

Martin Tr Kuiper

List of Publications by Year in descending order

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Version: 2024-02-01

101
papers

28,694
citations

87886

38
h-index

42393

92
g-index

106
all docs

106
docs citations

106
times ranked

39712
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | AFLP: a new technique for DNA fingerprinting. <i>Nucleic Acids Research</i> , 1995, 23, 4407-4414. | 14.5 | 10,873 |
| 2 | BiNGO: a Cytoscape plugin to assess overrepresentation of Gene Ontology categories in Biological Networks. <i>Bioinformatics</i> , 2005, 21, 3448-3449. | 4.1 | 3,901 |
| 3 | The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338. | 14.5 | 3,474 |
| 4 | The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334. | 14.5 | 2,416 |
| 5 | Integration of biological networks and gene expression data using Cytoscape. <i>Nature Protocols</i> , 2007, 2, 2366-2382. | 12.0 | 2,275 |
| 6 | Modeling gene and genome duplications in eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5454-5459. | 7.1 | 850 |
| 7 | Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896. | 17.5 | 506 |
| 8 | Development of an AFLP based linkage map of Ler, Col and Cvi <i>Arabidopsis thaliana</i> ecotypes and construction of a Ler/Cvi recombinant inbred line population. <i>Plant Journal</i> , 1998, 14, 259-271. | 5.7 | 355 |
| 9 | Combined mapping of AFLP and RFLP markers in barley. <i>Molecular Genetics and Genomics</i> , 1995, 249, 65-73. | 2.4 | 337 |
| 10 | Targeted interactomics reveals a complex core cell cycle machinery in <i>Arabidopsis thaliana</i> . <i>Molecular Systems Biology</i> , 2010, 6, 397. | 7.2 | 315 |
| 11 | Versatile Gene-Specific Sequence Tags for <i>Arabidopsis</i> Functional Genomics: Transcript Profiling and Reverse Genetics Applications. <i>Genome Research</i> , 2004, 14, 2176-2189. | 5.5 | 282 |
| 12 | The Cyclin-Dependent Kinase Inhibitor KRP2 Controls the Onset of the Endoreduplication Cycle during <i>Arabidopsis</i> Leaf Development through Inhibition of Mitotic CDKA;1 Kinase Complexes. <i>Plant Cell</i> , 2005, 17, 1723-1736. | 6.6 | 248 |
| 13 | Two high-density AFLP® linkage maps of <i>Zea mays</i> L.: analysis of distribution of AFLP markers. <i>Theoretical and Applied Genetics</i> , 1999, 99, 921-935. | 3.6 | 217 |
| 14 | Genetic diversity and its relationship to hybrid performance in maize as revealed by RFLP and AFLP markers. <i>Theoretical and Applied Genetics</i> , 1998, 96, 219-227. | 3.6 | 173 |
| 15 | AFLP® markers for DNA fingerprinting in cattle. <i>Animal Genetics</i> , 1997, 28, 418-426. | 1.7 | 147 |
| 16 | Biological knowledge management: the emerging role of the Semantic Web technologies. <i>Briefings in Bioinformatics</i> , 2009, 10, 392-407. | 6.5 | 126 |
| 17 | Discovery of Drug Synergies in Gastric Cancer Cells Predicted by Logical Modeling. <i>PLoS Computational Biology</i> , 2015, 11, e1004426. | 3.2 | 118 |
| 18 | Genetic Analysis of Variation in Gene Expression in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2005, 171, 1267-1275. | 2.9 | 116 |

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|----|--|------|-----------|
| 19 | A novel reverse transcriptase activity associated with mitochondrial plasmids of neurospora. <i>Cell</i> , 1988, 55, 693-704. | 28.9 | 109 |
| 20 | Phylogeny of bovine species based on AFLP fingerprinting. <i>Heredity</i> , 2002, 88, 46-51. | 2.6 | 93 |
| 21 | orthAogue: an agile tool for the rapid prediction of orthology relations. <i>Bioinformatics</i> , 2014, 30, 734-736. | 4.1 | 93 |
| 22 | Benchmarking the CATMA Microarray. A Novel Tool for Arabidopsis Transcriptome Analysis. <i>Plant Physiology</i> , 2005, 137, 588-601. | 4.8 | 91 |
| 23 | Integrated map of AFLP, SSLP and RFLP markers using a recombinant inbred population of rice (<i>Oryza</i>) Tj ETQq1 1 0,784314, 98 BT /Over | 3.6 | 90 |
| 24 | TFcheckpoint: a curated compendium of specific DNA-binding RNA polymerase II transcription factors. <i>Bioinformatics</i> , 2013, 29, 2519-2520. | 4.1 | 88 |
| 25 | Relationships among Early European Maize Inbreds: IV. Genetic Diversity Revealed with AFLP Markers and Comparison with RFLP, RAPD, and Pedigree Data. <i>Crop Science</i> , 2000, 40, 783-791. | 1.8 | 79 |
| 26 | Specific Impact of Tobamovirus Infection on the Arabidopsis Small RNA Profile. <i>PLoS ONE</i> , 2011, 6, e19549. | 2.5 | 70 |
| 27 | Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. <i>Plant Journal</i> , 2009, 57, 184-194. | 5.7 | 65 |
| 28 | Use of AFLP Markers for Gene Mapping and QTL Detection in the Rat. <i>Genomics</i> , 1996, 37, 289-294. | 2.9 | 64 |
| 29 | The VS catalytic RNA replicates by reverse transcription as a satellite of a retroplasmid.. <i>Genes and Development</i> , 1995, 9, 294-303. | 5.9 | 53 |
| 30 | BioGateway: a semantic systems biology tool for the life sciences. <i>BMC Bioinformatics</i> , 2009, 10, S11. | 2.6 | 53 |
| 31 | The Arabidopsis leaf as a model system for investigating the role of cell cycle regulation in organ growth. <i>Journal of Plant Research</i> , 2006, 119, 43-50. | 2.4 | 51 |
| 32 | Genetic Affinities Within the Herring Gull <i>Larus argentatus</i> Assemblage Revealed by AFLP Genotyping. <i>Journal of Molecular Evolution</i> , 2001, 52, 85-93. | 1.8 | 49 |
| 33 | Ontology Design Patterns for bio-ontologies: a case study on the Cell Cycle Ontology. <i>BMC Bioinformatics</i> , 2008, 9, S1. | 2.6 | 49 |
| 34 | Genetic dissection of transcriptional regulation by cDNA-AFLP. <i>Plant Journal</i> , 2006, 45, 439-446. | 5.7 | 46 |
| 35 | CATMA, a comprehensive genome-scale resource for silencing and transcript profiling of Arabidopsis genes. <i>BMC Bioinformatics</i> , 2007, 8, 400. | 2.6 | 46 |
| 36 | The gastrin and cholecystokinin receptors mediated signaling network: a scaffold for data analysis and new hypotheses on regulatory mechanisms. <i>BMC Systems Biology</i> , 2015, 9, 40. | 3.0 | 46 |

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|----|--|------|-----------|
| 37 | Chromosomal regions involved in hybrid performance and heterosis: their AFLP [®] -based identification and practical use in prediction models. <i>Heredity</i> , 2000, 85, 208-218. | 2.6 | 44 |
| 38 | European consortia building integrated resources for Arabidopsis functional genomics. <i>Current Opinion in Plant Biology</i> , 2003, 6, 426-429. | 7.1 | 44 |
| 39 | The Cell Cycle Ontology: An application ontology for the representation and integrated analysis of the cell cycle process. <i>Genome Biology</i> , 2009, 10, R58. | 9.6 | 38 |
| 40 | Validating module network learning algorithms using simulated data. <i>BMC Bioinformatics</i> , 2007, 8, S5. | 2.6 | 34 |
| 41 | Gene Ontology annotation of sequence-specific DNA binding transcription factors: setting the stage for a large-scale curation effort. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat062-bat062. | 3.0 | 33 |
| 42 | Title is missing!. <i>Molecular Breeding</i> , 2000, 6, 265-276. | 2.1 | 30 |
| 43 | Prediction of testcross means and variances among F3 progenies of F1 crosses from testcross means and genetic distances of their parents in maize. <i>Theoretical and Applied Genetics</i> , 1998, 96, 503-512. | 3.6 | 25 |
| 44 | Setting the basis of best practices and standards for curation and annotation of logical models in biology – highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. <i>Briefings in Bioinformatics</i> , 2021, 22, 1848-1859. | 6.5 | 25 |
| 45 | Reasoning with bio-ontologies: using relational closure rules to enable practical querying. <i>Bioinformatics</i> , 2011, 27, 1562-1568. | 4.1 | 24 |
| 46 | Genome-wide screening for cis-regulatory variation using a classical diallel crossing scheme. <i>Nucleic Acids Research</i> , 2006, 34, 3677-3686. | 14.5 | 20 |
| 47 | OLSVis: an animated, interactive visual browser for bio-ontologies. <i>BMC Bioinformatics</i> , 2012, 13, 116. | 2.6 | 20 |
| 48 | Network and Systems Medicine: Position Paper of the European Collaboration on Science and Technology Action on Open Multiscale Systems Medicine. <i>Network and Systems Medicine</i> , 2020, 3, 67-90. | 2.5 | 18 |
| 49 | Molecular cloning of pea mRNAs encoding a shoot-specific polypeptide and light-induced polypeptides. <i>Plant Molecular Biology</i> , 1983, 2, 295-303. | 3.9 | 17 |
| 50 | ONTO-PERL: An API for supporting the development and analysis of bio-ontologies. <i>Bioinformatics</i> , 2008, 24, 885-887. | 4.1 | 17 |
| 51 | Sequence-Dependent Promoter Escape Efficiency Is Strongly Influenced by Bias for the Pretranslocated State during Initial Transcription. <i>Biochemistry</i> , 2015, 54, 4267-4275. | 2.5 | 17 |
| 52 | Gene Ontology representation for transcription factor functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194752. | 1.9 | 17 |
| 53 | A recombinant plasmid carrying the mitochondrial plasmid sequence of <i>Neurospora intermedia</i> LaBelle yields new plasmid derivatives in <i>Neurospora crassa</i> transformants. <i>Current Genetics</i> , 1985, 9, 471-477. | 1.7 | 16 |
| 54 | Mapping of a QTL for Serum HDL Cholesterol in the Rabbit Using AFLP Technology. , 2001, 92, 322-326. | | 16 |

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|----|---|-----|-----------|
| 55 | Extracting expression modules from perturbational gene expression compendia. BMC Systems Biology, 2008, 2, 33. | 3.0 | 16 |
| 56 | Label-Free Quantitative Proteomic Analysis of Systemic Responses to Local Wounding and Virus Infection in <i>Arabidopsis thaliana</i> . Journal of Proteome Research, 2013, 12, 2491-2503. | 3.7 | 16 |
| 57 | The status of causality in biological databases: data resources and data retrieval possibilities to support logical modeling. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 15 |
| 58 | A GO catalogue of human DNA-binding transcription factors. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194765. | 1.9 | 15 |
| 59 | The Cytoscape BioGateway App: explorative network building from an RDF store. Bioinformatics, 2020, 36, 1966-1967. | 4.1 | 14 |
| 60 | The Minimum Information about a Molecular Interaction CAusal Statement (MI2CAST). Bioinformatics, 2021, 36, 5712-5718. | 4.1 | 14 |
| 61 | A Middle-Out Modeling Strategy to Extend a Colon Cancer Logical Model Improves Drug Synergy Predictions in Epithelial-Derived Cancer Cell Lines. Frontiers in Molecular Biosciences, 2020, 7, 502573. | 3.5 | 13 |
| 62 | Gene regulation knowledge commons: community action takes care of DNA binding transcription factors. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw088. | 3.0 | 12 |
| 63 | Gauging triple stores with actual biological data. BMC Bioinformatics, 2011, 13, S3. | 2.6 | 11 |
| 64 | Contributions of the EMERALD project to assessing and improving microarray data quality. BioTechniques, 2011, 50, 27-31. | 1.8 | 11 |
| 65 | Strategies to Enhance Logic Modeling-Based Cell Line-Specific Drug Synergy Prediction. Frontiers in Physiology, 2020, 11, 862. | 2.8 | 10 |
| 66 | Finding gene regulatory network candidates using the gene expression knowledge base. BMC Bioinformatics, 2014, 15, 386. | 2.6 | 8 |
| 67 | Simulating genetic networks made easy: network construction with simple building blocks. Bioinformatics, 2005, 21, 269-271. | 4.1 | 7 |
| 68 | ONTO-ToolKit: enabling bio-ontology engineering via Galaxy. BMC Bioinformatics, 2010, 11, S8. | 2.6 | 7 |
| 69 | A Cell-Cycle Knowledge Integration Framework. Lecture Notes in Computer Science, 2006, , 19-34. | 1.3 | 7 |
| 70 | Logical and experimental modeling of cytokine and eicosanoid signaling in psoriatic keratinocytes. IScience, 2021, 24, 103451. | 4.1 | 7 |
| 71 | ExTRI: Extraction of transcription regulation interactions from literature. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194778. | 1.9 | 7 |
| 72 | Reliable Self-assembly by Self-triggered Activation of Enveloped DNA Tiles. Lecture Notes in Computer Science, 2013, , 68-79. | 1.3 | 6 |

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|----|---|------|-----------|
| 73 | Formalization of gene regulation knowledge using ontologies and gene ontology causal activity models. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194766. | 1.9 | 6 |
| 74 | Systems Biology: A Promising Tool to Study Abiotic Stress Responses. , 2011, , 163-172. | | 6 |
| 75 | Gene expression trends and protein features effectively complement each other in gene function prediction. <i>Bioinformatics</i> , 2009, 25, 322-330. | 4.1 | 5 |
| 76 | DASS-GUI: a user interface for identification and analysis of significant patterns in non-sequential data. <i>Bioinformatics</i> , 2010, 26, 987-989. | 4.1 | 5 |
| 77 | Boolean function metrics can assist modelers to check and choose logical rules. <i>Journal of Theoretical Biology</i> , 2022, 538, 111025. | 1.7 | 5 |
| 78 | Network Building with the Cytoscape BioGateway App Explained in Five Use Cases. <i>Current Protocols in Bioinformatics</i> , 2020, 72, e106. | 25.8 | 4 |
| 79 | Silencing trust: confidence and familiarity in re-engineering knowledge infrastructures. <i>Medicine, Health Care and Philosophy</i> , 2020, 23, 471-484. | 1.8 | 4 |
| 80 | Genes2GO: A web application for querying gene sets for specific GO terms. <i>Bioinformatics</i> , 2016, 12, 231-232. | 0.5 | 4 |
| 81 | Initialization Dependence of Clustering Algorithms. <i>Lecture Notes in Computer Science</i> , 2009, , 615-622. | 1.3 | 4 |
| 82 | The emergence of Semantic Systems Biology. <i>New Biotechnology</i> , 2013, 30, 286-290. | 4.4 | 3 |
| 83 | Using the relation ontology Metarel for modelling Linked Data as multi-digraphs. <i>Semantic Web</i> , 2014, 5, 115-126. | 1.9 | 3 |
| 84 | CausalBuilder: bringing the MI2CAST causal interaction annotation standard to the curator. Database: the Journal of Biological Databases and Curation, 2021, 2021, . | 3.0 | 3 |
| 85 | Scientific knowledge in the age of computation: Explicated, computable and manageable?. <i>Theoria (Spain)</i> , 2019, 34, 213. | 0.4 | 3 |
| 86 | The gene regulation knowledge commons: the action area of GREEKC. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194768. | 1.9 | 3 |
| 87 | Dealing with different conceptions of pollution in the Gene Regulation Knowledge Commons. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194779. | 1.9 | 3 |
| 88 | Flexibility and utility of the cell cycle ontology. <i>Applied Ontology</i> , 2011, 6, 247-261. | 2.0 | 2 |
| 89 | Jointly creating digital abstracts: dealing with synonymy and polysemy. <i>BMC Research Notes</i> , 2012, 5, 601. | 1.4 | 2 |
| 90 | UniBioDicts: Unified access to Biological Dictionaries. <i>Bioinformatics</i> , 2021, 37, 143-144. | 4.1 | 2 |

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|-----|--|------|-----------|
| 91 | Integration and expression of 3â€²-truncated derivatives of the Neurospora crassa cyt-21 + gene, encoding a mitochondrial ribosomal protein, in Neurospora transformants. Molecular Genetics and Genomics, 1988, 213, 519-528. | 2.4 | 1 |
| 92 | WordVis: JavaScript and Animation to Visualize the WordNet Relational Dictionary. Advances in Intelligent Systems and Computing, 2013, , 137-145. | 0.6 | 1 |
| 93 | Clustering of gene expression profiles: creating initialization-independent clusterings by eliminating unstable genes. Journal of Integrative Bioinformatics, 2010, 7, . | 1.5 | 1 |
| 94 | Genome-wide screening for cis-regulatory variation using a classical diallel crossing scheme. Nucleic Acids Research, 2007, 35, 1038-1038. | 14.5 | 0 |
| 95 | Metarel: an Ontology to support the inferencing of Semantic Web relations within Biomedical Ontologies. Nature Precedings, 2009, , . | 0.1 | 0 |
| 96 | Validating clusterings of gene expression data. , 2010, , . | | 0 |
| 97 | Flexible network reconstruction from relational databases with Cytoscape and CytoSQL. BMC Bioinformatics, 2010, 11, 360. | 2.6 | 0 |
| 98 | Semantic systems biology. , 2011, , . | | 0 |
| 99 | The RDF foundry. , 2011, , . | | 0 |
| 100 | Cell Cycle Ontology (CCO). , 2013, , 305-309. | | 0 |
| 101 | emba: R package for analysis and visualization of biomarkers in boolean model ensembles. Journal of Open Source Software, 2020, 5, 2583. | 4.6 | 0 |