

Charlie T Hodgman

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Arabidopsis antibody resources for functional studies in plants. <i>Scientific Reports</i> , 2020 , 10, 21945	4.9	1
79	An Integrative Systems Perspective on Plant Phosphate Research. <i>Genes</i> , 2019 , 10,	4.2	11
78	Gsmodutils: a python based framework for test-driven genome scale metabolic model development. <i>Bioinformatics</i> , 2019 , 35, 3397-3403	7.2	2
77	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	1.1	17
76	Progress towards platform chemical production using. <i>Biochemical Society Transactions</i> , 2018 , 46, 523-535	1	15
75	Rice auxin influx carrier OsAUX1 facilitates root hair elongation in response to low external phosphate. <i>Nature Communications</i> , 2018 , 9, 1408	17.4	61
74	Regulatory feedback response mechanisms to phosphate starvation in rice. <i>Npj Systems Biology and Applications</i> , 2018 , 4, 4	5	5
73	Analysis of Gene Regulatory Networks of Maize in Response to Nitrogen. <i>Genes</i> , 2018 , 9,	4.2	18
72	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	4.9	6
71	A methodology for elucidating regulatory mechanisms leading to changes in lipid profiles. <i>Metabolomics</i> , 2017 , 13, 81	4.7	0
70	Genome-wide mapping of transcriptional enhancer candidates using DNA and chromatin features in maize. <i>Genome Biology</i> , 2017 , 18, 137	18.3	88
69	A Transcriptomic Comparison of Two Bambara Groundnut Landraces under Dehydration Stress. <i>Genes</i> , 2017 , 8,	4.2	18
68	The logic of the floral transition: Reverse-engineering the switch controlling the identity of lateral organs. <i>PLoS Computational Biology</i> , 2017 , 13, e1005744	5	4
67	DNA Methylation and Chromatin Regulation during Fleshy Fruit Development and Ripening. <i>Frontiers in Plant Science</i> , 2016 , 7, 807	6.2	73
66	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	4.9	17
65	The successful application of systems approaches in plant biology. <i>Progress in Biophysics and Molecular Biology</i> , 2015 , 117, 59-68	4.7	7
64	The circadian clock rephases during lateral root organ initiation in <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2015 , 6, 7641	17.4	83

63	Whole genome sequence and manual annotation of <i>Clostridium autoethanogenum</i> , an industrially relevant bacterium. <i>BMC Genomics</i> , 2015 , 16, 1085	4.5	37
62	A machine learning heuristic to identify biologically relevant and minimal biomarker panels from omics data. <i>BMC Genomics</i> , 2015 , 16 Suppl 1, S2	4.5	29
61	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	5.7	25
60	Lipidomic analysis of plasma samples from women with polycystic ovary syndrome. <i>Metabolomics</i> , 2015 , 11, 657-666	4.7	34
59	Modulation of <i>Arabidopsis</i> and monocot root architecture by CLAVATA3/EMBRYO SURROUNDING REGION 26 peptide. <i>Journal of Experimental Botany</i> , 2015 , 66, 5229-43	7	41
58	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, 10804-9	11.5	173
57	Metabolic differences in ripening of <i>Solanum lycopersicum</i> Wilsa Craig Vand three monogenic mutants. <i>Scientific Data</i> , 2014 , 1, 140029	8.2	9
56	Systems analysis of auxin transport in the <i>Arabidopsis</i> root apex. <i>Plant Cell</i> , 2014 , 26, 862-75	11.6	151
55	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, 857-62	11.5	79
54	Application of experimentally verified transcription factor binding sites models for computational analysis of ChIP-Seq data. <i>BMC Genomics</i> , 2014 , 15, 80	4.5	26
53	Mechanical modelling quantifies the functional importance of outer tissue layers during root elongation and bending. <i>New Phytologist</i> , 2014 , 202, 1212-1222	9.8	45
52	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, 213-6	2.4	5
51	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	4
50	Network inference analysis identifies an APRR2-like gene linked to pigment accumulation in tomato and pepper fruits. <i>Plant Physiology</i> , 2013 , 161, 1476-85	6.6	106
49	Parameter estimation using meta-heuristics in systems biology: a comprehensive review. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 185-202	3	85
48	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, 7577-82	11.5	82
47	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, 4668-73	11.5	240
46	Tackling drought stress: receptor-like kinases present new approaches. <i>Plant Cell</i> , 2012 , 24, 2262-78	11.6	118

45	Assessing the functional coherence of modules found in multiple-evidence networks from Arabidopsis. <i>BMC Bioinformatics</i> , 2011 , 12, 203	3.6	14
44	OscAND1 is required for crown root emergence in rice. <i>Molecular Plant</i> , 2011 , 4, 289-99	14.4	52
43	Unraveling the evolution of auxin signaling. <i>Plant Physiology</i> , 2011 , 155, 209-21	6.6	119
42	Sequence variants in the bovine gonadotrophin releasing hormone receptor gene and their associations with fertility. <i>Animal Genetics</i> , 2010 , 41, 329-31	2.5	30
41	Reduction of off-flavor generation in soybean homogenates: a mathematical model. <i>Journal of Food Science</i> , 2010 , 75, R131-8	3.4	9
40	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> , 2010 , 6, 9	5.8	11
39	Occurrence of a quadruplex motif in a unique insert within exon C of the bovine estrogen receptor alpha gene (ESR1). <i>Biochemistry</i> , 2010 , 49, 7625-33	3.2	18
38	Inference of gene regulatory networks using boolean-network inference methods. <i>Journal of Bioinformatics and Computational Biology</i> , 2009 , 7, 1013-29	1	36
37	Repression of translation of human estrogen receptor alpha by G-quadruplex formation. <i>Biochemistry</i> , 2009 , 48, 11487-95	3.2	67
36	A systems biology approach to modelling tea (<i>Camellia sinensis</i>). <i>BMC Systems Biology</i> , 2007 , 1,	3.5	2
35	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> , 2007 , 8, 481	3.6	26
34	Combined experimental and computational approaches to study the regulatory elements in eukaryotic genes. <i>Briefings in Bioinformatics</i> , 2007 , 8, 266-74	13.4	23
33	A bio-basis function neural network for protein peptide cleavage activity characterisation. <i>Neural Networks</i> , 2006 , 19, 401-7	9.1	6
32	Constructing an enzyme-centric view of metabolism. <i>Bioinformatics</i> , 2004 , 20, 2050-5	7.2	37
31	Characterizing proteolytic cleavage site activity using bio-basis function neural networks. <i>Bioinformatics</i> , 2003 , 19, 1741-7	7.2	82
30	Searching for discrimination rules in protease proteolytic cleavage activity using genetic programming with a min-max scoring function. <i>BioSystems</i> , 2003 , 72, 159-76	1.9	17
29	The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. <i>Bioinformatics</i> , 2003 , 19, 524-31	7.2	2324
28	Reconstructing whole-cell models. <i>Drug Discovery Today</i> , 2001 , 6, 109-112	8.8	3

27	An information-flow model of the pharmaceutical industry. <i>Drug Discovery Today</i> , 2001 , 6, 1256-1258	8.8	4
26	Simultaneous modelling of metabolic, genetic and product-interaction networks. <i>Briefings in Bioinformatics</i> , 2001 , 2, 223-32	13.4	9
25	A historical perspective on gene/protein functional assignment. <i>Bioinformatics</i> , 2000 , 16, 10-5	7.2	22
24	Comparison of functional annotation schemes for genomes. <i>Functional and Integrative Genomics</i> , 2000 , 1, 56-69	3.8	47
23	Mathematical simulation and analysis of cellular metabolism and regulation. <i>Bioinformatics</i> , 1999 , 15, 749-58	7.2	115
22	Nucleoprotein architecture and ColE1 dimer resolution: a hypothesis. <i>Molecular Microbiology</i> , 1998 , 29, 545-58	4.1	32
21	Automated management of gene discovery projects. <i>Bioinformatics</i> , 1998 , 14, 217-8	7.2	0
20	Lewis X biosynthesis in <i>Helicobacter pylori</i> . Molecular cloning of an alpha(1,3)-fucosyltransferase gene. <i>Journal of Biological Chemistry</i> , 1997 , 272, 21349-56	5.4	104
19	A new dynamic tool to perform assembly of expressed sequence tags (ESTs). <i>Bioinformatics</i> , 1997 , 13, 453-7	7.2	7
18	Cloning and analysis of the first cry gene from <i>Bacillus popilliae</i> . <i>Journal of Bacteriology</i> , 1997 , 179, 4336-41	3.5	80
17	Identification of the homologous beige and Chediak-Higashi syndrome genes. <i>Nature</i> , 1996 , 382, 262-5	50.4	444
16	Reported sequence homology between Alzheimer amyloid770 and the MRC OX-2 antigen does not predict function. <i>Brain Research Bulletin</i> , 1995 , 38, 305-6	3.9	4
15	pBR322 and other pSC101 derivatives have a gene fragment related to the mini-F plasmid resolvase. <i>Plasmid</i> , 1994 , 32, 333-5	3.3	
14	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	3.4	26
13	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	2.9	18
12	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	2.9	2
11	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, 23-9	2.9	2
10	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> , 1992 , 3, 213-20		2

9	The construction of <i>Bacillus thuringiensis</i> strains expressing novel entomocidal delta-endotoxin combinations. <i>Biochemical Journal</i> , 1990 , 270, 133-6	3.8	39
8	Models for the structure and function of the <i>Bacillus thuringiensis</i> delta-endotoxins determined by compilational analysis. <i>DNA Sequence</i> , 1990 , 1, 97-106		58
7	The elucidation of protein function by sequence motif analysis. <i>Bioinformatics</i> , 1989 , 5, 1-13	7.2	13
6	A new superfamily of replicative proteins. <i>Nature</i> , 1988 , 333, 22-3	50.4	407
5	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	20.1	11
4	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 (Pt 6), 1001-13	4.9	166
3	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	3.6	6
2	The elucidation of protein function from its amino acid sequence. <i>Bioinformatics</i> , 1986 , 2, 181-7	7.2	4
1	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, 647-55	6.6	73