

Martin Tr Kuiper

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2956018/publications.pdf>

Version: 2024-02-01

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	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

#	ARTICLE	IF	CITATIONS
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	orthAgoque: 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

#	ARTICLE	IF	CITATIONS
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

#	ARTICLE	IF	CITATIONS
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

#	ARTICLE	IF	CITATIONS
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

#	ARTICLE	IF	CITATIONS
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