# Gunnar W Klau

List of Publications by Year
in descending order

| 86 papers | 3,726 citations | 236833 25 h-index | 161767 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. Bioinformatics, 2008, 24, i223-i231. | 1.8 | 485 |
| 2 | WhatsHap: Weighted Haplotype Assembly for Future-Generation Sequencing Reads. Journal of Computational Biology, 2015, 22, 498-509. | 0.8 | 337 |
| 3 | BioNet: an R-Package for the functional analysis of biological networks. Bioinformatics, 2010, 26, 1129-1130. | 1.8 | 215 |
| 4 | Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089. | 3.2 | 207 |
| 5 | An Algorithmic Framework for the Exact Solution of the Prize-Collecting Steiner Tree Problem. Mathematical Programming, 2006, 105, 427-449. | 1.6 | 171 |
| 6 | A new graph-based method for pairwise global network alignment. BMC Bioinformatics, 2009, 10, S59. | 1.2 | 162 |
| 7 | Charge Group Partitioning in Biomolecular Simulation. Journal of Computational Biology, 2013, 20, 188-198. | 0.8 | 145 |
| 8 | Ancient Dispersal of the Human Fungal Pathogen Cryptococcus gattii from the Amazon Rainforest. PLoS ONE, 2013, 8, e71148. | 1.1 | 122 |
| 9 | CLEVER: clique-enumerating variant finder. Bioinformatics, 2012, 28, 2875-2882. | 1.8 | 101 |
| 10 | An integer linear programming approach for finding deregulated subgraphs in regulatory networks. Nucleic Acids Research, 2012, 40, e43-e43. | 6.5 | 84 |
| 11 | Optimal robust non-unique probe selection using Integer Linear Programming. Bioinformatics, 2004, 20, i186-i193. | 1.8 | 75 |
| 12 | Accurate multiple sequence-structure alignment of RNA sequences using combinatorial optimization. BMC Bioinformatics, 2007, 8, 271. | 1.2 | 74 |
| 13 | Exact Algorithms for Cluster Editing: Evaluation and Experiments. Algorithmica, 2011, 60, 316-334. | 1.0 | 71 |
| 14 | A Critical Evaluation of Network and Pathway-Based Classifiers for Outcome Prediction in Breast Cancer. PLoS ONE, 2012, 7, e34796. | 1.1 | 56 |
| 15 | Haplotype threading: accurate polyploid phasing from long reads. Genome Biology, 2020, 21, 252. | 3.8 | 50 |
| 16 | Human-guided search. Journal of Heuristics, 2010, 16, 289-310. | 1.1 | 47 |
| 17 | CIDANE: comprehensive isoform discovery and abundance estimation. Genome Biology, 2016, 17, 16. | 3.8 | 45 |
| 18 | Logic models to predict continuous outputs based on binary inputs with an application to personalized cancer therapy. Scientific Reports, 2016, 6, 36812. | 1.6 | 43 |

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|---|---------|----|-----------|
| 19 | Single-cell transcriptomics defines heterogeneity of epicardial cells and fibroblasts within the infarcted murine heart. ELife, 2021, 10, . | 2.8 | 42 |
| 20 | Current composite-feature classification methods do not outperform simple single-genes classifiers in breast cancer prognosis. Frontiers in Genetics, 2013, 4, 289. | 1.1 | 41 |
| 21 | HapCol: accurate and memory-efficient haplotype assembly from long reads. Bioinformatics, 2016, 32, 1610-1617. | 1.8 | 40 |
| 22 | Investigating human-computer optimization. , 2002, , . |  | 38 |
| 23 | Orthogonal Graph Drawing. Lecture Notes in Computer Science, 2001, , 121-171. | 1.0 | 31 |
| 24 | Using anticlustering to partition data sets into equivalent parts.. Psychological Methods, 2021, 26, 161-174. | 2.7 | 30 |
| 25 | Robustness and accuracy of functional modules in integrated network analysis. Bioinformatics, 2012, 28, 1887-1894. | 1.8 | 29 |
| 26 | On the Minimum Error Correction Problem for Haplotype Assembly in Diploid and Polyploid Genomes. Journal of Computational Biology, 2016, 23, 718-736. | 0.8 | 29 |
| 27 | Combining a Memetic Algorithm with Integer Programming to Solve the Prize-Collecting Steiner Tree Problem. Lecture Notes in Computer Science, 2004, , 1304-1315. | 1.0 | 29 |
| 28 | Lagrangian Relaxation Applied to Sparse Global Network Alignment. Lecture Notes in Computer Science, 2011, , 225-236. | 1.0 | 29 |
| 29 | Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. Journal of Computational Biology, 2018, 25, 689-708. | 0.8 | 28 |
| 30 | Optimal labeling of point features in rectangular labeling models. Mathematical Programming, 2003, 94, 435-458. | 1.6 | 25 |
| 31 | Robustness and Resilience. Lecture Notes in Computer Science, 2005, , 417-437. | 1.0 | 25 |
| 32 | Optimal Compaction of Orthogonal Grid Drawings (Extended Abstract). Lecture Notes in Computer Science, 1999, , 304-319. | 1.0 | 25 |
| 33 | Automated partial atomic charge assignment for drug-like molecules: a fast knapsack approach. Algorithms for Molecular Biology, 2019, 14, 1. | 0.3 | 24 |
| 34 | Integer linear programming approaches for non-unique probe selection. Discrete Applied Mathematics, 2007, 155, 840-856. | 0.5 | 22 |
| 35 | Natalie 2.0: Sparse Global Network Alignment as a Special Case of Quadratic Assignment. Algorithms, 2015, 8, 1035-1051. | 1.2 | 21 |
| 36 | metaModules identifies key functional subnetworks in microbiome-related disease. Bioinformatics, 2016, 32, 1678-1685. | 1.8 | 21 |

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|---|---------|----|-----------|
| 37 | Probing the Genome-Scale Metabolic Landscape of Bordetella pertussis, the Causative Agent of Whooping Cough. Applied and Environmental Microbiology, 2017, 83, . | 1.4 | 21 |
| 38 | WhatsHap: Haplotype Assembly for Future-Generation Sequencing Reads. Lecture Notes in Computer Science, 2014, , 237-249. | 1.0 | 20 |
| 39 | Combining Graph Labeling and Compaction. Lecture Notes in Computer Science, 1999, , 27-37. | 1.0 | 19 |
| 40 | A branch-and-cut approach to the crossing number problem. Discrete Optimization, 2008, 5, 373-388. | 0.6 | 19 |
| 41 | The HuGS platform. , 2002, , . |  | 19 |
| 42 | Towards optimal alignment of protein structure distance matrices. Bioinformatics, 2010, 26, 2273-2280. | 1.8 | 18 |
| 43 | The Fractional Prize-Collecting Steiner Tree Problem on Trees. Lecture Notes in Computer Science, 2003, , 691-702. | 1.0 | 17 |
| 44 | CSA: comprehensive comparison of pairwise protein structure alignments. Nucleic Acids Research, 2012, 40, W303-W309. | 6.5 | 17 |
| 45 | eXamine: Exploring annotated modules in networks. BMC Bioinformatics, 2014, 15, 201. | 1.2 | 16 |
| 46 | DALIX: Optimal DALI Protein Structure Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 26-36. | 1.9 | 14 |
| 47 | Integer Linear Programs for Discovering Approximate Gene Clusters. Lecture Notes in Computer Science, 2006, , 298-309. | 1.0 | 14 |
| 48 | The Generalized Robinson-Foulds Metric. Lecture Notes in Computer Science, 2013, , 156-169. | 1.0 | 14 |
| 49 | A Realistic Model Under Which the Genetic Code is Optimal. Journal of Molecular Evolution, 2013, 77, 170-184. | 0.8 | 13 |
| 50 | Exact Crossing Minimization. Lecture Notes in Computer Science, 2006, , 37-48. | 1.0 | 12 |
| 51 | Antilopeâ€"A Lagrangian Relaxation Approach to the de novo Peptide Sequencing Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 385-394. | 1.9 | 12 |
| 52 | Integrated pathway modules using time-course metabolic profiles and EST data from Milnesium tardigradum. BMC Systems Biology, 2012, 6, 72. | 3.0 | 11 |
| 53 | Optimal Labelling of Point Features in the Slider Model. Lecture Notes in Computer Science, 2000, , 340-350. | 1.0 | 10 |
| 54 | On the Fixed Parameter Tractability and Approximability of the Minimum Error Correction Problem. Lecture Notes in Computer Science, 2015, , 100-113. | 1.0 | 8 |

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|---|---------|----|-----------|
| 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. | 0.9 | 7 |
| 57 | Charge Group Partitioning in Biomolecular Simulation. Lecture Notes in Computer Science, 2012, , 29-43. | 1.0 | 7 |
| 58 | Bioinformatics Methods and Biological Interpretation for Next-Generation Sequencing Data. BioMed Research International, 2015, 2015, 1-2. | 0.9 | 7 |
| 59 | PAUL: protein structural alignment using integer linear programming and Lagrangian relaxation. BMC Bioinformatics, 2009, 10, . | 1.2 | 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. | 1.2 | 5 |
| 62 | Multiple Structural RNA Alignment with Lagrangian Relaxation. Lecture Notes in Computer Science, 2005, , 303-314. | 1.0 | 5 |
| 63 | Integer Linear Programming in Computational Biology. Lecture Notes in Computer Science, 2009, , 199-218. | 1.0 | 5 |
| 64 | On Tree-Constrained Matchings and Generalizations. Lecture Notes in Computer Science, 2011, , 98-109. | 1.0 | 5 |
| 65 | Graph Drawing Algorithm Engineering with AGD. Lecture Notes in Computer Science, 2002, , 307-323. | 1.0 | 5 |
| 66 | Fast and Accurate Structural RNA Alignment by Progressive Lagrangian Optimization. Lecture Notes in Computer Science, 2005, , 217-228. | 1.0 | 4 |
| 67 | An exact algorithm for side-chain placement in protein design. Optimization Letters, 2011, 5, 393-406. | 0.9 | 4 |
| 68 | Mapping proteins in the presence of paralogs using units of coevolution. BMC Bioinformatics, 2013, 14, S18. | 1.2 | 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. | 2.5 | 4 |
| 70 | Automatic Classification of Protein Structure Using the Maximum Contact Map Overlap Metric. Algorithms, 2015, 8, 850-869. | 1.2 | 4 |
| 71 | xHeinz: an algorithm for mining cross-species network modules under a flexible conservation model. Bioinformatics, 2015, 31, 3147-3155. | 1.8 | 4 |
| 72 | On Tree-Constrained Matchings and Generalizations. Algorithmica, 2015, 71, 98-119. | 1.0 | 4 |

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|---|---------|----|-----------|
| 73 | Structural Alignment of Two RNA Sequences with Lagrangian Relaxation. Lecture Notes in Computer Science, 2004, , 113-123. | 1.0 | 4 |
| 74 | A Guided Tour to Computational Haplotyping. Lecture Notes in Computer Science, 2017, , 50-63. | 1.0 | 3 |
| 75 | AGD â€" A Library of Algorithms for Graph Drawing. Mathematics and Visualization, 2004, , 149-172. | 0.4 | 3 |
| 76 | eXamine: Visualizing annotated networks in Cytoscape. F1000Research, 2018, 7, 519. | 0.8 | 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. | 1.0 | 2 |
| 79 | eXamine: Visualizing annotated networks in Cytoscape. F1000Research, 2018, 7, 519. | 0.8 | 2 |
| 80 | SuperDendrix algorithm integrates genetic dependencies and genomic alterations across pathways and cancer types. Cell Genomics, 2022, 2, 100099. | 3.0 | 2 |
| 81 | Using the longest run subsequence problem within homology-based scaffolding. Algorithms for Molecular Biology, 2021, 16, 11. | 0.3 | 1 |
| 82 | Graph-Drawing Contest Report. Lecture Notes in Computer Science, 2007, , 448-452. | 1.0 | 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. | 1.9 | 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. | 1.0 | 0 |