

# Shuhe Nasuda

## List of Publications by Year in descending order

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83  
papers

6,416  
citations

117625

34  
h-index

71685

76  
g-index

83  
all docs

83  
docs citations

83  
times ranked

5593  
citing authors

#	ARTICLE	IF	CITATIONS
1	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
2	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	27.8	513
3	Loss of centromeric histone H3 (CENH3) from centromeres precedes uniparental chromosome elimination in interspecific barley hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E498-505.	7.1	260
4	Structural dynamics of cereal mitochondrial genomes as revealed by complete nucleotide sequencing of the wheat mitochondrial genome. <i>Nucleic Acids Research</i> , 2005, 33, 6235-6250.	14.5	215
5	Stable barley chromosomes without centromeric repeats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 9842-9847.	7.1	199
6	A conserved repetitive DNA element located in the centromeres of cereal chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 14210-14213.	7.1	195
7	Durum wheat as a candidate for the unknown female progenitor of bread wheat: an empirical study with a highly fertile F1 hybrid with <i>Aegilops tauschii</i> Coss.. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1710-1717.	3.6	137
8	Localization of anchor loci representing five hundred annotated rice genes to wheat chromosomes using PLUG markers. <i>Theoretical and Applied Genetics</i> , 2009, 118, 499-514.	3.6	116
9	Transfer of rye chromosome segments to wheat by a gametocidal system. <i>Chromosome Research</i> , 2002, 10, 349-357.	2.2	109
10	The einkorn wheat ( <i>Triticum monococcum</i> ) mutant, maintained vegetative phase, is caused by a deletion in the VRN1 gene. <i>Genes and Genetic Systems</i> , 2007, 82, 167-170.	0.7	109
11	CENH3 interacts with the centromeric retrotransposon cereba and GC-rich satellites and locates to centromeric substructures in barley. <i>Chromosoma</i> , 2007, 116, 275-283.	2.2	107
12	Cytologically based physical maps of the group-2 chromosomes of wheat. <i>Theoretical and Applied Genetics</i> , 1995, 91, 568-573.	3.6	105
13	DArTseq-based analysis of genomic relationships among species of tribe Triticeae. <i>Scientific Reports</i> , 2018, 8, 16397.	3.3	101
14	Development of a complete set of <i>Triticum aestivum</i> - <i>Aegilops speltoides</i> chromosome addition lines. <i>Theoretical and Applied Genetics</i> , 2000, 101, 51-58.	3.6	91
15	A high-density genetic linkage map of <i>Aegilops tauschii</i> , the D-genome progenitor of bread wheat. <i>Theoretical and Applied Genetics</i> , 1999, 99, 16-26.	3.6	78
16	Novel QTLs for growth angle of seminal roots in wheat ( <i>Triticum aestivum</i> L.). <i>Plant and Soil</i> , 2012, 354, 395-405.	3.7	78
17	Three dominant awnless genes in common wheat: Fine mapping, interaction and contribution to diversity in awn shape and length. <i>PLoS ONE</i> , 2017, 12, e0176148.	2.5	78
18	Chromosomal assignment and deletion mapping of barley EST markers. <i>Genes and Genetic Systems</i> , 2005, 80, 357-366.	0.7	64

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19	Gametocidal Genes Induce Chromosome Breakage in the Interphase Prior to the First Mitotic Cell Division of the Male Gametophyte in Wheat. <i>Genetics</i> , 1998, 149, 1115-1124.	2.9	62
20	Global Wheat Head Detection 2021: An Improved Dataset for Benchmarking Wheat Head Detection Methods. <i>Plant Phenomics</i> , 2021, 2021, 9846158.	5.9	60
21	Cloning and characterization of a centromere-specific repetitive DNA element from Sorghum bicolor. <i>Theoretical and Applied Genetics</i> , 1998, 96, 832-839.	3.6	59
22	Origin of wheat B-genome chromosomes inferred from RNA sequencing analysis of leaf transcripts from section Sitopsis species of Aegilops. <i>DNA Research</i> , 2019, 26, 171-182.	3.4	58
23	Dissection of rye B chromosomes, and nondisjunction properties of the dissected segments in a common wheat background. <i>Genes and Genetic Systems</i> , 2008, 83, 23-30.	0.7	55
24	A wheat homologue of <i>PHYTOCLOCK 1</i> is a candidate gene conferring the early heading phenotype to einkorn wheat. <i>Genes and Genetic Systems</i> , 2012, 87, 357-367.	0.7	55
25	Genetic Basis for Spontaneous Hybrid Genome Doubling during Allopolyploid Speciation of Common Wheat Shown by Natural Variation Analyses of the Paternal Species. <i>PLoS ONE</i> , 2013, 8, e68310.	2.5	51
26	Detection of the Sec-1 locus of rye by a PCR-based method.. <i>Genes and Genetic Systems</i> , 1997, 72, 197-203.	0.7	47
27	Dissection of barley chromosome 3H in common wheat and a comparison of 3H physical and genetic maps. <i>Genes and Genetic Systems</i> , 2009, 84, 25-34.	0.7	45
28	Next-Generation Survey Sequencing and the Molecular Organization of Wheat Chromosome 6B. <i>DNA Research</i> , 2014, 21, 103-114.	3.4	45
29	Characterization of a knock-out mutation at the Gc2 locus in wheat. <i>Chromosoma</i> , 2003, 111, 509-517.	2.2	44
30	Dissection of barley chromosome 5H in common wheat. <i>Genes and Genetic Systems</i> , 2007, 82, 123-133.	0.7	43
31	Genome-wide marker development for the wheat D genome based on single nucleotide polymorphisms identified from transcripts in the wild wheat progenitor Aegilops tauschii. <i>Theoretical and Applied Genetics</i> , 2014, 127, 261-271.	3.6	43
32	The evolution of the hexaploid grass <i>Zingeria kochii</i> (Mez) Tzvel. (2n=12) was accompanied by complex hybridization and uniparental loss of ribosomal DNA. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 146-155.	2.7	41
33	A PCR-based marker for targeting small rye segments in wheat background. <i>Genes and Genetic Systems</i> , 2004, 79, 245-250.	0.7	36
34	Duplication of Centromeric Histone H3 (HTR12) Gene in Arabidopsis halleri and A. lyrata, Plant Species With Multiple Centromeric Satellite Sequences. <i>Genetics</i> , 2006, 174, 2021-2032.	2.9	36
35	Dissection of rye chromosome 1R in common wheat. <i>Genes and Genetic Systems</i> , 2008, 83, 43-53.	0.7	36
36	Homoeologous relationship of rye chromosome arms as detected with wheat PLUG markers. <i>Chromosoma</i> , 2013, 122, 555-564.	2.2	34

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37	Loss-of-Function Mutations in Three Homoeologous PHYTOCLOCK 1 Genes in Common Wheat Are Associated with the Extra-Early Flowering Phenotype. <i>PLoS ONE</i> , 2016, 11, e0165618.	2.5	34
38	A High-Density Genetic Map with Array-Based Markers Facilitates Structural and Quantitative Trait Locus Analyses of the Common Wheat Genome. <i>DNA Research</i> , 2014, 21, 555-567.	3.4	30
39	An alternative to radiation hybrid mapping for large-scale genome analysis in barley. <i>Molecular Genetics and Genomics</i> , 2005, 274, 589-594.	2.1	29
40	Discovery of High-Confidence Single Nucleotide Polymorphisms from Large-Scale De Novo Analysis of Leaf Transcripts of <i>Aegilops tauschii</i> , A Wild Wheat Progenitor. <i>DNA Research</i> , 2012, 19, 487-497.	3.4	29
41	Dissection of barley chromosome 4H in common wheat by the gametocidal system and cytological mapping of chromosome 4H with EST markers. <i>Genes and Genetic Systems</i> , 2010, 85, 19-29.	0.7	25
42	Resistance to wheat yellow mosaic virus in Madsen wheat is controlled by two major complementary QTLs. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1569-1578.	3.6	25
43	A direct repeat sequence associated with the centromeric retrotransposons in wheat. <i>Genome</i> , 2004, 47, 747-756.	2.0	24
44	Characterization of the genes encoding for MAD2 homologues in wheat. <i>Chromosome Research</i> , 2004, 12, 703-714.	2.2	23
45	Molecular cloning, sequencing, and chromosome mapping of a 1A-encoded P-type prolamin sequence from wheat. <i>Genome</i> , 2002, 45, 661-669.	2.0	22
46	Dissection and cytological mapping of barley chromosome 2H in the genetic background of common wheat. <i>Genes and Genetic Systems</i> , 2011, 86, 231-248.	0.7	20
47	Direct interaction between VRN1 protein and the promoter region of the wheat <i>FT</i> gene. <i>Genes and Genetic Systems</i> , 2018, 93, 25-29.	0.7	20
48	Structures of the three homoeologous loci of wheat benzoxazinone biosynthetic genes TaBx3 and TaBx4 and characterization of their promoter sequences. <i>Theoretical and Applied Genetics</i> , 2008, 116, 373-381.	3.6	19
49	Molecular Genetic Analysis of Domestication Traits in Emmer Wheat. I: Map Construction and QTL Analysis using an F <sub>2</sub> Population. <i>Biotechnology and Biotechnological Equipment</i> , 2013, 27, 3627-3637.	1.3	19
50	A high-resolution physical map integrating an anchored chromosome with the BAC physical maps of wheat chromosome 6B. <i>BMC Genomics</i> , 2015, 16, 595.	2.8	18
51	Dissection of barley chromosomes 1H and 6H by the gametocidal system. <i>Genes and Genetic Systems</i> , 2014, 89, 203-214.	0.7	17
52	Structural features of two major nucleolar organizer regions (NORs), <i>Nor1</i> and <i>Nor2</i> , and chromosome-specific rRNA gene expression in wheat. <i>Plant Journal</i> , 2018, 96, 1148-1159.	5.7	17
53	Identification of AFLP markers on the satellite region of chromosome 1BS in wheat. <i>Genome</i> , 2000, 43, 729-735.	2.0	16
54	De Novo Genome Assembly of the Japanese Wheat Cultivar Norin 61 Highlights Functional Variation in Flowering Time and Fusarium-Resistant Genes in East Asian Genotypes. <i>Plant and Cell Physiology</i> , 2021, 62, 8-27.	3.1	16

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55	Cytological dissection and molecular characterization of chromosome 1R derived from 'Burgas 2' common wheat. <i>Genes and Genetic Systems</i> , 2009, 84, 407-416.	0.7	15
56	Polymorphic Chromosomal Specificity of Centromere Satellite Families in <i>Arabidopsis halleri</i> ssp. <i>gemmaifera</i> . <i>Genetica</i> , 2006, 126, 335-342.	1.1	14
57	Dissection of rye chromosomes by the gametocidal system. <i>Genes and Genetic Systems</i> , 2013, 88, 321-327.	0.7	14
58	PCR and sequence analysis of barley chromosome 2H subjected to the gametocidal action of chromosome 2C. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2381-2390.	3.6	13
59	Genetic Mechanisms of Allopolyploid Speciation Through Hybrid Genome Doubling. <i>International Review of Cell and Molecular Biology</i> , 2014, 309, 199-258.	3.2	13
60	Population structure and association analyses of the core collection of hexaploid accessions conserved <i>ex situ</i> in the Japanese gene bank NBRP-Wheat. <i>Genes and Genetic Systems</i> , 2018, 93, 237-254.	0.7	13
61	QTL analysis of genetic loci affecting domestication-related spike characters in common wheat. <i>Genes and Genetic Systems</i> , 2014, 89, 121-131.	0.7	12
62	Level of <i>VERNALIZATION 1</i> expression is correlated with earliness in <i>extra early-flowering</i> mutant wheat lines. <i>Breeding Science</i> , 2014, 64, 213-221.	1.9	11
63	Variations in radioactive cesium accumulation in wheat germplasm from fields affected by the 2011 Fukushima nuclear power plant accident. <i>Scientific Reports</i> , 2020, 10, 3744.	3.3	11
64	Chromosomal locations of the genes for histones and a histone gene-binding protein family HBP-1 in common wheat. <i>Plant Molecular Biology</i> , 1993, 22, 603-614.	3.9	10
65	An early-flowering einkorn wheat mutant with deletions of <i>PHYTOCLOCK 1/LUX ARRHYTHMO</i> and <i>VERNALIZATION 2</i> exhibits a high level of <i>VERNALIZATION 1</i> expression induced by vernalization. <i>Journal of Plant Physiology</i> , 2018, 222, 28-38.	3.5	10
66	Genetic dissection of grain morphology in hexaploid wheat by analysis of the NBRP-Wheat core collection. <i>Genes and Genetic Systems</i> , 2019, 94, 35-49.	0.7	8
67	Differential contribution of two <i>Ppd-1</i> homoeoalleles to early-flowering phenotype in Nepalese and Japanese varieties of common wheat. <i>Breeding Science</i> , 2013, 63, 374-383.	1.9	7
68	Barley chromosome addition lines of wheat for screening of AFLP markers on barley chromosomes.. <i>Genes and Genetic Systems</i> , 2001, 76, 107-110.	0.7	5
69	Plant B Chromosomes. <i>Methods in Molecular Biology</i> , 2011, 701, 97-111.	0.9	5
70	Detection of terminal deletions in barley chromosomes by the PCR based method.. <i>Genes and Genetic Systems</i> , 1998, 73, 163-166.	0.7	4
71	Molecular mapping of the suppressor gene <i>lgc1</i> to the gametocidal gene <i>Gc3-C1</i> in common wheat. <i>Genes and Genetic Systems</i> , 2010, 85, 43-53.	0.7	4
72	Development of a self-fertile ditelosomic line for the long arm of chromosome 4B and its characterization using SSR markers. <i>Genes and Genetic Systems</i> , 2013, 88, 311-314.	0.7	4

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73	Comparative study of the structure of chromosome 1 <sup>R</sup> derived from <i>Scalecte montanum</i> and <i>Scalecte cereale</i> . <i>Plant Breeding</i> , 2015, 134, 675-683.	1.9	3
74	Variation in abscisic acid responsiveness at the early seedling stage is related to line differences in seed dormancy and in expression of genes involved in abscisic acid responses in common wheat. <i>Journal of Cereal Science</i> , 2016, 71, 167-176.	3.7	3
75	Chromosome-specific satellite sequences in <i>Turritis glabra</i> . <i>Genes and Genetic Systems</i> , 2006, 81, 287-290.	0.7	2
76	Cytological observation of chromosome breakage in wheat male gametophytes caused by gametocidal action of <i>Aegilops triuncialis</i> -derived chromosome 3C <sup>t</sup> . <i>Genes and Genetic Systems</i> , 2018, 93, 111-118.	0.7	2
77	A Review of Wheat Genome Sequencing and Perspectives for Breeding in Post-genome Era. <i>Journal of the Japanese Society for Food Science and Technology</i> , 2016, 63, 480-483.	0.1	1
78	Perspectives on the use of bioresources in breeding sciences: Lessons from successful studies. <i>Ikushugaku Kenkyu</i> , 2019, 21, 81-85.	0.3	0
79	Development of the BAC Physical Maps of Wheat Chromosome 6B for Its Genomic Sequencing. , 2015, , 101-107.		0
80	Sequencing of Wheat Chromosome 6B: Toward Functional Genomics. , 2015, , 111-116.		0
81	How to discover new genes in NGS era. <i>Ikushugaku Kenkyu</i> , 2016, 18, 62-66.	0.3	0
82	Toward a breakthrough in Triticeae breeding: searching for ways to connect genotype and phenotype. <i>Ikushugaku Kenkyu</i> , 2020, 22, 95-100.	0.3	0
83	Development of a high-throughput field phenotyping rover optimized for size-limited breeding fields as open-source hardware. <i>Breeding Science</i> , 2022, 72, .	1.9	0