

Yong-Bi Fu

List of Publications by Year in descending order

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120
papers

3,507
citations

126907

33
h-index

182427

51
g-index

121
all docs

121
docs citations

121
times ranked

3175
citing authors

#	ARTICLE	IF	CITATIONS
1	Understanding crop genetic diversity under modern plant breeding. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2131-2142.	3.6	195
2	Evolution of wild cereals during 28 years of global warming in Israel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3412-3415.	7.1	175
3	Evidence of the domestication history of flax (<i>Linum usitatissimum</i> L.) from genetic diversity of the <i>sad2</i> locus. <i>Theoretical and Applied Genetics</i> , 2005, 112, 58-65.	3.6	155
4	Genome-Wide Reduction of Genetic Diversity in Wheat Breeding. <i>Crop Science</i> , 2009, 49, 161-168.	1.8	124
5	Allelic Diversity Changes in 96 Canadian Oat Cultivars Released from 1886 to 2001. <i>Crop Science</i> , 2003, 43, 1989-1995.	1.8	93
6	Genotyping-By-Sequencing for Plant Genetic Diversity Analysis: A Lab Guide for SNP Genotyping. <i>Diversity</i> , 2014, 6, 665-680.	1.7	91
7	The Vulnerability of Plant Genetic Resources Conserved Ex Situ. <i>Crop Science</i> , 2017, 57, 2314-2328.	1.8	88
8	Allelic reduction and genetic shift in the Canadian hard red spring wheat germplasm released from 1845 to 2004. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1505-1516.	3.6	82
9	Towards a better monitoring of seed ageing under ex situ seed conservation. , 2015, 3, cov026.		78
10	Impact of plant breeding on genetic diversity of the Canadian hard red spring wheat germplasm as revealed by EST-derived SSR markers. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1239-1247.	3.6	77
11	The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119.	27.8	70
12	Genetic evidence for early flax domestication with capsular dehiscence. <i>Genetic Resources and Crop Evolution</i> , 2011, 58, 1119-1128.	1.6	67
13	Title is missing!. <i>Genetic Resources and Crop Evolution</i> , 2002, 49, 167-174.	1.6	65
14	Genetic diversity of cultivated flax (<i>Linum usitatissimum</i> L.) and its wild progenitor pale flax (<i>Linum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.6	63
15	On estimating the linkage of marker genes to viability genes controlling inbreeding depression. <i>Theoretical and Applied Genetics</i> , 1994, 88, 925-932.	3.6	60
16	Phylogenetic network of <i>Linum</i> species as revealed by non-coding chloroplast DNA sequences. <i>Genetic Resources and Crop Evolution</i> , 2010, 57, 667-677.	1.6	60
17	RAPD analysis of genetic relationships of seven flax species in the genus <i>Linum</i> L. <i>Genetic Resources and Crop Evolution</i> , 2002, 49, 253-259.	1.6	59
18	RAPD Analysis of 54 North American Flax Cultivars. <i>Crop Science</i> , 2003, 43, 1510-1515.	1.8	59

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19	Phenotypic and Molecular (RAPD) Differentiation of Four Intraspecific Groups of Cultivated Flax (<i>Linum usitatissimum</i> L. subsp. <i>usitatissimum</i>). <i>Genetic Resources and Crop Evolution</i> , 2006, 53, 77-90.	1.6	56
20	High-density marker profiling confirms ancestral genomes of <i>Avena</i> species and identifies D-genome chromosomes of hexaploid oat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2133-2149.	3.6	56
21	<i>Arabidopsis thaliana</i> differentially regulates two programmed cell death pathways in responses to pathogen and low temperature stress. <i>New Phytologist</i> , 2019, 221, 919-934.	7.3	56
22	Locus-specific view of flax domestication history. <i>Ecology and Evolution</i> , 2012, 2, 139-152.	1.9	53
23	Genetic Diversity Analysis of Highly Incomplete SNP Genotype Data with Imputations: An Empirical Assessment. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 891-900.	1.8	53
24	Redundancy and distinctness in flax germplasm as revealed by RAPD dissimilarity. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2006, 4, 117-124.	0.8	51
25	Increasing Genome Sampling and Improving SNP Genotyping for Genotyping-by-Sequencing with New Combinations of Restriction Enzymes. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 845-856.	1.8	51
26	Impact of plant breeding on genetic diversity of agricultural crops: searching for molecular evidence. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2006, 4, 71-78.	0.8	48
27	Morphological, Physiological, and Genetic Responses to Salt Stress in Alfalfa: A Review. <i>Agronomy</i> , 2020, 10, 577.	3.0	48
28	Geographic Patterns of RAPD Variation in Cultivated Flax. <i>Crop Science</i> , 2005, 45, 1084-1091.	1.8	46
29	Spatial patterns of tree height variations in a series of Douglas-fir progeny trials: implications for genetic testing. <i>Canadian Journal of Forest Research</i> , 1999, 29, 714-723.	1.7	45
30	Genetic Diversity Analysis with 454 Pyrosequencing and Genomic Reduction Confirmed the Eastern and Western Division in the Cultivated Barley Gene Pool. <i>Plant Genome</i> , 2011, 4, 226-237.	2.8	42
31	Genetic diversity analysis of yellow mustard (<i>Sinapis alba</i> L.) germplasm based on genotyping by sequencing. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 579-594.	1.6	41
32	Spatial variation in temperature thresholds during seed germination of remnant <i>Festuca hallii</i> populations across the Canadian prairie. <i>Environmental and Experimental Botany</i> , 2010, 67, 479-486.	4.2	40
33	AFLP variation in 25 <i>Avena</i> species. <i>Theoretical and Applied Genetics</i> , 2008, 117, 333-342.	3.6	36
34	Developing genomic resources in two <i>Linum</i> species via 454 pyrosequencing and genomic reduction. <i>Molecular Ecology Resources</i> , 2012, 12, 492-500.	4.8	35
35	Genetic Diversity of Canadian and Exotic Potato Germplasm Revealed by Simple Sequence Repeat Markers. <i>American Journal of Potato Research</i> , 2009, 86, 38-48.	0.9	34
36	Comparison of Breeding Strategies for Purging Inbreeding Depression via Simulation. <i>Conservation Biology</i> , 1998, 12, 856-864.	4.7	34

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37	Genetic Diversity of Canadian Soybean Cultivars and Exotic Germplasm Revealed by Simple Sequence Repeat Markers. <i>Crop Science</i> , 2007, 47, 1947-1954.	1.8	33
38	Genetic diversity of Canadian elite summer rape (<i>Brassica napus</i> L.) cultivars from the pre- to post-canola quality era. <i>Canadian Journal of Plant Science</i> , 2010, 90, 23-33.	0.9	32
39	Genetic Diversity in Natural Populations and Corresponding Seed Collections of Little Bluestem as Revealed by AFLP Markers. <i>Crop Science</i> , 2004, 44, 2254-2260.	1.8	31
40	Microsatellite variation in <i>Avena sterilis</i> oat germplasm. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1029-1038.	3.6	31
41	Oat evolution revealed in the maternal lineages of 25 <i>Avena</i> species. <i>Scientific Reports</i> , 2018, 8, 4252.	3.3	28
42	Allelic changes in bread wheat cultivars were associated with long-term wheat trait improvements. <i>Euphytica</i> , 2011, 179, 209-225.	1.2	27
43	Genetic diversity of Pakistan wheat germplasm as revealed by RAPD markers. <i>Genetic Resources and Crop Evolution</i> , 2005, 52, 239-244.	1.6	26
44	Extractions of High Quality RNA from the Seeds of Jerusalem Artichoke and Other Plant Species with High Levels of Starch and Lipid. <i>Plants</i> , 2013, 2, 302-316.	3.5	25
45	Long-Term Grazing Effects on Genetic Variability in Mountain Rough Fescue. <i>Rangeland Ecology and Management</i> , 2005, 58, 637-642.	2.3	24
46	Searching for an Accurate Marker-Based Prediction of an Individual Quantitative Trait in Molecular Plant Breeding. <i>Frontiers in Plant Science</i> , 2017, 8, 1182.	3.6	24
47	Population-based resequencing analysis of wild and cultivated barley revealed weak domestication signal of selection and bottleneck in the <i>Rrs2</i> scald resistance gene region. <i>Genome</i> , 2012, 55, 93-104.	2.0	23
48	Incomplete block designs for genetic testing: statistical efficiencies of estimating family means. <i>Canadian Journal of Forest Research</i> , 1998, 28, 977-986.	1.7	22
49	Genome resequencing and simple sequence repeat markers reveal the existence of divergent lineages in the Canadian <i>Puccinia striiformis</i> f. sp. <i>tritici</i> population with extensive DNA methylation. <i>Environmental Microbiology</i> , 2018, 20, 1498-1515.	3.8	21
50	Arabidopsis Seed Stored mRNAs are Degraded Constantly over Aging Time, as Revealed by New Quantification Methods. <i>Frontiers in Plant Science</i> , 2019, 10, 1764.	3.6	21
51	Applications of bulking in molecular characterization of plant germplasm: a critical review. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2003, 1, 161-167.	0.8	20
52	AFLP Variation in Four Blue Grama Seed Sources. <i>Crop Science</i> , 2004, 44, 283-288.	1.8	19
53	Variation in phenotypic characters of pale flax (<i>Linum bienne</i> Mill.) from Turkey. <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 19-30.	1.6	18
54	RNA-Seq analysis of gene expression for floral development in crested wheatgrass (<i>Agropyron</i>) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 62	2.5	18

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55	Elevated mutation and selection in wild emmer wheat in response to 28 years of global warming. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20002-20008.	7.1	18
56	Detecting Genetic Changes over Two Generations of Seed Increase in an Awned Slender Wheatgrass Population Using AFLP Markers. Crop Science, 2005, 45, 1064-1068.	1.8	17
57	fptest : a sas routine for testing differences in allelic count. Molecular Ecology Resources, 2010, 10, 389-392.	4.8	17
58	QTL mapping and molecular characterization of the classical D locus controlling seed and flower color in <i>Linum usitatissimum</i> (flax). Scientific Reports, 2017, 7, 15751.	3.3	17
59	Incomplete block designs for genetic testing: some practical considerations. Canadian Journal of Forest Research, 1999, 29, 1871-1878.	1.7	16
60	Characterization of expressed sequence tag-derived simple sequence repeat markers for 17 <i>Linum</i> species. Botany, 2010, 88, 537-543.	1.0	16
61	Thai elite cassava genetic diversity was fortuitously conserved through farming with different sets of varieties. Conservation Genetics, 2014, 15, 1463-1478.	1.5	16
62	Multiplexed shotgun sequencing reveals congruent three-genome phylogenetic signals for four botanical sections of the flax genus <i>Linum</i> . Molecular Phylogenetics and Evolution, 2016, 101, 122-132.	2.7	15
63	Point estimation and graphical inference of marginal dominance for two viability loci controlling inbreeding depression. Genetical Research, 1997, 70, 143-153.	0.9	14
64	Assessment of bulking strategies for RAPD analyses of flax germplasm. Genetic Resources and Crop Evolution, 2003, 50, 743-746.	1.6	14
65	Patterns of amplified restriction fragment polymorphism in natural populations and corresponding seed collections of plains rough fescue (<i>Festuca hallii</i>). Canadian Journal of Botany, 2007, 85, 484-492.	1.1	14
66	Genetic variation in remnant <i>Festuca hallii</i> populations is weakly differentiated, but geographically associated across the Canadian Prairie. Plant Species Biology, 2009, 24, 156-168.	1.0	14
67	An improved method with a wider applicability to isolate plant mitochondria for mtDNA extraction. Plant Methods, 2015, 11, 56.	4.3	14
68	The Associative Changes in Scutellum Nuclear Content and Morphology with Viability Loss of Naturally Aged and Accelerated Aging Wheat (<i>Triticum aestivum</i>) Seeds. Frontiers in Plant Science, 2016, 7, 1474.	3.6	14
69	Genotyping-by-Sequencing Enhances Genetic Diversity Analysis of Crested Wheatgrass [<i>Agropyron cristatum</i> (L.) Gaertn.]. International Journal of Molecular Sciences, 2018, 19, 2587.	4.1	14
70	Flax latitudinal adaptation at LuTFL1 altered architecture and promoted fiber production. Scientific Reports, 2019, 9, 976.	3.3	14
71	Marker-based inferences about fecundity genes contributing to inbreeding depression in <i>Mimulus guttatus</i> . Genome, 1994, 37, 1005-1010.	2.0	13
72	Genetic diversity of fringed brome (<i>Bromus ciliatus</i>) as determined by amplified fragment length polymorphism. Canadian Journal of Botany, 2005, 83, 1322-1328.	1.1	13

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73	Genetic Diversity in A Core Subset of Wild Barley Germplasm. <i>Diversity</i> , 2012, 4, 239-257.	1.7	12
74	Patterns of SSR variation in bread wheat (<i>Triticum aestivum</i> L.) seeds under ex situ genebank storage and accelerated ageing. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 277-290.	1.6	12
75	AveDissR: An R Function for Assessing Genetic Distinctness and Genetic Redundancy. <i>Applications in Plant Sciences</i> , 2017, 5, 1700018.	2.1	12
76	RAPD Variations in Selected and Unselected Blue Grama Populations. <i>Crop Science</i> , 2003, 43, 1852-1857.	1.8	11
77	Population-based resequencing analysis of improved wheat germplasm at wheat leaf rust resistance locus Lr21. <i>Theoretical and Applied Genetics</i> , 2010, 121, 271-281.	3.6	11
78	Biological and genetic characterisation of <i>Phoma macrostoma</i> isolates with bioherbicidal activity. <i>Biocontrol Science and Technology</i> , 2012, 22, 813-835.	1.3	11
79	Population-based resequencing revealed an ancestral winter group of cultivated flax: implication for flax domestication processes. <i>Ecology and Evolution</i> , 2012, 2, 622-635.	1.9	11
80	Tissue specific changes in elements and organic compounds of alfalfa (<i>Medicago sativa</i> L.) cultivars differing in salt tolerance under salt stress. <i>Journal of Plant Physiology</i> , 2021, 264, 153485.	3.5	11
81	Genetic variability of Canadian elite cultivars of summer turnip rape (<i>Brassica rapa</i> L.) revealed by simple sequence repeat markers. <i>Canadian Journal of Plant Science</i> , 2009, 89, 865-874.	0.9	10
82	Assessing Genetic Structure and Relatedness of Jerusalem Artichoke (<i>Helianthus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Plant Sciences, 2011, 02, 753-764.	0.8	10
83	Genetic Diversity of Kenyan Potato Germplasm Revealed by Simple Sequence Repeat Markers. <i>American Journal of Potato Research</i> , 2011, 88, 424-434.	0.9	10
84	<i>Arabidopsis</i> UBC22, an E2 able to catalyze lysine-11 specific ubiquitin linkage formation, has multiple functions in plant growth and immunity. <i>Plant Science</i> , 2020, 297, 110520.	3.6	10
85	Comparison of five DNA extraction methods for molecular analysis of Jerusalem artichoke (<i>Helianthus tuberosus</i>). <i>Genetics and Molecular Research</i> , 2012, 11, 572-581.	0.2	10
86	Genetic diversity of worldwide Jerusalem artichoke (<i>Helianthus tuberosus</i>) germplasm as revealed by RAPD markers. <i>Genetics and Molecular Research</i> , 2011, 10, 4012-4025.	0.2	9
87	Genotyping-by-Sequencing and Its Application to Oat Genomic Research. <i>Methods in Molecular Biology</i> , 2017, 1536, 169-187.	0.9	9
88	TUNEL Assay and DAPI Staining Revealed Few Alterations of Cellular Morphology in Naturally and Artificially Aged Seeds of Cultivated Flax. <i>Plants</i> , 2018, 7, 34.	3.5	9
89	Characterizing chloroplast genomes and inferring maternal divergence of the <i>Triticum</i> "Aegilops complex. <i>Scientific Reports</i> , 2021, 11, 15363.	3.3	8
90	Pollen pool heterogeneity in jack pine (<i>Pinus banksiana</i> Lamb.): a problem for estimating outcrossing rates?. <i>Theoretical and Applied Genetics</i> , 1992, 83, 500-508.	3.6	7

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91	Characterization of microsatellite markers for rough fescue species (<i>Festuca</i> spp.). <i>Molecular Ecology Notes</i> , 2006, 6, 894-896.	1.7	7
92	Genetic Variation and Relationships of Pedigree-Known Oat, Wheat, and Barley Cultivars Released by Bulking and Single-Plant Sampling. <i>Genetic Resources and Crop Evolution</i> , 2006, 53, 1153-1164.	1.6	7
93	Genetic diversity of <i>Sinapis alba</i> germplasm as revealed by AFLP markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2006, 4, 87-95.	0.8	7
94	Advancing Bromegrass Breeding Through Imaging Phenotyping and Genomic Selection: A Review. <i>Frontiers in Plant Science</i> , 2019, 10, 1673.	3.6	7
95	Genetic Erosion Under Modern Plant Breeding: Case Studies in Canadian Crop Gene Pools. <i>Sustainable Development and Biodiversity</i> , 2015, , 89-104.	1.7	7
96	RNA-Seq Analysis of Plant Maturity in Crested Wheatgrass (<i>Agropyron cristatum</i> L.). <i>Genes</i> , 2017, 8, 291.	2.4	6
97	Genetic diversity and relationship of sainfoin (<i>Onobrychis viciifolia</i> Scop.) germplasm as revealed by amplified fragment length polymorphism markers. <i>Canadian Journal of Plant Science</i> , 2018, 98, 543-551.	0.9	6
98	Advancing crested wheatgrass [<i>Agropyron cristatum</i> (L.) Gaertn.] breeding through genotyping-by-sequencing and genomic selection. <i>PLoS ONE</i> , 2020, 15, e0239609.	2.5	6
99	Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	6
100	Patterns of Genetic Variation in a Soybean Germplasm Collection as Characterized with Genotyping-by-Sequencing. <i>Plants</i> , 2021, 10, 1611.	3.5	6
101	Transcriptomic analysis of differentially expressed genes in leaves and roots of two alfalfa (<i>Medicago</i>) Tj ETQq1 1 0,784314 rgBT /Over	3.6	6
102	Evaluating genetic variation and relationships among <i>Puccinellia nuttalliana</i> populations using amplified fragment length polymorphism markers. <i>Canadian Journal of Plant Science</i> , 2013, 93, 1097-1104.	0.9	5
103	Genetic diversity of side-oats grama [<i>Bouteloua curtipendula</i> (Michx.) Torr.] populations as revealed by amplified fragment length polymorphism markers. <i>Canadian Journal of Plant Science</i> , 2013, 93, 1105-1114.	0.9	5
104	Genotyping-by-sequencing empowered genetic diversity analysis of Jordanian oat wild relative <i>Avena sterilis</i> . <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 2069-2082.	1.6	5
105	With a Little Help from My Cell Wall: Structural Modifications in Pectin May Play a Role to Overcome Both Dehydration Stress and Fungal Pathogens. <i>Plants</i> , 2022, 11, 385.	3.5	5
106	Marker-Based Inferences about the Genetic basis of Flowering time in <i>Mimulus Guttatus</i> . <i>Hereditas</i> , 2004, 121, 267-272.	1.4	4
107	Developing Chloroplast Genomic Resources from 25 <i>Avena</i> Species for the Characterization of Oat Wild Relative Germplasm. <i>Plants</i> , 2019, 8, 438.	3.5	4
108	Analysis of Stored mRNA Degradation in Accelerated Aged Seeds of Wheat and Canola in Comparison to <i>Arabidopsis</i> . <i>Plants</i> , 2020, 9, 1707.	3.5	4

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109	A Molecular View of Flax Gene Pool. <i>Plant Genetics and Genomics: Crops and Models</i> , 2019, , 17-37.	0.3	4
110	Comment-Enhanced heritabilities and best linear unbiased predictors through appropriate blocking of progeny trials. <i>Canadian Journal of Forest Research</i> , 1999, 29, 1633-1634.	1.7	3
111	Genetic Structure in a Core Subset of Cultivated Barley Germplasm. <i>Crop Science</i> , 2012, 52, 1195-1208.	1.8	3
112	Genetic Diversity of Northern Wheatgrass (<i>Elymus lanceolatus</i> ssp. <i>lanceolatus</i>) as Revealed by Genotyping-by-Sequencing. <i>Diversity</i> , 2018, 10, 23.	1.7	3
113	Genetic diversity of bluebunch wheatgrass (<i>Pseudoroegneria spicata</i>) in the Thompson River valley of British Columbia. <i>Canadian Journal of Botany</i> , 2006, 84, 1122-1128.	1.1	2
114	Genotyping-by-sequencing data of 272 crested wheatgrass (<i>Agropyron cristatum</i>) genotypes. <i>Data in Brief</i> , 2017, 15, 401-406.	1.0	2
115	An R version of FPTest for testing differences in allelic count. <i>Conservation Genetics Resources</i> , 2017, 9, 313-318.	0.8	2
116	Characterizing Molecular Quantitative Variability for Inbreeding Depression. <i>Plant Species Biology</i> , 1996, 11, 23-31.	1.0	1
117	Genetic Risk Assessment of a Threatened Remnant Population of Hairy Prairie-Clover (<i>Dalea villosa</i> var.) Tj ETQq1 1 0,784314,rgBT /O	1.7	1
118	Patterns of amplified restriction fragment polymorphism in the germination of <i>Festuca hallii</i> seeds. <i>Seed Science Research</i> , 2010, 20, 153-161.	1.7	0
119	Patterns of mitochondrial DNA fragmentation in bread wheat (<i>Triticum aestivum</i> L.) seeds under ex situ genebank storage and artificial aging. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 2023-2036.	1.6	0
120	Interpolating Genetic Variation in Natural Populations: A Case Study of Plains Rough Fescue (<i>Festuca</i>) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	0.2	0