

Taner Z Sen

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/5054458/taner-z-sen-publications-by-year.pdf>

Version: 2024-04-29

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

66
papers

1,577
citations

22
h-index

38
g-index

75
ext. papers

1,886
ext. citations

5.1
avg. IF

4.39
L-index

#	Paper	IF	Citations
66	Genome-wide discovery of G-quadruplexes in barley. <i>Scientific Reports</i> , 2021 , 11, 7876	4.9	6
65	FINDER: an automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences. <i>BMC Bioinformatics</i> , 2021 , 22, 205	3.6	5
64	mirMachine: A One-Stop Shop for Plant miRNA Annotation. <i>Journal of Visualized Experiments</i> , 2021 ,	1.6	5
63	LncMachine: a machine learning algorithm for long noncoding RNA annotation in plants. <i>Functional and Integrative Genomics</i> , 2021 , 21, 195-204	3.8	9
62	Building a successful international research community through data sharing: The case of the Wheat Information System (WheatIS). <i>F1000Research</i> , 2020 , 9, 536	3.6	1
61	Tissue-specific gene expression and protein abundance patterns are associated with fractionation bias in maize. <i>BMC Plant Biology</i> , 2020 , 20, 4	5.3	2
60	JBrowse Connect: A server API to connect JBrowse instances and users. <i>PLoS Computational Biology</i> , 2020 , 16, e1007261	5	1
59	Genome-Wide Discovery of G-Quadruplexes in Wheat: Distribution and Putative Functional Roles. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 2021-2032	3.2	7
58	PedigreeNet: a web-based pedigree viewer for biological databases. <i>Bioinformatics</i> , 2019 , 35, 4184-4186	7.2	0
57	GrainGenes: centralized small grain resources and digital platform for geneticists and breeders. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	27
56	MaizeGDB 2018: the maize multi-genome genetics and genomics database. <i>Nucleic Acids Research</i> , 2019 , 47, D1146-D1154	20.1	121
55	Structural dynamics of lytic polysaccharide monooxygenases reveals a highly flexible substrate binding region. <i>Journal of Molecular Graphics and Modelling</i> , 2019 , 88, 1-10	2.8	5
54	SNPiversity: a web-based tool for visualizing diversity. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	7
53	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	28
52	Application of Molecular Simulations Toward Understanding Cellulase Mechanisms. <i>Bioenergy Research</i> , 2018 , 11, 850-867	3.1	4
51	Surveying the Maize community for their diversity and pedigree visualization needs to prioritize tool development and curation. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	3
50	Predicting Protein Secondary Structure Using Consensus Data Mining (CDM) Based on Empirical Statistics and Evolutionary Information. <i>Methods in Molecular Biology</i> , 2017 , 1484, 35-44	1.4	6

49	The art of curation at a biological database: Principles and application. <i>Current Plant Biology</i> , 2017 , 11-12, 2-11	3.3	16
48	The quality of metabolic pathway resources depends on initial enzymatic function assignments: a case for maize. <i>BMC Systems Biology</i> , 2016 , 10, 129	3.5	11
47	MaizeGDB update: new tools, data and interface for the maize model organism database. <i>Nucleic Acids Research</i> , 2016 , 44, D1195-201	20.1	130
46	A Clade-Specific Arabidopsis Gene Connects Primary Metabolism and Senescence. <i>Frontiers in Plant Science</i> , 2016 , 7, 983	6.2	13
45	An adaptable pentaloop defines a robust neomycin-B RNA aptamer with conditional ligand-bound structures. <i>Rna</i> , 2014 , 20, 815-24	5.8	10
44	A computational platform to maintain and migrate manual functional annotations for BioCyc databases. <i>BMC Systems Biology</i> , 2014 , 8, 115	3.5	3
43	Sampling errors: Aristotle's suspect statistical skills. <i>Nature</i> , 2014 , 513, 315	50.4	
42	Endoglucanases: insights into thermostability for biofuel applications. <i>Biotechnology for Biofuels</i> , 2013 , 6, 136	7.8	59
41	Maize Metabolic Network Construction and Transcriptome Analysis. <i>Plant Genome</i> , 2013 , 6, plantgenome.2012.00025	11.9	25
40	Predicting the binding patterns of hub proteins: a study using yeast protein interaction networks. <i>PLoS ONE</i> , 2013 , 8, e56833	3.7	8
39	Molecular simulation of fibronectin adsorption onto polyurethane surfaces. <i>Langmuir</i> , 2012 , 28, 12619-28	4	22
38	A rigid network of long-range contacts increases thermostability in a mutant endoglucanase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012 , 30, 628-37	3.6	14
37	Plant Cytogenetics in Genome Databases 2012 , 311-322		
36	Thermostability in endoglucanases is fold-specific. <i>BMC Structural Biology</i> , 2011 , 11, 10	2.7	43
35	Dynamics of endoglucanase catalytic domains: implications towards thermostability. <i>Journal of Biomolecular Structure and Dynamics</i> , 2011 , 29, 509-26	3.6	4
34	MaizeGDB: curation and outreach go hand-in-hand. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar022	5	59
33	POPCorn: An Online Resource Providing Access to Distributed and Diverse Maize Project Data. <i>International Journal of Plant Genomics</i> , 2011 , 2011, 923035		17
32	The MaizeGDB Genome Browser tutorial: one example of database outreach to biologists via video. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar016	5	14

31	The Locus Lookup tool at MaizeGDB: identification of genomic regions in maize by integrating sequence information with physical and genetic maps. <i>Bioinformatics</i> , 2010 , 26, 434-6	7.2	60
30	Choosing a genome browser for a Model Organism Database: surveying the maize community. <i>Database: the Journal of Biological Databases and Curation</i> , 2010 , 2010, baq007	5	27
29	MaizeGDB becomes a sequence-centric Database: the Journal of Biological Databases and Curation, 2009 , 2009, bap020	5	40
28	Data Mining for Protein Secondary Structure Prediction. <i>Structure and Bonding</i> , 2009 , 135-167	0.9	1
27	Predicting the complex structure and functional motions of the outer membrane transporter and signal transducer FecA. <i>Biophysical Journal</i> , 2008 , 94, 2482-91	2.9	11
26	The ribosome structure controls and directs mRNA entry, translocation and exit dynamics. <i>Physical Biology</i> , 2008 , 5, 046005	3	50
25	Predicting the order in which contacts are broken during single molecule protein stretching experiments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 45-60	4.2	21
24	MaizeGDB: The maize model organism database for basic, translational, and applied research. <i>International Journal of Plant Genomics</i> , 2008 , 2008, 496957		74
23	Generation and enumeration of compact conformations on the two-dimensional triangular and three-dimensional fcc lattices. <i>Journal of Chemical Physics</i> , 2007 , 127, 044101	3.9	7
22	Consensus Data Mining (CDM) Protein Secondary Structure Prediction Server: combining GOR V and Fragment Database Mining (FDM). <i>Bioinformatics</i> , 2007 , 23, 2628-30	7.2	23
21	Monte Carlo Simulations on Nanoparticles in Elastomers. Effects of the Particles on the Dimensions of the Polymer Chains and the Mechanical Properties of the Networks. <i>Macromolecular Symposia</i> , 2007 , 256, 40-47	0.8	7
20	A DNA-centric look at protein-DNA complexes. <i>Structure</i> , 2006 , 14, 1341-2	5.2	3
19	Functional clustering of yeast proteins from the protein-protein interaction network. <i>BMC Bioinformatics</i> , 2006 , 7, 355	3.6	36
18	The Extent of Cooperativity of Protein Motions Observed with Elastic Network Models Is Similar for Atomic and Coarser-Grained Models. <i>Journal of Chemical Theory and Computation</i> , 2006 , 2, 696-704	6.4	77
17	Filler-induced deformations of amorphous polyethylene chains. The effects of the deformations on elastomeric properties, and some comparisons with experiments. <i>European Polymer Journal</i> , 2006 , 42, 796-806	5.2	19
16	A Consensus Data Mining secondary structure prediction by combining GOR V and Fragment Database Mining. <i>Protein Science</i> , 2006 , 15, 2499-506	6.3	20
15	Molecular modeling of matrix chain deformation in nanofiber filled composites. <i>Colloid and Polymer Science</i> , 2006 , 284, 700-709	2.4	2
14	Protein promiscuity: drug resistance and native functions--HIV-1 case. <i>Journal of Biomolecular Structure and Dynamics</i> , 2005 , 22, 615-24	3.6	19

13	The largest eigenvalue method for stereo-regular vinyl chains. <i>Polymer</i> , 2005 , 46, 4373-4383	3.9	6
12	Modeling the elastomeric properties of stereoregular polypropylenes in nanocomposites with spherical fillers. <i>Polymer</i> , 2005 , 46, 7301-7308	3.9	18
11	Some simulations on filler reinforcement in elastomers. <i>Polymer</i> , 2005 , 46, 8894-8904	3.9	61
10	Prediction of protein secondary structure by mining structural fragment database. <i>Polymer</i> , 2005 , 46, 4314-4321	3.9	25
9	GOR V server for protein secondary structure prediction. <i>Bioinformatics</i> , 2005 , 21, 2787-8	7.2	144
8	Optimizing the Parameters of the Gaussian Network Model for ATP-Binding Proteins. <i>Chapman & Hall/CRC Mathematical and Computational Biology Series</i> , 2005 , 171-186		2
7	Predicting binding sites of hydrolase-inhibitor complexes by combining several methods. <i>BMC Bioinformatics</i> , 2004 , 5, 205	3.6	18
6	The transfer matrix method for lattice proteins—An application with cooperative interactions. <i>Polymer</i> , 2004 , 45, 707-716	3.9	6
5	A Minimal Model for the Helix-Coil Transition of Wormlike Polymers. Insights from Monte Carlo Simulations and Theoretical Implications. <i>Macromolecules</i> , 2004 , 37, 8794-8804	5.5	18
4	The effect of natural rubber crosslink density on real time birefringence, true stress and true strain behavior. <i>Macromolecular Symposia</i> , 2002 , 185, 149-166	0.8	29
3	Modeling the deamidation of asparagine residues via succinimide intermediates. <i>Journal of Molecular Modeling</i> , 2001 , 7, 147-160	2	28
2	Local Dynamics of cis-1,4-Polybutadiene and cis-1,4-Polyisoprene. A Comparative Study Based on Cooperative Kinematics Theory and NMR Experiments. <i>Macromolecules</i> , 1999 , 32, 3017-3024	5.5	12
1	FINDER: An automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences		1