

Sophien Kamoun

List of Publications by Year in descending order

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261
papers

43,493
citations

1457

107
h-index

2617

194
g-index

355
all docs

355
docs citations

355
times ranked

25270
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence-Based Species Delimitation for the DNA Taxonomy of Undescribed Insects. <i>Systematic Biology</i> , 2006, 55, 595-609.	2.7	2,257
2	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	13.7	1,405
3	Genome sequencing reveals agronomically important loci in rice using MutMap. <i>Nature Biotechnology</i> , 2012, 30, 174-178.	9.4	1,087
4	<sc>QTL</sc>â€seq: rapid mapping of quantitative trait loci in rice by whole genome resequencing of <sc>DNA</sc> from two bulked populations. <i>Plant Journal</i> , 2013, 74, 174-183.	2.8	1,065
5	<i>Phytophthora</i> Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. <i>Science</i> , 2006, 313, 1261-1266.	6.0	1,059
6	Targeted mutagenesis in the model plant <i>Nicotiana benthamiana</i> using Cas9 RNA-guided endonuclease. <i>Nature Biotechnology</i> , 2013, 31, 691-693.	9.4	951
7	Genome evolution in filamentous plant pathogens: why bigger can be better. <i>Nature Reviews Microbiology</i> , 2012, 10, 417-430.	13.6	735
8	A Catalogue of the Effector Secretome of Plant Pathogenic Oomycetes. <i>Annual Review of Phytopathology</i> , 2006, 44, 41-60.	3.5	706
9	The Top 10 oomycete pathogens in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2015, 16, 413-434.	2.0	695
10	Emerging Concepts in Effector Biology of Plant-Associated Organisms. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 115-122.	1.4	631
11	From Guard to Decoy: A New Model for Perception of Plant Pathogen Effectors. <i>Plant Cell</i> , 2008, 20, 2009-2017.	3.1	626
12	Rapid generation of a transgene-free powdery mildew resistant tomato by genome deletion. <i>Scientific Reports</i> , 2017, 7, 482.	1.6	525
13	Plant genome editing made easy: targeted mutagenesis in model and crop plants using the CRISPR/Cas system. <i>Plant Methods</i> , 2013, 9, 39.	1.9	515
14	The two-speed genomes of filamentous pathogens: waltz with plants. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 57-65.	1.5	503
15	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. <i>Science</i> , 2010, 330, 1549-1551.	6.0	492
16	A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. <i>Nature Genetics</i> , 2013, 45, 1510-1515.	9.4	472
17	Editing plant genomes with CRISPR/Cas9. <i>Current Opinion in Biotechnology</i> , 2015, 32, 76-84.	3.3	456
18	Genome Evolution Following Host Jumps in the Irish Potato Famine Pathogen Lineage. <i>Science</i> , 2010, 330, 1540-1543.	6.0	440

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19	Differential Recognition of Highly Divergent Downy Mildew Avirulence Gene Alleles by RPP1 Resistance Genes from Two Arabidopsis Lines. <i>Plant Cell</i> , 2005, 17, 1839-1850.	3.1	416
20	An ancestral oomycete locus contains late blight avirulence gene Avr3a, encoding a protein that is recognized in the host cytoplasm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7766-7771.	3.3	414
21	<i>Phytophthora infestans</i> effector AVR3a is essential for virulence and manipulates plant immunity by stabilizing host E3 ligase CPMG1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9909-9914.	3.3	412
22	Association Genetics Reveals Three Novel Avirulence Genes from the Rice Blast Fungal Pathogen <i>Magnaporthe oryzae</i> . <i>Plant Cell</i> , 2009, 21, 1573-1591.	3.1	410
23	The C-terminal half of <i>Phytophthora infestans</i> RXLR effector AVR3a is sufficient to trigger R3a-mediated hypersensitivity and suppress INF1-induced cell death in <i>Nicotiana benthamiana</i> . <i>Plant Journal</i> , 2006, 48, 165-176.	2.8	402
24	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	13.9	391
25	In Planta Expression Screens of <i>Phytophthora infestans</i> RXLR Effectors Reveal Diverse Phenotypes, Including Activation of the <i>Solanum bulbocastanum</i> Disease Resistance Protein Rpi-blb2. <i>Plant Cell</i> , 2009, 21, 2928-2947.	3.1	376
26	Resistance of <i>Nicotiana benthamiana</i> to <i>Phytophthora infestans</i> Is Mediated by the Recognition of the Elicitor Protein INF1. <i>Plant Cell</i> , 1998, 10, 1413-1425.	3.1	371
27	Understanding and Exploiting Late Blight Resistance in the Age of Effectors. <i>Annual Review of Phytopathology</i> , 2011, 49, 507-531.	3.5	369
28	Effector Genomics Accelerates Discovery and Functional Profiling of Potato Disease Resistance and <i>Phytophthora infestans</i> Avirulence Genes. <i>PLoS ONE</i> , 2008, 3, e2875.	1.1	361
29	Effector Biology of Plant-Associated Organisms: Concepts and Perspectives. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2012, 77, 235-247.	2.0	355
30	Emergence of wheat blast in Bangladesh was caused by a South American lineage of <i>Magnaporthe oryzae</i> . <i>BMC Biology</i> , 2016, 14, 84.	1.7	355
31	The rise and fall of the <i>Phytophthora infestans</i> lineage that triggered the Irish potato famine. <i>ELife</i> , 2013, 2, e00731.	2.8	339
32	EST Mining and Functional Expression Assays Identify Extracellular Effector Proteins From the Plant Pathogen <i>Phytophthora</i> . <i>Genome Research</i> , 2003, 13, 1675-1685.	2.4	333
33	NLR network mediates immunity to diverse plant pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8113-8118.	3.3	330
34	Ancient class of translocated oomycete effectors targets the host nucleus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17421-17426.	3.3	326
35	Genome Analyses of an Aggressive and Invasive Lineage of the Irish Potato Famine Pathogen. <i>PLoS Pathogens</i> , 2012, 8, e1002940.	2.1	321
36	Adaptive Evolution Has Targeted the C-Terminal Domain of the RXLR Effectors of Plant Pathogenic Oomycetes. <i>Plant Cell</i> , 2007, 19, 2349-2369.	3.1	315

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37	Molecular Genetics of Pathogenic Oomycetes. <i>Eukaryotic Cell</i> , 2003, 2, 191-199.	3.4	302
38	A Kazal-like Extracellular Serine Protease Inhibitor from <i>Phytophthora infestans</i> Targets the Tomato Pathogenesis-related Protease P69B. <i>Journal of Biological Chemistry</i> , 2004, 279, 26370-26377.	1.6	301
39	Expression of a <i>Phytophthora sojae</i> necrosis-inducing protein occurs during transition from biotrophy to necrotrophy. <i>Plant Journal</i> , 2002, 32, 361-373.	2.8	299
40	A Common Signaling Process that Promotes Mycorrhizal and Oomycete Colonization of Plants. <i>Current Biology</i> , 2012, 22, 2242-2246.	1.8	291
41	<i>Phytophthora infestans</i> effector AVRblb2 prevents secretion of a plant immune protease at the haustorial interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20832-20837.	3.3	285
42	Trafficking arms: oomycete effectors enter host plant cells. <i>Trends in Microbiology</i> , 2006, 14, 8-11.	3.5	278
43	A <i>Phytophthora infestans</i> Cystatin-Like Protein Targets a Novel Tomato Papain-Like Apoplastic Protease. <i>Plant Physiology</i> , 2007, 143, 364-377.	2.3	277
44	Groovy times: filamentous pathogen effectors revealed. <i>Current Opinion in Plant Biology</i> , 2007, 10, 358-365.	3.5	274
45	Gene expression analysis of plant host-pathogen interactions by SuperSAGE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15718-15723.	3.3	273
46	MutMap+: Genetic Mapping and Mutant Identification without Crossing in Rice. <i>PLoS ONE</i> , 2013, 8, e68529.	1.1	267
47	MutMap accelerates breeding of a salt-tolerant rice cultivar. <i>Nature Biotechnology</i> , 2015, 33, 445-449.	9.4	265
48	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1350-1360.	1.4	264
49	Standards for plant synthetic biology: a common syntax for exchange of <i>scp</i> DNA parts. <i>New Phytologist</i> , 2015, 208, 13-19.	3.5	263
50	Apoplastic effectors secreted by two unrelated eukaryotic plant pathogens target the tomato defense protease Rcr3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1654-1659.	3.3	260
51	Structural basis of pathogen recognition by an integrated HMA domain in a plant NLR immune receptor. <i>ELife</i> , 2015, 4, .	2.8	246
52	Single Nucleus Genome Sequencing Reveals High Similarity among Nuclei of an Endomycorrhizal Fungus. <i>PLoS Genetics</i> , 2014, 10, e1004078.	1.5	238
53	Using Hierarchical Clustering of Secreted Protein Families to Classify and Rank Candidate Effectors of Rust Fungi. <i>PLoS ONE</i> , 2012, 7, e29847.	1.1	235
54	Genome analyses of the wheat yellow (stripe) rust pathogen <i>Puccinia striiformis</i> f. sp. <i>tritici</i> reveal polymorphic and haustorial expressed secreted proteins as candidate effectors. <i>BMC Genomics</i> , 2013, 14, 270.	1.2	235

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55	A Gene Encoding a Protein Elicitor of <i>Phytophthora infestans</i> Is Down-Regulated During Infection of Potato. <i>Molecular Plant-Microbe Interactions</i> , 1997, 10, 13-20.	1.4	233
56	Oomycetes, effectors, and all that jazz. <i>Current Opinion in Plant Biology</i> , 2012, 15, 483-492.	3.5	232
57	How Do Filamentous Pathogens Deliver Effector Proteins into Plant Cells?. <i>PLoS Biology</i> , 2014, 12, e1001801.	2.6	232
58	Fungal Effector Protein AVR2 Targets Diversifying Defense-Related Cys Proteases of Tomato. <i>Plant Cell</i> , 2008, 20, 1169-1183.	3.1	230
59	Elicitin recognition confers enhanced resistance to <i>Phytophthora infestans</i> in potato. <i>Nature Plants</i> , 2015, 1, 15034.	4.7	229
60	A Second Kazal-Like Protease Inhibitor from <i>Phytophthora infestans</i> Inhibits and Interacts with the Apoplastic Pathogenesis-Related Protease P69B of Tomato. <i>Plant Physiology</i> , 2005, 138, 1785-1793.	2.3	222
61	The hypersensitive response is associated with host and nonhost resistance to <i>Phytophthora infestans</i> . <i>Planta</i> , 2000, 210, 853-864.	1.6	217
62	Cytosolic HSP90 and HSP70 are essential components of INF1-mediated hypersensitive response and non-host resistance to <i>Pseudomonas cichorii</i> in <i>Nicotiana benthamiana</i> . <i>Molecular Plant Pathology</i> , 2003, 4, 383-391.	2.0	214
63	Oomyceteâ€“plant coevolution: recent advances and future prospects. <i>Current Opinion in Plant Biology</i> , 2010, 13, 427-433.	3.5	204
64	CRISPR Crops: Plant Genome Editing Toward Disease Resistance. <i>Annual Review of Phytopathology</i> , 2018, 56, 479-512.	3.5	197
65	<sc>M</sc>ut<sc>M</sc>apâ€“<sc>G</sc>ap: wholeâ€“genome resequencing of mutant <sc>F</sc>2 progeny bulk combined with <i>de novo</i> assembly of gap regions identifies the rice blast resistance gene <sc><i>Pii</i></sc>. <i>New Phytologist</i> , 2013, 200, 276-283.	3.5	196
66	AY-WB <i>Phytoplasma</i> Secretes a Protein That Targets Plant Cell Nuclei. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 18-30.	1.4	193
67	Systemic Modulation of Gene Expression in Tomato by <i>Trichoderma hamatum</i> 382. <i>Phytopathology</i> , 2007, 97, 429-437.	1.1	190
68	The Malarial Host-Targeting Signal Is Conserved in the Irish Potato Famine Pathogen. <i>PLoS Pathogens</i> , 2006, 2, e50.	2.1	189
69	An effector of the Irish potato famine pathogen antagonizes a host autophagy cargo receptor. <i>ELife</i> , 2016, 5, .	2.8	189
70	Analyses of genome architecture and gene expression reveal novel candidate virulence factors in the secretome of <i>Phytophthora infestans</i> . <i>BMC Genomics</i> , 2010, 11, 637.	1.2	188
71	<i>Phytophthora infestans</i> RXLR Effector PexRD2 Interacts with Host MAPKKÎ¼ to Suppress Plant Immune Signaling. <i>Plant Cell</i> , 2014, 26, 1345-1359.	3.1	188
72	NLR singletons, pairs, and networks: evolution, assembly, and regulation of the intracellular immunoreceptor circuitry of plants. <i>Current Opinion in Plant Biology</i> , 2019, 50, 121-131.	3.5	187

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73	Ten things to know about oomycete effectors. <i>Molecular Plant Pathology</i> , 2009, 10, 795-803.	2.0	185
74	Field pathogenomics reveals the emergence of a diverse wheat yellow rust population. <i>Genome Biology</i> , 2015, 16, 23.	3.8	185
75	Resistance to oomycetes: a general role for the hypersensitive response?. <i>Trends in Plant Science</i> , 1999, 4, 196-200.	4.3	183
76	Effector Specialization in a Lineage of the Irish Potato Famine Pathogen. <i>Science</i> , 2014, 343, 552-555.	6.0	179
77	Synergistic Interactions of the Plant Cell Death Pathways Induced by <i>Phytophthora infestans</i> Nep1-Like Protein PiNPP1.1 and INF1 Elicitin. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 854-863.	1.4	178
78	Structures of <i>Phytophthora</i> RXLR Effector Proteins. <i>Journal of Biological Chemistry</i> , 2011, 286, 35834-35842.	1.6	178
79	Candidate Effector Proteins of the Rust Pathogen <i>Melampsora larici-populina</i> Target Diverse Plant Cell Compartments. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 689-700.	1.4	172
80	The Receptor-Like Kinase SERK3/BAK1 Is Required for Basal Resistance against the Late Blight Pathogen <i>Phytophthora infestans</i> in <i>Nicotiana benthamiana</i> . <i>PLoS ONE</i> , 2011, 6, e16608.	1.1	170
81	Internuclear Gene Silencing in <i>Phytophthora infestans</i> . <i>Molecular Cell</i> , 1999, 3, 339-348.	4.5	168
82	An Effector-Targeted Protease Contributes to Defense against <i>Phytophthora infestans</i> and Is under Diversifying Selection in Natural Hosts. <i>Plant Physiology</i> , 2010, 154, 1794-1804.	2.3	166
83	Effectors of Filamentous Plant Pathogens: Commonalities amid Diversity. <i>Microbiology and Molecular Biology Reviews</i> , 2017, 81, .	2.9	166
84	Qualitative and Quantitative Late Blight Resistance in the Potato Cultivar Sarpo Mira Is Determined by the Perception of Five Distinct RXLR Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 910-919.	1.4	162
85	An N-terminal motif in NLR immune receptors is functionally conserved across distantly related plant species. <i>ELife</i> , 2019, 8, .	2.8	162
86	Large-Scale Gene Discovery in the Oomycete <i>Phytophthora infestans</i> Reveals Likely Components of Phytopathogenicity Shared with True Fungi. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 229-243.	1.4	160
87	Initial Assessment of Gene Diversity for the Oomycete Pathogen <i>Phytophthora infestans</i> Based on Expressed Sequences. <i>Fungal Genetics and Biology</i> , 1999, 28, 94-106.	0.9	159
88	Host specialization of the blast fungus <i>Magnaporthe oryzae</i> is associated with dynamic gain and loss of genes linked to transposable elements. <i>BMC Genomics</i> , 2016, 17, 370.	1.2	157
89	Sequence Divergent RXLR Effectors Share a Structural Fold Conserved across Plant Pathogenic Oomycete Species. <i>PLoS Pathogens</i> , 2012, 8, e1002400.	2.1	153
90	Independent pathways leading to apoptotic cell death, oxidative burst and defense gene expression in response to elicitor in tobacco cell suspension culture. <i>FEBS Journal</i> , 2000, 267, 5005-5013.	0.2	151

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91	Large-Scale Gene Disruption in <i>Magnaporthe oryzae</i> Identifies MC69, a Secreted Protein Required for Infection by Monocot and Dicot Fungal Pathogens. <i>PLoS Pathogens</i> , 2012, 8, e1002711.	2.1	150
92	Cellulose Binding Domains of a <i>Phytophthora</i> Cell Wall Protein Are Novel Pathogen-Associated Molecular Patterns. <i>Plant Cell</i> , 2006, 18, 1766-1777.	3.1	149
93	Receptor networks underpin plant immunity. <i>Science</i> , 2018, 360, 1300-1301.	6.0	149
94	Nonhost resistance to <i>Phytophthora</i> : novel prospects for a classical problem. <i>Current Opinion in Plant Biology</i> , 2001, 4, 295-300.	3.5	148
95	RXLN effectors of plant pathogenic oomycetes. <i>Current Opinion in Microbiology</i> , 2007, 10, 332-338.	2.3	148
96	Extracellular Protein Elicitors from <i>Phytophthora</i> : Host-Specificity and Induction of Resistance to Bacterial and Fungal Phytopathogens. <i>Molecular Plant-Microbe Interactions</i> , 1993, 6, 15.	1.4	144
97	Presence/absence, differential expression and sequence polymorphisms between <i>PiAVR2</i> and <i>PiAVR2</i> -like in <i>Phytophthora infestans</i> determine virulence on <i>R2</i> plants. <i>New Phytologist</i> , 2011, 191, 763-776.	3.5	142
98	Phosphatidylinositol monophosphate-binding interface in the oomycete RXLN effector AVR3a is required for its stability in host cells to modulate plant immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14682-14687.	3.3	141
99	Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of <i>Phytophthora infestans</i> . <i>Molecular Biology and Evolution</i> , 2005, 22, 659-672.	3.5	140
100	Editing of the urease gene by CRISPR-Cas in the diatom <i>Thalassiosira pseudonana</i> . <i>Plant Methods</i> , 2016, 12, 49.	1.9	137
101	Single Amino Acid Mutations in the Potato Immune Receptor R3a Expand Response to <i>Phytophthora</i> Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 624-637.	1.4	136
102	Genome analyses of the sunflower pathogen <i>Plasmopara halstedii</i> provide insights into effector evolution in downy mildews and <i>Phytophthora</i> . <i>BMC Genomics</i> , 2015, 16, 741.	1.2	135
103	Host Protein BSL1 Associates with <i>Phytophthora infestans</i> RXLN Effector AVR2 and the <i>Solanum demissum</i> Immune Receptor R2 to Mediate Disease Resistance. <i>Plant Cell</i> , 2012, 24, 3420-3434.	3.1	130
104	ATG8 Expansion: A Driver of Selective Autophagy Diversification?. <i>Trends in Plant Science</i> , 2017, 22, 204-214.	4.3	129
105	Rice Exo70 interacts with a fungal effector, <i>AVR</i> -Pi, and is required for <i>AVR</i> -Pi-triggered immunity. <i>Plant Journal</i> , 2015, 83, 875-887.	2.8	128
106	nQuire: a statistical framework for ploidy estimation using next generation sequencing. <i>BMC Bioinformatics</i> , 2018, 19, 122.	1.2	128
107	Polymorphic residues in rice NLRs expand binding and response to effectors of the blast pathogen. <i>Nature Plants</i> , 2018, 4, 576-585.	4.7	127
108	The genome sequence and effector complement of the flax rust pathogen <i>Melampsora lini</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 98.	1.7	126

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109	Protein engineering expands the effector recognition profile of a rice NLR immune receptor. <i>ELife</i> , 2019, 8, .	2.8	118
110	The Plant Membrane-Associated REMORIN1.3 Accumulates in Discrete Perihaustorial Domains and Enhances Susceptibility to <i>Phytophthora infestans</i> . <i>Plant Physiology</i> , 2014, 165, 1005-1018.	2.3	116
111	<i>Capsicum annuum</i> WRKY protein CaWRKY1 is a negative regulator of pathogen defense. <i>New Phytologist</i> , 2008, 177, 977-989.	3.5	114
112	Emerging oomycete threats to plants and animals. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150459.	1.8	114
113	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. <i>BMC Biology</i> , 2017, 15, 86.	1.7	114
114	A Gene Encoding a Host-Specific Elicitor Protein of <i>Phytophthora parasitica</i> . <i>Molecular Plant-Microbe Interactions</i> , 1993, 6, 573.	1.4	114
115	Patterns of plant subcellular responses to successful oomycete infections reveal differences in host cell reprogramming and endocytic trafficking. <i>Cellular Microbiology</i> , 2012, 14, 682-697.	1.1	111
116	Lessons in Effector and NLR Biology of Plant-Microbe Systems. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 34-45.	1.4	109
117	NbLRK1, a lectin-like receptor kinase protein of <i>Nicotiana benthamiana</i> , interacts with <i>Phytophthora infestans</i> INF1 elicitor and mediates INF1-induced cell death. <i>Planta</i> , 2008, 228, 977-987.	1.6	108
118	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 705-715.	1.1	108
119	Gene Expression Profiling During Asexual Development of the Late Blight Pathogen <i>Phytophthora infestans</i> Reveals a Highly Dynamic Transcriptome. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 433-447.	1.4	105
120	Comparative Genome Analysis Provides Insights into the Evolution and Adaptation of <i>Pseudomonas syringae</i> pv. <i>aesculi</i> on <i>Aesculus hippocastanum</i> . <i>PLoS ONE</i> , 2010, 5, e10224.	1.1	104
121	Rerouting of Plant Late Endocytic Trafficking Toward a Pathogen Interface. <i>Traffic</i> , 2015, 16, 204-226.	1.3	103
122	Discovery of single nucleotide polymorphisms in <i>Lycopersicon esculentum</i> by computer aided analysis of expressed sequence tags. <i>Molecular Breeding</i> , 2004, 14, 21-34.	1.0	101
123	Structure of the Glucanase Inhibitor Protein (GIP) Family from <i>Phytophthora</i> Species Suggests Coevolution with Plant Endo-1,3-Glucanases. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 820-830.	1.4	101
124	Late Blight of Potato and Tomato in the Genomics Era. <i>Plant Disease</i> , 2005, 89, 692-699.	0.7	99
125	Heterologous Expression Screens in <i>Nicotiana benthamiana</i> Identify a Candidate Effector of the Wheat Yellow Rust Pathogen that Associates with Processing Bodies. <i>PLoS ONE</i> , 2016, 11, e0149035.	1.1	99
126	Regulation of Transcription of Nucleotide-Binding Leucine-Rich Repeat-Encoding Genes SNC1 and RPP4 via H3K4 Trimethylation. <i>Plant Physiology</i> , 2013, 162, 1694-1705.	2.3	93

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127	Towards understanding the virulence functions of RXLR effectors of the oomycete plant pathogen <i>Phytophthora infestans</i> . <i>Journal of Experimental Botany</i> , 2009, 60, 1133-1140.	2.4	92
128	Helper NLR proteins NRC2a/b and NRC3 but not NRC1 are required for Pto-mediated cell death and resistance in <i>Nicotiana benthamiana</i> . <i>New Phytologist</i> , 2016, 209, 1344-1352.	3.5	92
129	The coming of age of EvoMPMI: evolutionary molecular plant-microbe interactions across multiple timescales. <i>Current Opinion in Plant Biology</i> , 2018, 44, 108-116.	3.5	92
130	Active defence responses associated with non-host resistance of <i>Arabidopsis thaliana</i> to the oomycete pathogen <i>Phytophthora infestans</i> . <i>Molecular Plant Pathology</i> , 2003, 4, 487-500.	2.0	90
131	Expressed sequence tags from the oomycete fish pathogen <i>Saprolegnia parasitica</i> reveal putative virulence factors. <i>BMC Microbiology</i> , 2005, 5, 46.	1.3	90
132	Common infection strategies of pathogenic eukaryotes. <i>Nature Reviews Microbiology</i> , 2006, 4, 922-931.	13.6	90
133	Purification of Effector-Target Protein Complexes via Transient Expression in <i>Nicotiana benthamiana</i> . <i>Methods in Molecular Biology</i> , 2011, 712, 181-194.	0.4	90
134	Rust fungal effectors mimic host transit peptides to translocate into chloroplasts. <i>Cellular Microbiology</i> , 2016, 18, 453-465.	1.1	90
135	A high-throughput screen of cell-death-inducing factors in <i>Nicotiana benthamiana</i> identifies a novel MAPKK that mediates INF1-induced cell death signaling and non-host resistance to <i>Pseudomonas cichorii</i> . <i>Plant Journal</i> , 2007, 49, 1030-1040.	2.8	86
136	Incompatible Interactions Between Crucifers and <i>Xanthomonas campestris</i> Involve a Vascular Hypersensitive Response: Role of the <i>hrpX</i> Locus. <i>Molecular Plant-Microbe Interactions</i> , 1992, 5, 22.	1.4	86
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