

# 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	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
2	Nitrate triggered phosphoproteome changes and a PIN2 phosphosite modulating root system architecture. <i>EMBO Reports</i> , 2021, 22, e51813.	4.5	22
3	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , 2021, 10, .	6.0	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, .	7.1	10
5	Wnt5a Induces ROR1 to Interact Grb2 to Enhance Ras Activation in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2021, 138, 247-247.	1.4	1
6	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
7	Current status of the multinational Arabidopsis community. <i>Plant Direct</i> , 2020, 4, e00248.	1.9	13
8	Genetic elucidation of interconnected antibiotic pathways mediating maize innate immunity. <i>Nature Plants</i> , 2020, 6, 1375-1388.	9.3	52
9	Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. <i>Plant Cell</i> , 2020, 32, 1377-1396.	6.6	60
10	Auxin Induces Widespread Proteome Remodeling in Arabidopsis Seedlings. <i>Proteomics</i> , 2019, 19, 1900199.	2.2	10
11	LIKE SEX4 1 Acts as a $\beta$ -Amylase-Binding Scaffold on Starch Granules during Starch Degradation. <i>Plant Cell</i> , 2019, 31, 2169-2186.	6.6	26
12	Front Cover: Auxin Induces Widespread Proteome Remodeling in Arabidopsis Seedlings. <i>Proteomics</i> , 2019, 19, 1970151.	2.2	0
13	Wnt5a induces ROR1 to recruit cortactin to promote breast-cancer migration and metastasis. <i>Npj Breast Cancer</i> , 2019, 5, 35.	5.2	18
14	Dynamic Patterns of Gene Expression Additivity and Regulatory Variation throughout Maize Development. <i>Molecular Plant</i> , 2019, 12, 410-425.	8.3	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.	6.6	17
16	Magnesium Flux Modulates Ribosomes to Increase Bacterial Survival. <i>Cell</i> , 2019, 177, 352-360.e13.	28.9	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.	3.8	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.	7.1	47

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19	Multiple genes recruited from hormone pathways partition maize diterpenoid defences. <i>Nature Plants</i> , 2019, 5, 1043-1056.	9.3	60
20	Discovery, Biosynthesis and Stress-Related Accumulation of Dolabradiene-Derived Defenses in Maize. <i>Plant Physiology</i> , 2018, 176, 2677-2690.	4.8	94
21	Wnt5a induces ROR1 to recruit DOCK2 to activate Rac1/2 in chronic lymphocytic leukemia. <i>Blood</i> , 2018, 132, 170-178.	1.4	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.	2.0	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.	7.1	71
24	Integration of omic networks in a developmental atlas of maize. <i>Science</i> , 2016, 353, 814-818.	12.6	411
25	The small GTPases Ras and Rap1 bind to and control TORC2 activity. <i>Scientific Reports</i> , 2016, 6, 25823.	3.3	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.	3.8	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.	1.4	2
28	Wnt5a Induces Association of ROR1 with 14-3-3 $\sigma$ to Enhance Chemotaxis and Proliferation in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2016, 128, 349-349.	1.4	1
29	Dual use of peptide mass spectra: Protein atlas and genome annotation. <i>Current Plant Biology</i> , 2015, 2, 21-24.	4.7	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.	5.2	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.	3.7	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.	4.8	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.	7.1	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.	12.8	64
35	Wnt5a induces ROR1/ROR2 heterooligomerization to enhance leukemia chemotaxis and proliferation. <i>Journal of Clinical Investigation</i> , 2015, 126, 585-598.	8.2	149
36	ROR1 can interact with TCL1 and enhance leukemogenesis in E $\mu$ -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

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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.	3.6	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.	3.8	79
39	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
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.	7.1	180
41	Parallel Proteomic and Phosphoproteomic Analyses of Successive Stages of Maize Leaf Development. <i>Plant Cell</i> , 2013, 25, 2798-2812.	6.6	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.	3.6	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.	3.8	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.	7.1	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.	7.1	179
46	ROR1 Can Interact With TCL1 and Enhance Leukemogenesis In E $\mu$ -TCL1 Transgenic Mice. <i>Blood</i> , 2013, 122, 868-868.	1.4	0
47	Accurate Mass Spectrometry Based Protein Quantification via Shared Peptides. <i>Journal of Computational Biology</i> , 2012, 19, 337-348.	1.6	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.	6.6	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.	3.4	80
50	Processing and Subcellular Trafficking of ER-Tethered EIN2 Control Response to Ethylene Gas. <i>Science</i> , 2012, 338, 390-393.	12.6	461
51	Biochemical and Phosphoproteomic Analysis of the Helix-Loop-Helix Protein E47. <i>Molecular and Cellular Biology</i> , 2012, 32, 1671-1682.	2.3	25
52	The HUPO initiative on Model Organism Proteomes, iMOP. <i>Proteomics</i> , 2012, 12, 340-345.	2.2	9
53	RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. <i>Nature Chemical Biology</i> , 2011, 7, 779-786.	8.0	286
54	MASCP Gator: An Aggregation Portal for the Visualization of Arabidopsis Proteomics Data. <i>Plant Physiology</i> , 2011, 155, 259-270.	4.8	94

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55	Nematode effectors and plant responses to infection. <i>Current Opinion in Plant Biology</i> , 2010, 13, 442-448.	7.1	40
56	Regulation of STIM1 and SOCE by the Ubiquitin-Proteasome System (UPS). <i>PLoS ONE</i> , 2010, 5, e13465.	2.5	39
57	Application of Proteomic Marker Ensembles to Subcellular Organelle Identification. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 388-402.	3.8	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.	7.1	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.	3.8	35
60	A Ras Signaling Complex Controls the RasC-TORC2 Pathway and Directed Cell Migration. <i>Developmental Cell</i> , 2010, 18, 737-749.	7.0	141
61	Sunday Driver Interacts with Two Distinct Classes of Axonal Organelles. <i>Journal of Biological Chemistry</i> , 2009, 284, 34628-34639.	3.4	54
62	Regulation of contractile vacuole formation and activity in <i>Dictyostelium</i> . <i>EMBO Journal</i> , 2008, 27, 2064-2076.	7.8	41
63	Accurate Annotation of Peptide Modifications through Unrestrictive Database Search. <i>Journal of Proteome Research</i> , 2008, 7, 170-181.	3.7	50
64	Clustering Millions of Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2008, 7, 113-122.	3.7	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.	4.7	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.	7.1	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.	4.7	174
68	Improving gene annotation using peptide mass spectrometry. <i>Genome Research</i> , 2007, 17, 231-239.	5.5	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.	7.1	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.	6.6	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.	3.5	97

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73	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
74	Genetic Networks. Plant Physiology, 2005, 138, 542-544.	4.8	3
75	Differential Expression Profile of the Proteome and Transcriptome in Aggressive and Indolent Chronic Lymphocytic Leukemia.. Blood, 2005, 106, 2101-2101.	1.4	0
76	Regulation of the endogenous VEGF-A gene by exogenous designed regulatory proteins. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15225-15230.	7.1	51
77	Loss of an MDR Transporter in Compact Stalks of Maize br2 and Sorghum dw3 Mutants. Science, 2003, 302, 81-84.	12.6	480
78	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
79	Heritable endogenous gene regulation in plants with designed polydactyl zinc finger transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13296-13301.	7.1	92
80	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
81	Membrane-mediated ultrafast restriction digestion and subsequent rapid gel microchip electrophoresis of DNA. Electrophoresis, 2002, 23, 1524.	2.4	15
82	The paradigm shift of genomics â€” a complement to traditional plant science. Current Opinion in Plant Biology, 1999, 2, 81-82.	7.1	6
83	Regulation of leaf initiation by the terminal ear 1 gene of maize. Nature, 1998, 393, 166-168.	27.8	141
84	Engineering new plant strains for commercial markets. Current Opinion in Biotechnology, 1998, 9, 233-235.	6.6	19
85	A Porphyrin Pathway Impairment Is Responsible for the Phenotype of a Dominant Disease Lesion Mimic Mutant of Maize. Plant Cell, 1998, 10, 1095.	6.6	33
86	The Maize Lethal Leaf Spot 1 Mutant Has Elevated Resistance to Fungal Infection at the Leaf Epidermis. Molecular Plant-Microbe Interactions, 1998, 11, 1110-1118.	2.6	46
87	Analysis of a Chemical Plant Defense Mechanism in Grasses. Science, 1997, 277, 696-699.	12.6	624
88	A Novel Suppressor of Cell Death in Plants Encoded by the Lls1 Gene of Maize. Cell, 1997, 89, 25-31.	28.9	268
89	Plant Disease Resistance: Grand unification theory in sight. Current Biology, 1995, 5, 128-131.	3.9	18
90	Disease lesion mimics of maize: A model for cell death in plants. BioEssays, 1995, 17, 685-692.	2.5	166

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91	Cloning and Characterization of the Maize An1 Gene. <i>Plant Cell</i> , 1995, 7, 75.	6.6	102
92	Genetic patterns of plant host-parasite interactions. <i>Trends in Genetics</i> , 1994, 10, 12-16.	6.7	34
93	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
94	Changes in Tobacco Cell Membrane Composition and Structure Caused by Cercosporin. <i>Plant Physiology</i> , 1983, 71, 763-766.	4.8	92
95	Localization of Spin Labels in Oat Leaf Protoplasts. <i>Plant Physiology</i> , 1982, 70, 662-667.	4.8	7
96	Interaction of Nitroxide Spin Labels with Chloroplasts. <i>Plant Physiology</i> , 1982, 70, 668-670.	4.8	3