Karambir Singh

List of Publications by Year
in descending order

128 papers	12,423 citations	30070 54 h-index	26613 107 g-index
137 all docs	137 docs citations	137 times ranked	12606 citing authors

#	Article	IF	Citations
1	Variability in an effector gene promoter of a necrotrophic fungal pathogen dictates epistasis and effector-triggered susceptibility in wheat. PLoS Pathogens, 2022, 18, e1010149.	4.7	9
2	The novel avirulence effector AlAvr1 from <i>Ascochyta lentis</i> mediates host cultivar specificity of ascochyta blight in lentil. Molecular Plant Pathology, 2022, , .	4.2	5
3	Insects Co-opt Host Genes to Overcome Plant Defences.. Faculty Reviews, 2022, 11, 10.	3.9	0
4	Transcription factor lineages in plant-pathogenic fungi, connecting diversity with fungal virulence. Fungal Genetics and Biology, 2022, 161, 103712.	2.1	4
5	Genomic resources for lupins are coming of age. , 2021, 3, e77.		5
6	Transcription factor control of virulence in phytopathogenic fungi. Molecular Plant Pathology, 2021, 22, 858-881.	4.2	50
7	A Trimethylguanosine Synthase1-like (TGS1) homologue is implicated in vernalisation and flowering time control. Theoretical and Applied Genetics, 2021, 134, 3411-3426.	3.6	9
8	The stem rust fungus Puccinia graminis f. sp. tritici induces centromeric small RNAs during late infection that are associated with genome-wide DNA methylation. BMC Biology, 2021, 19, 203.	3.8	15
9	A Plant Stress-Responsive Bioreporter Coupled With Transcriptomic Analysis Allows Rapid Screening for Biocontrols of Necrotrophic Fungal Pathogens. Frontiers in Molecular Biosciences, 2021, 8, 708530.	3.5	4
10	Foliar resistance to Rhizoctonia solani in Arabidopsis is compromised by simultaneous loss of ethylene, jasmonate and PEN2 mediated defense pathways. Scientific Reports, 2021, 11, 2546.	3.3	9
11	Editorial: Legumes for Global Food Security. Frontiers in Plant Science, 2020, 11, 926.	3.6	14
12	A functional genomics approach to dissect spotted alfalfa aphid resistance in Medicago truncatula. Scientific Reports, 2020, 10, 22159.	3.3	3
13	Ethylene Is Not Essential for R-Gene Mediated Resistance but Negatively Regulates Moderate Resistance to Some Aphids in Medicago truncatula. International Journal of Molecular Sciences, 2020, 21, 4657.	4.1	3
14	Overview of Genomic Resources Available for Lupins with a Focus on Narrow-Leafed Lupin (Lupinus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.5	1
15	Transcriptome Resources Paving the Way for Lupin Crop Improvement. Compendium of Plant Genomes, 2020, , 53-71.	0.5	3
16	An RNAi supplemented diet as a reverse genetics tool to control bluegreen aphid, a major pest of legumes. Scientific Reports, 2020, 10, 1604.	3.3	13
17	A specific fungal transcription factor controls effector gene expression and orchestrates the establishment of the necrotrophic pathogen lifestyle on wheat. Scientific Reports, 2019, 9, 15884.	3.3	34
18	A MYC2/MYC3/MYC4-dependent transcription factor network regulates water spray-responsive gene expression and jasmonate levels. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23345-23356.	7.1	95

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19	Additive and epistatic interactions between AKR and AIN loci conferring bluegreen aphid resistance and hypersensitivity in Medicago truncatula. Journal of Experimental Botany, 2019, 70, 4887-4902.	4.8	8
20	Transcriptome analysis reveals molecular mechanisms of sclerotial development in the rice sheath blight pathogen Rhizoctonia solani AG1-IA. Functional and Integrative Genomics, 2019, 19, 743-758.	3.5	28
21	The Arabidopsis altered in stress response2 is Impaired in Resistance to Root and Leaf Necrotrophic Fungal Pathogens. Plants, 2019, 8, 60.	3.5	1
22	The role of jasmonate signalling in quinolizidine alkaloid biosynthesis, wounding and aphid predation response in narrow-leafed lupin. Functional Plant Biology, 2019, 46, 443.	2.1	10
23	Identification and profiling of narrow-leafed lupin (Lupinus angustifolius) microRNAs during seed development. BMC Genomics, 2019, 20, 135.	2.8	22
24	INDEL variation in the regulatory region of the major flowering time gene <i>LanFTc1</i> is associated with vernalization response and flowering time in narrowâ€leafed lupin (<i>Lupinus angustifolius</i>) Tj ETQq0 0 0 rg BT /Overlock 10 Tf	5.7	51
25	Characterization of the genetic factors affecting quinolizidine alkaloid biosynthesis and its response to abiotic stress in narrowâ€leafed lupin (<scp><i>Lupinus angustifolius</i></scp>L.). Plant, Cell and Environment, 2018, 41, 2155-2168.	5.7	32
26	Improved prediction of fungal effector proteins from secretomes with EffectorP 2.0. Molecular Plant Pathology, 2018, 19, 2094-2110.	4.2	350
27	Ex vivo and in vitro assessment of anti-inflammatory activity of seed Î²-conglutin proteins from Lupinus angustifolius. Journal of Functional Foods, 2018, 40, 510-519.	3.4	22
28	Characterization of narrow-leaf lupin (Lupinus angustifolius L.) recombinant major allergen IgE-binding proteins and the natural Î²-conglutin counterparts in sweet lupin seed species. Food Chemistry, 2018, 244, 60-70.	8.2	21
29	<scp>ApoplastP</scp>: prediction of effectors and plant proteins in the apoplast using machine learning. New Phytologist, 2018, 217, 1764-1778.	7.3	180
30	The Arabidopsis RNA Polymerase II Carboxyl Terminal Domain (CTD) Phosphatase-Like1 (CPL1) is a biotic stress susceptibility gene. Scientific Reports, 2018, 8, 13454.	3.3	18
31	Exploring the genetic and adaptive diversity of a pan-Mediterranean crop wild relative: narrow-leafed lupin. Theoretical and Applied Genetics, 2018, 131, 887-901.	3.6	50
32	Transcriptome analysis reveals class IX ethylene response factors show specific up-regulation in resistant but not susceptible Medicago truncatula lines following infection with Rhizoctonia solani. European Journal of Plant Pathology, 2018, 152, 549-554.	1.7	5
33	Salicylic Acid-Dependent Plant Stress Signaling via Mitochondrial Succinate Dehydrogenase. Plant Physiology, 2017, 173, 2029-2040.	4.8	84
34	Ethylene Signaling Is Important for Isoflavonoid-Mediated Resistance to <i>Rhizoctonia solani</i> in Roots of <i>Medicago truncatula</i>. Molecular Plant-Microbe Interactions, 2017, 30, 691-700.	2.6	40
35	LOCALIZER: subcellular localization prediction of both plant and effector proteins in the plant cell. Scientific Reports, 2017, 7, 44598.	3.3	340
36	Narrowâ€leafed lupin (<i>Lupinus angustifolius</i> L.) Î²â€conglutin proteins modulate the insulin signaling pathway as potential type 2 diabetes treatment and inflammatoryâ€related disease amelioration. Molecular Nutrition and Food Research, 2017, 61, 1600819.	3.3	34

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37	Comparative secretome analysis of Rhizoctonia solani isolates with different host ranges reveals unique secretomes and cell death inducing effectors. Scientific Reports, 2017, 7, 10410.	3.3	62
38	A comprehensive draft genome sequence for lupin (<i>Lupinus angustifolius</i>), an emerging health food: insights into plantâ€“microbe interactions and legume evolution. Plant Biotechnology Journal, 2017, 15, 318-330.	8.3	153
39	Quinolizidine Alkaloid Biosynthesis in Lupins and Prospects for Grain Quality Improvement. Frontiers in Plant Science, 2017, 8, 87.	3.6	89
40	Genetic Mapping of a Major Resistance Gene to Pea Aphid (Acyrthosipon pisum) in the Model Legume Medicago truncatula. International Journal of Molecular Sciences, 2016, 17, 1224.	4.1	11
41	Narrow-Leafed Lupin (Lupinus angustifolius) Î²1- and Î²6-Conglutin Proteins Exhibit Antifungal Activity, Protecting Plants against Necrotrophic Pathogen Induced Damage from Sclerotinia sclerotiorum and Phytophthora nicotianae. Frontiers in Plant Science, 2016, 7, 1856.	3.6	17
42	Jasmonate Signalling and Defence Responses in the Model Legume Medicago truncatulaâ€"A Focus on Responses to Fusarium Wilt Disease. Plants, 2016, 5, 11.	3.5	9
43	Transcriptome analysis of the fungal pathogen Fusarium oxysporum f. sp. medicaginis during colonisation of resistant and susceptible Medicago truncatula hosts identifies differential pathogenicity profiles and novel candidate effectors. BMC Genomics, 2016, 17, 860.	2.8	42
44	Belowground Defence Strategies Against Rhizoctonia. Signaling and Communication in Plants, 2016, , 99-117.	0.7	0
45	Mass-spectrometry data for Rhizoctonia solani proteins produced during infection of wheat and vegetative growth. Data in Brief, 2016, 8, 267-271.	1.0	5
46	Comparative genomics and prediction of conditionally dispensable sequences in legumeâ€“infecting Fusarium oxysporum formae speciales facilitates identification of candidate effectors. BMC Genomics, 2016, 17, 191.	2.8	109
47	E<scp>ffector</scp>P: predicting fungal effector proteins from secretomes using machine learning. New Phytologist, 2016, 210, 743-761.	7.3	438
48	Proteomic Analysis of Rhizoctonia solani Identifies Infection-specific, Redox Associated Proteins and Insight into Adaptation to Different Plant Hosts. Molecular and Cellular Proteomics, 2016, 15, 1188-1203.	3.8	37
49	Reactive Oxygen Species Play a Role in the Infection of the Necrotrophic Fungi, Rhizoctonia solani in Wheat. PLoS ONE, 2016, 11, e0152548.	2.5	77
50	A rapid method for profiling of volatile and semi-volatile phytohormones using methyl chloroformate derivatisation and GCâ€“MS. Metabolomics, 2015, 11, 1922-1933.	3.0	26
51	Evaluation of Secretion Prediction Highlights Differing Approaches Needed for Oomycete and Fungal Effectors. Frontiers in Plant Science, 2015, 6, 1168.	3.6	85
52	Genome-Wide Analysis in Three Fusarium Pathogens Identifies Rapidly Evolving Chromosomes and Genes Associated with Pathogenicity. Genome Biology and Evolution, 2015, 7, 1613-1627.	2.5	77
53	Analysis of conglutin seed storage proteins across lupin species using transcriptomic, protein and comparative genomic approaches. BMC Plant Biology, 2015, 15, 106.	3.6	49
54	Advances and Challenges in Computational Prediction of Effectors from Plant Pathogenic Fungi. PLoS Pathogens, 2015, 11, e1004806.	4.7	197

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55	Characterization and mapping of LanrBo: a locus conferring anthracnose resistance in narrow-leafed lupin (Lupinus angustifolius L.). Theoretical and Applied Genetics, 2015, 128, 2121-2130.	3.6	25
56	Transcriptome sequencing of different narrowâ€leafed lupin tissue types provides a comprehensive uniâ€gene assembly and extensive geneâ€based molecular markers. Plant Biotechnology Journal, 2015, 13, 14-25.	8.3	70
57	Breeding Annual Grain Legumes for Sustainable Agriculture: New Methods to Approach Complex Traits and Target New Cultivar Ideotypes. Critical Reviews in Plant Sciences, 2015, 34, 381-411.	5.7	140
58	Achievements and Challenges in Legume Breeding for Pest and Disease Resistance. Critical Reviews in Plant Sciences, 2015, 34, 195-236.	5.7	153
59	Lupin Allergy: Uncovering Structural Features and Epitopes of Î²-conglutin Proteins in Lupinus Angustifolius L. with a Focus on Cross-allergenic Reactivity to Peanut and Other Legumes. Lecture Notes in Computer Science, 2015, , 96-107.	1.3	9
60	The Arabidopsis KH-Domain RNA-Binding Protein ESR1 Functions in Components of Jasmonate Signalling, Unlinking Growth Restraint and Resistance to Stress. PLoS ONE, 2015, 10, e0126978.	2.5	45
61	Diversifying selection in the wheat stem rust fungus acts predominantly on pathogen-associated gene families and reveals candidate effectors. Frontiers in Plant Science, 2014, 5, 372.	3.6	45
62	Genome Sequencing and Comparative Genomics of the Broad Host-Range Pathogen Rhizoctonia solani AG8. PLoS Genetics, 2014, 10, e1004281.	3.5	145
63	The mitochondrial outer membrane <scp>AAA ATP</scp>ase At<scp>OM</scp>66 affects cell death and pathogen resistance in <i><scp>A</scp>rabidopsis thaliana</i>. Plant Journal, 2014, 80, 709-727.	5.7	80
64	A chromosomal genomics approach to assess and validate the <i>desi</i> and <i>kabuli</i> draft chickpea genome assemblies. Plant Biotechnology Journal, 2014, 12, 778-786.	8.3	54
65	Draft genome sequence of chickpea (Cicer arietinum) provides a resource for trait improvement. Nature Biotechnology, 2013, 31, 240-246.	17.5	1,049
66	The essential role of genetic resources in narrow-leafed lupin improvement. Crop and Pasture Science, 2013, 64, 361.	1.5	44
67	<i>Medicago truncatula</i> as a model host for studying legume infecting <i><scp>R</scp>hizoctonia solani</i> and identification of a locus affecting resistance to root canker. Plant Pathology, 2013, 62, 908-921.	2.4	22
68	Characterization and genetic dissection of resistance to spotted alfalfa aphid (Therioaphis trifolii) in Medicago truncatula. Journal of Experimental Botany, 2013, 64, 5157-5172.	4.8	33
69	A comparative hidden Markov model analysis pipeline identifies proteins characteristic of cereal-infecting fungi. BMC Genomics, 2013, 14, 807.	2.8	26
70	Plantâ€"aphid interactions with a focus on legumes. Functional Plant Biology, 2013, 40, 1271.	2.1	40
71	Genetic and Genomic Analysis of Rhizoctonia solani Interactions with Arabidopsis; Evidence of Resistance Mediated through NADPH Oxidases. PLoS ONE, 2013, 8, e56814.	2.5	56
72	Identification of distinct quantitative trait loci associated with defence against the closely related aphids Acyrthosiphon pisum and A. kondoi in Medicago truncatula. Journal of Experimental Botany, 2012, 63, 3913-3922.	4.8	36

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73	Identification and characterization of resistance to cowpea aphid (Aphis craccivora Koch) in Medicago truncatula. BMC Plant Biology, 2012, 12, 101.	3.6	50
74	<i>Phoma medicaginis</i> stimulates the induction of the octadecanoid and phenylpropanoid pathways in <i>Medicago truncatula</i>. Molecular Plant Pathology, 2012, 13, 593-603.	4.2	25
75	Mitochondrial complex II has a key role in mitochondrial-derived reactive oxygen species influence on plant stress gene regulation and defense. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10768-10773.	7.1	206
76	Mutant Analysis in Arabidopsis Provides Insight into the Molecular Mode of Action of the Auxinic Herbicide Dicamba. PLoS ONE, 2011, 6, e17245.	2.5	59
77	Identification and characterisation of seed storage protein transcripts from Lupinus angustifolius. BMC Plant Biology, 2011, 11, 59.	3.6	71
78	Development of genomic resources for the narrow-leafed lupin (Lupinus angustifolius): construction of a bacterial artificial chromosome (BAC) library and BAC-end sequencing. BMC Genomics, 2011, 12, 521.	2.8	53
79	Interactions of Arabidopsis andM. truncatulawith the same pathogens differ in dependence on ethylene and ethylene response factors. Plant Signaling and Behavior, 2011, 6, 551-552.	2.4	17
80	Identification of potential early regulators of aphid resistance in <i>Medicago truncatula</i> via transcription factor expression profiling. New Phytologist, 2010, 186, 980-994.	7.3	36
81	Genome Sequence of the Pea Aphid Acyrthosiphon pisum. PLoS Biology, 2010, 8, e1000313.	5.6	913
82	The B-3 Ethylene Response Factor MtERF1-1 Mediates Resistance to a Subset of Root Pathogens in<i>Medicago truncatula</i>without Adversely Affecting Symbiosis with Rhizobia Â Â. Plant Physiology, 2010, 154, 861-873.	4.8	72
83	Plants versus pathogens: an evolutionary arms race. Functional Plant Biology, 2010, 37, 499.	2.1	156
84	Two independent resistance genes in the<i>Medicago truncatula</i>cultivar Jester confer resistance to two different aphid species of the genus<i>Acyrthosiphon</i>. Plant Signaling and Behavior, 2009, 4, 328-331.	2.4	25
85	A single gene, AIN, in Medicago truncatula mediates a hypersensitive response to both bluegreen aphid and pea aphid, but confers resistance only to bluegreen aphid. Journal of Experimental Botany, 2009, 60, 4115-4127.	4.8	65
86	The Arabidopsis glutathione transferase gene family displays complex stress regulation and coâ€silencing multiple genes results in altered metabolic sensitivity to oxidative stress. Plant Journal, 2009, 58, 53-68.	5.7	237
87	The <i>Medicago truncatula</i> ortholog of Arabidopsis EIN2, <i>sickle</i>, is a negative regulator of symbiotic and pathogenic microbial associations. Plant Journal, 2008, 55, 580-595.	5.7	272
88	Characterization of Pea Aphid Resistance in <i>Medicago truncatula</i> Â Â Â. Plant Physiology, 2008, 146, 996-1009.	4.8	87
89	AtERF14, a Member of the ERF Family of Transcription Factors, Plays a Nonredundant Role in Plant Defense. Plant Physiology, 2007, 143, 400-409.	4.8	188
90	Differential Gene Expression and Subcellular Targeting of Arabidopsis Glutathione S-Transferase F8 Is Achieved through Alternative Transcription Start Sites. Journal of Biological Chemistry, 2007, 282, 28915-28928.	3.4	69

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91	Characterization of resistance to multiple aphid species (Hemiptera: Aphididae) inMedicago truncatula. Bulletin of Entomological Research, 2007, 97, 41-48.	1.0	32
92	Involvement of the Octadecanoid Pathway in Bluegreen Aphid Resistance in Medicago truncatula. Molecular Plant-Microbe Interactions, 2007, 20, 82-93.	2.6	141
93	Independent action and contrasting phenotypes of resistance genes against spotted alfalfa aphid and bluegreen aphid in Medicago truncatula. New Phytologist, 2007, 173, 630-640.	7.3	52
94	The Medicago truncatula reference accession A17 has an aberrant chromosomal configuration. New Phytologist, 2007, 174, 299-303.	7.3	42
95	Resistance to insect pests: What do legumes have to offer?. Euphytica, 2006, 147, 273-285.	1.2	86
96	Biotechnology approaches to overcome biotic and abiotic stress constraints in legumes. Euphytica, 2006, 147, 1-24.	1.2	214
97	Desensitization of GSTF8 Induction by a Prior Chemical Treatment Is Long Lasting and Operates in a Tissue-Dependent Manner. Plant Physiology, 2006, 142, 245-253.	4.8	16
98	Plant defence responses: what have we learnt from Arabidopsis?. Functional Plant Biology, 2005, 32, 1.	2.1	136
99	Plant defence responses: conservation between models and crops. Functional Plant Biology, 2005, 32, 21.	2.1	39
100	Aphid Resistance in Medicago truncatula Involves Antixenosis and Phloem-Specific, Inducible Antibiosis, and Maps to a Single Locus Flanked by NBS-LRR Resistance Gene Analogs. Plant Physiology, 2005, 137, 1445-1455.	4.8	205
101	Proteomic Analysis of Glutathione S-Transferases of Arabidopsis thaliana Reveals Differential Salicylic Acid-Induced Expression of the Plant-Specific Phi and Tau Classes. Plant Molecular Biology, 2004, 54, 205-219.	3.9	116
102	TGA5 acts as a positive and TGA4 acts as a negative regulator of ocs element activity in Arabidopsis roots in response to defence signals. FEBS Letters, 2004, 563, 141-145.	2.8	27
103	Early Induction of the Arabidopsis GSTF8 Promoter by Specific Strains of the Fungal Pathogen Rhizoctonia solani. Molecular Plant-Microbe Interactions, 2004, 17, 70-80.	2.6	45
104	Target genes for OBP3, a Dof transcription factor, include novel basic helix-loop-helix domain proteins inducible by salicylic acid. Plant Journal, 2003, 35, 362-372.	5.7	107
105	Identification of Arabidopsis Ethylene-Responsive Element Binding Factors with Distinct Induction Kinetics after Pathogen Infection. Plant Physiology, 2002, 128, 1313-1322.	4.8	206
106	Transcription factors in plant defense and stress responses. Current Opinion in Plant Biology, 2002, 5, 430-436.	7.1	1,172
107	Characterization of salicylic acid-responsive, Arabidopsis Dof domain proteins: overexpression of OBP3 leads to growth defects. Plant Journal, 2000, 21, 329-339.	5.7	151
108	The auxin, hydrogen peroxide and salicylic acid induced expression of the Arabidopsis GST6 promoter is mediated in part by an ocs element. Plant Journal, 1999, 19, 667-677.	5.7	184

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109	A glucocorticoid-inducible transcription system causes severe growth defects in Arabidopsis and induces defense-related genes. Plant Journal, 1999, 20, 127-133.	5.7	138
110	Transcriptional Regulation in Plants: The Importance of Combinatorial Control. Plant Physiology, 1998, 118, 1111-1120.	4.8	198
111	Arabidopsis thaliana ethylene-responsive element binding protein (AtEBP), an ethylene-inducible, GCC box DNA-binding protein interacts with an ocs element binding protein. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 5961-5966.	7.1	338
112	Analysis of type 1 metallothionein cDNAs in Vicia faba. Plant Molecular Biology, 1997, 33, 583-591.	3.9	64
113	The promoter of a H2O2-inducible, Arabidopsis glutathione S-transferase gene contains closely linked OBF- and OBP1-binding sites. Plant Journal, 1996, 10, 955-966.	5.7	244
114	A novel phloem-specific gene is expressed preferentially in aerial portions of Vicia faba. Plant Molecular Biology, 1996, 30, 687-695.	3.9	2
115	Interactions between Distinct Types of DNA Binding Proteins Enhance Binding to ocs Element Promoter Sequences. Plant Cell, 1995, 7, 2241.	6.6	29
116	Isolation of a Vicia faba metallothionein-like gene: expression in foliar trichomes. Plant Molecular Biology, 1994, 26, 435-444.	3.9	81
117	ocs element promoter sequences are activated by auxin and salicylic acid in Arabidopsis.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 2507-2511.	7.1	87
118	Analysis of Ocs-Element Enhancer Sequences and Their Binding Factors. Results and Problems in Cell Differentiation, 1994, 20, 197-207.	0.7	4
119	Does the ocs-element occur as a functional component of the promoters of plant genes?. Plant Journal, 1993, 4, 433-443.	5.7	72
120	Isolation and characterization of two related Arabidopsis ocs-element bZIP binding proteins. Plant Journal, 1993, 4, 711-716.	5.7	66
121	Isolation of a maize bZIP protein subfamily: candidates for the ocs-element transcription factor. Plant Journal, 1993, 3, 669-679.	5.7	42
122	A DNA-Binding Protein Factor Recognizes Two Binding Domains within the Octopine Synthase Enhancer Element. Plant Cell, 1990, 2, 215.	6.6	0
123	Functional properties of the anaerobic responsive element of the maize Adh1 gene. Plant Molecular Biology, 1990, 15, 593-604.	3.9	91
124	OCSBF-1, a Maize Ocs Enhancer Binding Factor: Isolation and Expression during Development. Plant Cell, 1990, 2, 891.	6.6	0
125	Saturation mutagenesis of the octopine synthase enhancer: correlation of mutant phenotypes with binding of a nuclear protein factor.. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 3733-3737.	7.1	66
126	Enhanced B2 transcription in simian virus 40-transformed cells is mediated through the formation of RNA polymerase III transcription complexes on previously inactive genes.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 7059-7063.	7.1	28

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127	Expression of enhanced levels of small RNA polymerase III transcripts encoded by the B2 repeats in simian virus 40-transformed mouse cells. Nature, 1985, 314, 553-556.	27.8	149
128	Ethylene response factors and their role in plant defence.. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources, 0, , 1-12.	1.0	3