

# Charlie T Hodgman

## List of Publications by Citations

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80  
papers

6,297  
citations

33  
h-index

79  
g-index

88  
ext. papers

7,191  
ext. citations

7.4  
avg, IF

5.02  
L-index

#	Paper	IF	Citations
80	The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. <i>Bioinformatics</i> , <b>2003</b> , 19, 524-31	7.2	2324
79	Identification of the homologous beige and Chediak-Higashi syndrome genes. <i>Nature</i> , <b>1996</b> , 382, 262-5	50.4	444
78	A new superfamily of replicative proteins. <i>Nature</i> , <b>1988</b> , 333, 22-3	50.4	407
77	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> , <b>2012</b> , 109, 4668-73	11.5	240
76	A DEMETER-like DNA demethylase governs tomato fruit ripening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 10804-9	11.5	173
75	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> , <b>1986</b> , 67 ( Pt 6), 1001-13	4.9	166
74	Systems analysis of auxin transport in the Arabidopsis root apex. <i>Plant Cell</i> , <b>2014</b> , 26, 862-75	11.6	151
73	Unraveling the evolution of auxin signaling. <i>Plant Physiology</i> , <b>2011</b> , 155, 209-21	6.6	119
72	Tackling drought stress: receptor-like kinases present new approaches. <i>Plant Cell</i> , <b>2012</b> , 24, 2262-78	11.6	118
71	Mathematical simulation and analysis of cellular metabolism and regulation. <i>Bioinformatics</i> , <b>1999</b> , 15, 749-58	7.2	115
70	Network inference analysis identifies an APRR2-like gene linked to pigment accumulation in tomato and pepper fruits. <i>Plant Physiology</i> , <b>2013</b> , 161, 1476-85	6.6	106
69	Lewis X biosynthesis in <i>Helicobacter pylori</i> . Molecular cloning of an alpha(1,3)-fucosyltransferase gene. <i>Journal of Biological Chemistry</i> , <b>1997</b> , 272, 21349-56	5.4	104
68	Genome-wide mapping of transcriptional enhancer candidates using DNA and chromatin features in maize. <i>Genome Biology</i> , <b>2017</b> , 18, 137	18.3	88
67	Parameter estimation using meta-heuristics in systems biology: a comprehensive review. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2012</b> , 9, 185-202	3	85
66	The circadian clock rephases during lateral root organ initiation in <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , <b>2015</b> , 6, 7641	17.4	83
65	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> , <b>2012</b> , 109, 7577-82	11.5	82
64	Characterizing proteolytic cleavage site activity using bio-basis function neural networks. <i>Bioinformatics</i> , <b>2003</b> , 19, 1741-7	7.2	82

63	Cloning and analysis of the first cry gene from <i>Bacillus popilliae</i> . <i>Journal of Bacteriology</i> , <b>1997</b> , 179, 4336-41	8.0	80
62	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> , <b>2014</b> , 111, 857-62	11.5	79
61	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> , <b>1986</b> , 57, 647-55	6.6	73
60	DNA Methylation and Chromatin Regulation during Fleshy Fruit Development and Ripening. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 807	6.2	73
59	Repression of translation of human estrogen receptor alpha by G-quadruplex formation. <i>Biochemistry</i> , <b>2009</b> , 48, 11487-95	3.2	67
58	Rice auxin influx carrier OsAUX1 facilitates root hair elongation in response to low external phosphate. <i>Nature Communications</i> , <b>2018</b> , 9, 1408	17.4	61
57	Models for the structure and function of the <i>Bacillus thuringiensis</i> delta-endotoxins determined by compilational analysis. <i>DNA Sequence</i> , <b>1990</b> , 1, 97-106		58
56	OscAND1 is required for crown root emergence in rice. <i>Molecular Plant</i> , <b>2011</b> , 4, 289-99	14.4	52
55	Comparison of functional annotation schemes for genomes. <i>Functional and Integrative Genomics</i> , <b>2000</b> , 1, 56-69	3.8	47
54	Mechanical modelling quantifies the functional importance of outer tissue layers during root elongation and bending. <i>New Phytologist</i> , <b>2014</b> , 202, 1212-1222	9.8	45
53	Modulation of <i>Arabidopsis</i> and monocot root architecture by CLAVATA3/EMBRYO SURROUNDING REGION 26 peptide. <i>Journal of Experimental Botany</i> , <b>2015</b> , 66, 5229-43	7	41
52	The construction of <i>Bacillus thuringiensis</i> strains expressing novel entomocidal delta-endotoxin combinations. <i>Biochemical Journal</i> , <b>1990</b> , 270, 133-6	3.8	39
51	Whole genome sequence and manual annotation of <i>Clostridium autoethanogenum</i> , an industrially relevant bacterium. <i>BMC Genomics</i> , <b>2015</b> , 16, 1085	4.5	37
50	Constructing an enzyme-centric view of metabolism. <i>Bioinformatics</i> , <b>2004</b> , 20, 2050-5	7.2	37
49	Inference of gene regulatory networks using boolean-network inference methods. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2009</b> , 7, 1013-29	1	36
48	Lipidomic analysis of plasma samples from women with polycystic ovary syndrome. <i>Metabolomics</i> , <b>2015</b> , 11, 657-666	4.7	34
47	Nucleoprotein architecture and ColE1 dimer resolution: a hypothesis. <i>Molecular Microbiology</i> , <b>1998</b> , 29, 545-58	4.1	32
46	Sequence variants in the bovine gonadotrophin releasing hormone receptor gene and their associations with fertility. <i>Animal Genetics</i> , <b>2010</b> , 41, 329-31	2.5	30

45	A machine learning heuristic to identify biologically relevant and minimal biomarker panels from omics data. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 1, S2	4.5	29
44	Application of experimentally verified transcription factor binding sites models for computational analysis of ChIP-Seq data. <i>BMC Genomics</i> , <b>2014</b> , 15, 80	4.5	26
43	Effective transcription factor binding site prediction using a combination of optimization, a genetic algorithm and discriminant analysis to capture distant interactions. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 481	3.6	26
42	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> , <b>1994</b> , 11, 87-92	3.4	26
41	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> , <b>2015</b> , 3, 10	5.7	25
40	Combined experimental and computational approaches to study the regulatory elements in eukaryotic genes. <i>Briefings in Bioinformatics</i> , <b>2007</b> , 8, 266-74	13.4	23
39	A historical perspective on gene/protein functional assignment. <i>Bioinformatics</i> , <b>2000</b> , 16, 10-5	7.2	22
38	Analysis of Gene Regulatory Networks of Maize in Response to Nitrogen. <i>Genes</i> , <b>2018</b> , 9,	4.2	18
37	A Transcriptomic Comparison of Two Bambara Groundnut Landraces under Dehydration Stress. <i>Genes</i> , <b>2017</b> , 8,	4.2	18
36	Occurrence of a quadruplex motif in a unique insert within exon C of the bovine estrogen receptor alpha gene (ESR1). <i>Biochemistry</i> , <b>2010</b> , 49, 7625-33	3.2	18
35	Identification of a cryptic gene associated with an insertion sequence not previously identified in <i>Bacillus thuringiensis</i> . <i>FEMS Microbiology Letters</i> , <b>1993</b> , 114, 23-29	2.9	18
34	Searching for discrimination rules in protease proteolytic cleavage activity using genetic programming with a min-max scoring function. <i>BioSystems</i> , <b>2003</b> , 72, 159-76	1.9	17
33	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> , <b>2016</b> , 6, 28693	4.9	17
32	Genome-scale model of <i>C. autoethanogenum</i> reveals optimal bioprocess conditions for high-value chemical production from carbon monoxide. <i>Engineering Biology</i> , <b>2019</b> , 3, 32-40	1.1	17
31	Progress towards platform chemical production using. <i>Biochemical Society Transactions</i> , <b>2018</b> , 46, 523-535	5.1	15
30	Assessing the functional coherence of modules found in multiple-evidence networks from <i>Arabidopsis</i> . <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 203	3.6	14
29	The elucidation of protein function by sequence motif analysis. <i>Bioinformatics</i> , <b>1989</b> , 5, 1-13	7.2	13
28	An Integrative Systems Perspective on Plant Phosphate Research. <i>Genes</i> , <b>2019</b> , 10,	4.2	11

27	Statistical evaluation of transcriptomic data generated using the Affymetrix one-cycle, two-cycle and IVT-Express RNA labelling protocols with the Arabidopsis ATH1 microarray. <i>Plant Methods</i> , <b>2010</b> , 6, 9	5.8	11
26	An amino acid sequence motif linking viral DNA polymerases and plant virus proteins involved in RNA replication. <i>Nucleic Acids Research</i> , <b>1986</b> , 14, 6769	20.1	11
25	Metabolic differences in ripening of <i>Solanum lycopersicum</i> Wilsa Craig and three monogenic mutants. <i>Scientific Data</i> , <b>2014</b> , 1, 140029	8.2	9
24	Reduction of off-flavor generation in soybean homogenates: a mathematical model. <i>Journal of Food Science</i> , <b>2010</b> , 75, R131-8	3.4	9
23	Simultaneous modelling of metabolic, genetic and product-interaction networks. <i>Briefings in Bioinformatics</i> , <b>2001</b> , 2, 223-32	13.4	9
22	The successful application of systems approaches in plant biology. <i>Progress in Biophysics and Molecular Biology</i> , <b>2015</b> , 117, 59-68	4.7	7
21	A new dynamic tool to perform assembly of expressed sequence tags (ESTs). <i>Bioinformatics</i> , <b>1997</b> , 13, 453-7	7.2	7
20	A bio-basis function neural network for protein peptide cleavage activity characterisation. <i>Neural Networks</i> , <b>2006</b> , 19, 401-7	9.1	6
19	The herpes simplex virus type 2 equivalent of the herpes simplex virus type 1 US7 gene and its flanking sequences. <i>Virology</i> , <b>1986</b> , 153, 1-11	3.6	6
18	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> , <b>2018</b> , 8, 15915	4.9	6
17	Regulatory feedback response mechanisms to phosphate starvation in rice. <i>Npj Systems Biology and Applications</i> , <b>2018</b> , 4, 4	5	5
16	Validation of proteomic biomarkers previously found to be differentially expressed in women with polycystic ovary syndrome: a cross-sectional study. <i>Gynecological Endocrinology</i> , <b>2014</b> , 30, 213-6	2.4	5
15	Inference of the genetic network regulating lateral root initiation in <i>Arabidopsis thaliana</i> . <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2013</b> , 10, 50-60	3	4
14	An information-flow model of the pharmaceutical industry. <i>Drug Discovery Today</i> , <b>2001</b> , 6, 1256-1258	8.8	4
13	Reported sequence homology between Alzheimer amyloid770 and the MRC OX-2 antigen does not predict function. <i>Brain Research Bulletin</i> , <b>1995</b> , 38, 305-6	3.9	4
12	The elucidation of protein function from its amino acid sequence. <i>Bioinformatics</i> , <b>1986</b> , 2, 181-7	7.2	4
11	The logic of the floral transition: Reverse-engineering the switch controlling the identity of lateral organs. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005744	5	4
10	Reconstructing whole-cell models. <i>Drug Discovery Today</i> , <b>2001</b> , 6, 109-112	8.8	3

9	A systems biology approach to modelling tea ( <i>Camellia sinensis</i> ). <i>BMC Systems Biology</i> , <b>2007</b> , 1, 3-5	2
8	Secondary structure analysis identifies a putative mouse protein demonstrating similarity to the repeat units found in CDC4, the G protein beta subunits and related proteins. <i>DNA Sequence</i> , <b>1992</b> , 3, 213-20	2
7	Characterization of a <i>Bacillus thuringiensis</i> strain which is toxic to the housefly <i>Musca domestica</i> . <i>FEMS Microbiology Letters</i> , <b>1993</b> , 114, 17-22	2
6	Gsmodutils: a python based framework for test-driven genome scale metabolic model development. <i>Bioinformatics</i> , <b>2019</b> , 35, 3397-3403	2
5	Identification of a cryptic gene associated with an insertion sequence not previously identified in <i>Bacillus thuringiensis</i> . <i>FEMS Microbiology Letters</i> , <b>1993</b> , 114, 23-9	2
4	<i>Arabidopsis</i> antibody resources for functional studies in plants. <i>Scientific Reports</i> , <b>2020</b> , 10, 21945	1
3	A methodology for elucidating regulatory mechanisms leading to changes in lipid profiles. <i>Metabolomics</i> , <b>2017</b> , 13, 81	0
2	Automated management of gene discovery projects. <i>Bioinformatics</i> , <b>1998</b> , 14, 217-8	0
1	pBR322 and other pSC101 derivatives have a gene fragment related to the mini-F plasmid resolvase. <i>Plasmid</i> , <b>1994</b> , 32, 333-5	0