

Steven Briggs

List of Publications by Year in descending order

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96
papers

12,089
citations

43973

48
h-index

37111

96
g-index

101
all docs

101
docs citations

101
times ranked

15545
citing authors

#	ARTICLE	IF	CITATIONS
1	Age modifies both the maximal temperature and inflammatory response in patients with SARS-CoV-2 infection. <i>Clinical Medicine</i> , 2022, 22, 192-196.	0.8	2
2	Nitrate triggered phosphoproteome changes and a PIN2 phosphosite modulating root system architecture. <i>EMBO Reports</i> , 2021, 22, e51813.	2.0	22
3	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , 2021, 10, .	2.8	31
4	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, .	3.3	10
5	Wnt5a Induces ROR1 to Interact Grb2 to Enhance Ras Activation in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2021, 138, 247-247.	0.6	1
6	Dynamic regulation of Pep-induced immunity through post-translational control of defence transcript splicing. <i>Nature Plants</i> , 2020, 6, 1008-1019.	4.7	40
7	Current status of the multinational Arabidopsis community. <i>Plant Direct</i> , 2020, 4, e00248.	0.8	13
8	Genetic elucidation of interconnected antibiotic pathways mediating maize innate immunity. <i>Nature Plants</i> , 2020, 6, 1375-1388.	4.7	52
9	Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. <i>Plant Cell</i> , 2020, 32, 1377-1396.	3.1	60
10	Auxin Induces Widespread Proteome Remodeling in Arabidopsis Seedlings. <i>Proteomics</i> , 2019, 19, 1900199.	1.3	10
11	LIKE SEX4 1 Acts as a β -Amylase-Binding Scaffold on Starch Granules during Starch Degradation. <i>Plant Cell</i> , 2019, 31, 2169-2186.	3.1	26
12	Front Cover: Auxin Induces Widespread Proteome Remodeling in Arabidopsis Seedlings. <i>Proteomics</i> , 2019, 19, 1970151.	1.3	0
13	Wnt5a induces ROR1 to recruit cortactin to promote breast-cancer migration and metastasis. <i>Npj Breast Cancer</i> , 2019, 5, 35.	2.3	18
14	Dynamic Patterns of Gene Expression Additivity and Regulatory Variation throughout Maize Development. <i>Molecular Plant</i> , 2019, 12, 410-425.	3.9	69
15	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.	3.1	17
16	Magnesium Flux Modulates Ribosomes to Increase Bacterial Survival. <i>Cell</i> , 2019, 177, 352-360.e13.	13.5	77
17	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.	2.5	29
18	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.	3.3	47

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19	Multiple genes recruited from hormone pathways partition maize diterpenoid defences. <i>Nature Plants</i> , 2019, 5, 1043-1056.	4.7	60
20	Discovery, Biosynthesis and Stress-Related Accumulation of Dolabradiene-Derived Defenses in Maize. <i>Plant Physiology</i> , 2018, 176, 2677-2690.	2.3	94
21	Wnt5a induces ROR1 to recruit DOCK2 to activate Rac1/2 in chronic lymphocytic leukemia. <i>Blood</i> , 2018, 132, 170-178.	0.6	36
22	The Dictyostelium GSK3 kinase GlkA coordinates signal relay and chemotaxis in response to growth conditions. <i>Developmental Biology</i> , 2018, 435, 56-72.	0.9	6
23	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.	3.3	71
24	Integration of omic networks in a developmental atlas of maize. <i>Science</i> , 2016, 353, 814-818.	6.0	411
25	The small GTPases Ras and Rap1 bind to and control TORC2 activity. <i>Scientific Reports</i> , 2016, 6, 25823.	1.6	47
26	Identification of Evening Complex Associated Proteins in Arabidopsis by Affinity Purification and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 201-217.	2.5	170
27	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.	0.6	2
28	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.	0.6	1
29	Dual use of peptide mass spectra: Protein atlas and genome annotation. <i>Current Plant Biology</i> , 2015, 2, 21-24.	2.3	15
30	Stemness factor Sall4 is required for DNA damage response in embryonic stem cells. <i>Journal of Cell Biology</i> , 2015, 208, 513-520.	2.3	50
31	Potato Aphid Salivary Proteome: Enhanced Salivation Using Resorcinol and Identification of Aphid Phosphoproteins. <i>Journal of Proteome Research</i> , 2015, 14, 1762-1778.	1.8	60
32	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.	2.3	64
33	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.	3.3	82
34	The matrix protein Fibulin-5 is at the interface of tissue stiffness and inflammation in fibrosis. <i>Nature Communications</i> , 2015, 6, 8574.	5.8	64
35	Wnt5a induces ROR1/ROR2 heterooligomerization to enhance leukemia chemotaxis and proliferation. <i>Journal of Clinical Investigation</i> , 2015, 126, 585-598.	3.9	149
36	ROR1 can interact with TCL1 and enhance leukemogenesis in E μ -TCL1 transgenic mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 793-798.	3.3	75

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37	UV Irradiation Accelerates Amyloid Precursor Protein (APP) Processing and Disrupts APP Axonal Transport. <i>Journal of Neuroscience</i> , 2014, 34, 3320-3339.	1.7	37
38	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.	2.5	79
39	Response and Adaptation of <i>Escherichia coli</i> to Suppression of the Amber Stop Codon. <i>ChemBioChem</i> , 2014, 15, 1744-1749.	1.3	11
40	GroEL from the endosymbiont <i>Buchnera aphidicola</i> betrays the aphid by triggering plant defense. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8919-8924.	3.3	180
41	Parallel Proteomic and Phosphoproteomic Analyses of Successive Stages of Maize Leaf Development. <i>Plant Cell</i> , 2013, 25, 2798-2812.	3.1	94
42	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.	1.7	83
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.	2.5	62
44	Reconstruction of protein networks from an atlas of maize seed proteotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4808-17.	3.3	174
45	Plant elicitor peptides are conserved signals regulating direct and indirect antiherbivore defense. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5707-5712.	3.3	179
46	ROR1 Can Interact With TCL1 and Enhance Leukemogenesis In E μ -TCL1 Transgenic Mice. <i>Blood</i> , 2013, 122, 868-868.	0.6	0
47	Accurate Mass Spectrometry Based Protein Quantification via Shared Peptides. <i>Journal of Computational Biology</i> , 2012, 19, 337-348.	0.8	40
48	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.	3.1	82
49	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.	1.6	80
50	Processing and Subcellular Trafficking of ER-Tethered EIN2 Control Response to Ethylene Gas. <i>Science</i> , 2012, 338, 390-393.	6.0	461
51	Biochemical and Phosphoproteomic Analysis of the Helix-Loop-Helix Protein E47. <i>Molecular and Cellular Biology</i> , 2012, 32, 1671-1682.	1.1	25
52	The HUPO initiative on Model Organism Proteomes, iMOP. <i>Proteomics</i> , 2012, 12, 340-345.	1.3	9
53	RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. <i>Nature Chemical Biology</i> , 2011, 7, 779-786.	3.9	286
54	MASCP Gator: An Aggregation Portal for the Visualization of Arabidopsis Proteomics Data. <i>Plant Physiology</i> , 2011, 155, 259-270.	2.3	94

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55	Nematode effectors and plant responses to infection. <i>Current Opinion in Plant Biology</i> , 2010, 13, 442-448.	3.5	40
56	Regulation of STIM1 and SOCE by the Ubiquitin-Proteasome System (UPS). <i>PLoS ONE</i> , 2010, 5, e13465.	1.1	39
57	Application of Proteomic Marker Ensembles to Subcellular Organelle Identification. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 388-402.	2.5	49
58	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.	3.3	131
59	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.	2.5	35
60	A Ras Signaling Complex Controls the RasC-TORC2 Pathway and Directed Cell Migration. <i>Developmental Cell</i> , 2010, 18, 737-749.	3.1	141
61	Sunday Driver Interacts with Two Distinct Classes of Axonal Organelles. <i>Journal of Biological Chemistry</i> , 2009, 284, 34628-34639.	1.6	54
62	Regulation of contractile vacuole formation and activity in <i>Dictyostelium</i> . <i>EMBO Journal</i> , 2008, 27, 2064-2076.	3.5	41
63	Accurate Annotation of Peptide Modifications through Unrestrictive Database Search. <i>Journal of Proteome Research</i> , 2008, 7, 170-181.	1.8	50
64	Clustering Millions of Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2008, 7, 113-122.	1.8	230
65	Direct Identification of the <i>Meloidogyne incognita</i> Secretome Reveals Proteins with Host Cell Reprogramming Potential. <i>PLoS Pathogens</i> , 2008, 4, e1000192.	2.1	225
66	Discovery and revision of <i>Arabidopsis</i> genes by proteogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 21034-21038.	3.3	268
67	Activation of the Unfolded Protein Response Is Required for Defenses against Bacterial Pore-Forming Toxin In Vivo. <i>PLoS Pathogens</i> , 2008, 4, e1000176.	2.1	174
68	Improving gene annotation using peptide mass spectrometry. <i>Genome Research</i> , 2007, 17, 231-239.	2.4	157
69	ELYS is a dual nucleoporin/kinetochore protein required for nuclear pore assembly and proper cell division. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17801-17806.	3.3	247
70	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
71	Targeting the human genome. <i>Current Opinion in Biotechnology</i> , 2006, 17, 659-665.	3.3	9
72	A High-Resolution Map of <i>Arabidopsis</i> Recombinant Inbred Lines by Whole-Genome Exon Array Hybridization. <i>PLoS Genetics</i> , 2006, 2, e144.	1.5	97

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73	Comparative transcriptomics of rice reveals an ancient pattern of response to microbial colonization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 8066-8070.	3.3	368
74	Genetic Networks. <i>Plant Physiology</i> , 2005, 138, 542-544.	2.3	3
75	Differential Expression Profile of the Proteome and Transcriptome in Aggressive and Indolent Chronic Lymphocytic Leukemia.. <i>Blood</i> , 2005, 106, 2101-2101.	0.6	0
76	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.	3.3	51
77	Loss of an MDR Transporter in Compact Stalks of Maize br2 and Sorghum dw3 Mutants. <i>Science</i> , 2003, 302, 81-84.	6.0	480
78	Rice phosphate transporters include an evolutionarily divergent gene specifically activated in arbuscular mycorrhizal symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13324-13329.	3.3	565
79	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.	3.3	92
80	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. japonica). <i>Science</i> , 2002, 296, 92-100.	6.0	2,866
81	Membrane-mediated ultrafast restriction digestion and subsequent rapid gel microchip electrophoresis of DNA. <i>Electrophoresis</i> , 2002, 23, 1524.	1.3	15
82	The paradigm shift of genomics "a complement to traditional plant science. <i>Current Opinion in Plant Biology</i> , 1999, 2, 81-82.	3.5	6
83	Regulation of leaf initiation by the terminal ear 1 gene of maize. <i>Nature</i> , 1998, 393, 166-168.	13.7	141
84	Engineering new plant strains for commercial markets. <i>Current Opinion in Biotechnology</i> , 1998, 9, 233-235.	3.3	19
85	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.	3.1	33
86	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.	1.4	46
87	Analysis of a Chemical Plant Defense Mechanism in Grasses. <i>Science</i> , 1997, 277, 696-699.	6.0	624
88	A Novel Suppressor of Cell Death in Plants Encoded by the Lls1 Gene of Maize. <i>Cell</i> , 1997, 89, 25-31.	13.5	268
89	Plant Disease Resistance: Grand unification theory in sight. <i>Current Biology</i> , 1995, 5, 128-131.	1.8	18
90	Disease lesion mimics of maize: A model for cell death in plants. <i>BioEssays</i> , 1995, 17, 685-692.	1.2	166

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91	Cloning and Characterization of the Maize An1 Gene. <i>Plant Cell</i> , 1995, 7, 75.	3.1	102
92	Genetic patterns of plant host-parasite interactions. <i>Trends in Genetics</i> , 1994, 10, 12-16.	2.9	34
93	Selective Toxin of <i>Helminthosporium victoriae</i> : Thermal Relationships in Effects on Oat Tissues and Protoplasts. <i>Phytopathology</i> , 1984, 74, 768.	1.1	11
94	Changes in Tobacco Cell Membrane Composition and Structure Caused by Cercosporin. <i>Plant Physiology</i> , 1983, 71, 763-766.	2.3	92
95	Localization of Spin Labels in Oat Leaf Protoplasts. <i>Plant Physiology</i> , 1982, 70, 662-667.	2.3	7
96	Interaction of Nitroxide Spin Labels with Chloroplasts. <i>Plant Physiology</i> , 1982, 70, 668-670.	2.3	3