

Steven Briggs

List of Publications by Year in descending order

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96
papers

12,089
citations

44069

48
h-index

37204

96
g-index

101
all docs

101
docs citations

101
times ranked

15545
citing authors

#	ARTICLE	IF	CITATIONS
1	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. <i>japonica</i>). Science, 2002, 296, 92-100.	12.6	2,866
2	Analysis of a Chemical Plant Defense Mechanism in Grasses. Science, 1997, 277, 696-699.	12.6	624
3	Rice phosphate transporters include an evolutionarily divergent gene specifically activated in arbuscular mycorrhizal symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13324-13329.	7.1	565
4	Loss of an MDR Transporter in Compact Stalks of Maize br2 and Sorghum dw3 Mutants. Science, 2003, 302, 81-84.	12.6	480
5	Processing and Subcellular Trafficking of ER-Tethered EIN2 Control Response to Ethylene Gas. Science, 2012, 338, 390-393.	12.6	461
6	Integration of omic networks in a developmental atlas of maize. Science, 2016, 353, 814-818.	12.6	411
7	Comparative transcriptomics of rice reveals an ancient pattern of response to microbial colonization. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 8066-8070.	7.1	368
8	RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. Nature Chemical Biology, 2011, 7, 779-786.	8.0	286
9	A Novel Suppressor of Cell Death in Plants Encoded by the Lls1 Gene of Maize. Cell, 1997, 89, 25-31.	28.9	268
10	Discovery and revision of <i>Arabidopsis</i> genes by proteogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 21034-21038.	7.1	268
11	ELYS is a dual nucleoporin/kinetochore protein required for nuclear pore assembly and proper cell division. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17801-17806.	7.1	247
12	Clustering Millions of Tandem Mass Spectra. Journal of Proteome Research, 2008, 7, 113-122.	3.7	230
13	Direct Identification of the <i>Meloidogyne incognita</i> Secretome Reveals Proteins with Host Cell Reprogramming Potential. PLoS Pathogens, 2008, 4, e1000192.	4.7	225
14	GroEL from the endosymbiont <i>Buchnera aphidicola</i> betrays the aphid by triggering plant defense. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8919-8924.	7.1	180
15	Plant elicitor peptides are conserved signals regulating direct and indirect antiherbivore defense. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5707-5712.	7.1	179
16	Activation of the Unfolded Protein Response Is Required for Defenses against Bacterial Pore-Forming Toxin In Vivo. PLoS Pathogens, 2008, 4, e1000176.	4.7	174
17	Reconstruction of protein networks from an atlas of maize seed proteotypes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4808-17.	7.1	174
18	Identification of Evening Complex Associated Proteins in <i>Arabidopsis</i> by Affinity Purification and Mass Spectrometry. Molecular and Cellular Proteomics, 2016, 15, 201-217.	3.8	170

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19	Disease lesion mimics of maize: A model for cell death in plants. <i>BioEssays</i> , 1995, 17, 685-692.	2.5	166
20	Improving gene annotation using peptide mass spectrometry. <i>Genome Research</i> , 2007, 17, 231-239.	5.5	157
21	Wnt5a induces ROR1/ROR2 heterooligomerization to enhance leukemia chemotaxis and proliferation. <i>Journal of Clinical Investigation</i> , 2015, 126, 585-598.	8.2	149
22	Regulation of leaf initiation by the terminal ear 1 gene of maize. <i>Nature</i> , 1998, 393, 166-168.	27.8	141
23	A Ras Signaling Complex Controls the RasC-TORC2 Pathway and Directed Cell Migration. <i>Developmental Cell</i> , 2010, 18, 737-749.	7.0	141
24	Phosphorylation stabilizes Nanog by promoting its interaction with Pin1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13312-13317.	7.1	131
25	Cloning and Characterization of the Maize An1 Gene. <i>Plant Cell</i> , 1995, 7, 75.	6.6	102
26	A High-Resolution Map of Arabidopsis Recombinant Inbred Lines by Whole-Genome Exon Array Hybridization. <i>PLoS Genetics</i> , 2006, 2, e144.	3.5	97
27	MASCP Gator: An Aggregation Portal for the Visualization of Arabidopsis Proteomics Data. <i>Plant Physiology</i> , 2011, 155, 259-270.	4.8	94
28	Parallel Proteomic and Phosphoproteomic Analyses of Successive Stages of Maize Leaf Development. <i>Plant Cell</i> , 2013, 25, 2798-2812.	6.6	94
29	Discovery, Biosynthesis and Stress-Related Accumulation of Dolabradiene-Derived Defenses in Maize. <i>Plant Physiology</i> , 2018, 176, 2677-2690.	4.8	94
30	Changes in Tobacco Cell Membrane Composition and Structure Caused by Cercosporin. <i>Plant Physiology</i> , 1983, 71, 763-766.	4.8	92
31	Heritable endogenous gene regulation in plants with designed polydactyl zinc finger transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13296-13301.	7.1	92
32	Heterologous expression of the C-terminal antigenic domain of the malaria vaccine candidate Pfs48/45 in the green algae <i>Chlamydomonas reinhardtii</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 1987-1995.	3.6	83
33	Identification of PAN2 by Quantitative Proteomics as a Leucine-Rich Repeat Receptor-Like Kinase Acting Upstream of PAN1 to Polarize Cell Division in Maize. <i>Plant Cell</i> , 2012, 24, 4577-4589.	6.6	82
34	Plastid-produced interorgannellar stress signal MEcPP potentiates induction of the unfolded protein response in endoplasmic reticulum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6212-6217.	7.1	82
35	Expanding the Genetic Code of <i>Caenorhabditis elegans</i> Using Bacterial Aminoacyl-tRNA Synthetase/tRNA Pairs. <i>ACS Chemical Biology</i> , 2012, 7, 1292-1302.	3.4	80
36	An Automated Proteogenomic Method Uses Mass Spectrometry to Reveal Novel Genes in <i>Zea mays</i> . <i>Molecular and Cellular Proteomics</i> , 2014, 13, 157-167.	3.8	79

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37	Magnesium Flux Modulates Ribosomes to Increase Bacterial Survival. <i>Cell</i> , 2019, 177, 352-360.e13.	28.9	77
38	ROR1 can interact with TCL1 and enhance leukemogenesis in μ -TCL1 transgenic mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 793-798.	7.1	75
39	Fungal-induced protein hyperacetylation in maize identified by acetylome profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 210-215.	7.1	71
40	Dynamic Patterns of Gene Expression Additivity and Regulatory Variation throughout Maize Development. <i>Molecular Plant</i> , 2019, 12, 410-425.	8.3	69
41	A High-Resolution Tissue-Specific Proteome and Phosphoproteome Atlas of Maize Primary Roots Reveals Functional Gradients along the Root Axes. <i>Plant Physiology</i> , 2015, 168, 233-246.	4.8	64
42	The matrix protein Fibulin-5 is at the interface of tissue stiffness and inflammation in fibrosis. <i>Nature Communications</i> , 2015, 6, 8574.	12.8	64
43	Quantitative Proteomic and Functional Analysis of Liver Mitochondria from High Fat Diet (HFD) Diabetic Mice. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3744-3758.	3.8	62
44	Potato Aphid Salivary Proteome: Enhanced Salivation Using Resorcinol and Identification of Aphid Phosphoproteins. <i>Journal of Proteome Research</i> , 2015, 14, 1762-1778.	3.7	60
45	Multiple genes recruited from hormone pathways partition maize diterpenoid defences. <i>Nature Plants</i> , 2019, 5, 1043-1056.	9.3	60
46	Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. <i>Plant Cell</i> , 2020, 32, 1377-1396.	6.6	60
47	Sunday Driver Interacts with Two Distinct Classes of Axonal Organelles. <i>Journal of Biological Chemistry</i> , 2009, 284, 34628-34639.	3.4	54
48	Genetic elucidation of interconnected antibiotic pathways mediating maize innate immunity. <i>Nature Plants</i> , 2020, 6, 1375-1388.	9.3	52
49	Regulation of the endogenous VEGF-A gene by exogenous designed regulatory proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15225-15230.	7.1	51
50	Accurate Annotation of Peptide Modifications through Unrestrictive Database Search. <i>Journal of Proteome Research</i> , 2008, 7, 170-181.	3.7	50
51	Stemness factor Sall4 is required for DNA damage response in embryonic stem cells. <i>Journal of Cell Biology</i> , 2015, 208, 513-520.	5.2	50
52	Application of Proteomic Marker Ensembles to Subcellular Organelle Identification. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 388-402.	3.8	49
53	The small GTPases Ras and Rap1 bind to and control TORC2 activity. <i>Scientific Reports</i> , 2016, 6, 25823.	3.3	47
54	Identification of the expressome by machine learning on omics data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18119-18125.	7.1	47

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55	The Maize Lethal Leaf Spot 1 Mutant Has Elevated Resistance to Fungal Infection at the Leaf Epidermis. <i>Molecular Plant-Microbe Interactions</i> , 1998, 11, 1110-1118.	2.6	46
56	Regulation of contractile vacuole formation and activity in <i>Dictyostelium</i> . <i>EMBO Journal</i> , 2008, 27, 2064-2076.	7.8	41
57	Nematode effectors and plant responses to infection. <i>Current Opinion in Plant Biology</i> , 2010, 13, 442-448.	7.1	40
58	Accurate Mass Spectrometry Based Protein Quantification via Shared Peptides. <i>Journal of Computational Biology</i> , 2012, 19, 337-348.	1.6	40
59	Dynamic regulation of Pep-induced immunity through post-translational control of defence transcript splicing. <i>Nature Plants</i> , 2020, 6, 1008-1019.	9.3	40
60	Regulation of STIM1 and SOCE by the Ubiquitin-Proteasome System (UPS). <i>PLoS ONE</i> , 2010, 5, e13465.	2.5	39
61	UV Irradiation Accelerates Amyloid Precursor Protein (APP) Processing and Disrupts APP Axonal Transport. <i>Journal of Neuroscience</i> , 2014, 34, 3320-3339.	3.6	37
62	Wnt5a induces ROR1 to recruit DOCK2 to activate Rac1/2 in chronic lymphocytic leukemia. <i>Blood</i> , 2018, 132, 170-178.	1.4	36
63	Quantitative Proteome Analysis of Pluripotent Cells by iTRAQ Mass Tagging Reveals Post-transcriptional Regulation of Proteins Required for ES Cell Self-renewal. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2238-2251.	3.8	35
64	Genetic patterns of plant host-parasite interactions. <i>Trends in Genetics</i> , 1994, 10, 12-16.	6.7	34
65	A Porphyrin Pathway Impairment Is Responsible for the Phenotype of a Dominant Disease Lesion Mimic Mutant of Maize. <i>Plant Cell</i> , 1998, 10, 1095.	6.6	33
66	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , 2021, 10, .	6.0	31
67	Quantitative Early Auxin Root Proteomics Identifies GAUT10, a Galacturonosyltransferase, as a Novel Regulator of Root Meristem Maintenance. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1157-1170.	3.8	29
68	LIKE SEX4 1 Acts as a Î²-Amylase-Binding Scaffold on Starch Granules during Starch Degradation. <i>Plant Cell</i> , 2019, 31, 2169-2186.	6.6	26
69	Biochemical and Phosphoproteomic Analysis of the Helix-Loop-Helix Protein E47. <i>Molecular and Cellular Biology</i> , 2012, 32, 1671-1682.	2.3	25
70	Nitrate triggered phosphoproteome changes and a PIN2 phosphosite modulating root system architecture. <i>EMBO Reports</i> , 2021, 22, e51813.	4.5	22
71	Engineering new plant strains for commercial markets. <i>Current Opinion in Biotechnology</i> , 1998, 9, 233-235.	6.6	19
72	Plant Disease Resistance: Grand unification theory in sight. <i>Current Biology</i> , 1995, 5, 128-131.	3.9	18

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73	Wnt5a induces ROR1 to recruit cortactin to promote breast-cancer migration and metastasis. <i>Npj Breast Cancer</i> , 2019, 5, 35.	5.2	18
74	The Second Site Modifier, Sympathy for the ligule, Encodes a Homolog of Arabidopsis ENHANCED DISEASE RESISTANCE4 and Rescues the Liguleless narrow Maize Mutant. <i>Plant Cell</i> , 2019, 31, 1829-1844.	6.6	17
75	Membrane-mediated ultrafast restriction digestion and subsequent rapid gel microchip electrophoresis of DNA. <i>Electrophoresis</i> , 2002, 23, 1524.	2.4	15
76	Dual use of peptide mass spectra: Protein atlas and genome annotation. <i>Current Plant Biology</i> , 2015, 2, 21-24.	4.7	15
77	Current status of the multinational Arabidopsis community. <i>Plant Direct</i> , 2020, 4, e00248.	1.9	13
78	Response and Adaptation of <i>Escherichia coli</i> to Suppression of the Amber Stop Codon. <i>ChemBioChem</i> , 2014, 15, 1744-1749.	2.6	11
79	Selective Toxin of <i>Helminthosporium victoriae</i> : Thermal Relationships in Effects on Oat Tissues and Protoplasts. <i>Phytopathology</i> , 1984, 74, 768.	2.2	11
80	Auxin Induces Widespread Proteome Remodeling in Arabidopsis Seedlings. <i>Proteomics</i> , 2019, 19, 1900199.	2.2	10
81	Plant height heterosis is quantitatively associated with expression levels of plastid ribosomal proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	10
82	Targeting the human genome. <i>Current Opinion in Biotechnology</i> , 2006, 17, 659-665.	6.6	9
83	The HUPO initiative on Model Organism Proteomes, iMOP. <i>Proteomics</i> , 2012, 12, 340-345.	2.2	9
84	Localization of Spin Labels in Oat Leaf Protoplasts. <i>Plant Physiology</i> , 1982, 70, 662-667.	4.8	7
85	The paradigm shift of genomics â€” a complement to traditional plant science. <i>Current Opinion in Plant Biology</i> , 1999, 2, 81-82.	7.1	6
86	Use of high-throughput LC-MS/MS proteomics technologies in drug discovery. <i>Drug Discovery Today: Technologies</i> , 2006, 3, 301-306.	4.0	6
87	The Dictyostelium GSK3 kinase GlkA coordinates signal relay and chemotaxis in response to growth conditions. <i>Developmental Biology</i> , 2018, 435, 56-72.	2.0	6
88	Interaction of Nitroxide Spin Labels with Chloroplasts. <i>Plant Physiology</i> , 1982, 70, 668-670.	4.8	3
89	Genetic Networks. <i>Plant Physiology</i> , 2005, 138, 542-544.	4.8	3
90	Wnt5a Induces ROR1 to Complex with HS1, Which Undergoes Tyrosine Phosphorylation and Contributes to Planar-Cell-Polarity Migration in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2016, 128, 301-301.	1.4	2

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91	Age modifies both the maximal temperature and inflammatory response in patients with SARS-CoV-2 infection. <i>Clinical Medicine</i> , 2022, 22, 192-196.	1.9	2
92	Wnt5a Induces Association of ROR1 with 14-3-3 σ to Enhance Chemotaxis and Proliferation in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2016, 128, 349-349.	1.4	1
93	Wnt5a Induces ROR1 to Interact Grb2 to Enhance Ras Activation in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2021, 138, 247-247.	1.4	1
94	Front Cover: Auxin Induces Widespread Proteome Remodeling in Arabidopsis Seedlings. <i>Proteomics</i> , 2019, 19, 1970151.	2.2	0
95	Differential Expression Profile of the Proteome and Transcriptome in Aggressive and Indolent Chronic Lymphocytic Leukemia. <i>Blood</i> , 2005, 106, 2101-2101.	1.4	0
96	ROR1 Can Interact With TCL1 and Enhance Leukemogenesis In E μ -TCL1 Transgenic Mice. <i>Blood</i> , 2013, 122, 868-868.	1.4	0