

# Charlie T Hodgman

## List of Publications by Year in descending order

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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	Arabidopsis antibody resources for functional studies in plants. <i>Scientific Reports</i> , 2020, 10, 21945.	3.3	3
2	An Integrative Systems Perspective on Plant Phosphate Research. <i>Genes</i> , 2019, 10, 139.	2.4	24
3	Gsmodutils: a python based framework for test-driven genome scale metabolic model development. <i>Bioinformatics</i> , 2019, 35, 3397-3403.	4.1	2
4	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
5	Progress towards platform chemical production using <i>Clostridium autoethanogenum</i> . <i>Biochemical Society Transactions</i> , 2018, 46, 523-535.	3.4	25
6	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
7	Regulatory feedback response mechanisms to phosphate starvation in rice. <i>Npj Systems Biology and Applications</i> , 2018, 4, 4.	3.0	11
8	The Beta-adrenergic agonist, Ractopamine, increases skeletal muscle expression of Asparagine Synthetase as part of an integrated stress response gene program. <i>Scientific Reports</i> , 2018, 8, 15915.	3.3	12
9	Analysis of Gene Regulatory Networks of Maize in Response to Nitrogen. <i>Genes</i> , 2018, 9, 151.	2.4	30
10	A methodology for elucidating regulatory mechanisms leading to changes in lipid profiles. <i>Metabolomics</i> , 2017, 13, 81.	3.0	2
11	A Transcriptomic Comparison of Two Bambara Groundnut Landraces under Dehydration Stress. <i>Genes</i> , 2017, 8, 121.	2.4	23
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	The logic of the floral transition: Reverse-engineering the switch controlling the identity of lateral organs. <i>PLoS Computational Biology</i> , 2017, 13, e1005744.	3.2	7
14	DNA Methylation and Chromatin Regulation during Fleshy Fruit Development and Ripening. <i>Frontiers in Plant Science</i> , 2016, 7, 807.	3.6	106
15	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
16	Whole genome sequence and manual annotation of <i>Clostridium autoethanogenum</i> , an industrially relevant bacterium. <i>BMC Genomics</i> , 2015, 16, 1085.	2.8	56
17	A machine learning heuristic to identify biologically relevant and minimal biomarker panels from omics data. <i>BMC Genomics</i> , 2015, 16, S2.	2.8	43
18	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

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19	Lipidomic analysis of plasma samples from women with polycystic ovary syndrome. <i>Metabolomics</i> , 2015, 11, 657-666.	3.0	44
20	Modulation of <i>Arabidopsis</i> and monocot root architecture by CLAVATA3/EMBRYO SURROUNDING REGION 26 peptide. <i>Journal of Experimental Botany</i> , 2015, 66, 5229-5243.	4.8	62
21	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
22	The successful application of systems approaches in plant biology. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 117, 59-68.	2.9	9
23	The circadian clock rephases during lateral root organ initiation in <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2015, 6, 7641.	12.8	119
24	Systems Analysis of Auxin Transport in the <i>Arabidopsis</i> Root Apex. <i>Plant Cell</i> , 2014, 26, 862-875.	6.6	190
25	Integration of hormonal signaling networks and mobile microRNAs is required for vascular patterning in <i>Arabidopsis</i> roots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 857-862.	7.1	98
26	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
27	Mechanical modelling quantifies the functional importance of outer tissue layers during root elongation and bending. <i>New Phytologist</i> , 2014, 202, 1212-1222.	7.3	53
28	Validation of proteomic biomarkers previously found to be differentially expressed in women with Polycystic Ovary Syndrome: a cross-sectional study. <i>Gynecological Endocrinology</i> , 2014, 30, 213-216.	1.7	6
29	Metabolic differences in ripening of <i>Solanum lycopersicum</i> 'Ailsa Craig'™ and three monogenic mutants. <i>Scientific Data</i> , 2014, 1, 140029.	5.3	12
30	Computational Prediction of Domain-domain Interactions: Factor-graph Based Modelling and Inference. <i>Current Chemical Biology</i> , 2014, 7, 234-240.	0.5	0
31	Inference of the Genetic Network Regulating Lateral Root Initiation in <i>Arabidopsis thaliana</i> . <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 50-60.	3.0	6
32	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
33	Growth-induced hormone dilution can explain the dynamics of plant root cell elongation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7577-7582.	7.1	95
34	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
35	Tackling Drought Stress: RECEPTOR-LIKE KINASES Present New Approaches. <i>Plant Cell</i> , 2012, 24, 2262-2278.	6.6	155
36	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

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37	Assessing the functional coherence of modules found in multiple-evidence networks from Arabidopsis. BMC Bioinformatics, 2011, 12, 203.	2.6	14
38	OsCAND1 Is Required for Crown Root Emergence in Rice. Molecular Plant, 2011, 4, 289-299.	8.3	75
39	Unraveling the Evolution of Auxin Signaling. Plant Physiology, 2011, 155, 209-221.	4.8	140
40	Sequence variants in the bovine gonadotrophin releasing hormone receptor gene and their associations with fertility. Animal Genetics, 2010, 41, 329-331.	1.7	32
41	Reduction of Off-Flavor Generation in Soybean Homogenates: A Mathematical Model. Journal of Food Science, 2010, 75, R131-8.	3.1	13
42	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
43	Occurrence of a Quadruplex Motif in a Unique Insert within Exon C of the Bovine Estrogen Receptor Gene (ESR1). Biochemistry, 2010, 49, 7625-7633.	2.5	19
44	INFERENCE OF GENE REGULATORY NETWORKS USING BOOLEAN-NETWORK INFERENCE METHODS. Journal of Bioinformatics and Computational Biology, 2009, 07, 1013-1029.	0.8	47
45	Repression of Translation of Human Estrogen Receptor by G-Quadruplex Formation. Biochemistry, 2009, 48, 11487-11495.	2.5	70
46	Integrative biology the way forward. Briefings in Bioinformatics, 2007, 8, 208-209.	6.5	5
47	Combined experimental and computational approaches to study the regulatory elements in eukaryotic genes. Briefings in Bioinformatics, 2007, 8, 266-274.	6.5	28
48	A systems biology approach to modelling tea (Camellia sinensis). BMC Systems Biology, 2007, 1, .	3.0	3
49	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
50	A bio-basis function neural network for protein peptide cleavage activity characterisation. Neural Networks, 2006, 19, 401-407.	5.9	9
51	The informatics of post-translational modification and its implications for systems biology. Briefings in Bioinformatics, 2004, 5, 104-105.	6.5	0
52	Constructing an enzyme-centric view of metabolism. Bioinformatics, 2004, 20, 2050-2055.	4.1	45
53	Searching for discrimination rules in protease proteolytic cleavage activity using genetic programming with a min-max scoring function. BioSystems, 2003, 72, 159-176.	2.0	19
54	The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. Bioinformatics, 2003, 19, 524-531.	4.1	2,811

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55	Characterizing proteolytic cleavage site activity using bio-basis function neural networks. <i>Bioinformatics</i> , 2003, 19, 1741-1747.	4.1	92
56	Reconstructing whole-cell models. <i>Drug Discovery Today</i> , 2001, 6, 109-112.	6.4	3
57	An information-flow model of the pharmaceutical industry. <i>Drug Discovery Today</i> , 2001, 6, 1256-1258.	6.4	6
58	Simultaneous modelling of metabolic, genetic and product-interaction networks. <i>Briefings in Bioinformatics</i> , 2001, 2, 223-232.	6.5	13
59	A historical perspective on gene/protein functional assignment. <i>Bioinformatics</i> , 2000, 16, 10-15.	4.1	29
60	Comparison of functional annotation schemes for genomes. <i>Functional and Integrative Genomics</i> , 2000, 1, 56-69.	3.5	60
61	Mathematical simulation and analysis of cellular metabolism and regulation. <i>Bioinformatics</i> , 1999, 15, 749-758.	4.1	135
62	Nucleoprotein architecture and ColE1 dimer resolution: a hypothesis. <i>Molecular Microbiology</i> , 1998, 29, 545-558.	2.5	36
63	Automated management of gene discovery projects. <i>Bioinformatics</i> , 1998, 14, 217-218.	4.1	2
64	Lewis X Biosynthesis in <i>Helicobacter pylori</i> . <i>Journal of Biological Chemistry</i> , 1997, 272, 21349-21356.	3.4	123
65	A new dynamic tool to perform assembly of Expressed Sequence Tags (ESTs). <i>Bioinformatics</i> , 1997, 13, 453-457.	4.1	12
66	Cloning and analysis of the first cry gene from <i>Bacillus popilliae</i> . <i>Journal of Bacteriology</i> , 1997, 179, 4336-4341.	2.2	92
67	Identification of the homologous beige and Chediak-Higashi syndrome genes. <i>Nature</i> , 1996, 382, 262-265.	27.8	501
68	Reported sequence homology between Alzheimer amyloid770 and the MRC OX-2 antigen does not predict function. <i>Brain Research Bulletin</i> , 1995, 38, 305-306.	3.0	5
69	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
70	Structural and functional studies of a synthetic peptide mimicking a proposed membrane inserting region of a <i>Bacillus thuringiensis</i> $\delta$ -endotoxin. <i>Molecular Membrane Biology</i> , 1994, 11, 87-92.	2.0	30
71	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
72	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

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73	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	7
74	Secondary structure analysis identifies a putative mouse protein demonstrating similarity to the repeat units found in CDC4, the G protein $\beta^2$ subunits and related proteins. <i>DNA Sequence</i> , 1992, 3, 213-220.	0.7	2
75	The construction of <i>Bacillus thuringiensis</i> strains expressing novel entomocidal $\delta$ -endotoxin combinations. <i>Biochemical Journal</i> , 1990, 270, 133-136.	3.7	45
76	Models for the structure and function of the <i>Bacillus thuringiensis</i> $\delta$ -endotoxins determined by computational analysis. <i>DNA Sequence</i> , 1990, 1, 97-106.	0.7	67
77	The elucidation of protein function by sequence motif analysis. <i>Bioinformatics</i> , 1989, 5, 1-13.	4.1	18
78	A new superfamily of replicative proteins. <i>Nature</i> , 1988, 333, 22-23.	27.8	515
79	The herpes simplex virus type 2 equivalent of the herpes simplex virus type 1 US7 gene and its flanking sequences. <i>Virology</i> , 1986, 153, 1-11.	2.4	10
80	The elucidation of protein function from its amino acid sequence. <i>Bioinformatics</i> , 1986, 2, 181-187.	4.1	10
81	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
82	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
83	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