

Bret Cooper

List of Publications by Year in descending order

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56
papers

5,561
citations

249298

26
h-index

175968

55
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56
all docs

56
docs citations

56
times ranked

7972
citing authors

#	ARTICLE	IF	CITATIONS
1	Salicylic Acid and Phytoalexin Induction by a Bacterium that Causes Halo Blight in Beans. <i>Phytopathology</i> , 2022, , .	1.1	3
2	Proteomic Identification and Meta-Analysis in <i>Salvia hispanica</i> RNA-Seq de novo Assemblies. <i>Plants</i> , 2021, 10, 765.	1.6	2
3	Genomic Resources for <i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> Races 5 and 8. <i>Phytopathology</i> , 2021, 111, 893-895.	1.1	3
4	Bacterial Immobilization and Toxicity Induced by a Bean Plant Immune System. <i>Journal of Proteome Research</i> , 2021, 20, 3664-3677.	1.8	6
5	Blistering1 Modulates <i>Penicillium expansum</i> Virulence Via Vesicle-mediated Protein Secretion. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 344-361.	2.5	22
6	The Proteomics of Resistance to Halo Blight in Common Bean. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1161-1175.	1.4	12
7	Benzothiadiazole Conditions the Bean Proteome for Immunity to Bean Rust. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 600-611.	1.4	8
8	Quantitative Proteomics Reveals a Role for SERINE/ARGININE-Rich 45 in Regulating RNA Metabolism and Modulating Transcriptional Suppression via the ASAP Complex in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1116.	1.7	16
9	Quantitative Proteomic Analysis of <i>Staphylococcus aureus</i> Treated With Punicalagin, a Natural Antibiotic From Pomegranate That Disrupts Iron Homeostasis and Induces SOS. <i>Proteomics</i> , 2018, 18, e1700461.	1.3	28
10	A Proteomic Network for Symbiotic Nitrogen Fixation Efficiency in <i>Bradyrhizobium elkanii</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 334-343.	1.4	5
11	Protection Against Common Bean Rust Conferred by a Gene-Silencing Method. <i>Phytopathology</i> , 2017, 107, 920-927.	1.1	23
12	Putative Rust Fungal Effector Proteins in Infected Bean and Soybean Leaves. <i>Phytopathology</i> , 2016, 106, 491-499.	1.1	31
13	Different Cellular Origins and Functions of Extracellular Proteins from <i>Escherichia coli</i> O157:H7 and O104:H4 as Determined by Comparative Proteomic Analysis. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4371-4378.	1.4	13
14	Doubling down on phosphorylation as a variable peptide modification. <i>Proteomics</i> , 2016, 16, 2444-2447.	1.3	3
15	Expression of a synthetic rust fungal virus cDNA in yeast. <i>Archives of Virology</i> , 2016, 161, 111-123.	0.9	3
16	Proteomics of Nitrogen Remobilization in Poplar Bark. <i>Journal of Proteome Research</i> , 2015, 14, 1112-1126.	1.8	16
17	Phosphothreonine 218 is required for the function of SR45.1 in regulating flower petal development in <i>Arabidopsis</i> . <i>Plant Signaling and Behavior</i> , 2014, 9, e29134.	1.2	36
18	The haustorial transcriptomes of <i>Uromyces appendiculatus</i> and <i>Puccinia hakopsora pachyrhizi</i> and their candidate effector families. <i>Molecular Plant Pathology</i> , 2014, 15, 379-393.	2.0	67

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19	Proof by synthesis of Tobacco mosaic virus. <i>Genome Biology</i> , 2014, 15, R67.	13.9	20
20	Disruption of <i>Rpp1</i> -mediated soybean rust immunity by virus-induced gene silencing. <i>Plant Signaling and Behavior</i> , 2013, 8, e27543.	1.2	20
21	Separation anxiety. <i>Plant Signaling and Behavior</i> , 2013, 8, e24721.	1.2	6
22	CTR1 phosphorylates the central regulator EIN2 to control ethylene hormone signaling from the ER membrane to the nucleus in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19486-19491.	3.3	539
23	Proteomic Pleiotropy of <i>OpgGH</i> , an Operon Necessary for Efficient Growth of <i>Salmonella enterica</i> serovar Typhimurium under Low-Osmotic Conditions. <i>Journal of Proteome Research</i> , 2012, 11, 1720-1727.	1.8	11
24	The Problem with Peptide Presumption and the Downfall of Targetâ€˜Decoy False Discovery Rates. <i>Analytical Chemistry</i> , 2012, 84, 9663-9667.	3.2	13
25	Nuclear proteomic changes linked to soybean rust resistance. <i>Molecular BioSystems</i> , 2011, 7, 773-783.	2.9	39
26	Proteomic responses in <i>Arabidopsis thaliana</i> seedlings treated with ethylene. <i>Molecular BioSystems</i> , 2011, 7, 2637.	2.9	71
27	The Problem with Peptide Presumption and Low Mascot Scoring. <i>Journal of Proteome Research</i> , 2011, 10, 1432-1435.	1.8	32
28	A Parallelized Binary Search Tree. <i>Journal of Information Technology & Software Engineering</i> , 2011, 01, .	0.3	2
29	Affinity Purification and Mass Spectrometry: An Attractive Choice to Investigate Protein-Protein Interactions in Plant Immunity. <i>Current Proteomics</i> , 2010, 7, 258-264.	0.1	11
30	Relative, label-free protein quantitation: Spectral counting error statistics from nine replicate MudPIT samples. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1534-1546.	1.2	46
31	Quantitative Proteomic Analysis of Bean Plants Infected by a Virulent and Avirulent Obligate Rust Fungus. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 19-31.	2.5	61
32	Generation of <i>Phaseolus vulgaris</i> ESTs and investigation of their regulation upon <i>Uromyces appendiculatus</i> infection. <i>BMC Plant Biology</i> , 2009, 9, 46.	1.6	34
33	Establishment of a Protein Reference Map for Soybean Root Hair Cells. <i>Plant Physiology</i> , 2009, 149, 670-682.	2.3	95
34	Correlation of Multiple Peptide Mass Spectra for Phosphoprotein Identification. <i>Journal of Proteome Research</i> , 2009, 8, 5396-5405.	1.8	8
35	Coding DNA repeated throughout intergenic regions of the <i>Arabidopsis thaliana</i> genome: evolutionary footprints of RNA silencing. <i>Molecular BioSystems</i> , 2009, 5, 1679.	2.9	11
36	Combined Dynamic Arrays for Storing and Searching Semi-Ordered Tandem Mass Spectrometry Data. <i>Journal of Computational Biology</i> , 2008, 15, 457-468.	0.8	2

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37	Probability-based pattern recognition and statistical framework for randomization: modeling tandem mass spectrum/peptide sequence false match frequencies. <i>Bioinformatics</i> , 2007, 23, 2210-2217.	1.8	39
38	Protein Accumulation in the Germinating <i>Uromyces appendiculatus</i> Uredospore. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 857-866.	1.4	37
39	Probability Model for Assessing Proteins Assembled from Peptide Sequences Inferred from Tandem Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2007, 79, 3901-3911.	3.2	58
40	Shotgun proteomic analysis of <i>Arabidopsis thaliana</i> leaves. <i>Journal of Separation Science</i> , 2007, 30, 2225-2230.	1.3	31
41	Tandem mass spectrometry for the detection of plant pathogenic fungi and the effects of database composition on protein inferences. <i>Proteomics</i> , 2007, 7, 3932-3942.	1.3	22
42	Alternative workflows for plant proteomic analysis. <i>Molecular BioSystems</i> , 2006, 2, 621.	2.9	24
43	Shotgun identification of proteins from uredospores of the bean rust <i>Uromyces appendiculatus</i> . <i>Proteomics</i> , 2006, 6, 2477-2484.	1.3	44
44	Mass spectrometry-based proteomics for the detection of plant pathogens. <i>Proteomics</i> , 2006, 6, 4069-4075.	1.3	27
45	Identification of rice (<i>Oryza sativa</i>) proteins linked to the cyclin-mediated regulation of the cell cycle. <i>Plant Molecular Biology</i> , 2003, 53, 273-279.	2.0	17
46	Investigative proteomics: Identification of an unknown plant virus from infected plants using mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 736-741.	1.2	79
47	Diverse RNA viruses elicit the expression of common sets of genes in susceptible <i>Arabidopsis thaliana</i> plants. <i>Plant Journal</i> , 2003, 33, 271-283.	2.8	323
48	A network of rice genes associated with stress response and seed development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4945-4950.	3.3	228
49	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
50	Collateral gene expression changes induced by distinct plant viruses during the hypersensitive resistance reaction in <i>Chenopodium amaranticolor</i> . <i>Plant Journal</i> , 2001, 26, 339-349.	2.8	41
51	Constitutive salicylic acid-dependent signaling in <i>cpr1</i> and <i>cpr6</i> mutants requires PAD4. <i>Plant Journal</i> , 2001, 26, 395-407.	2.8	113
52	Genetic Mechanisms for Engineering Host Resistance to Plant Viruses. , 1999, , 557-574.		1
53	Domains of the TMV movement protein involved in subcellular localization. <i>Plant Journal</i> , 1998, 15, 15-25.	2.8	81
54	Defective Movement of Viruses in the Family Bromoviridae Is Differentially Complemented in <i>Nicotiana benthamiana</i> Expressing Tobamovirus or Dianthovirus Movement Proteins. <i>Phytopathology</i> , 1998, 88, 666-672.	1.1	26

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55	Cell-to-Cell Transport of Movement-Defective Cucumber Mosaic and Tobacco Mosaic Viruses in Transgenic Plants Expressing Heterologous Movement Protein Genes. <i>Virology</i> , 1996, 216, 208-213.	1.1	36
56	A defective movement protein of TMV in transgenic plants confers resistance to multipleviruses whereas the functional analog increases susceptibility. <i>Virology</i> , 1995, 206, 307-313.	1.1	150