

# Gunnar W Klau

## List of Publications by Year in descending order

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86  
papers

3,726  
citations

236925

25  
h-index

161849

54  
g-index

106  
all docs

106  
docs citations

106  
times ranked

4896  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identifying functional modules in protein-protein interaction networks: an integrated exact approach. <i>Bioinformatics</i> , 2008, 24, i223-i231.	4.1	485
2	W <sub>H</sub> ap: Weighted Haplotype Assembly for Future-Generation Sequencing Reads. <i>Journal of Computational Biology</i> , 2015, 22, 498-509.	1.6	337
3	BioNet: an R-Package for the functional analysis of biological networks. <i>Bioinformatics</i> , 2010, 26, 1129-1130.	4.1	215
4	Computational pan-genomics: status, promises and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw089.	6.5	207
5	An Algorithmic Framework for the Exact Solution of the Prize-Collecting Steiner Tree Problem. <i>Mathematical Programming</i> , 2006, 105, 427-449.	2.4	171
6	A new graph-based method for pairwise global network alignment. <i>BMC Bioinformatics</i> , 2009, 10, S59.	2.6	162
7	Charge Group Partitioning in Biomolecular Simulation. <i>Journal of Computational Biology</i> , 2013, 20, 188-198.	1.6	145
8	Ancient Dispersal of the Human Fungal Pathogen <i>Cryptococcus gattii</i> from the Amazon Rainforest. <i>PLoS ONE</i> , 2013, 8, e71148.	2.5	122
9	CLEVER: clique-enumerating variant finder. <i>Bioinformatics</i> , 2012, 28, 2875-2882.	4.1	101
10	An integer linear programming approach for finding deregulated subgraphs in regulatory networks. <i>Nucleic Acids Research</i> , 2012, 40, e43-e43.	14.5	84
11	Optimal robust non-unique probe selection using Integer Linear Programming. <i>Bioinformatics</i> , 2004, 20, i186-i193.	4.1	75
12	Accurate multiple sequence-structure alignment of RNA sequences using combinatorial optimization. <i>BMC Bioinformatics</i> , 2007, 8, 271.	2.6	74
13	Exact Algorithms for Cluster Editing: Evaluation and Experiments. <i>Algorithmica</i> , 2011, 60, 316-334.	1.3	71
14	A Critical Evaluation of Network and Pathway-Based Classifiers for Outcome Prediction in Breast Cancer. <i>PLoS ONE</i> , 2012, 7, e34796.	2.5	56
15	Haplotype threading: accurate polyploid phasing from long reads. <i>Genome Biology</i> , 2020, 21, 252.	8.8	50
16	Human-guided search. <i>Journal of Heuristics</i> , 2010, 16, 289-310.	1.4	47
17	CIDANE: comprehensive isoform discovery and abundance estimation. <i>Genome Biology</i> , 2016, 17, 16.	8.8	45
18	Logic models to predict continuous outputs based on binary inputs with an application to personalized cancer therapy. <i>Scientific Reports</i> , 2016, 6, 36812.	3.3	43

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19	Single-cell transcriptomics defines heterogeneity of epicardial cells and fibroblasts within the infarcted murine heart. <i>ELife</i> , 2021, 10, .	6.0	42
20	Current composite-feature classification methods do not outperform simple single-genes classifiers in breast cancer prognosis. <i>Frontiers in Genetics</i> , 2013, 4, 289.	2.3	41
21	H <sub>ap</sub> C <sub>ol</sub> : accurate and memory-efficient haplotype assembly from long reads. <i>Bioinformatics</i> , 2016, 32, 1610-1617.	4.1	40
22	Investigating human-computer optimization. , 2002, , .		38
23	Orthogonal Graph Drawing. <i>Lecture Notes in Computer Science</i> , 2001, , 121-171.	1.3	31
24	Using anticlustering to partition data sets into equivalent parts.. <i>Psychological Methods</i> , 2021, 26, 161-174.	3.5	30
25	Robustness and accuracy of functional modules in integrated network analysis. <i>Bioinformatics</i> , 2012, 28, 1887-1894.	4.1	29
26	On the Minimum Error Correction Problem for Haplotype Assembly in Diploid and Polyploid Genomes. <i>Journal of Computational Biology</i> , 2016, 23, 718-736.	1.6	29
27	Combining a Memetic Algorithm with Integer Programming to Solve the Prize-Collecting Steiner Tree Problem. <i>Lecture Notes in Computer Science</i> , 2004, , 1304-1315.	1.3	29
28	Lagrangian Relaxation Applied to Sparse Global Network Alignment. <i>Lecture Notes in Computer Science</i> , 2011, , 225-236.	1.3	29
29	Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. <i>Journal of Computational Biology</i> , 2018, 25, 689-708.	1.6	28
30	Optimal labeling of point features in rectangular labeling models. <i>Mathematical Programming</i> , 2003, 94, 435-458.	2.4	25
31	Robustness and Resilience. <i>Lecture Notes in Computer Science</i> , 2005, , 417-437.	1.3	25
32	Optimal Compaction of Orthogonal Grid Drawings (Extended Abstract). <i>Lecture Notes in Computer Science</i> , 1999, , 304-319.	1.3	25
33	Automated partial atomic charge assignment for drug-like molecules: a fast knapsack approach. <i>Algorithms for Molecular Biology</i> , 2019, 14, 1.	1.2	24
34	Integer linear programming approaches for non-unique probe selection. <i>Discrete Applied Mathematics</i> , 2007, 155, 840-856.	0.9	22
35	Natalie 2.0: Sparse Global Network Alignment as a Special Case of Quadratic Assignment. <i>Algorithms</i> , 2015, 8, 1035-1051.	2.1	21
36	metaModules identifies key functional subnetworks in microbiome-related disease. <i>Bioinformatics</i> , 2016, 32, 1678-1685.	4.1	21

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37	Probing the Genome-Scale Metabolic Landscape of <i>Bordetella pertussis</i> , the Causative Agent of Whooping Cough. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	21
38	WhatsHap: Haplotype Assembly for Future-Generation Sequencing Reads. <i>Lecture Notes in Computer Science</i> , 2014, , 237-249.	1.3	20
39	Combining Graph Labeling and Compaction. <i>Lecture Notes in Computer Science</i> , 1999, , 27-37.	1.3	19
40	A branch-and-cut approach to the crossing number problem. <i>Discrete Optimization</i> , 2008, 5, 373-388.	0.9	19
41	The HuGS platform. , 2002, , .		19
42	Towards optimal alignment of protein structure distance matrices. <i>Bioinformatics</i> , 2010, 26, 2273-2280.	4.1	18
43	The Fractional Prize-Collecting Steiner Tree Problem on Trees. <i>Lecture Notes in Computer Science</i> , 2003, , 691-702.	1.3	17
44	CSA: comprehensive comparison of pairwise protein structure alignments. <i>Nucleic Acids Research</i> , 2012, 40, W303-W309.	14.5	17
45	eXamine: Exploring annotated modules in networks. <i>BMC Bioinformatics</i> , 2014, 15, 201.	2.6	16
46	DALIX: Optimal DALI Protein Structure Alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 26-36.	3.0	14
47	Integer Linear Programs for Discovering Approximate Gene Clusters. <i>Lecture Notes in Computer Science</i> , 2006, , 298-309.	1.3	14
48	The Generalized Robinson-Foulds Metric. <i>Lecture Notes in Computer Science</i> , 2013, , 156-169.	1.3	14
49	A Realistic Model Under Which the Genetic Code is Optimal. <i>Journal of Molecular Evolution</i> , 2013, 77, 170-184.	1.8	13
50	Exact Crossing Minimization. <i>Lecture Notes in Computer Science</i> , 2006, , 37-48.	1.3	12
51	Antilopeâ€™ A 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
52	Integrated pathway modules using time-course metabolic profiles and EST data from <i>Milnesium tardigradum</i> . <i>BMC Systems Biology</i> , 2012, 6, 72.	3.0	11
53	Optimal Labelling of Point Features in the Slider Model. <i>Lecture Notes in Computer Science</i> , 2000, , 340-350.	1.3	10
54	On the Fixed Parameter Tractability and Approximability of the Minimum Error Correction Problem. <i>Lecture Notes in Computer Science</i> , 2015, , 100-113.	1.3	8

#	ARTICLE	IF	CITATIONS
55	Exact Algorithms for Cluster Editing: Evaluation and Experiments. , 2008, , 289-302.		8
56	Algorithm engineering for optimal alignment of protein structure distance matrices. Optimization Letters, 2011, 5, 421-433.	1.6	7
57	Charge Group Partitioning in Biomolecular Simulation. Lecture Notes in Computer Science, 2012, , 29-43.	1.3	7
58	Bioinformatics Methods and Biological Interpretation for Next-Generation Sequencing Data. BioMed Research International, 2015, 2015, 1-2.	1.9	7
59	PAUL: protein structural alignment using integer linear programming and Lagrangian relaxation. BMC Bioinformatics, 2009, 10, .	2.6	6
60	NatalieQ: A web server for protein-protein interaction network querying. BMC Systems Biology, 2014, 8, 40.	3.0	6
61	On optimal comparability editing with applications to molecular diagnostics. BMC Bioinformatics, 2009, 10, S61.	2.6	5
62	Multiple Structural RNA Alignment with Lagrangian Relaxation. Lecture Notes in Computer Science, 2005, , 303-314.	1.3	5
63	Integer Linear Programming in Computational Biology. Lecture Notes in Computer Science, 2009, , 199-218.	1.3	5
64	On Tree-Constrained Matchings and Generalizations. Lecture Notes in Computer Science, 2011, , 98-109.	1.3	5
65	Graph Drawing Algorithm Engineering with AGD. Lecture Notes in Computer Science, 2002, , 307-323.	1.3	5
66	Fast and Accurate Structural RNA Alignment by Progressive Lagrangian Optimization. Lecture Notes in Computer Science, 2005, , 217-228.	1.3	4
67	An exact algorithm for side-chain placement in protein design. Optimization Letters, 2011, 5, 393-406.	1.6	4
68	Mapping proteins in the presence of paralogs using units of coevolution. BMC Bioinformatics, 2013, 14, S18.	2.6	4
69	Functional Module Search in Protein Networks based on Semantic Similarity Improves the Analysis of Proteomics Data. Molecular and Cellular Proteomics, 2014, 13, 1877-1889.	3.8	4
70	Automatic Classification of Protein Structure Using the Maximum Contact Map Overlap Metric. Algorithms, 2015, 8, 850-869.	2.1	4
71	xHeinz: an algorithm for mining cross-species network modules under a flexible conservation model. Bioinformatics, 2015, 31, 3147-3155.	4.1	4
72	On Tree-Constrained Matchings and Generalizations. Algorithmica, 2015, 71, 98-119.	1.3	4

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73	Structural Alignment of Two RNA Sequences with Lagrangian Relaxation. Lecture Notes in Computer Science, 2004, , 113-123.	1.3	4
74	A Guided Tour to Computational Haplotyping. Lecture Notes in Computer Science, 2017, , 50-63.	1.3	3
75	AGD " A Library of Algorithms for Graph Drawing. Mathematics and Visualization, 2004, , 149-172.	0.6	3
76	eXamine: Visualizing annotated networks in Cytoscape. F1000Research, 2018, 7, 519.	1.6	3
77	A Combinatorial Approach to Orthogonal Placement Problems. , 2003, , 26-32.		3
78	Label Number Maximization in the Slider Model. Lecture Notes in Computer Science, 2005, , 144-154.	1.3	2
79	eXamine: Visualizing annotated networks in Cytoscape. F1000Research, 2018, 7, 519.	1.6	2
80	SuperDendrix algorithm integrates genetic dependencies and genomic alterations across pathways and cancer types. Cell Genomics, 2022, 2, 100099.	6.5	2
81	Using the longest run subsequence problem within homology-based scaffolding. Algorithms for Molecular Biology, 2021, 16, 11.	1.2	1
82	Graph-Drawing Contest Report. Lecture Notes in Computer Science, 2007, , 448-452.	1.3	1
83	Accelerated microRNA-Precursor Detection Using the Smith-Waterman Algorithm on FPGAs. , 2007, , 19-32.		1
84	Genetic polyploid phasing from low-depth progeny samples. IScience, 2022, 25, 104461.	4.1	1
85	Automatic Layout and Labelling of State Diagrams. , 2003, , 584-608.		0
86	The Lost Recipes from the Four Schools of Amathus. Lecture Notes in Computer Science, 2020, , 16-23.	1.3	0