

# Yong-Bi Fu

## List of Publications by Year in descending order

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120  
papers

3,507  
citations

145106

33  
h-index

206121

51  
g-index

121  
all docs

121  
docs citations

121  
times ranked

3516  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.6	5
2	The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119.	13.7	70
3	Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	6
4	Characterizing chloroplast genomes and inferring maternal divergence of the Triticum-Aegilops complex. <i>Scientific Reports</i> , 2021, 11, 15363.	1.6	8
5	Patterns of Genetic Variation in a Soybean Germplasm Collection as Characterized with Genotyping-by-Sequencing. <i>Plants</i> , 2021, 10, 1611.	1.6	6
6	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.	1.6	11
7	Transcriptomic analysis of differentially expressed genes in leaves and roots of two alfalfa ( <i>Medicago</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.6	8
8	Advancing crested wheatgrass [ <i>Agropyron cristatum</i> (L.) Gaertn.] breeding through genotyping-by-sequencing and genomic selection. <i>PLoS ONE</i> , 2020, 15, e0239609.	1.1	6
9	Analysis of Stored mRNA Degradation in Accelerated Aged Seeds of Wheat and Canola in Comparison to Arabidopsis. <i>Plants</i> , 2020, 9, 1707.	1.6	4
10	Arabidopsis 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.	1.7	10
11	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.	0.8	0
12	Morphological, Physiological, and Genetic Responses to Salt Stress in Alfalfa: A Review. <i>Agronomy</i> , 2020, 10, 577.	1.3	48
13	Developing Chloroplast Genomic Resources from 25 Avena Species for the Characterization of Oat Wild Relative Germplasm. <i>Plants</i> , 2019, 8, 438.	1.6	4
14	Flax latitudinal adaptation at LuTFL1 altered architecture and promoted fiber production. <i>Scientific Reports</i> , 2019, 9, 976.	1.6	14
15	Elevated mutation and selection in wild emmer wheat in response to 28 years of global warming. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20002-20008.	3.3	18
16	Arabidopsis <i>UBC13</i> differentially regulates two programmed cell death pathways in responses to pathogen and low temperature stress. <i>New Phytologist</i> , 2019, 221, 919-934.	3.5	56
17	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.	1.7	21
18	Advancing Bromegrass Breeding Through Imaging Phenotyping and Genomic Selection: A Review. <i>Frontiers in Plant Science</i> , 2019, 10, 1673.	1.7	7

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19	A Molecular View of Flax Gene Pool. <i>Plant Genetics and Genomics: Crops and Models</i> , 2019, , 17-37.	0.3	4
20	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.	0.3	6
21	Oat evolution revealed in the maternal lineages of 25 <i>Avena</i> species. <i>Scientific Reports</i> , 2018, 8, 4252.	1.6	28
22	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.	1.8	21
23	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.	1.6	9
24	Genotyping-by-Sequencing Enhances Genetic Diversity Analysis of Crested Wheatgrass [ <i>Agropyron cristatum</i> (L.) Gaertn.]. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2587.	1.8	14
25	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.	0.7	3
26	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.	0.8	5
27	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.	0.8	12
28	Genotyping-by-Sequencing and Its Application to Oat Genomic Research. <i>Methods in Molecular Biology</i> , 2017, 1536, 169-187.	0.4	9
29	Genotyping-by-sequencing data of 272 crested wheatgrass ( <i>Agropyron cristatum</i> ) genotypes. <i>Data in Brief</i> , 2017, 15, 401-406.	0.5	2
30	QTL mapping and molecular characterization of the classical D locus controlling seed and flower color in <i>Linum usitatissimum</i> (flax). <i>Scientific Reports</i> , 2017, 7, 15751.	1.6	17
31	An R version of FPTest for testing differences in allelic count. <i>Conservation Genetics Resources</i> , 2017, 9, 313-318.	0.4	2
32	AveDissR: An R Function for Assessing Genetic Distinctness and Genetic Redundancy. <i>Applications in Plant Sciences</i> , 2017, 5, 1700018.	0.8	12
33	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.	1.7	24
34	RNA-Seq analysis of gene expression for floral development in crested wheatgrass ( <i>Agropyron</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142	1.1	18
35	The Vulnerability of Plant Genetic Resources Conserved Ex Situ. <i>Crop Science</i> , 2017, 57, 2314-2328.	0.8	88
36	RNA-Seq Analysis of Plant Maturity in Crested Wheatgrass ( <i>Agropyron cristatum</i> L.). <i>Genes</i> , 2017, 8, 291.	1.0	6

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37	The Associative Changes in Scutellum Nuclear Content and Morphology with Viability Loss of Naturally Aged and Accelerated Aging Wheat ( <i>Triticum aestivum</i> ) Seeds. <i>Frontiers in Plant Science</i> , 2016, 7, 1474.	1.7	14
38	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.	0.8	51
39	Multiplexed shotgun sequencing reveals congruent three-genome phylogenetic signals for four botanical sections of the flax genus <i>Linum</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 122-132.	1.2	15
40	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.	1.8	56
41	An improved method with a wider applicability to isolate plant mitochondria for mtDNA extraction. <i>Plant Methods</i> , 2015, 11, 56.	1.9	14
42	Towards a better monitoring of seed ageing under <i>ex situ</i> seed conservation. , 2015, 3, cov026.		78
43	Understanding crop genetic diversity under modern plant breeding. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2131-2142.	1.8	195
44	Genetic Erosion Under Modern Plant Breeding: Case Studies in Canadian Crop Gene Pools. <i>Sustainable Development and Biodiversity</i> , 2015, , 89-104.	1.4	7
45	Thai elite cassava genetic diversity was fortuitously conserved through farming with different sets of varieties. <i>Conservation Genetics</i> , 2014, 15, 1463-1478.	0.8	16
46	Genetic Diversity Analysis of Highly Incomplete SNP Genotype Data with Imputations: An Empirical Assessment. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 891-900.	0.8	53
47	Genotyping-By-Sequencing for Plant Genetic Diversity Analysis: A Lab Guide for SNP Genotyping. <i>Diversity</i> , 2014, 6, 665-680.	0.7	91
48	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.	0.8	41
49	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.	0.3	5
50	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.	0.3	5
51	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.	1.6	25
52	Genetic Structure in a Core Subset of Cultivated Barley Germplasm. <i>Crop Science</i> , 2012, 52, 1195-1208.	0.8	3
53	Biological and genetic characterisation of <i>Phoma macrostoma</i> isolates with bioherbicidal activity. <i>Biocontrol Science and Technology</i> , 2012, 22, 813-835.	0.5	11
54	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.	0.9	23

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55	Evolution of wild cereals during 28 years of global warming in Israel. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3412-3415.	3.3	175
56	Genetic Diversity in A Core Subset of Wild Barley Germplasm. Diversity, 2012, 4, 239-257.	0.7	12
57	Population-based resequencing revealed an ancestral winter group of cultivated flax: implication for flax domestication processes. Ecology and Evolution, 2012, 2, 622-635.	0.8	11
58	Locus-specific view of flax domestication history. Ecology and Evolution, 2012, 2, 139-152.	0.8	53
59	Developing genomic resources in two <i>Linum</i> species via 454 pyrosequencing and genomic reduction. Molecular Ecology Resources, 2012, 12, 492-500.	2.2	35
60	Variation in phenotypic characters of pale flax ( <i>Linum bienne</i> Mill.) from Turkey. Genetic Resources and Crop Evolution, 2012, 59, 19-30.	0.8	18
61	Comparison of five DNA extraction methods for molecular analysis of Jerusalem artichoke ( <i>Helianthus tuberosus</i> ). Genetics and Molecular Research, 2012, 11, 572-581.	0.3	10
62	Assessing Genetic Structure and Relatedness of Jerusalem Artichoke ( <i>Helianthus tuberosus</i> ) Plant Sciences, 2011, 02, 753-764.	0.3	10
63	Genetic Diversity Analysis with 454 Pyrosequencing and Genomic Reduction Confirmed the Eastern and Western Division in the Cultivated Barley Gene Pool. Plant Genome, 2011, 4, 226-237.	1.6	42
64	Genetic diversity of worldwide Jerusalem artichoke ( <i>Helianthus tuberosus</i> ) germplasm as revealed by RAPD markers. Genetics and Molecular Research, 2011, 10, 4012-4025.	0.3	9
65	Allelic changes in bread wheat cultivars were associated with long-term wheat trait improvements. Euphytica, 2011, 179, 209-225.	0.6	27
66	Genetic evidence for early flax domestication with capsular dehiscence. Genetic Resources and Crop Evolution, 2011, 58, 1119-1128.	0.8	67
67	Genetic Diversity of Kenyan Potato Germplasm Revealed by Simple Sequence Repeat Markers. American Journal of Potato Research, 2011, 88, 424-434.	0.5	10
68	Genetic Risk Assessment of a Threatened Remnant Population of Hairy Prairie-Clover ( <i>Dalea villosa</i> var.)	0.7	10
69	Genetic diversity of Canadian elite summer rape ( <i>Brassica napus</i> L.) cultivars from the pre- to post-canola quality era. Canadian Journal of Plant Science, 2010, 90, 23-33.	0.3	32
70	Population-based resequencing analysis of improved wheat germplasm at wheat leaf rust resistance locus Lr21. Theoretical and Applied Genetics, 2010, 121, 271-281.	1.8	11
71	Phylogenetic network of <i>Linum</i> species as revealed by non-coding chloroplast DNA sequences. Genetic Resources and Crop Evolution, 2010, 57, 667-677.	0.8	60
72	Genetic diversity of cultivated flax ( <i>Linum usitatissimum</i> L.) and its wild progenitor pale flax ( <i>Linum catharticum</i> L.)	0.8	63

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73	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.	2.0	40
74	Patterns of amplified restriction fragment polymorphism in the germination of <i>Festuca hallii</i> seeds. <i>Seed Science Research</i> , 2010, 20, 153-161.	0.8	0
75	fptest : a sas routine for testing differences in allelic count. <i>Molecular Ecology Resources</i> , 2010, 10, 389-392.	2.2	17
76	Characterization of expressed sequence tag-derived simple sequence repeat markers for 17 <i>Linum</i> species. <i>Botany</i> , 2010, 88, 537-543.	0.5	16
77	Genome-Wide Reduction of Genetic Diversity in Wheat Breeding. <i>Crop Science</i> , 2009, 49, 161-168.	0.8	124
78	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.	0.5	34
79	Genetic variation in remnant <i>Festuca hallii</i> populations is weakly differentiated, but geographically associated across the Canadian Prairie. <i>Plant Species Biology</i> , 2009, 24, 156-168.	0.6	14
80	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.	0.3	10
81	AFLP variation in 25 <i>Avena</i> species. <i>Theoretical and Applied Genetics</i> , 2008, 117, 333-342.	1.8	36
82	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
83	Patterns of amplified restriction fragment polymorphism in natural populations and corresponding seed collections of plains rough fescue ( <i>Festuca hallii</i> ). <i>Canadian Journal of Botany</i> , 2007, 85, 484-492.	1.2	14
84	Genetic Diversity of Canadian Soybean Cultivars and Exotic Germplasm Revealed by Simple Sequence Repeat Markers. <i>Crop Science</i> , 2007, 47, 1947-1954.	0.8	33
85	Microsatellite variation in <i>Avena sterilis</i> oat germplasm. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1029-1038.	1.8	31
86	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.	1.2	2
87	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.	0.4	48
88	Characterization of microsatellite markers for rough fescue species ( <i>Festuca</i> spp.). <i>Molecular Ecology Notes</i> , 2006, 6, 894-896.	1.7	7
89	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.	0.8	56
90	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.	0.8	7

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91	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.	1.8	77
92	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.	0.4	7
93	Redundancy and distinctness in flax germplasm as revealed by RAPD dissimilarity. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2006, 4, 117-124.	0.4	51
94	Geographic Patterns of RAPD Variation in Cultivated Flax. <i>Crop Science</i> , 2005, 45, 1084-1091.	0.8	46
95	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.	1.8	155
96	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.	1.8	82
97	Genetic diversity of Pakistan wheat germplasm as revealed by RAPD markers. <i>Genetic Resources and Crop Evolution</i> , 2005, 52, 239-244.	0.8	26
98	Detecting Genetic Changes over Two Generations of Seed Increase in an Awned Slender Wheatgrass Population Using AFLP Markers. <i>Crop Science</i> , 2005, 45, 1064-1068.	0.8	17
99	Genetic diversity of fringed brome ( <i>Bromus ciliatus</i> ) as determined by amplified fragment length polymorphism. <i>Canadian Journal of Botany</i> , 2005, 83, 1322-1328.	1.2	13
100	Long-Term Grazing Effects on Genetic Variability in Mountain Rough Fescue. <i>Rangeland Ecology and Management</i> , 2005, 58, 637-642.	1.1	24
101	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.	0.8	31
102	AFLP Variation in Four Blue Grama Seed Sources. <i>Crop Science</i> , 2004, 44, 283-288.	0.8	19
103	Marker-Based Inferences about the Genetic basis of Flowering time in <i>Mimulus Guttatus</i> . <i>Hereditas</i> , 2004, 121, 267-272.	0.5	4
104	Assessment of bulking strategies for RAPD analyses of flax germplasm. <i>Genetic Resources and Crop Evolution</i> , 2003, 50, 743-746.	0.8	14
105	Applications of bulking in molecular characterization of plant germplasm: a critical review. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2003, 1, 161-167.	0.4	20
106	Allelic Diversity Changes in 96 Canadian Oat Cultivars Released from 1886 to 2001. <i>Crop Science</i> , 2003, 43, 1989-1995.	0.8	93
107	RAPD Analysis of 54 North American Flax Cultivars. <i>Crop Science</i> , 2003, 43, 1510-1515.	0.8	59
108	RAPD Variations in Selected and Unselected Blue Grama Populations. <i>Crop Science</i> , 2003, 43, 1852-1857.	0.8	11

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109	Title is missing!. Genetic Resources and Crop Evolution, 2002, 49, 167-174.	0.8	65
110	RAPD analysis of genetic relationships of seven flax species in the genus <i>Linum</i> L. Genetic Resources and Crop Evolution, 2002, 49, 253-259.	0.8	59
111	Incomplete block designs for genetic testing: some practical considerations. Canadian Journal of Forest Research, 1999, 29, 1871-1878.	0.8	16
112	Spatial patterns of tree height variations in a series of Douglas-fir progeny trials: implications for genetic testing. Canadian Journal of Forest Research, 1999, 29, 714-723.	0.8	45
113	Comment-Enhanced heritabilities and best linear unbiased predictors through appropriate blocking of progeny trials. Canadian Journal of Forest Research, 1999, 29, 1633-1634.	0.8	3
114	Incomplete block designs for genetic testing: statistical efficiencies of estimating family means. Canadian Journal of Forest Research, 1998, 28, 977-986.	0.8	22
115	Comparison of Breeding Strategies for Purging Inbreeding Depression via Simulation. Conservation Biology, 1998, 12, 856-864.	2.4	34
116	Point estimation and graphical inference of marginal dominance for two viability loci controlling inbreeding depression. Genetical Research, 1997, 70, 143-153.	0.3	14
117	Characterizing Molecular Quantitative Variability for Inbreeding Depression. Plant Species Biology, 1996, 11, 23-31.	0.6	1
118	On estimating the linkage of marker genes to viability genes controlling inbreeding depression. Theoretical and Applied Genetics, 1994, 88, 925-932.	1.8	60
119	Marker-based inferences about fecundity genes contributing to inbreeding depression in <i>Mimulus guttatus</i> . Genome, 1994, 37, 1005-1010.	0.9	13
120	Pollen pool heterogeneity in jack pine ( <i>Pinus banksiana</i> Lamb.): a problem for estimating outcrossing rates?. Theoretical and Applied Genetics, 1992, 83, 500-508.	1.8	7