Gunnar W Klau

List of Publications by Year
in descending order

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	SuperDendrix algorithm integrates genetic dependencies and genomic alterations across pathways and cancer types. Cell Genomics, 2022, 2, 100099.	6.5	2
2	Genetic polyploid phasing from low-depth progeny samples. IScience, 2022, 25, 104461.	4.1	1
3	Using anticlustering to partition data sets into equivalent parts.. Psychological Methods, 2021, 26, 161-174.	3.5	30
4	Single-cell transcriptomics defines heterogeneity of epicardial cells and fibroblasts within the infarcted murine heart. ELife, 2021, 10, .	6.0	42
5	Using the longest run subsequence problem within homology-based scaffolding. Algorithms for Molecular Biology, 2021, 16, 11.	1.2	1
6	Haplotype threading: accurate polyploid phasing from long reads. Genome Biology, 2020, 21, 252.	8.8	50
7	The Lost Recipes from the Four Schools of Amathus. Lecture Notes in Computer Science, 2020, , 16-23.	1.3	0
8	Automated partial atomic charge assignment for drug-like molecules: a fast knapsack approach. Algorithms for Molecular Biology, 2019, 14, 1.	1.2	24
9	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	6.5	207
10	Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. Journal of Computational Biology, 2018, 25, 689-708.	1.6	28
11	eXamine: Visualizing annotated networks in Cytoscape. F1000Research, 2018, 7, 519.	1.6	3
12	eXamine: Visualizing annotated networks in Cytoscape. F1000Research, 2018, 7, 519.	1.6	2
13	A Guided Tour to Computational Haplotyping. Lecture Notes in Computer Science, 2017, , 50-63.	1.3	3
14	Probing the Genome-Scale Metabolic Landscape of Bordetella pertussis, the Causative Agent of Whooping Cough. Applied and Environmental Microbiology, 2017, 83, .	3.1	21
15	On the Minimum Error Correction Problem for Haplotype Assembly in Diploid and Polyploid Genomes. Journal of Computational Biology, 2016, 23, 718-736.	1.6	29
16	Logic models to predict continuous outputs based on binary inputs with an application to personalized cancer therapy. Scientific Reports, 2016, 6, 36812.	3.3	43
17	CIDANE: comprehensive isoform discovery and abundance estimation. Genome Biology, 2016, 17, 16.	8.8	45
18	metaModules identifies key functional subnetworks in microbiome-related disease. Bioinformatics, 2016, 32, 1678-1685.	4.1	21

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19	HapCol: accurate and memory-efficient haplotype assembly from long reads. Bioinformatics, 2016, 32, 1610-1617.	4.1	40
20	Automatic Classification of Protein Structure Using the Maximum Contact Map Overlap Metric. Algorithms, 2015, 8, 850-869.	2.1	4
21	Natalie 2.0: Sparse Global Network Alignment as a Special Case of Quadratic Assignment. Algorithms, 2015, 8, 1035-1051.	2.1	21
22	Bioinformatics Methods and Biological Interpretation for Next-Generation Sequencing Data. BioMed Research International, 2015, 2015, 1-2.	1.9	7
23	xHeinz: an algorithm for mining cross-species network modules under a flexible conservation model. Bioinformatics, 2015, 31, 3147-3155.	4.1	4
24	On the Fixed Parameter Tractability and Approximability of the Minimum Error Correction Problem. Lecture Notes in Computer Science, 2015, , 100-113.	1.3	8
25	WhatsHap: Weighted Haplotype Assembly for Future-Generation Sequencing Reads. Journal of Computational Biology, 2015, 22, 498-509.	1.6	337
26	On Tree-Constrained Matchings and Generalizations. Algorithmica, 2015, 71, 98-119.	1.3	4
27	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
28	eXamine: Exploring annotated modules in networks. BMC Bioinformatics, 2014, 15, 201.	2.6	16
29	NatalieQ: A web server for protein-protein interaction network querying. BMC Systems Biology, 2014, 8, 40.	3.0	6
30	WhatsHap: Haplotype Assembly for Future-Generation Sequencing Reads. Lecture Notes in Computer Science, 2014, , 237-249.	1.3	20
31	A Realistic Model Under Which the Genetic Code is Optimal. Journal of Molecular Evolution, 2013, 77, 170-184.	1.8	13
32	Mapping proteins in the presence of paralogs using units of coevolution. BMC Bioinformatics, 2013, 14, S18.	2.6	4
33	Charge Group Partitioning in Biomolecular Simulation. Journal of Computational Biology, 2013, 20, 188-198.	1.6	145
34	DALIX: Optimal DALI Protein Structure Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 26-36.	3.0	14
35	Ancient Dispersal of the Human Fungal Pathogen Cryptococcus gattii from the Amazon Rainforest. PLoS ONE, 2013, 8, e71148.	2.5	122
36	Current composite-feature classification methods do not outperform simple single-genes classifiers in breast cancer prognosis. Frontiers in Genetics, 2013, 4, 289.	2.3	41

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37	The Generalized Robinson-Foulds Metric. Lecture Notes in Computer Science, 2013, , 156-169.	1.3	14
38	An integer linear programming approach for finding deregulated subgraphs in regulatory networks. Nucleic Acids Research, 2012, 40, e43-e43.	14.5	84
39	Robustness and accuracy of functional modules in integrated network analysis. Bioinformatics, 2012, 28, 1887-1894.	4.1	29
40	CSA: comprehensive comparison of pairwise protein structure alignments. Nucleic Acids Research, 2012, 40, W303-W309.	14.5	17
41	CLEVER: clique-enumerating variant finder. Bioinformatics, 2012, 28, 2875-2882.	4.1	101
42	Antilopeâ€"A Lagrangian Relaxation Approach to the de novo Peptide Sequencing Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 385-394.	3.0	12
43	Integrated pathway modules using time-course metabolic profiles and EST data from Milnesium tardigradum. BMC Systems Biology, 2012, 6, 72.	3.0	11
44	Charge Group Partitioning in Biomolecular Simulation. Lecture Notes in Computer Science, 2012, , 29-43.	1.3	7
45	A Critical Evaluation of Network and Pathway-Based Classifiers for Outcome Prediction in Breast Cancer. PLoS ONE, 2012, 7, e34796.	2.5	56
46	Exact Algorithms for Cluster Editing: Evaluation and Experiments. Algorithmica, 2011, 60, 316-334.	1.3	71
47	An exact algorithm for side-chain placement in protein design. Optimization Letters, 2011, 5, 393-406.	1.6	4
48	Algorithm engineering for optimal alignment of protein structure distance matrices. Optimization Letters, 2011, 5, 421-433.	1.6	7
49	On Tree-Constrained Matchings and Generalizations. Lecture Notes in Computer Science, 2011, , 98-109.	1.3	5
50	Lagrangian Relaxation Applied to Sparse Global Network Alignment. Lecture Notes in Computer Science, 2011, , 225-236.	1.3	29
51	Human-guided search. Journal of Heuristics, 2010, 16, 289-310.	1.4	47
52	Towards optimal alignment of protein structure distance matrices. Bioinformatics, 2010, 26, 2273-2280.	4.1	18
53	BioNet: an R-Package for the functional analysis of biological networks. Bioinformatics, 2010, 26, 1129-1130.	4.1	215
54	A new graph-based method for pairwise global network alignment. BMC Bioinformatics, 2009, 10, S59.	2.6	162

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55	On optimal comparability editing with applications to molecular diagnostics. BMC Bioinformatics, 2009, 10, S61.	2.6	5
56	PAUL: protein structural alignment using integer linear programming and Lagrangian relaxation. BMC Bioinformatics, 2009, 10, .	2.6	6
57	Integer Linear Programming in Computational Biology. Lecture Notes in Computer Science, 2009, , 199-218.	1.3	5
58	A branch-and-cut approach to the crossing number problem. Discrete Optimization, 2008, 5, 373-388.	0.9	19
59	Identifying functional modules in protein–protein interaction networks: an integrated exact approach. Bioinformatics, 2008, 24, i223-i231.	4.1	485
60	Exact Algorithms for Cluster Editing: Evaluation and Experiments. , 2008, , 289-302.		8
61	Integer linear programming approaches for non-unique probe selection. Discrete Applied Mathematics, 2007, 155, 840-856.	0.9	22
62	Accurate multiple sequence-structure alignment of RNA sequences using combinatorial optimization. BMC Bioinformatics, 2007, 8, 271.	2.6	74
63	Graph-Drawing Contest Report. Lecture Notes in Computer Science, 2007, , 448-452.	1.3	1
64	Accelerated microRNA-Precursor Detection Using the Smith-Waterman Algorithm on FPGAs. , 2007, , 19-32.		1
65	An Algorithmic Framework for the Exact Solution of the Prize-Collecting Steiner Tree Problem. Mathematical Programming, 2006, 105, 427-449.	2.4	171
66	Exact Crossing Minimization. Lecture Notes in Computer Science, 2006, , 37-48.	1.3	12
67	Integer Linear Programs for Discovering Approximate Gene Clusters. Lecture Notes in Computer Science, 2006, , 298-309.	1.3	14
68	Robustness and Resilience. Lecture Notes in Computer Science, 2005, , 417-437.	1.3	25
69	Fast and Accurate Structural RNA Alignment by Progressive Lagrangian Optimization. Lecture Notes in Computer Science, 2005, , 217-228.	1.3	4
70	Multiple Structural RNA Alignment with Lagrangian Relaxation. Lecture Notes in Computer Science, 2005, , 303-314.	1.3	5
71	Label Number Maximization in the Slider Model. Lecture Notes in Computer Science, 2005, , 144-154.	1.3	2
72	Optimal robust non-unique probe selection using Integer Linear Programming. Bioinformatics, 2004, 20, i186-i193.	4.1	75

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73	Combining a Memetic Algorithm with Integer Programming to Solve the Prize-Collecting Steiner Tree Problem. Lecture Notes in Computer Science, 2004, , 1304-1315.	1.3	29
74	Structural Alignment of Two RNA Sequences with Lagrangian Relaxation. Lecture Notes in Computer Science, 2004, , 113-123.	1.3	4
75	AGD â€" A Library of Algorithms for Graph Drawing. Mathematics and Visualization, 2004, , 149-172.	0.6	3
76	Optimal labeling of point features in rectangular labeling models. Mathematical Programming, 2003, 94, 435-458.	2.4	25
77	The Fractional Prize-Collecting Steiner Tree Problem on Trees. Lecture Notes in Computer Science, 2003, , 691-702.	1.3	17
78	Automatic Layout and Labelling of State Diagrams. , 2003, , 584-608.		0
79	A Combinatorial Approach to Orthogonal Placement Problems. , 2003, , 26-32.		3
80	Investigating human-computer optimization. , 2002, , .		38
81	The HuGS platform. , 2002, , .		19
82	Graph Drawing Algorithm Engineering with AGD. Lecture Notes in Computer Science, 2002, , 307-323.	1.3	5
83	Orthogonal Graph Drawing. Lecture Notes in Computer Science, 2001, , 121-171.	1.3	31
84	Optimal Labelling of Point Features in the Slider Model. Lecture Notes in Computer Science, 2000, , 340-350.	1.3	10
85	Combining Graph Labeling and Compaction. Lecture Notes in Computer Science, 1999, , 27-37.	1.3	19
86	Optimal Compaction of Orthogonal Grid Drawings (Extended Abstract). Lecture Notes in Computer Science, 1999, , 304-319.	1.3	25