Shigeo Takumi

List of Publications by Citations

153 papers	4,221 citations	37 h-index	57 g-index
155 ext. papers	4,834 ext. citations	3.6 avg, IF	5.35 L-index

#	Paper	IF	Citations
153	Differential regulation of transcript accumulation and alternative splicing of a DREB2 homolog under abiotic stress conditions in common wheat. *Genes and Genetic Systems*, **2006**, 81, 77-91	1.4	195
152	Structural dynamics of cereal mitochondrial genomes as revealed by complete nucleotide sequencing of the wheat mitochondrial genome. *Nucleic Acids Research*, **2005**, 33, 6235-50	20.1	176
151	WAP1, a wheat APETALA1 homolog, plays a central role in the phase transition from vegetative to reproductive growth. *Plant and Cell Physiology*, **2003**, 44, 1255-65	4.9	166
150	Superoxide and Singlet Oxygen Produced within the Thylakoid Membranes Both Cause Photosystem I Photoinhibition. *Plant Physiology*, **2016**, 171, 1626-34	6.6	154
149	Pistillody, homeotic transformation of stamens into pistil-like structures, caused by nuclear-cytoplasm interaction in wheat. *Plant Journal*, **2002**, 29, 169-81	6.9	121
148	Genetic and epigenetic alteration among three homoeologous genes of a class E MADS box gene in hexaploid wheat. *Plant Cell*, **2007**, 19, 1723-37	11.6	119
147	The einkorn wheat (Triticum monococcum) mutant, maintained vegetative phase, is caused by a deletion in the VRN1 gene. *Genes and Genetic Systems*, **2007**, 82, 167-70	1.4	98
146	Development of abiotic stress tolerance via bZIP-type transcription factor LIP19 in common wheat. *Journal of Experimental Botany*, **2008**, 59, 891-905	7	93
145	Population structure of wild wheat D-genome progenitor Aegilops tauschii Coss.: implications for intraspecific lineage diversification and evolution of common wheat. *Molecular Ecology*, **2010**, 19, 999-1013	5.7	88
144	Pistillody is caused by alterations to the class-B MADS-box gene expression pattern in alloplasmic wheats. *Planta*, **2004**, 218, 712-20	4.7	88
143	Positive role of a wheat HvABI5 ortholog in abiotic stress response of seedlings. *Physiologia Plantarum*, **2008**, 134, 74-86	4.6	82
142	Differential and coordinated expression of Cbf and Cor/Lea genes during long-term cold acclimation in two wheat cultivars showing distinct levels of freezing tolerance. *Genes and Genetic Systems*, **2005**, 80, 185-97	1.4	79
141	Regulation by Vrn-1/Fr-1 chromosomal intervals of CBF-mediated Cor/Lea gene expression and freezing tolerance in common wheat. *Journal of Experimental Botany*, **2005**, 56, 887-95	7	78
140	Comparative study of the expression profiles of the Cor/Lea gene family in two wheat cultivars with contrasting levels of freezing tolerance. *Physiologia Plantarum*, **2004**, 120, 585-594	4.6	73
139	Overexpression of wheat alternative oxidase gene Waox1a alters respiration capacity and response to reactive oxygen species under low temperature in transgenic Arabidopsis. *Genes and Genetic Systems*, **2006**, 81, 349-54	1.4	64
138	Hypersensitive response-like reaction is associated with hybrid necrosis in interspecific crosses between tetraploid wheat and Aegilops tauschii coss. *PLoS ONE*, **2010**, 5, e11326	3.7	62
137	Transcriptional activation of Cor/Lea genes and increase in abiotic stress tolerance through expression of a wheat DREB2 homolog in transgenic tobacco. *Transgenic Research*, **2008**, 17, 755-67	3.3	62

136	Natural variation for fertile triploid F1 hybrid formation in allohexaploid wheat speciation. *Theoretical and Applied Genetics*, **2007**, 115, 509-18	6	61
135	New members of a cold-responsive group-3 Lea/Rab-related Cor gene family from common wheat (Triticum aestivum L.). *Genes and Genetic Systems*, **2000**, 75, 179-88	1.4	58
134	Flowering time diversification and dispersal in central Eurasian wild wheat Aegilops tauschii Coss.: genealogical and ecological framework. *PLoS ONE*, **2008**, 3, e3138	3.7	57
133	Kinetics of transcript and protein accumulation of a low-molecular-weight wheat LEA D-11 dehydrin in response to low temperature. *Journal of Plant Physiology*, **2003**, 160, 193-200	3.6	57
132	Rmg8, a New Gene for Resistance to Triticum Isolates of Pyricularia oryzae in Hexaploid Wheat. *Phytopathology*, **2015**, 105, 1568-72	3.8	50
131	Identification of quantitative trait loci controlling grain size and shape in the D genome of synthetic hexaploid wheat lines. *Breeding Science*, **2013**, 63, 423-9	2	49
130	Chinese spring wheat (Triticum aestivum L.) chloroplast genome: Complete sequence and contig clones. *Plant Molecular Biology Reporter*, **2000**, 18, 243-253	1.7	49
129	WAG, a wheat AGAMOUS homolog, is associated with development of pistil-like stamens in alloplasmic wheats. *Sexual Plant Reproduction*, **2003**, 15, 221-230		44
128	RFLP mapping of a brown planthopper (Nilaparvata lugens Stal) resistance gene bph2 of indica rice introgressed into a japonica breeding line ‘Norin-PL4’. *Genes and Genetic Systems*, **1998**, 73, 359-364	1.4	42
127	A cold-responsive wheat (Triticum aestivum L.) gene wcor14 identified in a winter-hardy cultivar ‘Mironovska 808’. *Genes and Genetic Systems*, **2000**, 75, 49-57	1.4	42
126	Genealogical analysis of subspecies divergence and spikelet-shape diversification in central Eurasian wild wheat Aegilops tauschii Coss.. *Plant Systematics and Evolution*, **2009**, 279, 233-244	1.3	41
125	Distinct genetic regulation of flowering time and grain-filling period based on empirical study of D-genome diversity in synthetic hexaploid wheat lines. *Breeding Science*, **2011**, 61, 130-141	2	41
124	Mitochondrial alternative pathway is associated with development of freezing tolerance in common wheat. *Journal of Plant Physiology*, **2008**, 165, 462-7	3.6	41
123	Improvement of freezing tolerance in tobacco plants expressing a cold-responsive and chloroplast-targeting protein WCOR15 of wheat. *Journal of Plant Physiology*, **2006**, 163, 213-9	3.6	41
122	Class D and B(sister) MADS-box genes are associated with ectopic ovule formation in the pistil-like stamens of alloplasmic wheat (Triticum aestivum L.). *Plant Molecular Biology*, **2009**, 71, 1-14	4.6	40
121	WFL, a wheat FLORICAULA/LEAFY ortholog, is associated with spikelet formation as lateral branch of the inflorescence meristem. *Genes and Genetic Systems*, **2006**, 81, 13-20	1.4	40
120	Genetic basis for spontaneous hybrid genome doubling during allopolyploid speciation of common wheat shown by natural variation analyses of the paternal species. *PLoS ONE*, **2013**, 8, e68310	3.7	39
119	Characterization of two non-homoeologous nuclear genes encoding mitochondrial alternative oxidase in common wheat. *Genes and Genetic Systems*, **2002**, 77, 81-8	1.4	38

118	Production of transgenic wheat through particle bombardment of scutellar tissues: Frequency is influenced by culture duration. *Journal of Plant Physiology*, **1996**, 149, 418-423	3.6	38
117	Autoimmune response and repression of mitotic cell division occur in inter-specific crosses between tetraploid wheat and Aegilops tauschii Coss. that show low temperature-induced hybrid necrosis. *Plant Journal*, **2011**, 68, 114-28	6.9	37
116	Isolation, identification and characterization of disomic and translocated barley chromosome addition lines of common wheat. *Euphytica*, **1997**, 96, 289-296	2.1	37
115	Effect of six promoter-intron combinations on transient reporter gene expression in einkorn, emmer and common wheat cells by particle bombardment. *Plant Science*, **1994**, 103, 161-166	5.3	37
114	Genome-wide marker development for the wheat D genome based on single nucleotide polymorphisms identified from transcripts in the wild wheat progenitor Aegilops tauschii. *Theoretical and Applied Genetics*, **2014**, 127, 261-71	6	36
113	Heterochronic development of the floret meristem determines grain number per spikelet in diploid, tetraploid and hexaploid wheats. *Annals of Botany*, **2009**, 104, 243-51	4.1	36
112	Identification of quantitative trait loci for ABA responsiveness at the seedling stage associated with ABA-regulated gene expression in common wheat. *Theoretical and Applied Genetics*, **2010**, 121, 629-41	6	35
111	Mitochondrial DNA heteroplasmy in wheat, Aegilops and their nucleus-cytoplasm hybrids. *Genetics*, **2002**, 160, 1619-30	4	35
110	Natural variation of morphological traits in wild wheat progenitor Aegilops tauschii Coss.. *Breeding Science*, **2009**, 59, 579-588	2	33
109	Variation in dehydration tolerance, ABA sensitivity and related gene expression patterns in D-genome progenitor and synthetic hexaploid wheat lines. *International Journal of Molecular Sciences*, **2009**, 10, 2733-51	6.3	32
108	Increased freezing tolerance in an ABA-hypersensitive mutant of common wheat. *Journal of Plant Physiology*, **2008**, 165, 224-32	3.6	32
107	Wheat SOC1 functions independently of WAP1/VRN1, an integrator of vernalization and photoperiod flowering promotion pathways. *Physiologia Plantarum*, **2007**, 130, 627-636	4.6	32
106	Increased freezing tolerance through up-regulation of downstream genes via the wheat CBF gene in transgenic tobacco. *Plant Physiology and Biochemistry*, **2008**, 46, 205-11	5.4	31
105	Expression patterns of low temperature responsive genes in a dominant ABA-less-sensitive mutant line of common wheat. *Physiologia Plantarum*, **2006**, 127, 612-623	4.6	31
104	Mapping of a brown planthopper (Nilaparvata lugens Stl) resistance gene Bph9 on the long arm of rice chromosome 12. *Cereal Research Communications*, **2001**, 29, 245-250	1.1	31
103	Evidence from principal component analysis for improvement of grain shape- and spikelet morphology-related traits after hexaploid wheat speciation. *Genes and Genetic Systems*, **2012**, 87, 299-310	1.4	29
102	Discovery of high-confidence single nucleotide polymorphisms from large-scale de novo analysis of leaf transcripts of Aegilops tauschii, a wild wheat progenitor. *DNA Research*, **2012**, 19, 487-97	4.5	29
101	A high-density genetic map with array-based markers facilitates structural and quantitative trait locus analyses of the common wheat genome. *DNA Research*, **2014**, 21, 555-67	4.5	28

100	Variation in transformation frequencies among six common wheat cultivars through particle bombardment of scutellar tissues. *Genes and Genetic Systems*, **1997**, 72, 63-9	1.4	28
99	Allopolyploidization reduces alternative splicing efficiency for transcripts of the wheat DREB2 homolog, WDREB2. *Genome*, **2009**, 52, 100-5	2.4	27
98	Three dominant awnless genes in common wheat: Fine mapping, interaction and contribution to diversity in awn shape and length. *PLoS ONE*, **2017**, 12, e0176148	3.7	27
97	Intraspecific lineage divergence and its association with reproductive trait change during species range expansion in central Eurasian wild wheat Aegilops tauschii Coss. (Poaceae). *BMC Evolutionary Biology*, **2015**, 15, 213	3	26
96	Intragenic diversity and functional conservation of the three homoeologous loci of the KN1-type homeobox gene Wknox1 in common wheat. *Plant Molecular Biology*, **2005**, 57, 907-24	4.6	26
95	orf260cra, a novel mitochondrial gene, is associated with the homeotic transformation of stamens into pistil-like structures (pistillody) in alloplasmic wheat. *Plant and Cell Physiology*, **2008**, 49, 1723-33	4.9	25
94	Origin of wheat B-genome chromosomes inferred from RNA sequencing analysis of leaf transcripts from section Sitopsis species of Aegilops. *DNA Research*, **2019**, 26, 171-182	4.5	24
93	Identification of quantitative trait locus for abscisic acid responsiveness on chromosome 5A and association with dehydration tolerance in common wheat seedlings. *Journal of Plant Physiology*, **2014**, 171, 25-34	3.6	23
92	Semi-real time imaging of the expression of a maize polyubiquitin promoter-GFP gene in transgenic rice. *Plant Science*, **1997**, 124, 49-56	5.3	23
91	Alteration of respiration capacity and transcript accumulation level of alternative oxidase genes in necrosis lines of common wheat. *Genes and Genetic Systems*, **2007**, 82, 231-9	1.4	23
90	A major quantitative trait locus for cold-responsive gene expression is linked to frost-resistance gene Fr-A2 in common wheat. *Breeding Science*, **2013**, 63, 58-67	2	22
89	Chloroplast and nuclear DNA variation in common wheat: insight into the origin and evolution of common wheat. *Genes and Genetic Systems*, **2004**, 79, 271-82	1.4	22
88	Molecular cloning of three homoeologous cDNAs encoding orthologs of the maize KNOTTED1 homeobox protein from young spikes of hexaploid wheat. *Gene*, **2000**, 249, 171-81	3.8	22
87	Altered expression of wheat AINTEGUMENTA homolog, WANT-1, in pistil and pistil-like transformed stamen of an alloplasmic line with Aegilops crassa cytoplasm. *Development Genes and Evolution*, **2009**, 219, 175-87	1.8	21
86	Nuclear and chloroplast genome genetic diversity in the wild einkorn wheat, Triticum urartu, revealed by AFLP and SSLP analyses. *Hereditas*, **2002**, 137, 208-214	2.4	21
85	Utility of leaf senescence-associated gene homologs as developmental markers in common wheat. *Plant Physiology and Biochemistry*, **2010**, 48, 851-9	5.4	20
84	Dysfunction of mitotic cell division at shoot apices triggered severe growth abortion in interspecific hybrids between tetraploid wheat and Aegilops tauschii. *New Phytologist*, **2012**, 194, 1143-1154	9.8	19
83	Identification of paternal mitochondrial DNA sequences in the nucleus-cytoplasm hybrids of tetraploid and hexaploid wheat with D and D2 plasmons from Aegilops species. *Current Genetics*, **2000**, 38, 208-17	2.9	19

82	The cuticular wax inhibitor locus Iw2 in wild diploid wheat Aegilops tauschii: phenotypic survey, genetic analysis, and implications for the evolution of common wheat. *BMC Plant Biology*, **2014**, 14, 246	5.3	18
81	Identification of a protein kinase gene associated with pistillody, homeotic transformation of stamens into pistil-like structures, in alloplasmic wheat. *Planta*, **2007**, 227, 211-21	4.7	17
80	Mapping of QTLs for low temperature response in seedlings of rice (Oryza sativa L.). *Cereal Research Communications*, **2000**, 28, 33-40	1.1	17
79	A high-resolution physical map integrating an anchored chromosome with the BAC physical maps of wheat chromosome 6B. *BMC Genomics*, **2015**, 16, 595	4.5	16
78	Variation in abscisic acid responsiveness of Aegilops tauschii and hexaploid wheat synthetics due to the D-genome diversity. *Genes and Genetic Systems*, **2012**, 87, 9-18	1.4	16
77	Pleiotropic effects of the elongated glume gene P1 on grain and spikelet shape-related traits in tetraploid wheat. *Euphytica*, **2013**, 194, 207-218	2.1	16
76	Genome-wide identification of novel genetic markers from RNA sequencing assembly of diverse Aegilops tauschii accessions. *Molecular Genetics and Genomics*, **2016**, 291, 1681-94	3.1	16
75	RNA-seq analysis reveals considerable genetic diversity and provides genetic markers saturating all chromosomes in the diploid wild wheat relative Aegilops umbellulata. *BMC Plant Biology*, **2018**, 18, 271	5.3	16
74	Line differences in Cor/Lea and fructan biosynthesis-related gene transcript accumulation are related to distinct freezing tolerance levels in synthetic wheat hexaploids. *Journal of Plant Physiology*, **2015**, 176, 78-88	3.6	15
73	Salt tolerance during germination and seedling growth of wild wheat Aegilops tauschii and its impact on the species range expansion. *Scientific Reports*, **2016**, 6, 38554	4.9	15
72	Growth Light Environment Changes the Sensitivity of Photosystem I Photoinhibition Depending on Common Wheat Cultivars. *Frontiers in Plant Science*, **2019**, 10, 686	6.2	14
71	Segregation distortion caused by weak hybrid necrosis in recombinant inbred lines of common wheat. *Genetica*, **2013**, 141, 463-70	1.5	14
70	Evidence of paternal transmission of mitochondrial DNA in a nucleus-cytoplasm hybrid of timopheevi wheat. *Genes and Genetic Systems*, **2002**, 77, 243-50	1.4	14
69	Quantitative trait locus analysis for spikelet shape-related traits in wild wheat progenitor Aegilops tauschii: Implications for intraspecific diversification and subspecies differentiation. *PLoS ONE*, **2017**, 12, e0173210	3.7	14
68	Hybrid incompatibilities in interspecific crosses between tetraploid wheat and its wild diploid relative Aegilops umbellulata. *Plant Molecular Biology*, **2017**, 95, 625-645	4.6	13
67	Identification of quantitative trait loci for abscisic acid responsiveness in the D-genome of hexaploid wheat. *Journal of Plant Physiology*, **2014**, 171, 830-41	3.6	13
66	Application of real-time PCR-based SNP detection for mapping of Net2, a causal D-genome gene for hybrid necrosis in interspecific crosses between tetraploid wheat and Aegilops tauschii. *Genes and Genetic Systems*, **2012**, 87, 137-43	1.4	13
65	Identification of quantitative trait loci for flowering-related traits in the D genome of synthetic hexaploid wheat lines. *Euphytica*, **2013**, 192, 401-412	2.1	12

64	Functional conservation of wheat orthologs of maize rough sheath1 and rough sheath2 genes. *Plant Molecular Biology*, **2009**, 69, 273-85	4.6	12
63	Variations in the maize Ac transposase transcript level and the Ds excision frequency in transgenic wheat callus lines. *Genome*, **1999**, 42, 1234-41	2.4	12
62	Genetic mechanisms of allopolyploid speciation through hybrid genome doubling: novel insights from wheat (Triticum and Aegilops) studies. *International Review of Cell and Molecular Biology*, **2014**, 309, 199-258	6	11
61	Characterization of three VERNALIZATION INSENSITIVE3-like (VIL) homologs in wild wheat, Aegilops tauschii Coss. *Hereditas*, **2012**, 149, 62-71	2.4	11
60	Accelerated senescence and enhanced disease resistance in hybrid chlorosis lines derived from interspecific crosses between tetraploid wheat and Aegilops tauschii. *PLoS ONE*, **2015**, 10, e0121583	3.7	11
59	Characterization of wheat Bell1-type homeobox genes in floral organs of alloplasmic lines with Aegilops crassa cytoplasm. *BMC Plant Biology*, **2011**, 11, 2	5.3	11
58	Preferential expression of a HLP homolog encoding a mitochondrial L14 ribosomal protein in stamens of common wheat. *Gene*, **2004**, 343, 281-9	3.8	11
57	Identification of a large deletion in the first intron of the Vrn-D1 locus, associated with loss of vernalization requirement in wild wheat progenitor Aegilops tauschii Coss. *Genes and Genetic Systems*, **2011**, 86, 183-95	1.4	10
56	Segregation Distortion Through Female Gametophytes in Interspecific Hybrids of Tetraploid Wheat as Revealed by RAPD Analysis. *Hereditas*, **2004**, 131, 47-53	2.4	10
55	Nicotiana tabacum cDNAs encoding alpha and beta subunits of a heterotrimeric GTP-binding protein isolated from hairy root tissues. *Genes and Genetic Systems*, **2000**, 75, 211-21	1.4	10
54	Genome-wide polymorphisms from RNA sequencing assembly of leaf transcripts facilitate phylogenetic analysis and molecular marker development in wild einkorn wheat. *Molecular Genetics and Genomics*, **2019**, 294, 1327-1341	3.1	9
53	Comparison of gene expression profiles and responses to zinc chloride among inter- and intraspecific hybrids with growth abnormalities in wheat and its relatives. *Plant Molecular Biology*, **2015**, 88, 487-502	4.6	9
52	Heterologous expression of wheat WRKY transcription factor genes transcriptionally activated in hybrid necrosis strains alters abiotic and biotic stress tolerance in transgenic Arabidopsis. *Plant Physiology and Biochemistry*, **2020**, 150, 71-79	5.4	9
51	Identification of a novel homolog for a calmodulin-binding protein that is upregulated in alloplasmic wheat showing pistillody. *Planta*, **2013**, 237, 1001-13	4.7	9
50	Differential effects of Aegilops tauschii genotypes on maturing-time in synthetic hexaploid wheats. *Breeding Science*, **2010**, 60, 286-292	2	9
49	Fine mapping and genetic association analysis of Net2, the causative D-genome locus of low temperature-induced hybrid necrosis in interspecific crosses between tetraploid wheat and Aegilops tauschii. *Genetica*, **2016**, 144, 523-533	1.5	8
48	Low temperature-induced necrosis shows phenotypic plasticity in wheat triploid hybrids. *Plant Signaling and Behavior*, **2011**, 6, 1431-3	2.5	8
47	Selective transcription and post-transcriptional processing of the heteroplasmic mitochondrial orf156 copies in the nucleus-cytoplasm hybrids of wheat. *Plant Molecular Biology*, **2003**, 53, 609-19	4.6	8

46	Appraisal of wheat genomics for gene discovery and breeding applications: a special emphasis on advances in Asia. *Theoretical and Applied Genetics*, **2020**, 133, 1503-1520	6	8
45	GRAS-Di system facilitates high-density genetic map construction and QTL identification in recombinant inbred lines of the wheat progenitor Aegilops tauschii. *Scientific Reports*, **2020**, 10, 21455	4.9	7
44	Effect of the U genome on grain hardness in nascent synthetic hexaploids derived from interspecific hybrids between durum wheat and Aegilops umbellulata. *Journal of Cereal Science*, **2018**, 83, 153-161	3.8	7
43	The role of reproductive isolation in allopolyploid speciation patterns: empirical insights from the progenitors of common wheat. *Scientific Reports*, **2017**, 7, 16004	4.9	7
42	Identification of chromosomes controlling abscisic acid responsiveness and transcript accumulation of Cor-Lea genes in common wheat seedlings. *Functional Plant Biology*, **2011**, 38, 758-766	2.7	7
41	Epigenetic silencing and unstable inheritance of MuDR activity monitored at four bz2-mu alleles in maize (Zea mays L.). *Genes and Genetic Systems*, **2007**, 82, 387-401	1.4	7
40	Genetic mapping reveals a dominant awn-inhibiting gene related to differentiation of the variety anathera in the wild diploid wheat Aegilops tauschii. *Genetica*, **2018**, 146, 75-84	1.5	7
39	RNA Sequencing-Based Bulked Segregant Analysis Facilitates Efficient D-genome Marker Development for a Specific Chromosomal Region of Synthetic Hexaploid Wheat. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	7
38	QTL analysis of genetic loci affecting domestication-related spike characters in common wheat. *Genes and Genetic Systems*, **2014**, 89, 121-31	1.4	6
37	Quantitative trait locus analysis for flowering-related traits using two F2 populations derived from crosses between Japanese common wheat cultivars and synthetic hexaploids. *Genes and Genetic Systems*, **2015**, 90, 89-98	1.4	6
36	Differential contribution of two Ppd-1 homoeoalleles to early-flowering phenotype in Nepalese and Japanese varieties of common wheat. *Breeding Science*, **2013**, 63, 374-83	2	6
35	Genomic structure and homoeologous relationship of the two alpha-subunit genes of a heterotrimeric GTP-binding protein in tobacco. *Genome*, **2002**, 45, 626-33	2.4	6
34	Introgression of chromosomal segments conferring early heading date from wheat diploid progenitor, Aegilops tauschii Coss., into Japanese elite wheat cultivars. *PLoS ONE*, **2020**, 15, e0228397	3.7	5
33	Fine mapping of Hch1, the causal D-genome gene for hybrid chlorosis in interspecific crosses between tetraploid wheat and Aegilops tauschii. *Genes and Genetic Systems*, **2015**, 90, 283-91	1.4	4
32	Natural variation in photoperiodic flowering pathway and identification of photoperiod-insensitive accessions in wild wheat, Aegilops tauschii. *Euphytica*, **2018**, 214, 1	2.1	4
31	Experimental evolutionary studies on the genetic autonomy of the cytoplasmic genome "plasmon" in the (wheat)- complex. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 3082-3090	11.5	3
30	Diploid genome differentiation conferred by RNA sequencing-based survey of genome-wide polymorphisms throughout homoeologous loci in Triticum and Aegilops. *BMC Genomics*, **2020**, 21, 246	4.5	3
29	Genetic mapping of a novel recessive allele for non-glaucousness in wild diploid wheat Aegilops tauschii: implications for the evolution of common wheat. *Genetica*, **2018**, 146, 249-254	1.5	3

28	Origin, dispersal and genomic structure of a low-copy-number hypervariable RFLP clone in Triticum and Aegilops species. *Genes and Genetic Systems*, **2003**, 78, 291-300	1.4	3
27	Global gene expression profiling related to temperature-sensitive growth abnormalities in interspecific crosses between tetraploid wheat and Aegilops tauschii. *PLoS ONE*, **2017**, 12, e0176497	3.7	3
26	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. *Journal of Cereal Science*, **2016**, 71, 167-176	3.8	3
25	Phenotypic effects of the U-genome variation in nascent synthetic hexaploids derived from interspecific crosses between durum wheat and its diploid relative Aegilops umbellulata. *PLoS ONE*, **2020**, 15, e0231129	3.7	3
24	Differences in glucose yield of residues from among varieties of rice, wheat, and sorghum after dilute acid pretreatment. *Bioscience, Biotechnology and Biochemistry*, **2017**, 81, 1650-1656	2.1	2
23	Production and phenotypic characterization of nascent synthetic decaploids derived from interspecific crosses between a durum wheat cultivar and hexaploid Aegilops species. *Genetic Resources and Crop Evolution*, **2020**, 67, 1905-1917	2	2
22	Identification of a hard kernel texture line of synthetic allohexaploid wheat reducing the puroindoline accumulation on the D genome from Aegilops tauschii. *Journal of Cereal Science*, **2020**, 93, 102964	3.8	2
21	Implications of an inverted duplication in the wheat KN1-type homeobox gene Wknox1 for theorigin of Persian wheat. *Genes and Genetic Systems*, **2015**, 90, 115-20	1.4	2
20	Extracellular trafficking of a wheat cold-responsive protein, WLT10. *Journal of Plant Physiology*, **2015**, 174, 71-4	3.6	2
19	Detection of splicing variants in the leaf and spike transcripts of wild diploid wheat Aegilops tauschii and transmission of the splicing patterns to synthetic hexaploid wheat. *Plant Gene*, **2017**, 9, 6-12	3.1	1
18	Characterization of three homoeologous cDNAs encoding chloroplast-targeted aminolevulinic acid dehydratase in common wheat. *Journal of Integrative Plant Biology*, **2011**, 53, 942-50	8.3	1
17	Genetic Transformation of Durum Wheat (Triticum durum Desf.) through Particle Bombardment of Scutellar Tissues.. *Plant Biotechnology*, **1997**, 14, 151-156	1.3	1
16	Genome sequencing-based coverage analyses facilitate high-resolution detection of deletions linked to phenotypes of gamma-irradiated wheat mutants.. *BMC Genomics*, **2022**, 23, 111	4.5	0
15	Segregation distortion caused by weak hybrid necrosis in recombinant inbred lines of common wheat **2013**, 141, 463		0
14	RNA-Seq-based DNA marker analysis of the genetics and molecular evolution of Triticeae species. *Functional and Integrative Genomics*, **2021**, 21, 535-542	3.8	0
13	Gene Expression Profiles Involved in Development of Freezing Tolerance in Common Wheat **2015**, 247-252		
12	Genetic effect of the Aegilops caudata plasmon on the manifestation of the Ae. cylindrica genome. *Genes and Genetic Systems*, **2014**, 89, 195-202	1.4	
11	????. *Ikushugaku Kenkyu*, **2000**, 2, 165-166	0.1	

10 Association of Wheat miRNAs with Hybrid Incompatibility in Interspecific Crosses of Triticum and Aegilops **2015**, 159-165

9 Abiotic Stress Signal Network with Expression QTLs for Cold-Responsive Genes in Common Wheat **2013**, 219-229

8 Introgression of chromosomal segments conferring early heading date from wheat diploid progenitor, Aegilops tauschii Coss., into Japanese elite wheat cultivars **2020**, 15, e0228397

7 Introgression of chromosomal segments conferring early heading date from wheat diploid progenitor, Aegilops tauschii Coss., into Japanese elite wheat cultivars **2020**, 15, e0228397

6 Introgression of chromosomal segments conferring early heading date from wheat diploid progenitor, Aegilops tauschii Coss., into Japanese elite wheat cultivars **2020**, 15, e0228397

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4 Phenotypic effects of the U-genome variation in nascent synthetic hexaploids derived from interspecific crosses between durum wheat and its diploid relative Aegilops umbellulata **2020**, 15, e0231129

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1 Phenotypic effects of the U-genome variation in nascent synthetic hexaploids derived from interspecific crosses between durum wheat and its diploid relative Aegilops umbellulata **2020**, 15, e0231129