

Taner Z Sen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5054458/publications.pdf>

Version: 2024-02-01

72
papers

2,135
citations

279778

23
h-index

254170

43
g-index

75
all docs

75
docs citations

75
times ranked

3238
citing authors

#	ARTICLE	IF	CITATIONS
1	MaizeGDB 2018: the maize multi-genome genetics and genomics database. <i>Nucleic Acids Research</i> , 2019, 47, D1146-D1154.	14.5	235
2	GOR V server for protein secondary structure prediction. <i>Bioinformatics</i> , 2005, 21, 2787-2788.	4.1	179
3	MaizeGDB update: new tools, data and interface for the maize model organism database. <i>Nucleic Acids Research</i> , 2016, 44, D1195-D1201.	14.5	170
4	MaizeGDB: The Maize Model Organism Database for Basic, Translational, and Applied Research. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-10.	2.2	95
5	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.	5.3	84
6	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, 434-436.	4.1	83
7	Endoglucanases: insights into thermostability for biofuel applications. <i>Biotechnology for Biofuels</i> , 2013, 6, 136.	6.2	72
8	MaizeGDB: curation and outreach go hand-in-hand. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar022-bar022.	3.0	66
9	Some simulations on filler reinforcement in elastomers. <i>Polymer</i> , 2005, 46, 8894-8904.	3.8	65
10	Maize Metabolic Network Construction and Transcriptome Analysis. <i>Plant Genome</i> , 2013, 6, plantgenome2012.09.0025.	2.8	63
11	The ribosome structure controls and directs mRNA entry, translocation and exit dynamics. <i>Physical Biology</i> , 2008, 5, 046005.	1.8	61
12	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	52
13	OUP accepted manuscript. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	50
14	Thermostability in endoglucanases is fold-specific. <i>BMC Structural Biology</i> , 2011, 11, 10.	2.3	49
15	MaizeGDB becomes 'sequence-centric'. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2009, bap020-bap020.	3.0	44
16	Functional clustering of yeast proteins from the protein-protein interaction network. <i>BMC Bioinformatics</i> , 2006, 7, 355.	2.6	40
17	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.	0.7	31
18	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.	3.0	31

#	ARTICLE	IF	CITATIONS
19	Consensus Data Mining (CDM) Protein Secondary Structure Prediction Server: Combining GOR V and Fragment Database Mining (FDM). <i>Bioinformatics</i> , 2007, 23, 2628-2630.	4.1	30
20	The art of curation at a biological database: Principles and application. <i>Current Plant Biology</i> , 2017, 11-12, 2-11.	4.7	30
21	Modeling the deamidation of asparagine residues via succinimide intermediates. <i>Journal of Molecular Modeling</i> , 2001, 7, 147-160.	1.8	29
22	Prediction of protein secondary structure by mining structural fragment database. <i>Polymer</i> , 2005, 46, 4314-4321.	3.8	28
23	Predicting binding sites of hydrolase-inhibitor complexes by combining several methods. <i>BMC Bioinformatics</i> , 2004, 5, 205.	2.6	27
24	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.	2.6	26
25	Molecular Simulation of Fibronectin Adsorption onto Polyurethane Surfaces. <i>Langmuir</i> , 2012, 28, 12619-12628.	3.5	24
26	A Clade-Specific Arabidopsis Gene Connects Primary Metabolism and Senescence. <i>Frontiers in Plant Science</i> , 2016, 7, 983.	3.6	24
27	Protein Promiscuity: Drug Resistance and Native Functionsâ€™HIV-1 Case. <i>Journal of Biomolecular Structure and Dynamics</i> , 2005, 22, 615-624.	3.5	22
28	A Consensus Data Mining secondary structure prediction by combining GOR V and Fragment Database Mining. <i>Protein Science</i> , 2006, 15, 2499-2506.	7.6	22
29	Genome-Wide Discovery of G-Quadruplexes in Wheat: Distribution and Putative Functional Roles. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2021-2032.	1.8	22
30	GrainGenes: a data-rich repository for small grains genetics and genomics. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	22
31	Modeling the elastomeric properties of stereoregular polypropylenes in nanocomposites with spherical fillers. <i>Polymer</i> , 2005, 46, 7301-7308.	3.8	21
32	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.	5.4	21
33	POPCorn: An Online Resource Providing Access to Distributed and Diverse Maize Project Data. <i>International Journal of Plant Genomics</i> , 2011, 2011, 1-10.	2.2	20
34	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.	4.8	19
35	A rigid network of long-range contacts increases thermostability in a mutant endoglucanase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 30, 628-637.	3.5	17
36	LncMachine: a machine learning algorithm for long noncoding RNA annotation in plants. <i>Functional and Integrative Genomics</i> , 2021, 21, 195-204.	3.5	17

#	ARTICLE	IF	CITATIONS
37	FINDER: an automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences. BMC Bioinformatics, 2021, 22, 205.	2.6	17
38	Genome-wide discovery of G-quadruplexes in barley. Scientific Reports, 2021, 11, 7876.	3.3	16
39	The quality of metabolic pathway resources depends on initial enzymatic function assignments: a case for maize. BMC Systems Biology, 2016, 10, 129.	3.0	15
40	The MaizeGDB Genome Browser tutorial: one example of database outreach to biologists via video. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar016-bar016.	3.0	14
41	Predicting the Binding Patterns of Hub Proteins: A Study Using Yeast Protein Interaction Networks. PLoS ONE, 2013, 8, e56833.	2.5	13
42	Local Dynamics of cis-1,4-Polybutadiene and cis-1,4-Polyisoprene. A Comparative Study Based on Cooperative Kinematics Theory and NMR Experiments. Macromolecules, 1999, 32, 3017-3024.	4.8	12
43	An adaptable pentaloop defines a robust neomycin-B RNA aptamer with conditional ligand-bound structures. Rna, 2014, 20, 815-824.	3.5	12
44	Predicting the Complex Structure and Functional Motions of the Outer Membrane Transporter and Signal Transducer FecA. Biophysical Journal, 2008, 94, 2482-2491.	0.5	11
45	Structural dynamics of lytic polysaccharide monooxygenases reveals a highly flexible substrate binding region. Journal of Molecular Graphics and Modelling, 2019, 88, 1-10.	2.4	11
46	Tissue-specific gene expression and protein abundance patterns are associated with fractionation bias in maize. BMC Plant Biology, 2020, 20, 4.	3.6	10
47	Generation and enumeration of compact conformations on the two-dimensional triangular and three-dimensional fcc lattices. Journal of Chemical Physics, 2007, 127, 044101.	3.0	9
48	SNPiversity: a web-based tool for visualizing diversity. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	9
49	The transfer matrix method for lattice proteins— an application with cooperative interactions. Polymer, 2004, 45, 707-716.	3.8	8
50	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. Macromolecular Symposia, 2007, 256, 40-47.	0.7	8
51	The largest eigenvalue method for stereo-regular vinyl chains. Polymer, 2005, 46, 4373-4383.	3.8	7
52	Predicting Protein Secondary Structure Using Consensus Data Mining (CDM) Based on Empirical Statistics and Evolutionary Information. Methods in Molecular Biology, 2017, 1484, 35-44.	0.9	7
53	Application of Molecular Simulations Toward Understanding Cellulase Mechanisms. Bioenergy Research, 2018, 11, 850-867.	3.9	7
54	mirMachine: A One-Stop Shop for Plant miRNA Annotation. Journal of Visualized Experiments, 2021, .	0.3	7

#	ARTICLE	IF	CITATIONS
55	C4Boost: a machine learning-based tool for quadruplex identification and stability prediction. BMC Bioinformatics, 2022, 23, .	2.6	7
56	Dynamics of Endoglucanase Catalytic Domains: Implications Towards Thermostability. Journal of Biomolecular Structure and Dynamics, 2011, 29, 509-526.	3.5	5
57	Building a successful international research community through data sharing: The case of the Wheat Information System (WheatIS). F1000Research, 2020, 9, 536.	1.6	5
58	A DNA-Centric Look at Protein-DNA Complexes. Structure, 2006, 14, 1341-1342.	3.3	4
59	A computational platform to maintain and migrate manual functional annotations for BioCyc databases. BMC Systems Biology, 2014, 8, 115.	3.0	4
60	Surveying the Maize community for their diversity and pedigree visualization needs to prioritize tool development and curation. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	4
61	Molecular modeling of matrix chain deformation in nanofiber filled composites. Colloid and Polymer Science, 2006, 284, 700-709.	2.1	3
62	PedigreeNet: a web-based pedigree viewer for biological databases. Bioinformatics, 2019, 35, 4184-4186.	4.1	3
63	Data Mining for Protein Secondary Structure Prediction. Structure and Bonding, 2009, , 135-167.	1.0	3
64	GrainGenes: Tools and Content to Assist Breeders Improving Oat Quality. Foods, 2022, 11, 914.	4.3	2
65	Experimental and computational studies of cellulases as bioethanol enzymes. Bioengineered, 2022, 13, 14028-14046.	3.2	2
66	JBrowse Connect: A server API to connect JBrowse instances and users. PLoS Computational Biology, 2020, 16, e1007261.	3.2	1
67	Multiple Variant Calling Pipelines in Wheat Whole Exome Sequencing. International Journal of Molecular Sciences, 2021, 22, 10400.	4.1	1
68	MaizeGDB , maize genetics cooperation and the ~2500MB B73 genome generated tsunami. Nature Precedings, 2010, , .	0.1	0
69	Plant Cytogenetics in Genome Databases. , 2012, , 311-322.		0
70	Aristotle's suspect statistical skills. Nature, 2014, 513, 315-315.	27.8	0
71	Data Mining for Protein Secondary Structure Prediction. Structure and Bonding, 2009, , 135-167.	1.0	0
72	Predicting Tissue-Specific mRNA and Protein Abundance in Maize: A Machine Learning Approach. Frontiers in Artificial Intelligence, 2022, 5, .	3.4	0