Martin Tr Kuiper

List of Publications by Citations

96 papers	21,642 citations	38 h-index	106 g-index
106 ext. papers	25,651 ext. citations	7.2 avg, IF	7.65 L-index

#	Paper	IF	Citations
96	AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Research*, **1995**, 23, 4407-14	20.1	9655
95	BiNGO: a Cytoscape plugin to assess overrepresentation of gene ontology categories in biological networks. *Bioinformatics*, **2005**, 21, 3448-9	7.2	3065
94	The Gene Ontology Resource: 20 years and still GOing strong. *Nucleic Acids Research*, **2019**, 47, D330-D338	20.1	1962
93	Integration of biological networks and gene expression data using Cytoscape. *Nature Protocols*, **2007**, 2, 2366-82	18.8	1798
92	Modeling gene and genome duplications in eukaryotes. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 5454-9	11.5	670
91	The Gene Ontology resource: enriching a GOld mine. *Nucleic Acids Research*, **2021**, 49, D325-D334	20.1	494
90	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. *Nature Biotechnology*, **2008**, 26, 889-96	44.5	417
89	Development of an AFLP based linkage map of Ler, Col and Cvi Arabidopsis thaliana ecotypes and construction of a Ler/Cvi recombinant inbred line population. *Plant Journal*, **1998**, 14, 259-71	6.9	293
88	Versatile gene-specific sequence tags for Arabidopsis functional genomics: transcript profiling and reverse genetics applications. *Genome Research*, **2004**, 14, 2176-89	9.7	265
87	Targeted interactomics reveals a complex core cell cycle machinery in Arabidopsis thaliana. *Molecular Systems Biology*, **2010**, 6, 397	12.2	254
86	The cyclin-dependent kinase inhibitor KRP2 controls the onset of the endoreduplication cycle during Arabidopsis leaf development through inhibition of mitotic CDKA;1 kinase complexes. *Plant Cell*, **2005**, 17, 1723-36	11.6	216
85	Combined mapping of AFLP and RFLP markers in barley. *Molecular Genetics and Genomics*, **1995**, 249, 65-73		213
84	Two high-density AFLP linkage maps of Zea mays L.: analysis of distribution of AFLP markers. *Theoretical and Applied Genetics*, **1999**, 99, 921-935	6	201
83	Genetic diversity and its relationship to hybrid performance in maize as revealed by RFLP and AFLP markers. *Theoretical and Applied Genetics*, **1998**, 96, 219-227	6	140
82	AFLP markers for DNA fingerprinting in cattle. *Animal Genetics*, **1997**, 28, 418-26	2.5	116
81	Biological knowledge management: the emerging role of the Semantic Web technologies. *Briefings in Bioinformatics*, **2009**, 10, 392-407	13.4	107
80	Genetic analysis of variation in gene expression in Arabidopsis thaliana. *Genetics*, **2005**, 171, 1267-75	4	106

79	A novel reverse transcriptase activity associated with mitochondrial plasmids of Neurospora. *Cell*, **1988**, 55, 693-704	56.2	102
78	Phylogeny of bovine species based on AFLP fingerprinting. *Heredity*, **2002**, 88, 46-51	3.6	85
77	Benchmarking the CATMA microarray. A novel tool for Arabidopsis transcriptome analysis. *Plant Physiology*, **2005**, 137, 588-601	6.6	84
76	Genome-wide screening for cis -regulatory variation using a classical diallel crossing scheme. *Nucleic Acids Research*, **2007**, 35, 1038-1038	20.1	78
75	orthAgogue: an agile tool for the rapid prediction of orthology relations. *Bioinformatics*, **2014**, 30, 734-6	7.2	66
74	TFcheckpoint: a curated compendium of specific DNA-binding RNA polymerase II transcription factors. *Bioinformatics*, **2013**, 29, 2519-20	7.2	66
73	Relationships among Early European Maize Inbreds: IV. Genetic Diversity Revealed with AFLP Markers and Comparison with RFLP, RAPD, and Pedigree Data. *Crop Science*, **2000**, 40, 783-791	2.4	64
72	Discovery of Drug Synergies in Gastric Cancer Cells Predicted by Logical Modeling. *PLoS Computational Biology*, **2015**, 11, e1004426	5	63
71	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. *Plant Journal*, **2009**, 57, 184-94	6.9	56
70	Integrated map of AFLP, SSLP and RFLP markers using a recombinant inbred population of rice (Oryza sativa L.). *Theoretical and Applied Genetics*, **1998**, 97, 370-380	6	56
69	Specific impact of tobamovirus infection on the Arabidopsis small RNA profile. *PLoS ONE*, **2011**, 6, e19549	3.7	54
68	Use of AFLP markers for gene mapping and QTL detection in the rat. *Genomics*, **1996**, 37, 289-94	4.3	53
67	The VS catalytic RNA replicates by reverse transcription as a satellite of a retroplasmid. *Genes and Development*, **1995**, 9, 294-303	12.6	46
66	The Arabidopsis leaf as a model system for investigating the role of cell cycle regulation in organ growth. *Journal of Plant Research*, **2006**, 119, 43-50	2.6	45
65	Genetic affinities within the herring gull Larus argentatus assemblage revealed by AFLP genotyping. *Journal of Molecular Evolution*, **2001**, 52, 85-93	3.1	45
64	BioGateway: a semantic systems biology tool for the life sciences. *BMC Bioinformatics*, **2009**, 10 Suppl 10, S11	3.6	43
63	Genetic dissection of transcriptional regulation by cDNA-AFLP. *Plant Journal*, **2006**, 45, 439-46	6.9	42
62	CATMA, a comprehensive genome-scale resource for silencing and transcript profiling of Arabidopsis genes. *BMC Bioinformatics*, **2007**, 8, 400	3.6	40

61	European consortia building integrated resources for Arabidopsis functional genomics. *Current Opinion in Plant Biology*, **2003**, 6, 426-9	9.9	40
60	Ontology Design Patterns for bio-ontologies: a case study on the Cell Cycle Ontology. *BMC Bioinformatics*, **2008**, 9 Suppl 5, S1	3.6	39
59	Chromosomal regions involved in hybrid performance and heterosis: their AFLP(R)-based identification and practical use in prediction models. *Heredity*, **2000**, 85 Pt 3, 208-18	3.6	39
58	The gastrin and cholecystokinin receptors mediated signaling network: a scaffold for data analysis and new hypotheses on regulatory mechanisms. *BMC Systems Biology*, **2015**, 9, 40	3.5	36
57	Validating module network learning algorithms using simulated data. *BMC Bioinformatics*, **2007**, 8 Suppl 2, S5	3.6	30
56	Further characterization of AFLP data as a tool in genetic diversity assessments among maize (Zea mays L.) inbred lines. *Molecular Breeding*, **2000**, 6, 265-276	3.4	27
55	The Cell Cycle Ontology: an application ontology for the representation and integrated analysis of the cell cycle process. *Genome Biology*, **2009**, 10, R58	18.3	26
54	Prediction of testcross means and variances among F3 progenies of F1 crosses from testcross means and genetic distances of their parents in maize. *Theoretical and Applied Genetics*, **1998**, 96, 503-12	6	24
53	Gene Ontology annotation of sequence-specific DNA binding transcription factors: setting the stage for a large-scale curation effort. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat062	5	22
52	Reasoning with bio-ontologies: using relational closure rules to enable practical querying. *Bioinformatics*, **2011**, 27, 1562-8	7.2	21
51	Genome-wide screening for cis-regulatory variation using a classical diallel crossing scheme. *Nucleic Acids Research*, **2006**, 34, 3677-86	20.1	19
50	OLSVis: an animated, interactive visual browser for bio-ontologies. *BMC Bioinformatics*, **2012**, 13, 116	3.6	16
49	Sequence-Dependent Promoter Escape Efficiency Is Strongly Influenced by Bias for the Pretranslocated State during Initial Transcription. *Biochemistry*, **2015**, 54, 4267-75	3.2	15
48	Label-free quantitative proteomic analysis of systemic responses to local wounding and virus infection in Arabidopsis thaliana. *Journal of Proteome Research*, **2013**, 12, 2491-503	5.6	15
47	ONTO-PERL: an API for supporting the development and analysis of bio-ontologies. *Bioinformatics*, **2008**, 24, 885-7	7.2	15
46	Molecular cloning of pea mRNAs encoding a shoot-specific polypeptide and light-induced polypeptides. *Plant Molecular Biology*, **1983**, 2, 295-303	4.6	15
45	Extracting expression modules from perturbational gene expression compendia. *BMC Systems Biology*, **2008**, 2, 33	3.5	14
44	A recombinant plasmid carrying the mitochondrial plasmid sequence of Neurospora intermedia LaBelle yields new plasmid derivatives in Neurospora crassa transformants. *Current Genetics*, **1985**, 9, 471-477	2.9	14

43	Mapping of a QTL for serum HDL cholesterol in the rabbit using AFLP technology. *Journal of Heredity*, **2001**, 92, 322-6	2.4	12
42	Gene regulation knowledge commons: community action takes care of DNA binding transcription factors. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	10
41	Network and Systems Medicine: Position Paper of the European Collaboration on Science and Technology Action on Open Multiscale Systems Medicine. *Network and Systems Medicine*, **2020**, 3, 67-90	4	10
40	Gauging triple stores with actual biological data. *BMC Bioinformatics*, **2012**, 13 Suppl 1, S3	3.6	9
39	Contributions of the EMERALD project to assessing and improving microarray data quality. *BioTechniques*, **2011**, 50, 27-31	2.5	9
38	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. *Briefings in Bioinformatics*, **2021**, 22, 1848-1859	13.4	9
37	Finding gene regulatory network candidates using the gene expression knowledge base. *BMC Bioinformatics*, **2014**, 15, 386	3.6	7
36	The status of causality in biological databases: data resources and data retrieval possibilities to support logical modeling. *Briefings in Bioinformatics*, **2021**, 22,	13.4	7
35	The Cytoscape BioGateway App: explorative network building from the BioGateway triple store. *Bioinformatics*, **2019**,	7.2	7
34	Simulating genetic networks made easy: network construction with simple building blocks. *Bioinformatics*, **2005**, 21, 269-71	7.2	6
33	Gene expression trends and protein features effectively complement each other in gene function prediction. *Bioinformatics*, **2009**, 25, 322-30	7.2	5
32	Reliable Self-assembly by Self-triggered Activation of Enveloped DNA Tiles. *Lecture Notes in Computer Science*, **2013**, 68-79	0.9	5
31	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). *Bioinformatics*, **2021**, 36, 5712-5718	7.2	5
30	A Cell-Cycle Knowledge Integration Framework. *Lecture Notes in Computer Science*, **2006**, 19-34	0.9	5
29	Strategies to Enhance Logic Modeling-Based Cell Line-Specific Drug Synergy Prediction. *Frontiers in Physiology*, **2020**, 11, 862	4.6	4
28	ONTO-ToolKit: enabling bio-ontology engineering via Galaxy. *BMC Bioinformatics*, **2010**, 11 Suppl 12, S8	3.6	4
27	A GO catalogue of human DNA-binding transcription factors		4
26	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	5.6	4

25	DASS-GUI: a user interface for identification and analysis of significant patterns in non-sequential data. *Bioinformatics*, **2010**, 26, 987-9	7.2	3
24	Formalization of gene regulation knowledge using ontologies and gene ontology causal activity models. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1864, 194766	6	3
23	Initialization Dependence of Clustering Algorithms. *Lecture Notes in Computer Science*, **2009**, 615-622	0.9	3
22	Silencing trust: confidence and familiarity in re-engineering knowledge infrastructures. *Medicine, Health Care and Philosophy*, **2020**, 23, 471-484	2	2
21	The emergence of Semantic Systems Biology. *New Biotechnology*, **2013**, 30, 286-90	6.4	2
20	Using the relation ontology Metarel for modelling Linked Data as multi-digraphs. *Semantic Web*, **2014**, 5, 115-126	2.4	2
19	Jointly creating digital abstracts: dealing with synonymy and polysemy. *BMC Research Notes*, **2012**, 5, 601	2.3	2
18	Systems Biology: A Promising Tool to Study Abiotic Stress Responses **2011**, 163-172		2
17	Gene Ontology representation for transcription factor functions. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1864, 194752	6	2
16	UniBioDicts: Unified access to biological dictionaries. *Bioinformatics*, **2020**,	7.2	2
15	Flexibility and utility of the cell cycle ontology. *Applied Ontology*, **2011**, 6, 247-261	1.4	1
14	Technologies and Best Practices for Building Bio-Ontologies **2010**, 67-86		1
13	Integration and expression of 3?-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		1
12	Boolean function metrics can assist modelers to check and choose logical rules.. *Journal of Theoretical Biology*, **2022**, 538, 111025	2.3	1
11	ExTRI: Extraction of transcription regulation interactions from literature. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 194778	6	1
10	Genes2GO: A web application for querying gene sets for specific GO terms. *Bioinformation*, **2016**, 12, 231-232	1.1	1
9	The gene regulation knowledge commons: the action area of GREEKC. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1865, 194768	6	1
8	CausalBuilder: bringing the MI2CAST causal interaction annotation standard to the curator. *Database: the Journal of Biological Databases and Curation*, **2021**, 2021,	5	1

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7	Network Building with the Cytoscape BioGateway App Explained in Five Use Cases. *Current Protocols in Bioinformatics*, **2020**, 72, e106	24.2	0
6	Dealing with different conceptions of pollution in the Gene Regulation Knowledge Commons.. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 194779	6	0
5	Logical and experimental modeling of cytokine and eicosanoid signaling in psoriatic keratinocytes. *IScience*, **2021**, 24, 103451	6.1	0
4	A GO catalogue of human DNA-binding transcription factors. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1864, 194765	6	0
3	Flexible network reconstruction from relational databases with Cytoscape and CytoSQL. *BMC Bioinformatics*, **2010**, 11, 360	3.6	
2	emba: R package for analysis and visualization of biomarkers in boolean model ensembles. *Journal of Open Source Software*, **2020**, 5, 2583	5.2	
1	WordVis: JavaScript and Animation to Visualize the WordNet Relational Dictionary. *Advances in Intelligent Systems and Computing*, **2013**, 137-145	0.4	