

Charlie T Hodgman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/412896/publications.pdf>

Version: 2024-02-01

83
papers

7,962
citations

117625
34
h-index

58581
82
g-index

88
all docs

88
docs citations

88
times ranked

9682
citing authors

#	ARTICLE	IF	CITATIONS
1	The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. <i>Bioinformatics</i> , 2003, 19, 524-531.	4.1	2,811
2	A new superfamily of replicative proteins. <i>Nature</i> , 1988, 333, 22-23.	27.8	515
3	Identification of the homologous beige and Chediak-Higashi syndrome genes. <i>Nature</i> , 1996, 382, 262-265.	27.8	501
4	Root gravitropism is regulated by a transient lateral auxin gradient controlled by a tipping-point mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4668-4673.	7.1	304
5	A DEMETER-like DNA demethylase governs tomato fruit ripening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10804-10809.	7.1	256
6	An Analysis of the Biological Properties of Monoclonal Antibodies against Glycoprotein D of Herpes Simplex Virus and Identification of Amino Acid Substitutions that Confer Resistance to Neutralization. <i>Journal of General Virology</i> , 1986, 67, 1001-1013.	2.9	226
7	Systems Analysis of Auxin Transport in the <i>Arabidopsis</i> Root Apex. <i>Plant Cell</i> , 2014, 26, 862-875.	6.6	190
8	Network Inference Analysis Identifies an <i>APRR2-Like</i> Gene Linked to Pigment Accumulation in Tomato and Pepper Fruits. <i>Plant Physiology</i> , 2013, 161, 1476-1485.	4.8	166
9	Tackling Drought Stress: RECEPTOR-LIKE KINASES Present New Approaches. <i>Plant Cell</i> , 2012, 24, 2262-2278.	6.6	155
10	Unraveling the Evolution of Auxin Signaling. <i>Plant Physiology</i> , 2011, 155, 209-221.	4.8	140
11	Mathematical simulation and analysis of cellular metabolism and regulation. <i>Bioinformatics</i> , 1999, 15, 749-758.	4.1	135
12	Genome-wide mapping of transcriptional enhancer candidates using DNA and chromatin features in maize. <i>Genome Biology</i> , 2017, 18, 137.	8.8	134
13	Lewis X Biosynthesis in <i>Helicobacter pylori</i> . <i>Journal of Biological Chemistry</i> , 1997, 272, 21349-21356.	3.4	123
14	The circadian clock rephases during lateral root organ initiation in <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2015, 6, 7641.	12.8	119
15	Identification of a new glycoprotein of herpes simplex virus type 1 and genetic mapping of the gene that codes for it. <i>Journal of Virology</i> , 1986, 57, 647-655.	3.4	117
16	Parameter Estimation Using Metaheuristics in Systems Biology: A Comprehensive Review. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 185-202.	3.0	112
17	Rice auxin influx carrier OsAUX1 facilitates root hair elongation in response to low external phosphate. <i>Nature Communications</i> , 2018, 9, 1408.	12.8	110
18	DNA Methylation and Chromatin Regulation during Fleshy Fruit Development and Ripening. <i>Frontiers in Plant Science</i> , 2016, 7, 807.	3.6	106

#	ARTICLE	IF	CITATIONS
19	Integration of hormonal signaling networks and mobile microRNAs is required for vascular patterning in <i>Arabidopsis</i> roots. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 857-862.	7.1	98
20	Growth-induced hormone dilution can explain the dynamics of plant root cell elongation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7577-7582.	7.1	95
21	Cloning and analysis of the first cry gene from <i>Bacillus popilliae</i> . Journal of Bacteriology, 1997, 179, 4336-4341.	2.2	92
22	Characterizing proteolytic cleavage site activity using bio-basis function neural networks. Bioinformatics, 2003, 19, 1741-1747.	4.1	92
23	OsCAND1 Is Required for Crown Root Emergence in Rice. Molecular Plant, 2011, 4, 289-299.	8.3	75
24	Repression of Translation of Human Estrogen Receptor β by G-Quadruplex Formation. Biochemistry, 2009, 48, 11487-11495.	2.5	70
25	Models for the structure and function of the <i>Bacillus thuringiensis</i> δ -endotoxins determined by compilational analysis. DNA Sequence, 1990, 1, 97-106.	0.7	67
26	Modulation of <i>Arabidopsis</i> and monocot root architecture by CLAVATA3/EMBRYO SURROUNDING REGION 26 peptide. Journal of Experimental Botany, 2015, 66, 5229-5243.	4.8	62
27	Comparison of functional annotation schemes for genomes. Functional and Integrative Genomics, 2000, 1, 56-69.	3.5	60
28	Whole genome sequence and manual annotation of <i>Clostridium autoethanogenum</i> , an industrially relevant bacterium. BMC Genomics, 2015, 16, 1085.	2.8	56
29	Mechanical modelling quantifies the functional importance of outer tissue layers during root elongation and bending. New Phytologist, 2014, 202, 1212-1222.	7.3	53
30	INFERENCE OF GENE REGULATORY NETWORKS USING BOOLEAN-NETWORK INFERENCE METHODS. Journal of Bioinformatics and Computational Biology, 2009, 07, 1013-1029.	0.8	47
31	The construction of <i>Bacillus thuringiensis</i> strains expressing novel entomocidal δ -endotoxin combinations. Biochemical Journal, 1990, 270, 133-136.	3.7	45
32	Constructing an enzyme-centric view of metabolism. Bioinformatics, 2004, 20, 2050-2055.	4.1	45
33	Lipidomic analysis of plasma samples from women with polycystic ovary syndrome. Metabolomics, 2015, 11, 657-666.	3.0	44
34	A machine learning heuristic to identify biologically relevant and minimal biomarker panels from omics data. BMC Genomics, 2015, 16, S2.	2.8	43
35	Nucleoprotein architecture and ColE1 dimer resolution: a hypothesis. Molecular Microbiology, 1998, 29, 545-558.	2.5	36
36	Effective transcription factor binding site prediction using a combination of optimization, a genetic algorithm and discriminant analysis to capture distant interactions. BMC Bioinformatics, 2007, 8, 481.	2.6	35

#	ARTICLE	IF	CITATIONS
37	Sequence variants in the bovine <i>gonadotrophin releasing hormone receptor</i> gene and their associations with fertility. <i>Animal Genetics</i> , 2010, 41, 329-331.	1.7	32
38	Application of experimentally verified transcription factor binding sites models for computational analysis of ChIP-Seq data. <i>BMC Genomics</i> , 2014, 15, 80.	2.8	31
39	Structural and functional studies of a synthetic peptide mimicking a proposed membrane inserting region of a <i>Bacillus thuringiensis</i> δ -endotoxin. <i>Molecular Membrane Biology</i> , 1994, 11, 87-92.	2.0	30
40	Multi-omics analysis identifies genes mediating the extension of cell walls in the <i>Arabidopsis thaliana</i> root elongation zone. <i>Frontiers in Cell and Developmental Biology</i> , 2015, 3, 10.	3.7	30
41	Analysis of Gene Regulatory Networks of Maize in Response to Nitrogen. <i>Genes</i> , 2018, 9, 151.	2.4	30
42	A historical perspective on gene/protein functional assignment. <i>Bioinformatics</i> , 2000, 16, 10-15.	4.1	29
43	Mitochondrial phosphoenolpyruvate carboxykinase (PEPCK-M) and serine biosynthetic pathway genes are co-ordinately increased during anabolic agent-induced skeletal muscle growth. <i>Scientific Reports</i> , 2016, 6, 28693.	3.3	29
44	Combined experimental and computational approaches to study the regulatory elements in eukaryotic genes. <i>Briefings in Bioinformatics</i> , 2007, 8, 266-274.	6.5	28
45	Progress towards platform chemical production using <i>Clostridium autoethanogenum</i> . <i>Biochemical Society Transactions</i> , 2018, 46, 523-535.	3.4	25
46	An Integrative Systems Perspective on Plant Phosphate Research. <i>Genes</i> , 2019, 10, 139.	2.4	24
47	A Transcriptomic Comparison of Two Bambara Groundnut Landraces under Dehydration Stress. <i>Genes</i> , 2017, 8, 121.	2.4	23
48	Searching for discrimination rules in protease proteolytic cleavage activity using genetic programming with a min-max scoring function. <i>BioSystems</i> , 2003, 72, 159-176.	2.0	19
49	Occurrence of a Quadruplex Motif in a Unique Insert within Exon C of the Bovine Estrogen Receptor β Gene (ESR1). <i>Biochemistry</i> , 2010, 49, 7625-7633.	2.5	19
50	Genome-scale model of <i>C. autoethanogenum</i> reveals optimal bioprocess conditions for high-value chemical production from carbon monoxide. <i>Engineering Biology</i> , 2019, 3, 32-40.	1.8	19
51	The elucidation of protein function by sequence motif analysis. <i>Bioinformatics</i> , 1989, 5, 1-13.	4.1	18
52	Identification of a cryptic gene associated with an insertion sequence not previously identified in <i>Bacillus thuringiensis</i> . <i>FEMS Microbiology Letters</i> , 1993, 114, 23-29.	1.8	18
53	An amino acid sequence motif linking viral DNA polymerases and plant virus proteins involved in RNA replication. <i>Nucleic Acids Research</i> , 1986, 14, 6769-6769.	14.5	17
54	Assessing the functional coherence of modules found in multiple-evidence networks from <i>Arabidopsis</i> . <i>BMC Bioinformatics</i> , 2011, 12, 203.	2.6	14

#	ARTICLE	IF	CITATIONS
55	Simultaneous modelling of metabolic, genetic and product-interaction networks. Briefings in Bioinformatics, 2001, 2, 223-232.	6.5	13
56	Reduction of Off-flavor Generation in Soybean Homogenates: A Mathematical Model. Journal of Food Science, 2010, 75, R131-8.	3.1	13
57	A new dynamic tool to perform assembly of Expressed Sequence Tags (ESTs). Bioinformatics, 1997, 13, 453-457.	4.1	12
58	Metabolic differences in ripening of <i>Solanum lycopersicum</i> 'Ailsa Craig'™ and three monogenic mutants. Scientific Data, 2014, 1, 140029.	5.3	12
59	The Beta-adrenergic agonist, Ractopamine, increases skeletal muscle expression of Asparagine Synthetase as part of an integrated stress response gene program. Scientific Reports, 2018, 8, 15915.	3.3	12
60	Statistical evaluation of transcriptomic data generated using the Affymetrix one-cycle, two-cycle and IVT-Express RNA labelling protocols with the Arabidopsis ATH1 microarray. Plant Methods, 2010, 6, 9.	4.3	11
61	Regulatory feedback response mechanisms to phosphate starvation in rice. Npj Systems Biology and Applications, 2018, 4, 4.	3.0	11
62	The herpes simplex virus type 2 equivalent of the herpes simplex virus type 1 US7 gene and its flanking sequences. Virology, 1986, 153, 1-11.	2.4	10
63	The elucidation of protein function from its amino acid sequence. Bioinformatics, 1986, 2, 181-187.	4.1	10
64	A bio-basis function neural network for protein peptide cleavage activity characterisation. Neural Networks, 2006, 19, 401-407.	5.9	9
65	The successful application of systems approaches in plant biology. Progress in Biophysics and Molecular Biology, 2015, 117, 59-68.	2.9	9
66	The logic of the floral transition: Reverse-engineering the switch controlling the identity of lateral organs. PLoS Computational Biology, 2017, 13, e1005744.	3.2	7
67	Identification of a cryptic gene associated with an insertion sequence not previously identified in <i>Bacillus thuringiensis</i> . FEMS Microbiology Letters, 1993, 114, 23-29.	1.8	7
68	An information-flow model of the pharmaceutical industry. Drug Discovery Today, 2001, 6, 1256-1258.	6.4	6
69	Inference of the Genetic Network Regulating Lateral Root Initiation in <i>Arabidopsis thaliana</i> . IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 50-60.	3.0	6
70	Validation of proteomic biomarkers previously found to be differentially expressed in women with Polycystic Ovary Syndrome: a cross-sectional study. Gynecological Endocrinology, 2014, 30, 213-216.	1.7	6
71	Reported sequence homology between Alzheimer amyloid770 and the MRC OX-2 antigen does not predict function. Brain Research Bulletin, 1995, 38, 305-306.	3.0	5
72	Integrative biology the way forward. Briefings in Bioinformatics, 2007, 8, 208-209.	6.5	5

#	ARTICLE	IF	CITATIONS
73	Reconstructing whole-cell models. <i>Drug Discovery Today</i> , 2001, 6, 109-112.	6.4	3
74	A systems biology approach to modelling tea (<i>Camellia sinensis</i>). <i>BMC Systems Biology</i> , 2007, 1, .	3.0	3
75	Characterization of a <i>Bacillus thuringiensis</i> strain which is toxic to the housefly <i>Musca domestica</i> . <i>FEMS Microbiology Letters</i> , 1993, 114, 17-22.	1.8	3
76	Arabidopsis antibody resources for functional studies in plants. <i>Scientific Reports</i> , 2020, 10, 21945.	3.3	3
77	Secondary structure analysis identifies a putative mouse protein demonstrating similarity to the repeat units found in CDC4, the G protein β^2 subunits and related proteins. <i>DNA Sequence</i> , 1992, 3, 213-220.	0.7	2
78	Automated management of gene discovery projects. <i>Bioinformatics</i> , 1998, 14, 217-218.	4.1	2
79	A methodology for elucidating regulatory mechanisms leading to changes in lipid profiles. <i>Metabolomics</i> , 2017, 13, 81.	3.0	2
80	Gsmodutils: a python based framework for test-driven genome scale metabolic model development. <i>Bioinformatics</i> , 2019, 35, 3397-3403.	4.1	2
81	pBR322 and Other pSC101 Derivatives Have a Gene Fragment Related to the Mini-F Plasmid Resolvase. <i>Plasmid</i> , 1994, 32, 333-335.	1.4	0
82	The informatics of post-translational modification and its implications for systems biology. <i>Briefings in Bioinformatics</i> , 2004, 5, 104-105.	6.5	0
83	Computational Prediction of Domain-domain Interactions: Factor-graph Based Modelling and Inference. <i>Current Chemical Biology</i> , 2014, 7, 234-240.	0.5	0