

Knut Hj Reinert

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8654817/publications.pdf>

Version: 2024-02-01

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	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	12.6	12,623
2	The Genome Sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000, 287, 2185-2195.	12.6	5,566
3	A Whole-Genome Assembly of <i>Drosophila</i> . <i>Science</i> , 2000, 287, 2196-2204.	12.6	1,449
4	Recent Segmental Duplications in the Human Genome. <i>Science</i> , 2002, 297, 1003-1007.	12.6	1,238
5	OpenMS – An open-source software framework for mass spectrometry. <i>BMC Bioinformatics</i> , 2008, 9, 163.	2.6	556
6	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748.	19.0	537
7	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. <i>Science</i> , 2002, 296, 1661-1671.	12.6	344
8	SeqAn An efficient, generic C++ library for sequence analysis. <i>BMC Bioinformatics</i> , 2008, 9, 11.	2.6	287
9	TOPP–the OpenMS proteomics pipeline. <i>Bioinformatics</i> , 2007, 23, e191-e197.	4.1	249
10	Computational pan-genomics: status, promises and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw089.	6.5	207
11	Tools for Label-free Peptide Quantification. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 549-556.	3.8	198
12	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, 1916-1921.	7.1	164
13	Flexbar 3.0 – SIMD and multicore parallelization. <i>Bioinformatics</i> , 2017, 33, 2941-2942.	4.1	150
14	RazerS 3: Faster, fully sensitive read mapping. <i>Bioinformatics</i> , 2012, 28, 2592-2599.	4.1	128
15	RazerS – fast read mapping with sensitivity control. <i>Genome Research</i> , 2009, 19, 1646-1654.	5.5	125
16	Approaching clinical proteomics: current state and future fields of application in fluid proteomics. <i>Clinical Chemistry and Laboratory Medicine</i> , 2009, 47, 724-44.	2.3	112
17	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.	6.5	110
18	GenMap: ultra-fast computation of genome mappability. <i>Bioinformatics</i> , 2020, 36, 3687-3692.	4.1	107

#	ARTICLE	IF	CITATIONS
19	IMSEQ—a fast and error aware approach to immunogenetic sequence analysis. <i>Bioinformatics</i> , 2015, 31, 2963-2971.	4.1	98
20	Detecting genomic indel variants with exact breakpoints in single- and paired-end sequencing data using SplazerS. <i>Bioinformatics</i> , 2012, 28, 619-627.	4.1	95
21	Alignment of Next-Generation Sequencing Reads. <i>Annual Review of Genomics and Human Genetics</i> , 2015, 16, 133-151.	6.2	91
22	The SeqAn C++ template library for efficient sequence analysis: A resource for programmers. <i>Journal of Biotechnology</i> , 2017, 261, 157-168.	3.8	90
23	OpenMS — A platform for reproducible analysis of mass spectrometry data. <i>Journal of Biotechnology</i> , 2017, 261, 142-148.	3.8	85
24	A geometric approach for the alignment of liquid chromatography—mass spectrometry data. <i>Bioinformatics</i> , 2007, 23, i273-i281.	4.1	78
25	The greedy path-merging algorithm for contig scaffolding. <i>Journal of the ACM</i> , 2002, 49, 603-615.	2.2	77
26	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, 414-421.	3.7	77
27	Fast and accurate read mapping with approximate seeds and multiple backtracking. <i>Nucleic Acids Research</i> , 2013, 41, e78-e78.	14.5	77
28	Optimal robust non-unique probe selection using Integer Linear Programming. <i>Bioinformatics</i> , 2004, 20, i186-i193.	4.1	75
29	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, 138-165.	2.4	75
30	Accurate multiple sequence-structure alignment of RNA sequences using combinatorial optimization. <i>BMC Bioinformatics</i> , 2007, 8, 271.	2.6	74
31	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.	4.7	72
32	OpenMS and TOPP: Open Source Software for LC-MS Data Analysis. <i>Methods in Molecular Biology</i> , 2011, 696, 353-367.	0.9	68
33	A novel and well-defined benchmarking method for second generation read mapping. <i>BMC Bioinformatics</i> , 2011, 12, 210.	2.6	63
34	Lambda: the local aligner for massive biological data. <i>Bioinformatics</i> , 2014, 30, i349-i355.	4.1	60
35	Fiona: a parallel and automatic strategy for read error correction. <i>Bioinformatics</i> , 2014, 30, i356-i363.	4.1	59
36	Design of a compartmentalized shotgun assembler for the human genome. <i>Bioinformatics</i> , 2001, 17, S132-S139.	4.1	56

#	ARTICLE	IF	CITATIONS
37	NetCoffee: a fast and accurate global alignment approach to identify functionally conserved proteins in multiple networks. <i>Bioinformatics</i> , 2014, 30, 540-548.	4.1	56
38	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. <i>Journal of Proteomics</i> , 2017, 150, 170-182.	2.4	56
39	An iterative method for faster sum-of-pairs multiple sequence alignment. <i>Bioinformatics</i> , 2000, 16, 808-814.	4.1	54
40	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, 75A, 816-832.	1.5	52
41	TOPPAS: A Graphical Workflow Editor for the Analysis of High-Throughput Proteomics Data. <i>Journal of Proteome Research</i> , 2012, 11, 3914-3920.	3.7	50
42	A Polyhedral Approach to RNA Sequence Structure Alignment. <i>Journal of Computational Biology</i> , 1998, 5, 517-530.	1.6	48
43	A polyhedral approach to sequence alignment problems. <i>Discrete Applied Mathematics</i> , 2000, 104, 143-186.	0.9	48
44	Gustaf: Detecting and correctly classifying SVs in the NGS twilight zone. <i>Bioinformatics</i> , 2014, 30, 3484-3490.	4.1	46
45	CIDANE: comprehensive isoform discovery and abundance estimation. <i>Genome Biology</i> , 2016, 17, 16.	8.8	45
46	Segment-based multiple sequence alignment. <i>Bioinformatics</i> , 2008, 24, i187-i192.	4.1	44
47	LC-MSsim – a simulation software for liquid chromatography mass spectrometry data. <i>BMC Bioinformatics</i> , 2008, 9, 423.	2.6	42
48	MSSimulator: Simulation of Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2011, 10, 2922-2929.	3.7	42
49	ganon: precise metagenomics classification against large and up-to-date sets of reference sequences. <i>Bioinformatics</i> , 2020, 36, i12-i20.	4.1	39
50	MicroRazerS: rapid alignment of small RNA reads. <i>Bioinformatics</i> , 2010, 26, 123-124.	4.1	37
51	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.	9.8	37
52	An exact solution for the segment-to-segment multiple sequence alignment problem. <i>Bioinformatics</i> , 1999, 15, 203-210.	4.1	35
53	HIGH-ACCURACY PEAK PICKING OF PROTEOMICS DATA USING WAVELET TECHNIQUES. , 2005, , .		33
54	Journalized string tree – a scalable data structure for analyzing thousands of similar genomes on your laptop. <i>Bioinformatics</i> , 2014, 30, 3499-3505.	4.1	32

#	ARTICLE	IF	CITATIONS
55	Genome alignment with graph data structures: a comparison. BMC Bioinformatics, 2014, 15, 99.	2.6	32
56	Workflows for automated downstream data analysis and visualization in large-scale computational mass spectrometry. Proteomics, 2015, 15, 1443-1447.	2.2	32
57	LocalAli: an evolutionary-based local alignment approach to identify functionally conserved modules in multiple networks. Bioinformatics, 2015, 31, 363-372.	4.1	32
58	A consistency-based consensus algorithm for de novo and reference-guided sequence assembly of short reads. Bioinformatics, 2009, 25, 1118-1124.	4.1	30
59	Generic accelerated sequence alignment in SeqAn using vectorization and multi-threading. Bioinformatics, 2018, 34, 3437-3445.	4.1	30
60	DREAM-Yara: an exact read mapper for very large databases with short update time. Bioinformatics, 2018, 34, i766-i772.	4.1	29
61	SLIMM: species level identification of microorganisms from metagenomes. PeerJ, 2017, 5, e3138.	2.0	29
62	STELLAR: fast and exact local alignments. BMC Bioinformatics, 2011, 12, S15.	2.6	28
63	OpenMS and TOPP: Open Source Software for LC-MS Data Analysis. Methods in Molecular Biology, 2010, 604, 201-211.	0.9	27
64	The Practical Use of the A* Algorithm for Exact Multiple Sequence Alignment. Journal of Computational Biology, 2000, 7, 655-671.	1.6	25
65	Analytical model of peptide mass cluster centres with applications. Proteome Science, 2006, 4, 18.	1.7	25
66	Fast Structural Alignment of Biomolecules Using a Hash Table, N-Grams and String Descriptors. Algorithms, 2009, 2, 692-709.	2.1	23
67	Statistical quality assessment and outlier detection for liquid chromatography-mass spectrometry experiments. BioData Mining, 2009, 2, 4.	4.0	23
68	Ranbow: A fast and accurate method for polyploid haplotype reconstruction. PLoS Computational Biology, 2020, 16, e1007843.	3.2	23
69	Multiple sequence alignment with arbitrary gap costs: Computing an optimal solution using polyhedral combinatorics. Bioinformatics, 2002, 18, S4-S16.	4.1	22
70	Integer linear programming approaches for non-unique probe selection. Discrete Applied Mathematics, 2007, 155, 840-856.	0.9	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.	2.6	21

#	ARTICLE	IF	CITATIONS
73	EPIFANY: A Method for Efficient High-Confidence Protein Inference. <i>Journal of Proteome Research</i> , 2020, 19, 1060-1072.	3.7	20
74	An Iterative Strategy for Precursor Ion Selection for LC-MS/MS Based Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2009, 8, 3239-3251.	3.7	18
75	Methods for the detection and assembly of novel sequence in high-throughput sequencing data. <i>Bioinformatics</i> , 2015, 31, 1904-1912.	4.1	18
76	Formula Feeding Predisposes Neonatal Piglets to <i>Clostridium difficile</i> Gut Infection. <i>Journal of Infectious Diseases</i> , 2018, 217, 1442-1452.	4.0	18
77	Transformation and other factors of the peptide mass spectrometry pairwise peak-list comparison process. <i>BMC Bioinformatics</i> , 2005, 6, 285.	2.6	17
78	Rapid and Comprehensive Impurity Profiling of Synthetic Thyroxine by Ultrahigh-Performance Liquid Chromatography-High-Resolution Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 3309-3317.	6.5	17
79	A branch-and-cut algorithm for multiple sequence alignment. <i>Mathematical Programming</i> , 2006, 105, 387-425.	2.4	16
80	Alternate-locus aware variant calling in whole genome sequencing. <i>Genome Medicine</i> , 2016, 8, 130.	8.2	16
81	Comparing Assemblies Using Fragments and Mate-Pairs. <i>Lecture Notes in Computer Science</i> , 2001, , 294-306.	1.3	16
82	Fast and Adaptive Variable Order Markov Chain Construction. <i>Lecture Notes in Computer Science</i> , 2008, , 306-317.	1.3	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. <i>Journal of Computational Biology</i> , 2008, 15, 685-704.	1.6	12
86	AntilopeA Lagrangian Relaxation Approach to the de novo Peptide Sequencing Problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 385-394.	3.0	12
87	From the desktop to the grid: scalable bioinformatics via workflow conversion. <i>BMC Bioinformatics</i> , 2016, 17, 127.	2.6	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. <i>Analytical Chemistry</i> , 2013, 85, 2385-2390.	6.5	11
89	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.	1.3	11
90	A Fast and Accurate Algorithm for the Quantification of Peptides from Mass Spectrometry Data. <i>Lecture Notes in Computer Science</i> , 2007, , 473-487.	1.3	9

#	ARTICLE	IF	CITATIONS
91	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.	2.5	9
92	VARSCOT: variant-aware detection and scoring enables sensitive and personalized off-target detection for CRISPR-Cas9. <i>BMC Biotechnology</i> , 2019, 19, 40.	3.3	9
93	Rapid and Culture Free Identification of Francisella in Hare Carcasses by High-Resolution Tandem Mass Spectrometry Proteotyping. <i>Frontiers in Microbiology</i> , 2020, 11, 636.	3.5	8
94	Segment Match Refinement and Applications. <i>Lecture Notes in Computer Science</i> , 2002, , 126-139.	1.3	7
95	Optimal Decharging and Clustering of Charge Ladders Generated in ESI-MS. <i>Journal of Proteome Research</i> , 2010, 9, 2688-2695.	3.7	7
96	The Duplication-Loss Small Phylogeny Problem: From Cherries to Trees. <i>Journal of Computational Biology</i> , 2013, 20, 643-659.	1.6	7
97	Raptor: A fast and space-efficient pre-filter for querying very large collections of nucleotide sequences. <i>IScience</i> , 2021, 24, 102782.	4.1	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. <i>Journal of Chromatography A</i> , 2014, 1371, 196-203.	3.7	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. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 989-997.	3.7	6
100	Profiling of Sub-Lethal in Vitro Effects of Multi-Walled Carbon Nanotubes Reveals Changes in Chemokines and Chemokine Receptors. <i>Nanomaterials</i> , 2021, 11, 883.	4.1	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. <i>BMC Bioinformatics</i> , 2011, 12, 140.	2.6	5
103	Optimal precursor ion selection for LC-MALDI MS/MS. <i>BMC Bioinformatics</i> , 2013, 14, 56.	2.6	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. <i>Bioinformatics</i> , 2021, 37, 3934-3935.	4.1	5
106	Multiple Structural RNA Alignment with Lagrangian Relaxation. <i>Lecture Notes in Computer Science</i> , 2005, , 303-314.	1.3	5
107	Integer Linear Programming in Computational Biology. <i>Lecture Notes in Computer Science</i> , 2009, , 199-218.	1.3	5
108	Fast and Accurate Structural RNA Alignment by Progressive Lagrangian Optimization. <i>Lecture Notes in Computer Science</i> , 2005, , 217-228.	1.3	4

#	ARTICLE	IF	CITATIONS
109	Bioinformatics for Qualitative and Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2011, 719, 331-349.	0.9	4
110	PPINGUIN: Peptide Profiling Guided Identification of Proteins improves quantitation of iTRAQ ratios. <i>BMC Bioinformatics</i> , 2012, 13, 34.	2.6	4
111	Algorithms for the Automated Absolute Quantification of Diagnostic Markers in Complex Proteomics Samples. <i>Lecture Notes in Computer Science</i> , 2005, , 151-162.	1.3	4
112	Robust consensus computation. <i>BMC Bioinformatics</i> , 2008, 9, .	2.6	3
113	LaRA 2: parallel and vectorized program for sequenceâ€“structure alignment of RNA sequences. <i>BMC Bioinformatics</i> , 2022, 23, 18.	2.6	3
114	Inferring Proteolytic Processes from Mass Spectrometry Time Series Data Using Degradation Graphs. <i>PLoS ONE</i> , 2012, 7, e40656.	2.5	2
115	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.	0.8	2
116	Testing assembly strategies of <i>Francisella tularensis</i> genomes to infer an evolutionary conservation analysis of genomic structures. <i>BMC Genomics</i> , 2021, 22, 822.	2.8	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). <i>IT - Information Technology</i> , 2004, 46, 31-38.	0.9	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. <i>Lecture Notes in Computer Science</i> , 2012, , 391-403.	1.3	0