

# Narayana M Upadhyaya

## List of Publications by Year in descending order

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71  
papers

3,858  
citations

117571

34  
h-index

133188

59  
g-index

76  
all docs

76  
docs citations

76  
times ranked

4185  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rice Mutant Resources for Gene Discovery. <i>Plant Molecular Biology</i> , 2004, 54, 325-334.	2.0	221
2	Over-expression of miR172 causes loss of spikelet determinacy and floral organ abnormalities in rice ( <i>Oryza sativa</i> ). <i>BMC Plant Biology</i> , 2009, 9, 149.	1.6	210
3	Loss of <i>AvrSr50</i> by somatic exchange in stem rust leads to virulence for <i>Sr50</i> resistance in wheat. <i>Science</i> , 2017, 358, 1607-1610.	6.0	206
4	Mutant Resources in Rice for Functional Genomics of the Grasses. <i>Plant Physiology</i> , 2009, 149, 165-170.	2.3	167
5	The ANTHR INDEHISCENCE1 Gene Encoding a Single MYB Domain Protein Is Involved in Anther Development in Rice. <i>Plant Physiology</i> , 2004, 135, 1514-1525.	2.3	152
6	Antisense suppression of the rice transporter gene, OsSUT1, leads to impaired grain filling and germination but does not affect photosynthesis. <i>Functional Plant Biology</i> , 2002, 29, 815.	1.1	143
7	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
8	Functional characterization of the rice kaurene synthase-like gene family. <i>Phytochemistry</i> , 2007, 68, 312-326.	1.4	124
9	Emergence of the Ug99 lineage of the wheat stem rust pathogen through somatic hybridisation. <i>Nature Communications</i> , 2019, 10, 5068.	5.8	121
10	The redistribution of protein sulfur in transgenic rice expressing a gene for a foreign, sulfur-rich protein. <i>Plant Journal</i> , 2003, 34, 1-11.	2.8	119
11	A Bacterial Type III Secretion Assay for Delivery of Fungal Effector Proteins into Wheat. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 255-264.	1.4	111
12	Strategies for Wheat Stripe Rust Pathogenicity Identified by Transcriptome Sequencing. <i>PLoS ONE</i> , 2013, 8, e67150.	1.1	110
13	Comparative genomics of Australian isolates of the wheat stem rust pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> reveals extensive polymorphism in candidate effector genes. <i>Frontiers in Plant Science</i> , 2014, 5, 759.	1.7	98
14	The wheat durable, multipathogen resistance gene <i>Lr34</i> confers partial blast resistance in rice. <i>Plant Biotechnology Journal</i> , 2016, 14, 1261-1268.	4.1	98
15	A five-transgene cassette confers broad-spectrum resistance to a fungal rust pathogen in wheat. <i>Nature Biotechnology</i> , 2021, 39, 561-566.	9.4	94
16	The Ins and Outs of Rust Haustoria. <i>PLoS Pathogens</i> , 2014, 10, e1004329.	2.1	90
17	Reciprocal control of flowering time by OsSOC1 in transgenic <i>Arabidopsis</i> and by FLC in transgenic rice. <i>Plant Biotechnology Journal</i> , 2003, 1, 361-369.	4.1	81
18	Over-expression of the rice OsAMT1-1 gene increases ammonium uptake and content, but impairs growth and development of plants under high ammonium nutrition. <i>Functional Plant Biology</i> , 2006, 33, 153.	1.1	77

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19	Ds tagging of BRANCHED FLORETLESS 1 (BFL1) that mediates the transition from spikelet to floret meristem in rice ( <i>Oryza sativa</i> L). <i>BMC Plant Biology</i> , 2003, 3, 6.	1.6	67
20	Genomics accelerated isolation of a new stem rust avirulence gene–wheat resistance gene pair. <i>Nature Plants</i> , 2021, 7, 1220-1228.	4.7	67
21	An iAc/Ds gene and enhancer trapping system for insertional mutagenesis in rice. <i>Functional Plant Biology</i> , 2002, 29, 547.	1.1	65
22	Isolation and characterization of a Ds-tagged rice ( <i>Oryza sativa</i> L.) GA-responsive dwarf mutant defective in an early step of the gibberellin biosynthesis pathway. <i>Plant Cell Reports</i> , 2005, 23, 819-833.	2.8	61
23	Genome analysis and avirulence gene cloning using a high-density RADseq linkage map of the flax rust fungus, <i>Melampsora lini</i> . <i>BMC Genomics</i> , 2016, 17, 667.	1.2	59
24	Comparison of promoters and selectable marker genes for use in Indica rice transformation. <i>Molecular Breeding</i> , 1997, 3, 1-14.	1.0	58
25	<i>De Novo</i> Assembly and Phasing of Dikaryotic Genomes from Two Isolates of <i>Puccinia coronata</i> f. sp. <i>avenae</i> , the Causal Agent of Oat Crown Rust. <i>MBio</i> , 2018, 9, .	1.8	57
26	Protein extraction from mature rice leaves for two-dimensional gel electrophoresis and its application in proteome analysis. <i>Proteomics</i> , 2004, 4, 1903-1908.	1.3	54
27	Stem rust resistance in wheat is suppressed by a subunit of the mediator complex. <i>Nature Communications</i> , 2020, 11, 1123.	5.8	52
28	Dissociation (Ds) constructs, mapped Ds launch pads and a transiently-expressed transposase system suitable for localized insertional mutagenesis in rice. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1326-1341.	1.8	51
29	SHOEBOX Modulates Root Meristem Size in Rice through Dose-Dependent Effects of Gibberellins on Cell Elongation and Proliferation. <i>PLoS Genetics</i> , 2015, 11, e1005464.	1.5	51
30	Diversifying selection in the wheat stem rust fungus acts predominantly on pathogen-associated gene families and reveals candidate effectors. <i>Frontiers in Plant Science</i> , 2014, 5, 372.	1.7	45
31	Changing the Game: Using Integrative Genomics to Probe Virulence Mechanisms of the Stem Rust Pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 205.	1.7	45
32	A bidirectional gene trap construct suitable for T-DNA and Ds-mediated insertional mutagenesis in rice ( <i>Oryza sativa</i> L.). <i>Plant Biotechnology Journal</i> , 2004, 2, 367-380.	4.1	40
33	Genomic Analysis of <i>Xanthomonas translucens</i> Pathogenic on Wheat and Barley Reveals Cross-Kingdom Gene Transfer Events and Diverse Protein Delivery Systems. <i>PLoS ONE</i> , 2014, 9, e84995.	1.1	39
34	The different effects of starch synthase IIa mutations or variation on endosperm amylose content of barley, wheat and rice are determined by the distribution of starch synthase I and starch branching enzyme IIb between the starch granule and amyloplast stroma. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1407-1419.	1.8	39
35	A recombined Sr26 and Sr61 disease resistance gene stack in wheat encodes unrelated NLR genes. <i>Nature Communications</i> , 2021, 12, 3378.	5.8	39
36	Agrobacterium-mediated transformation of Australian rice cultivars Jarrah and Amaro using modified promoters and selectable markers. <i>Functional Plant Biology</i> , 2000, 27, 201.	1.1	38

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37	Major haplotype divergence including multiple germin-like protein genes, at the wheat Sr2 adult plant stem rust resistance locus. <i>BMC Plant Biology</i> , 2014, 14, 379.	1.6	36
38	Transgene structures suggest that multiple mechanisms are involved in T-DNA integration in plants. <i>Plant Science</i> , 2006, 171, 308-322.	1.7	34
39	The stem rust effector protein AvrSr50 escapes Sr50 recognition by a substitution in a single surface-exposed residue. <i>New Phytologist</i> , 2022, 234, 592-606.	3.5	32
40	Physical separation of haplotypes in dikaryons allows benchmarking of phasing accuracy in Nanopore and HiFi assemblies with Hi-C data. <i>Genome Biology</i> , 2022, 23, 84.	3.8	31
41	Evidence for Cytokinin Involvement in Rhizobium (IC3342)-Induced Leaf Curl Syndrome of Pigeonpea ( <i>Cajanus cajan</i> Millsp.). <i>Plant Physiology</i> , 1991, 95, 1019-1025.	2.3	26
42	Title is missing!. <i>Molecular Breeding</i> , 2003, 11, 295-301.	1.0	26
43	<i>De Novo</i> Genome Assembly and Comparative Genomics of the Barley Leaf Rust Pathogen <i>Puccinia hordei</i> Identifies Candidates for Three Avirulence Genes. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3263-3271.	0.8	25
44	Rice ragged stunt oryzavirus genome segment S4 could encode an RNA dependent RNA polymerase and a second protein of unknown function. <i>Archives of Virology</i> , 1998, 143, 1815-1822.	0.9	23
45	Factors affecting nitrogenase activity ( $C_2H_4$ reduction) associated with sorghum and millet estimated using the soil core assay. <i>Canadian Journal of Microbiology</i> , 1983, 29, 1063-1069.	0.8	22
46	Molecular analysis of rice ragged stunt oryzavirus segment 9 and sequence conservation among isolates from Thailand and India. <i>Archives of Virology</i> , 1995, 140, 1945-1956.	0.9	22
47	The Mr 43K major capsid protein of rice ragged stunt oryzavirus is a post-translationally processed product of a Mr 67 348 polypeptide encoded by genome segment 8. <i>Archives of Virology</i> , 1996, 141, 1689-1701.	0.9	22
48	Rice ragged stunt oryzavirus genome segments S7 and S10 encode non-structural proteins of Mr 68 025 (Pns7) and Mr 32 364 (Pns10). <i>Archives of Virology</i> , 1997, 142, 1719-1726.	0.9	22
49	An intact plant assay for estimating nitrogenase activity ( $C_2H_2$ reduction) of sorghum and millet plants grown in pots. <i>Plant and Soil</i> , 1984, 82, 15-29.	1.8	21
50	Decreased accumulation of glutelin types in rice grains constitutively expressing a sunflower seed albumin gene. <i>Phytochemistry</i> , 2005, 66, 2534-2539.	1.4	21
51	Generation of selectable marker-free transgenic rice using double right-border (DRB) binary vectors. <i>Functional Plant Biology</i> , 2001, 28, 241.	1.1	19
52	<i>Agrobacterium tumefaciens</i> -mediated transformation of wheat using suspension cells as a model system and green fluorescent protein as a visual marker. <i>Functional Plant Biology</i> , 2001, 28, 807.	1.1	19
53	<i>Agrobacterium tumefaciens</i> -mediated transformation of an elite Australian barley cultivar with virus resistance and reporter genes. <i>Functional Plant Biology</i> , 2001, 28, 149.	1.1	18
54	A novel T-DNA vector design for selection of transgenic lines with simple transgene integration and stable transgene expression. <i>Functional Plant Biology</i> , 2005, 32, 671.	1.1	18

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55	Genome segment 5 of rice ragged stunt virus encodes avirion protein. <i>Journal of General Virology</i> , 1996, 77, 3155-3160.	1.3	17
56	A Bacterial Type III Secretion-Based Delivery System for Functional Assays of Fungal Effectors in Cereals. <i>Methods in Molecular Biology</i> , 2014, 1127, 277-290.	0.4	15
57	The stem rust fungus <i>Puccinia graminis</i> f. sp. <i>tritici</i> induces centromeric small RNAs during late infection that are associated with genome-wide DNA methylation. <i>BMC Biology</i> , 2021, 19, 203.	1.7	15
58	Thetms2 gene as a negative selection marker in rice. <i>Plant Molecular Biology Reporter</i> , 2000, 18, 227-233.	1.0	12
59	Transposon Insertional Mutants: A Resource for Rice Functional Genomics. , 2007, , 223-271.		12
60	compact shoot and leafy head 1, a mutation affects leaf initiation and developmental transition in rice ( <i>Oryza sativa</i> L.). <i>Plant Cell Reports</i> , 2007, 26, 421-427.	2.8	12
61	Identification of a <i>Serratia entomophila</i> genetic locus encoding amber disease in New Zealand grass grub ( <i>Costelytra zealandica</i> ). <i>Journal of Bacteriology</i> , 1992, 174, 1020-1028.	1.0	8
62	Transposon Insertional Mutagenesis in Rice. <i>Methods in Molecular Biology</i> , 2011, 678, 147-177.	0.4	8
63	Isolation and Characterization of <i>Rhizobium</i> (IC3342) Genes that Determine Leaf Curl Induction in Pigeon Pea. <i>Molecular Plant-Microbe Interactions</i> , 1992, 5, 129.	1.4	7
64	Mutant Resources for Functional Analysis of the Rice Genome. , 2013, , 81-115.		6
65	Leaf curl syndrome of pigeonpea ( <i>Cajanus cajan</i> (L.) Millsp.) is a systemic response to effective nodulation by the <i>Rhizobium</i> strain IC3342. <i>Physiological and Molecular Plant Pathology</i> , 1991, 38, 357-373.	1.3	4
66	Rice Gene Machine: A Vehicle for Finding Functions of Cereal Genes. <i>Asia Pacific Biotech News</i> , 2002, 06, 936-942.	0.5	4
67	RGMIMS: a web-based Laboratory Information Management System for plant functional genomics research. <i>Molecular Breeding</i> , 2008, 22, 151-157.	1.0	4
68	Rice Gene Machine: A Vehicle for Finding Functions of Cereal Genes. , 2003, , 79-92.		1
69	A gene machine for rice. , 2008, , 352-355.		1
70	Biotech Crops and Functional Genomics. , 2010, , 359-390.		0
71	Rice Genomics. , 2010, , 257-279.		0