Knut Hj Reinert

List of Publications by Citations

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	The sequence of the human genome. *Science*, **2001**, 291, 1304-51	33.3	10609
125	The genome sequence of Drosophila melanogaster. *Science*, **2000**, 287, 2185-95	33.3	4857
124	A whole-genome assembly of Drosophila. *Science*, **2000**, 287, 2196-204	33.3	1204
123	Recent segmental duplications in the human genome. *Science*, **2002**, 297, 1003-7	33.3	1051
122	OpenMS - an open-source software framework for mass spectrometry. *BMC Bioinformatics*, **2008**, 9, 163	3.6	474
121	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. *Nature Methods*, **2016**, 13, 741-8	21.6	337
120	A comparison of whole-genome shotgun-derived mouse chromosome 16 and the human genome. *Science*, **2002**, 296, 1661-71	33.3	305
119	TOPP--the OpenMS proteomics pipeline. *Bioinformatics*, **2007**, 23, e191-7	7.2	216
118	SeqAn an efficient, generic C++ library for sequence analysis. *BMC Bioinformatics*, **2008**, 9, 11	3.6	210
117	Tools for label-free peptide quantification. *Molecular and Cellular Proteomics*, **2013**, 12, 549-56	7.6	171
116	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, 1916-21	11.5	142
115	Computational pan-genomics: status, promises and challenges. *Briefings in Bioinformatics*, **2018**, 19, 118-135	7.4	130
114	RazerS--fast read mapping with sensitivity control. *Genome Research*, **2009**, 19, 1646-54	9.7	104
113	Approaching clinical proteomics: current state and future fields of application in fluid proteomics. *Clinical Chemistry and Laboratory Medicine*, **2009**, 47, 724-44	5.9	94
112	RazerS 3: faster, fully sensitive read mapping. *Bioinformatics*, **2012**, 28, 2592-9	7.2	91
111	Detecting genomic indel variants with exact breakpoints in single- and paired-end sequencing data using SplazerS. *Bioinformatics*, **2012**, 28, 619-27	7.2	84
110	Flexbar 3.0 - SIMD and multicore parallelization. *Bioinformatics*, **2017**, 33, 2941-2942	7.2	74

109	Alignment of Next-Generation Sequencing Reads. *Annual Review of Genomics and Human Genetics*, **2015**, 16, 133-51	9.7	72
108	A geometric approach for the alignment of liquid chromatography-mass spectrometry data. *Bioinformatics*, **2007**, 23, i273-81	7.2	68
107	Absolute myoglobin quantitation in serum by combining two-dimensional liquid chromatography-electrospray ionization mass spectrometry and novel data analysis algorithms. *Journal of Proteome Research*, **2006**, 5, 414-21	5.6	68
106	IMSEQ--a fast and error aware approach to immunogenetic sequence analysis. *Bioinformatics*, **2015**, 31, 2963-71	7.2	67
105	Fast and accurate read mapping with approximate seeds and multiple backtracking. *Nucleic Acids Research*, **2013**, 41, e78	20.1	63
104	Accurate multiple sequence-structure alignment of RNA sequences using combinatorial optimization. *BMC Bioinformatics*, **2007**, 8, 271	3.6	63
103	Optimal robust non-unique probe selection using Integer Linear Programming. *Bioinformatics*, **2004** , 20 Suppl 1, i186-93	7.2	62
102	OpenMS - A platform for reproducible analysis of mass spectrometry data. *Journal of Biotechnology* , **2017**, 261, 142-148	3.7	61
101	OpenMS and TOPP: open source software for LC-MS data analysis. *Methods in Molecular Biology*, **2011**, 696, 353-67	1.4	61
100	The greedy path-merging algorithm for contig scaffolding. *Journal of the ACM*, **2002**, 49, 603-615	2	61
99	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. *Briefings in Bioinformatics*, **2021**, 22, 642-663	13.4	56
98	Integration preferences of wildtype AAV-2 for consensus rep-binding sites at numerous loci in the human genome. *PLoS Pathogens*, **2010**, 6, e1000985	7.6	53
97	Evaluation of drug-induced neurotoxicity based on metabolomics, proteomics and electrical activity measurements in complementary CNS in vitro models. *Toxicology in Vitro*, **2015**, 30, 138-65	3.6	51
96	A novel and well-defined benchmarking method for second generation read mapping. *BMC Bioinformatics*, **2011**, 12, 210	3.6	51
95	The SeqAn C++ template library for efficient sequence analysis: A resource for programmers. *Journal of Biotechnology*, **2017**, 261, 157-168	3.7	49
94	Design of a compartmentalized shotgun assembler for the human genome. *Bioinformatics*, **2001**, 17 Suppl 1, S132-9	7.2	46
93	Lambda: the local aligner for massive biological data. *Bioinformatics*, **2014**, 30, i349-55	7.2	44
92	An iterative method for faster sum-of-pairs multiple sequence alignment. *Bioinformatics*, **2000**, 16, 808-14	7.2	44

91	TOPPAS: a graphical workflow editor for the analysis of high-throughput proteomics data. *Journal of Proteome Research*, **2012**, 11, 3914-20	5.6	43
90	NetCoffee: a fast and accurate global alignment approach to identify functionally conserved proteins in multiple networks. *Bioinformatics*, **2014**, 30, 540-8	7.2	42
89	Fiona: a parallel and automatic strategy for read error correction. *Bioinformatics*, **2014**, 30, i356-63	7.2	42
88	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**, 75, 816-32	4.6	41
87	LC-MSsim--a simulation software for liquid chromatography mass spectrometry data. *BMC Bioinformatics*, **2008**, 9, 423	3.6	40
86	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. *Journal of Proteomics*, **2017**, 150, 170-182	3.9	39
85	Segment-based multiple sequence alignment. *Bioinformatics*, **2008**, 24, i187-92	7.2	39
84	MSSimulator: Simulation of mass spectrometry data. *Journal of Proteome Research*, **2011**, 10, 2922-9	5.6	36
83	MicroRazerS: rapid alignment of small RNA reads. *Bioinformatics*, **2010**, 26, 123-4	7.2	36
82	CIDANE: comprehensive isoform discovery and abundance estimation. *Genome Biology*, **2016**, 17, 16	18.3	34
81	A polyhedral approach to RNA sequence structure alignment. *Journal of Computational Biology*, **1998**, 5, 517-30	1.7	34
80	A polyhedral approach to sequence alignment problems. *Discrete Applied Mathematics*, **2000**, 104, 143-186	1.8	33
79	Gustaf: Detecting and correctly classifying SVs in the NGS twilight zone. *Bioinformatics*, **2014**, 30, 3484-90	7.2	31
78	An exact solution for the segment-to-segment multiple sequence alignment problem. *Bioinformatics*, **1999**, 15, 203-10	7.2	29
77	GenMap: ultra-fast computation of genome mappability. *Bioinformatics*, **2020**, 36, 3687-3692	7.2	27
76	Genome alignment with graph data structures: a comparison. *BMC Bioinformatics*, **2014**, 15, 99	3.6	26
75	Workflows for automated downstream data analysis and visualization in large-scale computational mass spectrometry. *Proteomics*, **2015**, 15, 1443-7	4.8	26
74	LocalAli: an evolutionary-based local alignment approach to identify functionally conserved modules in multiple networks. *Bioinformatics*, **2015**, 31, 363-72	7.2	25

73	A consistency-based consensus algorithm for de novo and reference-guided sequence assembly of short reads. *Bioinformatics*, **2009**, 25, 1118-24	7.2	24
72	Journaled string tree-a scalable data structure for analyzing thousands of similar genomes on your laptop. *Bioinformatics*, **2014**, 30, 3499-505	7.2	23
71	High-accuracy peak picking of proteomics data using wavelet techniques. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2006**, 243-54	1.3	21
70	Fast Structural Alignment of Biomolecules Using a Hash Table, N-Grams and String Descriptors. *Algorithms*, **2009**, 2, 692-709	1.8	20
69	Statistical quality assessment and outlier detection for liquid chromatography-mass spectrometry experiments. *BioData Mining*, **2009**, 2, 4	4.3	20
68	Analytical model of peptide mass cluster centres with applications. *Proteome Science*, **2006**, 4, 18	2.6	20
67	SLIMM: species level identification of microorganisms from metagenomes. *PeerJ*, **2017**, 5, e3138	3.1	20
66	STELLAR: fast and exact local alignments. *BMC Bioinformatics*, **2011**, 12 Suppl 9, S15	3.6	19
65	Multiple sequence alignment with arbitrary gap costs: computing an optimal solution using polyhedral combinatorics. *Bioinformatics*, **2002**, 18 Suppl 2, S4-S16	7.2	19
64	Calibration of mass spectrometric peptide mass fingerprint data without specific external or internal calibrants. *BMC Bioinformatics*, **2005**, 6, 203	3.6	18
63	Generic accelerated sequence alignment in SeqAn using vectorization and multi-threading. *Bioinformatics*, **2018**, 34, 3437-3445	7.2	17
62	OpenMS and TOPP: open source software for LC-MS data analysis. *Methods in Molecular Biology*, **2010**, 604, 201-11	1.4	16
61	An iterative strategy for precursor ion selection for LC-MS/MS based shotgun proteomics. *Journal of Proteome Research*, **2009**, 8, 3239-51	5.6	16
60	Integer linear programming approaches for non-unique probe selection. *Discrete Applied Mathematics*, **2007**, 155, 840-856	1	16
59	The practical use of the A* algorithm for exact multiple sequence alignment. *Journal of Computational Biology*, **2000**, 7, 655-71	1.7	16
58	DREAM-Yara: an exact read mapper for very large databases with short update time. *Bioinformatics*, **2018**, 34, i766-i772	7.2	16
57	Rapid and comprehensive impurity profiling of synthetic thyroxine by ultrahigh-performance liquid chromatography-high-resolution mass spectrometry. *Analytical Chemistry*, **2013**, 85, 3309-17	7.8	15
56	Transformation and other factors of the peptide mass spectrometry pairwise peak-list comparison process. *BMC Bioinformatics*, **2005**, 6, 285	3.6	15

55	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	11.9	15
54	Formula Feeding Predisposes Neonatal Piglets to Clostridium difficile Gut Infection. *Journal of Infectious Diseases*, **2018**, 217, 1442-1452	7	14
53	ganon: precise metagenomics classification against large and up-to-date sets of reference sequences. *Bioinformatics*, **2020**, 36, i12-i20	7.2	14
52	Comparing Assemblies Using Fragments and Mate-Pairs. *Lecture Notes in Computer Science*, **2001**, 294-306	0.9	14
51	A polyhedral approach to RNA sequence structure alignment **1998**,		13
50	Methods for the detection and assembly of novel sequence in high-throughput sequencing data. *Bioinformatics*, **2015**, 31, 1904-12	7.2	12
49	Ranbow: A fast and accurate method for polyploid haplotype reconstruction. *PLoS Computational Biology*, **2020**, 16, e1007843	5	11
48	From the desktop to the grid: scalable bioinformatics via workflow conversion. *BMC Bioinformatics*, **2016**, 17, 127	3.6	11
47	Computational quantification of peptides from LC-MS data. *Journal of Computational Biology*, **2008**, 15, 685-704	1.7	11
46	A branch-and-cut algorithm for multiple sequence alignment. *Mathematical Programming*, **2006**, 105, 387-425	2.1	11
45	Fast and Adaptive Variable Order Markov Chain Construction. *Lecture Notes in Computer Science*, **2008**, 306-317	0.9	11
44	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	0.9	10
43	Antilope--a Lagrangian relaxation approach to the de novo peptide sequencing problem. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2012**, 9, 385-94	3	9
42	HIGH-ACCURACY PEAK PICKING OF PROTEOMICS DATA USING WAVELET TECHNIQUES **2005**,		9
41	The greedy path-merging algorithm for sequence assembly **2001**,		9
40	Alternate-locus aware variant calling in whole genome sequencing. *Genome Medicine*, **2016**, 8, 130	14.4	9
39	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, 2385-90	7.8	8
38	EPIFANY: A Method for Efficient High-Confidence Protein Inference. *Journal of Proteome Research*, **2020**, 19, 1060-1072	5.6	6

37	High-performance liquid chromatography with electrospray ionization ion mobility spectrometry: Characterization, data management, and applications. *Journal of Separation Science*, **2016**, 39, 4756-4764	2.4	6
36	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	4.5	6
35	The duplication-loss small phylogeny problem: from cherries to trees. *Journal of Computational Biology*, **2013**, 20, 643-59	1.7	6
34	A Fast and Accurate Algorithm for the Quantification of Peptides from Mass Spectrometry Data. *Lecture Notes in Computer Science*, **2007**, 473-487	0.9	6
33	Segment Match Refinement and Applications. *Lecture Notes in Computer Science*, **2002**, 126-139	0.9	6
32	Computational Pan-Genomics: Status, Promises and Challenges		6
31	VARSCOT: variant-aware detection and scoring enables sensitive and personalized off-target detection for CRISPR-Cas9. *BMC Biotechnology*, **2019**, 19, 40	3.5	5
30	Optimal precursor ion selection for LC-MALDI MS/MS. *BMC Bioinformatics*, **2013**, 14, 56	3.6	5
29	Biomarker discovery and redundancy reduction towards classification using a multi-factorial MALDI-TOF MS T2DM mouse model dataset. *BMC Bioinformatics*, **2011**, 12, 140	3.6	5
28	Integer Linear Programming in Computational Biology. *Lecture Notes in Computer Science*, **2009**, 199-218	0.9	5
27	Multiple Structural RNA Alignment with Lagrangian Relaxation. *Lecture Notes in Computer Science*, **2005**, 303-314	0.9	5
26	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	4.4	4
25	PPINGUIN: Peptide Profiling Guided Identification of Proteins improves quantitation of iTRAQ ratios. *BMC Bioinformatics*, **2012**, 13, 34	3.6	4
24	Optimal decharging and clustering of charge ladders generated in ESI-MS. *Journal of Proteome Research*, **2010**, 9, 2688-95	5.6	4
23	Fast and Accurate Structural RNA Alignment by Progressive Lagrangian Optimization. *Lecture Notes in Computer Science*, **2005**, 217-228	0.9	4
22	Visualization challenges for a new cyber-pharmaceutical computing paradigm		4
21	GenMap: Fast and Exact Computation of Genome Mappability		4
20	Scalable string similarity search/join with approximate seeds and multiple backtracking **2013**,		3

19	Bioinformatics for qualitative and quantitative proteomics. *Methods in Molecular Biology*, **2011**, 719, 331-49	1.4	3
18	Rapid and Culture Free Identification of in Hare Carcasses by High-Resolution Tandem Mass Spectrometry Proteotyping. *Frontiers in Microbiology*, **2020**, 11, 636	5.7	2
17	Predict-IV project overview (EU grant 202222): non animal-based toxicity profiling by integrating toxico dynamics and biokinetics. *Toxicology Letters*, **2013**, 221, S7	4.4	2
16	Inferring proteolytic processes from mass spectrometry time series data using degradation graphs. *PLoS ONE*, **2012**, 7, e40656	3.7	2
15	Robust consensus computation. *BMC Bioinformatics*, **2008**, 9,	3.6	2
14	Biological Sequence Analysis Using the SeqAn C++ Library		2
13	Profiling of Sub-Lethal in Vitro Effects of Multi-Walled Carbon Nanotubes Reveals Changes in Chemokines and Chemokine Receptors. *Nanomaterials*, **2021**, 11,	5.4	2
12	Algorithms for the Automated Absolute Quantification of Diagnostic Markers in Complex Proteomics Samples. *Lecture Notes in Computer Science*, **2005**, 151-162	0.9	2
11	PriSeT: Efficient De Novo Primer Discovery		1
10	Optimum Search Schemes for Approximate String Matching Using Bidirectional FM-Index		1
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8	LaRA 2: parallel and vectorized program for sequence-structure alignment of RNA sequences.. *BMC Bioinformatics*, **2022**, 23, 18	3.6	0
7	Testing assembly strategies of Francisella tularensis genomes to infer an evolutionary conservation analysis of genomic structures. *BMC Genomics*, **2021**, 22, 822	4.5	0
6	Raptor: A fast and space-efficient pre-filter for querying very large collections of nucleotide sequences. *IScience*, **2021**, 24, 102782	6.1	0
5	UHPLC-HRMS-Experimente planen und auswerten Beispiel Thyroxin. *Nachrichten Aus Der Chemie* , **2013**, 61, 455-458	0.1	
4	Bioinformatics Support for Genome-Sequencing Projects25-55		
3	Differenzielle Proteomanalyse Experimentelle Methoden, algorithmische Herausforderungen (Differential Analysis in Proteomics: Experimental Methods, Algorithmic Challenges). *IT - Information Technology*, **2004**, 46, 31-38	0.4	
2	Practical Multiple Sequence Alignment **2010**, 21-43		

1 Hidden Breakpoints in Genome Alignments. *Lecture Notes in Computer Science*, **2012**, 391-403 0.9