Martin Tr Kuiper

List of Publications by Year
in descending order

101 papers	28,694 citations	87888 38 h-index	42399 92 g-index
106 all docs	106 docs citations	106 times ranked	39712 citing authors

#	Article	IF	Citations
1	The gene regulation knowledge commons: the action area of GREEKC. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194768.	1.9	3
2	Dealing with different conceptions of pollution in the Gene Regulation Knowledge Commons. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194779.	1.9	3
3	Boolean function metrics can assist modelers to check and choose logical rules. Journal of Theoretical Biology, 2022, 538, 111025.	1.7	5
4	ExTRI: Extraction of transcription regulation interactions from literature. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194778.	1.9	7
5	Setting the basis of best practices and standards for curation and annotation of logical models in biologyâ€"highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. Briefings in Bioinformatics, 2021, 22, 1848-1859.	6.5	25
6	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). Bioinformatics, 2021, 36, 5712-5718.	4.1	14
7	CausalBuilder: bringing the MI2CAST causal interaction annotation standard to the curator. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	3
8	Gene Ontology representation for transcription factor functions. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194752.	1.9	17
9	UniBioDicts: Unified access to Biological Dictionaries. Bioinformatics, 2021, 37, 143-144.	4.1	2
10	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
11	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
12	Formalization of gene regulation knowledge using ontologies and gene ontology causal activity models. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194766.	1.9	6
13	A GO catalogue of human DNA-binding transcription factors. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194765.	1.9	15
14	Logical and experimental modeling of cytokine and eicosanoid signaling in psoriatic keratinocytes. IScience, 2021, 24, 103451.	4.1	7
15	The Cytoscape BioGateway App: explorative network building from an RDF store. Bioinformatics, 2020, 36, 1966-1967.	4.1	14
16	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.	2.5	18
17	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
18	Network Building with the Cytoscape BioGateway App Explained in Five Use Cases. Current Protocols in Bioinformatics, 2020, 72, e106.	25.8	4

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19	Strategies to Enhance Logic Modeling-Based Cell Line-Specific Drug Synergy Prediction. Frontiers in Physiology, 2020, 11, 862.	2.8	10
20	Silencing trust: confidence and familiarity in re-engineering knowledge infrastructures. Medicine, Health Care and Philosophy, 2020, 23, 471-484.	1.8	4
21	emba: R package for analysis and visualization of biomarkers in boolean model ensembles. Journal of Open Source Software, 2020, 5, 2583.	4.6	0
22	The Gene Ontology Resource: 20 years and still GOing strong. Nucleic Acids Research, 2019, 47, D330-D338.	14.5	3,474
23	Scientific knowledge in the age of computation: Explicated, computable and manageable?. Theoria (Spain), 2019, 34, 213.	0.4	3
24	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
25	Genes2GO: A web application for querying gene sets for specific GO terms. Bioinformation, 2016, 12, 231-232.	0.5	4
26	Sequence-Dependent Promoter Escape Efficiency Is Strongly Influenced by Bias for the Pretranslocated State during Initial Transcription. Biochemistry, 2015, 54, 4267-4275.	2.5	17
27	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.	3.0	46
28	Discovery of Drug Synergies in Gastric Cancer Cells Predicted by Logical Modeling. PLoS Computational Biology, 2015, 11, e1004426.	3.2	118
29	Using the relation ontology Metarel for modelling Linked Data as multi-digraphs. Semantic Web, 2014, 5, 115-126.	1.9	3
30	Finding gene regulatory network candidates using the gene expression knowledge base. BMC Bioinformatics, 2014, 15, 386.	2.6	8
31	orthAgogue: an agile tool for the rapid prediction of orthology relations. Bioinformatics, 2014, 30, 734-736.	4.1	93
32	The emergence of Semantic Systems Biology. New Biotechnology, 2013, 30, 286-290.	4.4	3
33	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
34	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-bat062.	3.0	33
35	TFcheckpoint: a curated compendium of specific DNA-binding RNA polymerase II transcription factors. Bioinformatics, 2013, 29, 2519-2520.	4.1	88
36	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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37	WordVis: JavaScript and Animation to Visualize the WordNet Relational Dictionary. Advances in Intelligent Systems and Computing, 2013, , 137-145.	0.6	1
38	Cell Cycle Ontology (CCO). , 2013, , 305-309.		0
39	OLSVis: an animated, interactive visual browser for bio-ontologies. BMC Bioinformatics, 2012, 13, 116.	2.6	20
40	Jointly creating digital abstracts: dealing with synonymy and polysemy. BMC Research Notes, 2012, 5, 601.	1.4	2
41	Specific Impact of Tobamovirus Infection on the Arabidopsis Small RNA Profile. PLoS ONE, 2011, 6, e19549.	2.5	70
42	Flexibility and utility of the cell cycle ontology. Applied Ontology, 2011, 6, 247-261.	2.0	2
43	Gauging triple stores with actual biological data. BMC Bioinformatics, 2011, 13, S3.	2.6	11
44	Semantic systems biology. , 2011, , .		0
45	Reasoning with bio-ontologies: using relational closure rules to enable practical querying. Bioinformatics, 2011, 27, 1562-1568.	4.1	24
46	Contributions of the EMERALD project to assessing and improving microarray data quality. BioTechniques, 2011, 50, 27-31.	1.8	11
47	Systems Biology: A Promising Tool to Study Abiotic Stress Responses. , 2011, , 163-172.		6
48	The RDF foundry. , 2011, , .		0
49	Validating clusterings of gene expression data. , 2010, , .		0
50	Flexible network reconstruction from relational databases with Cytoscape and CytoSQL. BMC Bioinformatics, 2010, 11, 360.	2.6	0
51	ONTO-ToolKit: enabling bio-ontology engineering via Galaxy. BMC Bioinformatics, 2010, 11, S8.	2.6	7
52	DASS-GUI: a user interface for identification and analysis of significant patterns in non-sequential data. Bioinformatics, 2010, 26, 987-989.	4.1	5
53	Targeted interactomics reveals a complex core cell cycle machinery in <i>Arabidopsis thaliana</i>. Molecular Systems Biology, 2010, 6, 397.	7.2	315
54	Clustering of gene expression profiles: creating initialization-independent clusterings by eliminating unstable genes. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	1

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55	Metarel: an Ontology to support the inferencing of Semantic Web relations within Biomedical Ontologies. Nature Precedings, 2009, , .	0.1	0
56	Gene expression trends and protein features effectively complement each other in gene function prediction. Bioinformatics, 2009, 25, 322-330.	4.1	5
57	Biological knowledge management: the emerging role of the Semantic Web technologies. Briefings in Bioinformatics, 2009, 10, 392-407.	6.5	126
58	BioGateway: a semantic systems biology tool for the life sciences. BMC Bioinformatics, 2009, 10, S11.	2.6	53
59	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. Plant Journal, 2009, 57, 184-194.	5.7	65
60	The Cell Cycle Ontology: An application ontology for the representation and integrated analysis of the cell cycle process. Genome Biology, 2009, 10, R58.	9.6	38
61	Initialization Dependence of Clustering Algorithms. Lecture Notes in Computer Science, 2009, , 615-622.	1.3	4
62	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	17.5	506
63	Ontology Design Patterns for bio-ontologies: a case study on the Cell Cycle Ontology. BMC Bioinformatics, 2008, 9, S1.	2.6	49
64	Extracting expression modules from perturbational gene expression compendia. BMC Systems Biology, 2008, 2, 33.	3.0	16
65	ONTO-PERL: An API for supporting the development and analysis of bio-ontologies. Bioinformatics, 2008, 24, 885-887.	4.1	17
66	Genome-wide screening for cis-regulatory variation using a classical diallel crossing scheme. Nucleic Acids Research, 2007, 35, 1038-1038.	14.5	0
67	Integration of biological networks and gene expression data using Cytoscape. Nature Protocols, 2007, 2, 2366-2382.	12.0	2,275
68	CATMA, a comprehensive genome-scale resource for silencing and transcript profiling of Arabidopsis genes. BMC Bioinformatics, 2007, 8, 400.	2.6	46
69	Validating module network learning algorithms using simulated data. BMC Bioinformatics, 2007, 8, S5.	2.6	34
70	Genetic dissection of transcriptional regulation by cDNA-AFLP. Plant Journal, 2006, 45, 439-446.	5.7	46
71	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.	2.4	51
72	Genome-wide screening for cis-regulatory variation using a classical diallel crossing scheme. Nucleic Acids Research, 2006, 34, 3677-3686.	14.5	20

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73	A Cell-Cycle Knowledge Integration Framework. Lecture Notes in Computer Science, 2006, , 19-34.	1.3	7
74	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, 1723-1736.	6.6	248
75	Modeling gene and genome duplications in eukaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5454-5459.	7.1	850
76	Genetic Analysis of Variation in Gene Expression in Arabidopsis thaliana. Genetics, 2005, 171, 1267-1275.	2.9	116
77	Benchmarking the CATMA Microarray. A Novel Tool forArabidopsis Transcriptome Analysis. Plant Physiology, 2005, 137, 588-601.	4.8	91
78	Simulating genetic networks made easy: network construction with simple building blocks. Bioinformatics, 2005, 21, 269-271.	4.1	7
79	BiNGO: a Cytoscape plugin to assess overrepresentation of Gene Ontology categories in Biological Networks. Bioinformatics, 2005, 21, 3448-3449.	4.1	3,901
80	Versatile Gene-Specific Sequence Tags for Arabidopsis Functional Genomics: Transcript Profiling and Reverse Genetics Applications. Genome Research, 2004, 14, 2176-2189.	5.5	282
81	European consortia building integrated resources for Arabidopsis functional genomics. Current Opinion in Plant Biology, 2003, 6, 426-429.	7.1	44
82	Phylogeny of bovine species based on AFLP fingerprinting. Heredity, 2002, 88, 46-51.	2.6	93
83	Genetic Affinities Within the Herring Gull Larus argentatus Assemblage Revealed by AFLP Genotyping. Journal of Molecular Evolution, 2001, 52, 85-93.	1.8	49
84	Mapping of a QTL for Serum HDL Cholesterol in the Rabbit Using AFLP Technology. , 2001, 92, 322-326.		16
85	Chromosomal regions involved in hybrid performance and heterosis: their AFLPÂ®-based identification and practical use in prediction models. Heredity, 2000, 85, 208-218.	2.6	44
86	Title is missing!. Molecular Breeding, 2000, 6, 265-276.	2.1	30
87	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.	1.8	79
88	Two high-density AFLPÂ® linkage maps of Zea mays L.: analysis of distribution of AFLP markers. Theoretical and Applied Genetics, 1999, 99, 921-935.	3.6	217
89	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.	3.6	173
90	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, 503-512.	3.6	25

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91	Integrated map of AFLP, SSLP and RFLP markers using a recombinant inbred population of rice (Oryza) Tj ETQq1 1 0.784314 rgBT /Over	3.6	90
92	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, 259-271.	5.7	355
93	AFLPâ„¢ markers for DNA fingerprinting in cattle. Animal Genetics, 1997, 28, 418-426.	1.7	147
94	Use of AFLP Markers for Gene Mapping and QTL Detection in the Rat. Genomics, 1996, 37, 289-294.	2.9	64
95	Combined mapping of AFLP and RFLP markers in barley. Molecular Genetics and Genomics, 1995, 249, 65-73.	2.4	337
96	The VS catalytic RNA replicates by reverse transcription as a satellite of a retroplasmid.. Genes and Development, 1995, 9, 294-303.	5.9	53
97	AFLP: a new technique for DNA fingerprinting. Nucleic Acids Research, 1995, 23, 4407-4414.	14.5	10,873
98	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
99	A novel reverse transcriptase activity associated with mitochondrial plasmids of neurospora. Cell, 1988, 55, 693-704.	28.9	109
100	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.	1.7	16
101	Molecular cloning of pea mRNAs encoding a shoot-specific polypeptide and light-induced polypeptides. Plant Molecular Biology, 1983, 2, 295-303.	3.9	17