Taner Z Sen

List of Publications by Citations

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	GOR V server for protein secondary structure prediction. *Bioinformatics*, **2005**, 21, 2787-8	7.2	144
65	MaizeGDB update: new tools, data and interface for the maize model organism database. *Nucleic Acids Research*, **2016**, 44, D1195-201	20.1	130
64	MaizeGDB 2018: the maize multi-genome genetics and genomics database. *Nucleic Acids Research*, **2019**, 47, D1146-D1154	20.1	121
63	The Extent of Cooperativity of Protein Motions Observed with Elastic Network Models Is Similar for Atomic and Coarser-Grained Models. *Journal of Chemical Theory and Computation*, **2006**, 2, 696-704	6.4	77
62	MaizeGDB: The maize model organism database for basic, translational, and applied research. *International Journal of Plant Genomics*, **2008**, 2008, 496957		74
61	Some simulations on filler reinforcement in elastomers. *Polymer*, **2005**, 46, 8894-8904	3.9	61
60	The Locus Lookup tool at MaizeGDB: identification of genomic regions in maize by integrating sequence information with physical and genetic maps. *Bioinformatics*, **2010**, 26, 434-6	7.2	60
59	Endoglucanases: insights into thermostability for biofuel applications. *Biotechnology for Biofuels*, **2013**, 6, 136	7.8	59
58	MaizeGDB: curation and outreach go hand-in-hand. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, bar022	5	59
57	Maize Metabolic Network Construction and Transcriptome Analysis. *Plant Genome*, **2013**, 6, plantgenome2012.09.0025	4.4	50
56	The ribosome structure controls and directs mRNA entry, translocation and exit dynamics. *Physical Biology*, **2008**, 5, 046005	3	50
55	Thermostability in endoglucanases is fold-specific. *BMC Structural Biology*, **2011**, 11, 10	2.7	43
54	MaizeGDB becomes ᵁsequence-centricᵁ *Database: the Journal of Biological Databases and Curation*, **2009**, 2009, bap020	5	40
53	Functional clustering of yeast proteins from the protein-protein interaction network. *BMC Bioinformatics*, **2006**, 7, 355	3.6	36
52	The effect of natural rubber crosslink density on real time birefringence, true stress and true strain behavior. *Macromolecular Symposia*, **2002**, 185, 149-166	0.8	29
51	Modeling the deamidation of asparagine residues via succinimide intermediates. *Journal of Molecular Modeling*, **2001**, 7, 147-160	2	28
50	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018,	5	28

49	Choosing a genome browser for a Model Organism Database: surveying the maize community. *Database: the Journal of Biological Databases and Curation*, **2010**, 2010, baq007	5	27
48	GrainGenes: centralized small grain resources and digital platform for geneticists and breeders. *Database: the Journal of Biological Databases and Curation*, **2019**, 2019,	5	27
47	Prediction of protein secondary structure by mining structural fragment database. *Polymer*, **2005**, 46, 4314-4321	3.9	25
46	Consensus Data Mining (CDM) Protein Secondary Structure Prediction Server: combining GOR V and Fragment Database Mining (FDM). *Bioinformatics*, **2007**, 23, 2628-30	7.2	23
45	Molecular simulation of fibronectin adsorption onto polyurethane surfaces. *Langmuir*, **2012**, 28, 12619-28	4	22
44	Predicting the order in which contacts are broken during single molecule protein stretching experiments. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 45-60	4.2	21
43	A Consensus Data Mining secondary structure prediction by combining GOR V and Fragment Database Mining. *Protein Science*, **2006**, 15, 2499-506	6.3	20
42	Protein promiscuity: drug resistance and native functions--HIV-1 case. *Journal of Biomolecular Structure and Dynamics*, **2005**, 22, 615-24	3.6	19
41	Filler-induced deformations of amorphous polyethylene chains. The effects of the deformations on elastomeric properties, and some comparisons with experiments. *European Polymer Journal*, **2006**, 42, 796-806	5.2	19
40	Predicting binding sites of hydrolase-inhibitor complexes by combining several methods. *BMC Bioinformatics*, **2004**, 5, 205	3.6	18
39	A Minimal Model for the Helix Coil Transition of Wormlike Polymers. Insights from Monte Carlo Simulations and Theoretical Implications. *Macromolecules*, **2004**, 37, 8794-8804	5.5	18
38	Modeling the elastomeric properties of stereoregular polypropylenes in nanocomposites with spherical fillers. *Polymer*, **2005**, 46, 7301-7308	3.9	18
37	POPcorn: An Online Resource Providing Access to Distributed and Diverse Maize Project Data. *International Journal of Plant Genomics*, **2011**, 2011, 923035		17
36	The art of curation at a biological database: Principles and application. *Current Plant Biology*, **2017**, 11-12, 2-11	3.3	16
35	A rigid network of long-range contacts increases thermostability in a mutant endoglucanase. *Journal of Biomolecular Structure and Dynamics*, **2012**, 30, 628-37	3.6	14
34	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	5	14
33	A Clade-Specific Arabidopsis Gene Connects Primary Metabolism and Senescence. *Frontiers in Plant Science*, **2016**, 7, 983	6.2	13
32	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	5.5	12

31	The quality of metabolic pathway resources depends on initial enzymatic function assignments: a case for maize. *BMC Systems Biology*, **2016**, 10, 129	3.5	11
30	Predicting the complex structure and functional motions of the outer membrane transporter and signal transducer FecA. *Biophysical Journal*, **2008**, 94, 2482-91	2.9	11
29	An adaptable pentaloop defines a robust neomycin-B RNA aptamer with conditional ligand-bound structures. *Rna*, **2014**, 20, 815-24	5.8	10
28	LncMachine: a machine learning algorithm for long noncoding RNA annotation in plants. *Functional and Integrative Genomics*, **2021**, 21, 195-204	3.8	9
27	Predicting the binding patterns of hub proteins: a study using yeast protein interaction networks. *PLoS ONE*, **2013**, 8, e56833	3.7	8
26	Generation and enumeration of compact conformations on the two-dimensional triangular and three-dimensional fcc lattices. *Journal of Chemical Physics*, **2007**, 127, 044101	3.9	7
25	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	0.8	7
24	Genome-Wide Discovery of G-Quadruplexes in Wheat: Distribution and Putative Functional Roles. *G3: Genes, Genomes, Genetics*, **2020**, 10, 2021-2032	3.2	7
23	SNPversity: a web-based tool for visualizing diversity. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018,	5	7
22	Predicting Protein Secondary Structure Using Consensus Data Mining (CDM) Based on Empirical Statistics and Evolutionary Information. *Methods in Molecular Biology*, **2017**, 1484, 35-44	1.4	6
21	The transfer matrix method for lattice proteins—an application with cooperative interactions. *Polymer*, **2004**, 45, 707-716	3.9	6
20	The largest eigenvalue method for stereo-regular vinyl chains. *Polymer*, **2005**, 46, 4373-4383	3.9	6
19	Genome-wide discovery of G-quadruplexes in barley. *Scientific Reports*, **2021**, 11, 7876	4.9	6
18	FINDER: an automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences. *BMC Bioinformatics*, **2021**, 22, 205	3.6	5
17	mirMachine: A One-Stop Shop for Plant miRNA Annotation. *Journal of Visualized Experiments*, **2021**,	1.6	5
16	Structural dynamics of lytic polysaccharide monoxygenases reveals a highly flexible substrate binding region. *Journal of Molecular Graphics and Modelling*, **2019**, 88, 1-10	2.8	5
15	Dynamics of endoglucanase catalytic domains: implications towards thermostability. *Journal of Biomolecular Structure and Dynamics*, **2011**, 29, 509-26	3.6	4
14	Application of Molecular Simulations Toward Understanding Cellulase Mechanisms. *Bioenergy Research*, **2018**, 11, 850-867	3.1	4

List of Publications

13	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,	5	3
12	A computational platform to maintain and migrate manual functional annotations for BioCyc databases. *BMC Systems Biology*, **2014**, 8, 115	3.5	3
11	A DNA-centric look at protein-DNA complexes. *Structure*, **2006**, 14, 1341-2	5.2	3
10	Molecular modeling of matrix chain deformation in nanofiber filled composites. *Colloid and Polymer Science*, **2006**, 284, 700-709	2.4	2
9	Optimizing the Parameters of the Gaussian Network Model for ATP-Binding Proteins. *Chapman & Hall/CRC Mathematical and Computational Biology Series*, **2005**, 171-186		2
8	Tissue-specific gene expression and protein abundance patterns are associated with fractionation bias in maize. *BMC Plant Biology*, **2020**, 20, 4	5.3	2
7	Building a successful international research community through data sharing: The case of the Wheat Information System (WheatIS). *F1000Research*, **2020**, 9, 536	3.6	1
6	Data Mining for Protein Secondary Structure Prediction. *Structure and Bonding*, **2009**, 135-167	0.9	1
5	JBrowse Connect: A server API to connect JBrowse instances and users. *PLoS Computational Biology*, **2020**, 16, e1007261	5	1
4	FINDER: An automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences		1
3	PedigreeNet: a web-based pedigree viewer for biological databases. *Bioinformatics*, **2019**, 35, 4184-4186	7.2	0
2	Sampling errors: Aristotle's suspect statistical skills. *Nature*, **2014**, 513, 315	50.4	
1	Plant Cytogenetics in Genome Databases **2012**, 311-322		