 2016 , 17, 16	18.3	34
99	Alternate-locus aware variant calling in whole genome sequencing. <i>Genome Medicine</i> , 2016 , 8, 130	14.4	9
98	Alignment of Next-Generation Sequencing Reads. <i>Annual Review of Genomics and Human Genetics</i> , 2015 , 16, 133-51	9.7	72
97	LocalAli: an evolutionary-based local alignment approach to identify functionally conserved modules in multiple networks. <i>Bioinformatics</i> , 2015 , 31, 363-72	7.2	25
96	IMSEQ--a fast and error aware approach to immunogenetic sequence analysis. <i>Bioinformatics</i> , 2015 , 31, 2963-71	7.2	67
95	Evaluation of drug-induced neurotoxicity based on metabolomics, proteomics and electrical activity measurements in complementary CNS in vitro models. <i>Toxicology in Vitro</i> , 2015 , 30, 138-65	3.6	51
94	Methods for the detection and assembly of novel sequence in high-throughput sequencing data. <i>Bioinformatics</i> , 2015 , 31, 1904-12	7.2	12
93	Workflows for automated downstream data analysis and visualization in large-scale computational mass spectrometry. <i>Proteomics</i> , 2015 , 15, 1443-7	4.8	26
92	NetCoffee: a fast and accurate global alignment approach to identify functionally conserved proteins in multiple networks. <i>Bioinformatics</i> , 2014 , 30, 540-8	7.2	42

91	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. <i>Journal of Chromatography A</i> , 2014 , 1371, 196-203	4.5	6
90	Journalized string tree-a scalable data structure for analyzing thousands of similar genomes on your laptop. <i>Bioinformatics</i> , 2014 , 30, 3499-505	7.2	23
89	Gustaf: Detecting and correctly classifying SVs in the NGS twilight zone. <i>Bioinformatics</i> , 2014 , 30, 3484-90.	9.2	31
88	Genome alignment with graph data structures: a comparison. <i>BMC Bioinformatics</i> , 2014 , 15, 99	3.6	26
87	Lambda: the local aligner for massive biological data. <i>Bioinformatics</i> , 2014 , 30, i349-55	7.2	44
86	Fiona: a parallel and automatic strategy for read error correction. <i>Bioinformatics</i> , 2014 , 30, i356-63	7.2	42
85	Rapid and comprehensive impurity profiling of synthetic thyroxine by ultrahigh-performance liquid chromatography-high-resolution mass spectrometry. <i>Analytical Chemistry</i> , 2013 , 85, 3309-17	7.8	15
84	Optimal precursor ion selection for LC-MALDI MS/MS. <i>BMC Bioinformatics</i> , 2013 , 14, 56	3.6	5
83	The duplication-loss small phylogeny problem: from cherries to trees. <i>Journal of Computational Biology</i> , 2013 , 20, 643-59	1.7	6
82	Tools for label-free peptide quantification. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 549-56	7.6	171
81	Predict-IV project overview (EU grant 202222): non animal-based toxicity profiling by integrating toxico dynamics and biokinetics. <i>Toxicology Letters</i> , 2013 , 221, S7	4.4	2
80	UHPLC-HRMS-Experimente planen und auswerten [Beispiel Thyroxin. <i>Nachrichten Aus Der Chemie</i> , 2013 , 61, 455-458	0.1	
79	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. <i>Analytical Chemistry</i> , 2013 , 85, 2385-90	7.8	8
78	Scalable string similarity search/join with approximate seeds and multiple backtracking 2013 ,		3
77	Fast and accurate read mapping with approximate seeds and multiple backtracking. <i>Nucleic Acids Research</i> , 2013 , 41, e78	20.1	63
76	Antilope--a Lagrangian relaxation approach to the de novo peptide sequencing problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 385-94	3	9
75	RazerS 3: faster, fully sensitive read mapping. <i>Bioinformatics</i> , 2012 , 28, 2592-9	7.2	91
74	PPINGUIN: Peptide Profiling Guided Identification of Proteins improves quantitation of iTRAQ ratios. <i>BMC Bioinformatics</i> , 2012 , 13, 34	3.6	4

73	Inferring proteolytic processes from mass spectrometry time series data using degradation graphs. <i>PLoS ONE</i> , 2012 , 7, e40656	3.7	2
72	TOPPAS: a graphical workflow editor for the analysis of high-throughput proteomics data. <i>Journal of Proteome Research</i> , 2012 , 11, 3914-20	5.6	43
71	Detecting genomic indel variants with exact breakpoints in single- and paired-end sequencing data using SplazerS. <i>Bioinformatics</i> , 2012 , 28, 619-27	7.2	84
70	Hidden Breakpoints in Genome Alignments. <i>Lecture Notes in Computer Science</i> , 2012 , 391-403	0.9	
69	OpenMS and TOPP: open source software for LC-MS data analysis. <i>Methods in Molecular Biology</i> , 2011 , 696, 353-67	1.4	61
68	Bioinformatics for qualitative and quantitative proteomics. <i>Methods in Molecular Biology</i> , 2011 , 719, 331-49	1.4	3
67	MSSimulator: Simulation of mass spectrometry data. <i>Journal of Proteome Research</i> , 2011 , 10, 2922-9	5.6	36
66	Biomarker discovery and redundancy reduction towards classification using a multi-factorial MALDI-TOF MS T2DM mouse model dataset. <i>BMC Bioinformatics</i> , 2011 , 12, 140	3.6	5
65	A novel and well-defined benchmarking method for second generation read mapping. <i>BMC Bioinformatics</i> , 2011 , 12, 210	3.6	51
64	STELLAR: fast and exact local alignments. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 9, S15	3.6	19
63	MicroRazerS: rapid alignment of small RNA reads. <i>Bioinformatics</i> , 2010 , 26, 123-4	7.2	36
62	Integration preferences of wildtype AAV-2 for consensus rep-binding sites at numerous loci in the human genome. <i>PLoS Pathogens</i> , 2010 , 6, e1000985	7.6	53
61	Optimal decharging and clustering of charge ladders generated in ESI-MS. <i>Journal of Proteome Research</i> , 2010 , 9, 2688-95	5.6	4
60	OpenMS and TOPP: open source software for LC-MS data analysis. <i>Methods in Molecular Biology</i> , 2010 , 604, 201-11	1.4	16
59	Practical Multiple Sequence Alignment 2010 , 21-43		
58	Fast Structural Alignment of Biomolecules Using a Hash Table, N-Grams and String Descriptors. <i>Algorithms</i> , 2009 , 2, 692-709	1.8	20
57	Approaching clinical proteomics: current state and future fields of application in fluid proteomics. <i>Clinical Chemistry and Laboratory Medicine</i> , 2009 , 47, 724-44	5.9	94
56	RazerS--fast read mapping with sensitivity control. <i>Genome Research</i> , 2009 , 19, 1646-54	9.7	104

55	A consistency-based consensus algorithm for de novo and reference-guided sequence assembly of short reads. <i>Bioinformatics</i> , 2009 , 25, 1118-24	7.2	24
54	Approaching clinical proteomics: current state and future fields of application in cellular proteomics. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2009 , 75, 816-32	4.6	41
53	Statistical quality assessment and outlier detection for liquid chromatography-mass spectrometry experiments. <i>BioData Mining</i> , 2009 , 2, 4	4.3	20
52	An iterative strategy for precursor ion selection for LC-MS/MS based shotgun proteomics. <i>Journal of Proteome Research</i> , 2009 , 8, 3239-51	5.6	16
51	Integer Linear Programming in Computational Biology. <i>Lecture Notes in Computer Science</i> , 2009 , 199-218	0.9	5
50	SeqAn an efficient, generic C++ library for sequence analysis. <i>BMC Bioinformatics</i> , 2008 , 9, 11	3.6	210
49	OpenMS - an open-source software framework for mass spectrometry. <i>BMC Bioinformatics</i> , 2008 , 9, 163	3.6	474
48	LC-MSsim--a simulation software for liquid chromatography mass spectrometry data. <i>BMC Bioinformatics</i> , 2008 , 9, 423	3.6	40
47	Robust consensus computation. <i>BMC Bioinformatics</i> , 2008 , 9,	3.6	2
46	Segment-based multiple sequence alignment. <i>Bioinformatics</i> , 2008 , 24, i187-92	7.2	39
45	Computational quantification of peptides from LC-MS data. <i>Journal of Computational Biology</i> , 2008 , 15, 685-704	1.7	11
44	Fast and Adaptive Variable Order Markov Chain Construction. <i>Lecture Notes in Computer Science</i> , 2008 , 306-317	0.9	11
43	Integer linear programming approaches for non-unique probe selection. <i>Discrete Applied Mathematics</i> , 2007 , 155, 840-856	1	16
42	Accurate multiple sequence-structure alignment of RNA sequences using combinatorial optimization. <i>BMC Bioinformatics</i> , 2007 , 8, 271	3.6	63
41	TOPP--the OpenMS proteomics pipeline. <i>Bioinformatics</i> , 2007 , 23, e191-7	7.2	216
40	A geometric approach for the alignment of liquid chromatography-mass spectrometry data. <i>Bioinformatics</i> , 2007 , 23, i273-81	7.2	68
39	A Fast and Accurate Algorithm for the Quantification of Peptides from Mass Spectrometry Data. <i>Lecture Notes in Computer Science</i> , 2007 , 473-487	0.9	6
38	Analytical model of peptide mass cluster centres with applications. <i>Proteome Science</i> , 2006 , 4, 18	2.6	20

37	Absolute myoglobin quantitation in serum by combining two-dimensional liquid chromatography-electrospray ionization mass spectrometry and novel data analysis algorithms. <i>Journal of Proteome Research</i> , 2006 , 5, 414-21	5.6	68
36	A branch-and-cut algorithm for multiple sequence alignment. <i>Mathematical Programming</i> , 2006 , 105, 387-425	2.1	11
35	High-accuracy peak picking of proteomics data using wavelet techniques. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006 , 243-54	1.3	21
34	Fast and Accurate Structural RNA Alignment by Progressive Lagrangian Optimization. <i>Lecture Notes in Computer Science</i> , 2005 , 217-228	0.9	4
33	HIGH-ACCURACY PEAK PICKING OF PROTEOMICS DATA USING WAVELET TECHNIQUES 2005 ,		9
32	Calibration of mass spectrometric peptide mass fingerprint data without specific external or internal calibrants. <i>BMC Bioinformatics</i> , 2005 , 6, 203	3.6	18
31	Transformation and other factors of the peptide mass spectrometry pairwise peak-list comparison process. <i>BMC Bioinformatics</i> , 2005 , 6, 285	3.6	15
30	Multiple Structural RNA Alignment with Lagrangian Relaxation. <i>Lecture Notes in Computer Science</i> , 2005 , 303-314	0.9	5
29	Algorithms for the Automated Absolute Quantification of Diagnostic Markers in Complex Proteomics Samples. <i>Lecture Notes in Computer Science</i> , 2005 , 151-162	0.9	2
28	Differenzielle Proteomanalyse [Experimentelle Methoden, algorithmische Herausforderungen (Differential Analysis in Proteomics: Experimental Methods, Algorithmic Challenges)]. <i>IT - Information Technology</i> , 2004 , 46, 31-38	0.4	
27	Whole-genome shotgun assembly and comparison of human genome assemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 1916-21	11.5	142
26	Optimal robust non-unique probe selection using Integer Linear Programming. <i>Bioinformatics</i> , 2004 , 20 Suppl 1, i186-93	7.2	62
25	A comparison of whole-genome shotgun-derived mouse chromosome 16 and the human genome. <i>Science</i> , 2002 , 296, 1661-71	33.3	305
24	The greedy path-merging algorithm for contig scaffolding. <i>Journal of the ACM</i> , 2002 , 49, 603-615	2	61
23	Multiple sequence alignment with arbitrary gap costs: computing an optimal solution using polyhedral combinatorics. <i>Bioinformatics</i> , 2002 , 18 Suppl 2, S4-S16	7.2	19
22	Segment Match Refinement and Applications. <i>Lecture Notes in Computer Science</i> , 2002 , 126-139	0.9	6
21	Recent segmental duplications in the human genome. <i>Science</i> , 2002 , 297, 1003-7	33.3	1051
20	The sequence of the human genome. <i>Science</i> , 2001 , 291, 1304-51	33.3	10609

19	Design of a compartmentalized shotgun assembler for the human genome. <i>Bioinformatics</i> , 2001 , 17 Suppl 1, S132-9	7.2	46
18	The greedy path-merging algorithm for sequence assembly 2001 ,		9
17	Comparing Assemblies Using Fragments and Mate-Pairs. <i>Lecture Notes in Computer Science</i> , 2001 , 294-306	9	14
16	A polyhedral approach to sequence alignment problems. <i>Discrete Applied Mathematics</i> , 2000 , 104, 143-186	186	33
15	The genome sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000 , 287, 2185-95	33.3	4857
14	An iterative method for faster sum-of-pairs multiple sequence alignment. <i>Bioinformatics</i> , 2000 , 16, 808-142	142	44
13	A whole-genome assembly of <i>Drosophila</i> . <i>Science</i> , 2000 , 287, 2196-204	33.3	1204
12	The practical use of the A* algorithm for exact multiple sequence alignment. <i>Journal of Computational Biology</i> , 2000 , 7, 655-71	1.7	16
11	An exact solution for the segment-to-segment multiple sequence alignment problem. <i>Bioinformatics</i> , 1999 , 15, 203-10	7.2	29
10	A polyhedral approach to RNA sequence structure alignment 1998 ,		13
9	A polyhedral approach to RNA sequence structure alignment. <i>Journal of Computational Biology</i> , 1998 , 5, 517-30	1.7	34
8	Bioinformatics Support for Genome-Sequencing Projects 25-55		
7	Visualization challenges for a new cyber-pharmaceutical computing paradigm		4
6	Biological Sequence Analysis Using the SeqAn C++ Library		2
5	PriSeT: Efficient De Novo Primer Discovery		1
4	Optimum Search Schemes for Approximate String Matching Using Bidirectional FM-Index		1
3	ganon: precise metagenomics classification against large and up-to-date sets of reference sequences		1
2	Computational Pan-Genomics: Status, Promises and Challenges		6

1 GenMap: Fast and Exact Computation of Genome Mappability

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