

Konstantin Krutovsky

List of Publications by Citations

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112
papers

2,117
citations

24
h-index

43
g-index

129
ext. papers

2,613
ext. citations

3
avg, IF

5.05
L-index

#	Paper	IF	Citations
112	Association genetics of coastal Douglas fir (<i>Pseudotsuga menziesii</i> var. <i>menziesii</i> , Pinaceae). I. Cold-hardiness related traits. <i>Genetics</i> , 2009 , 182, 1289-302	4	168
111	Forest-tree population genomics and adaptive evolution. <i>New Phytologist</i> , 2006 , 170, 227-38	9.8	168
110	Nucleotide diversity and linkage disequilibrium in cold-hardiness- and wood quality-related candidate genes in Douglas fir. <i>Genetics</i> , 2005 , 171, 2029-41	4	132
109	Comparative mapping in the Pinaceae. <i>Genetics</i> , 2004 , 168, 447-61	4	103
108	Mixed-species versus monocultures in plantation forestry: Development, benefits, ecosystem services and perspectives for the future. <i>Global Ecology and Conservation</i> , 2018 , 15, e00419	2.8	100
107	RAPDs and allozymes exhibit similar levels of diversity and differentiation among populations and races of Douglas-fir. <i>Heredity</i> , 1998 , 81, 69-78	3.6	93
106	Multilocus patterns of nucleotide diversity and divergence reveal positive selection at candidate genes related to cold hardiness in coastal Douglas Fir (<i>Pseudotsuga menziesii</i> var. <i>menziesii</i>). <i>Genetics</i> , 2009 , 183, 289-98	4	79
105	Introgressive hybridization and phylogenetic relationships between Norway, <i>Picea abies</i> (L.) Karst., and Siberian, <i>P. obovata</i> Ledeb., spruce species studied by isozyme loci. <i>Heredity</i> , 1995 , 74, 464-480	3.6	66
104	Structure and expression of duplicate AGAMOUS orthologues in poplar. <i>Plant Molecular Biology</i> , 2000 , 44, 619-34	4.6	65
103	Nuclear DNA diversity, population differentiation, and phylogenetic relationships in the California closed-cone pines based on RAPD and allozyme markers. <i>Genome</i> , 1999 , 42, 893-908	2.4	65
102	A DEFICIENS homolog from the dioecious tree black cottonwood is expressed in female and male floral meristems of the two-whorled, unisexual flowers. <i>Plant Physiology</i> , 2000 , 124, 627-40	6.6	51
101	An annotated genetic map of loblolly pine based on microsatellite and cDNA markers. <i>BMC Genetics</i> , 2011 , 12, 17	2.6	50
100	Evolution of exon-intron structure and alternative splicing. <i>PLoS ONE</i> , 2011 , 6, e18055	3.7	50
99	Mapping of quantitative trait loci controlling adaptive traits in coastal Douglas-fir. IV. Cold-hardiness QTL verification and candidate gene mapping. <i>Molecular Breeding</i> , 2005 , 15, 145-156	3.4	46
98	Highly variable SSR markers in Douglas-fir: Mendelian inheritance and map locations. <i>Theoretical and Applied Genetics</i> , 2004 , 108, 873-80	6	39
97	Genetic structure and association mapping of adaptive and selective traits in the east Texas loblolly pine (<i>Pinus taeda</i> L.) breeding populations. <i>Tree Genetics and Genomes</i> , 2013 , 9, 1161-1178	2.1	36
96	Self-citation can inflate h-index. <i>Scientometrics</i> , 2008 , 77, 373-375	3	36

95	Exome genotyping, linkage disequilibrium and population structure in loblolly pine (<i>Pinus taeda</i> L.). <i>BMC Genomics</i> , 2016 , 17, 730	4.5	35
94	RAPD Genome maps of Douglas-fir 1998 , 89, 197-205		35
93	Estimation of population structure in coastal Douglas-fir [<i>Pseudotsuga menziesii</i> (Mirb.) Franco var. <i>menziesii</i>] using allozyme and microsatellite markers. <i>Tree Genetics and Genomes</i> , 2009 , 5, 641-658	2.1	34
92	Relationships among the Spruces (<i>Picea</i> , Pinaceae) of Southwestern North America. <i>Systematic Botany</i> , 2004 , 29, 275-295	0.7	33
91	A Reference Genome Sequence for the European Silver Fir (Mill.): A Community-Generated Genomic Resource. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2039-2049	3.2	29
90	RAPD markers of mitochondrial origin exhibit lower population diversity and higher differentiation than RAPDs of nuclear origin in Douglas fir. <i>Molecular Ecology</i> , 1998 , 7, 801-812	5.7	25
89	Mobile genetic elements explain size variation in the mitochondrial genomes of four closely-related <i>Armillaria</i> species. <i>BMC Genomics</i> , 2019 , 20, 351	4.5	24
88	Stepwise large genome assembly approach: a case of Siberian larch (<i>Larix sibirica</i> Ledeb). <i>BMC Bioinformatics</i> , 2019 , 20, 37	3.6	24
87	Development of genetic markers in Eucalyptus species by target enrichment and exome sequencing. <i>PLoS ONE</i> , 2015 , 10, e0116528	3.7	24
86	Landscape Genomics: Understanding Relationships Between Environmental Heterogeneity and Genomic Characteristics of Populations. <i>Population Genomics</i> , 2017 , 261-322	1.4	23
85	Association genetics of growth and adaptive traits in loblolly pine (<i>Pinus taeda</i> L.) using whole-exome-discovered polymorphisms. <i>Tree Genetics and Genomes</i> , 2017 , 13, 1	2.1	21
84	Seed dispersal at alpine treeline: an assessment of seed movement within the alpine treeline ecotone. <i>Ecosphere</i> , 2017 , 8, e01649	3.1	20
83	Landscape genomic insights into the historic migration of mountain hemlock in response to Holocene climate change. <i>American Journal of Botany</i> , 2017 , 104, 439-450	2.7	20
82	Isolation of a full-length CCNBS-RR resistance gene analog candidate from sugar pine showing low nucleotide diversity. <i>Tree Genetics and Genomes</i> , 2006 , 2, 76-85	2.1	20
81	Genetic variation and signatures of natural selection in populations of European beech (<i>Fagus sylvatica</i> L.) along precipitation gradients. <i>Tree Genetics and Genomes</i> , 2018 , 14, 1	2.1	20
80	Conserved ortholog sets in forest trees. <i>Tree Genetics and Genomes</i> , 2006 , 3, 61-70	2.1	18
79	Response of Four Tree Species to Changing Climate in a Moisture-Limited Area of South Siberia. <i>Forests</i> , 2019 , 10, 999	2.8	15
78	Integrating DNA Barcoding and Traditional Taxonomy for the Identification of Dipterocarps in Remnant Lowland Forests of Sumatra. <i>Plants</i> , 2019 , 8,	4.5	14

77	Detecting the genetic basis of local adaptation in loblolly pine (L.) using whole exome-wide genotyping and an integrative landscape genomics analysis approach. <i>Ecology and Evolution</i> , 2019 , 9, 6798-6809	2.8	12
76	Gene Flow, Spatial Structure, Local Adaptation, and Assisted Migration in Trees 2012 , 71-116		12
75	Transferability and Polymorphism of SSR Markers Located in Flavonoid Pathway Genes in and Species. <i>Genes</i> , 2019 , 11,	4.2	12
74	Population Epigenomics: Advancing Understanding of Phenotypic Plasticity, Acclimation, Adaptation and Diseases. <i>Population Genomics</i> , 2018 , 179-260	1.4	12
73	Colonization history of Scots pine in Eastern Europe and North Asia based on mitochondrial DNA variation. <i>Tree Genetics and Genomes</i> , 2018 , 14, 1	2.1	10
72	The effect of individual genetic heterozygosity on general homeostasis, heterosis and resilience in Siberian larch (<i>Larix sibirica</i> Ledeb.) using dendrochronology and microsatellite loci genotyping. <i>Dendrochronologia</i> , 2016 , 38, 26-37	2.8	10
71	Somaclonal variation of haploid in vitro tissue culture obtained from Siberian larch (<i>Larix sibirica</i> Ledeb.) megagametophytes for whole genome de novo sequencing. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2014 , 50, 655-664	2.3	10
70	Saving the world's ash forests calls for international cooperation now. <i>Nature Ecology and Evolution</i> , 2019 , 3, 141-144	12.3	10
69	Predicting Adaptive Genetic Variation of Loblolly Pine (<i>Pinus taeda</i> L.) Populations Under Projected Future Climates Based on Multivariate Models. <i>Journal of Heredity</i> , 2019 , 110, 857-865	2.4	9
68	De novo assembling and primary analysis of genome and transcriptome of gray whale <i>Eschrichtius robustus</i> . <i>BMC Evolutionary Biology</i> , 2017 , 17, 258	3	9
67	Development of new mitochondrial DNA markers in Scots pine (<i>Pinus sylvestris</i> L.) for population and phylogeographic studies. <i>Russian Journal of Genetics</i> , 2015 , 51, 1199-1203	0.6	9
66	Genetic diversity and differentiation of introduced red oak (<i>Quercus rubra</i>) in Germany in comparison with reference native North American populations. <i>European Journal of Forest Research</i> , 2019 , 138, 275-285	2.7	8
65	From population genetics to population genomics of forest trees: Integrated population genomics approach. <i>Russian Journal of Genetics</i> , 2006 , 42, 1088-1100	0.6	8
64	Exploring the genetic basis of gene transcript abundance and metabolite levels in loblolly pine (<i>Pinus taeda</i> L.) using association mapping and network construction. <i>BMC Genetics</i> , 2018 , 19, 100	2.6	8
63	Siberian larch (<i>Larix sibirica</i> Ledeb.) chloroplast genome and development of polymorphic chloroplast markers. <i>BMC Bioinformatics</i> , 2019 , 20, 38	3.6	7
62	Morphological and genetic diversity of shea tree (<i>Vitellaria paradoxa</i>) in the savannah regions of Ghana. <i>Genetic Resources and Crop Evolution</i> , 2017 , 64, 1253-1268	2	7
61	Growth and Its Relationship to Individual Genetic Diversity of Mountain Hemlock (<i>Tsuga mertensiana</i>) at Alpine Treeline in Alaska: Combining Dendrochronology and Genomics. <i>Forests</i> , 2017 , 8, 418	2.8	7
60	Allozyme evidence for polyzygotic polyembryony in Siberian stone pine (<i>Pinus sibirica</i> Du Tour). <i>Theoretical and Applied Genetics</i> , 1995 , 90, 811-8	6	7

59	Genetic structure of coast redwood (<i>Sequoia sempervirens</i> [D. Don] Endl.) populations in and outside of the natural distribution range based on nuclear and chloroplast microsatellite markers. <i>PLoS ONE</i> , 2020 , 15, e0243556	3.7	7
58	High Morphological Differentiation in Crown Architecture Contrasts with Low Population Genetic Structure of German Norway Spruce Stands. <i>Forests</i> , 2018 , 9, 752	2.8	7
57	Bell Upas Sits, the Hydra-Tree of Death , or the Phytotoxicity of Trees. <i>Molecules</i> , 2019 , 24,	4.8	6
56	Conservation genetics and evolutionary history of <i>Gleditsia caspica</i> : Inferences from allozyme diversity in populations from Azerbaijan. <i>Conservation Genetics</i> , 2004 , 5, 195-204	2.6	6
55	Siberian larch (<i>Larix sibirica</i> Ledeb.) mitochondrial genome assembled using both short and long nucleotide sequence reads is currently the largest known mitogenome. <i>BMC Genomics</i> , 2020 , 21, 654	4.5	6
54	Development of microsatellite genetic markers in Siberian stone pine (<i>Pinus sibirica</i> Du Tour) based on the de novo whole genome sequencing. <i>Russian Journal of Genetics</i> , 2016 , 52, 1263-1271	0.6	6
53	Plant responses to global change: next generation biogeography. <i>Physical Geography</i> , 2016 , 37, 93-119	1.8	6
52	Differential expression of flowering genes in <i>Arabidopsis thaliana</i> under chronic and acute ionizing radiation. <i>International Journal of Radiation Biology</i> , 2019 , 95, 626-634	2.9	6
51	Morphological and Genetic Diversity of Sea Buckthorn (<i>Hippophae rhamnoides</i> L.) in the Karakoram Mountains of Northern Pakistan. <i>Diversity</i> , 2018 , 10, 76	2.5	6
50	Genetic variation of introduced red oak (<i>Quercus rubra</i>) stands in Germany compared to North American populations. <i>European Journal of Forest Research</i> , 2020 , 139, 321-331	2.7	5
49	Crown morphology in Norway spruce (<i>Picea abies</i> [Karst.] L.) as adaptation to mountainous environments is associated with single nucleotide polymorphisms (SNPs) in genes regulating seasonal growth rhythm. <i>Tree Genetics and Genomes</i> , 2020 , 16,	2.1	5
48	Selenium Nanocomposites in Natural Matrices as Potato Recovery Agent. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	5
47	Development of novel polymorphic nuclear and chloroplast microsatellite markers in coast redwood (<i>Sequoia sempervirens</i>). <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2019 , 17, 293-297	1.97	5
46	A candidate gene association analysis identifies SNPs potentially involved in drought tolerance in European beech (<i>Fagus sylvatica</i> L.). <i>Scientific Reports</i> , 2021 , 11, 2386	4.9	5
45	Genetic Variation of European Beech Populations and Their Progeny from Northeast Germany to Southwest Switzerland. <i>Forests</i> , 2018 , 9, 469	2.8	5
44	Assessment of Genetic Diversity in Differently Colored Raspberry Cultivars Using SSR Markers Located in Flavonoid Biosynthesis Genes. <i>Agronomy</i> , 2019 , 9, 518	3.6	4
43	Mitochondrial DNA in Siberian conifers indicates multiple postglacial colonization centers. <i>Canadian Journal of Forest Research</i> , 2019 , 49, 875-883	1.9	4
42	Gene-specific sex-linked genetic markers in date palm (<i>Phoenix dactylifera</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2018 , 65, 1-10	2	4

41	Advancing Biogeography Through Population Genomics. <i>Population Genomics</i> , 2018 , 539-585	1.4	4
40	Molecular evolution of drought tolerance and wood strength related candidate genes in loblolly pine (<i>Pinus taeda</i> L.). <i>Silvae Genetica</i> , 2014 , 63, 59-66	1.1	4
39	Development of novel <i>Quercus rubra</i> chloroplast genome CAPS markers for haplotype identification. <i>Silvae Genetica</i> , 2020 , 69, 78-85	1.1	4
38	Mass spectrometry reveals the presence of specific set of epigenetic DNA modifications in the Norway spruce genome. <i>Scientific Reports</i> , 2019 , 9, 19314	4.9	4
37	Development of microsatellite genetic markers in Siberian larch (<i>Larix sibirica</i> Ledeb.) based on the de novo whole genome sequencing. <i>Russian Journal of Genetics</i> , 2017 , 53, 1194-1199	0.6	3
36	Comparative Genetic Mapping in Trees: The Group of Conifers. <i>Biotechnology in Agriculture and Forestry</i> , 2004 , 267-277		3
35	Novel Nanobiocomposites Based on Natural Polysaccharides as Universal Trophic Low-Dose Micronutrients. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
34	Assignment of frost tolerant coast redwood trees of unknown origin to populations within their natural range using nuclear and chloroplast microsatellite genetic markers		3
33	De novo transcriptome assembly of cold stressed clones of the hexaploid <i>Sequoia sempervirens</i> (D. Don) Endl. <i>Scientific Data</i> , 2020 , 7, 239	8.2	3
32	De novo sequencing, assembly and functional annotation of <i>Armillaria borealis</i> genome. <i>BMC Genomics</i> , 2020 , 21, 534	4.5	3
31	Early Detection and Identification of the Main Fungal Pathogens for Resistance Evaluation of New Genotypes of Forest Trees. <i>Forests</i> , 2018 , 9, 732	2.8	3
30	Effect of Natural Polysaccharide Matrix-Based Selenium Nanocomposites on and Rhizospheric Microorganisms. <i>Nanomaterials</i> , 2021 , 11,	5.4	3
29	Structural and Functional Organization of the Mitochondrial DNA Control Region in the Woolly Mammoth (<i>Mammuthus primigenius</i>). <i>Molecular Biology</i> , 2019 , 53, 560-570	1.2	2
28	Taxonomy of dark- and white-barked birches related to <i>Betula pendula</i> and <i>B. pubescens</i> (Betulaceae) in Ukraine based on both morphological traits and DNA markers. <i>Botanical Journal of the Linnean Society</i> , 2019 , 191, 142-154	2.2	2
27	Effects of megagametophyte removal on DNA yield and early seedling growth in coastal Douglas-fir. <i>Canadian Journal of Forest Research</i> , 1997 , 27, 964-968	1.9	2
26	Various effects of the expression of the xyloglucanase gene from <i>Penicillium canescens</i> in transgenic aspen under semi-natural conditions. <i>BMC Plant Biology</i> , 2020 , 20, 251	5.3	2
25	Genetic diversity of common guava in Kenya: an underutilized naturalized fruit species. <i>Fruits</i> , 2019 , 74, 236-248	0.3	2
24	Targeted re-sequencing and genome-wide association analysis for wood property traits in breeding population of <i>Eucalyptus tereticornis</i> [E. grandis]. <i>Genomics</i> , 2021 , 113, 4276-4292	4.3	2

23	Conflicting genomic signals affect phylogenetic inference in four species of North American pines. <i>AoB PLANTS</i> , 2016 , 8,	2.9	2
22	De Novo Assembly and Cluster Analysis of Siberian Larch Transcriptome and Genome. <i>Lecture Notes in Computer Science</i> , 2016 , 455-464	0.9	2
21	Effect of Phosphinothricin on Transgenic Downy Birch (<i>Betula pubescens</i> Ehrh.) Containing bar or GS1 Genes. <i>Forests</i> , 2019 , 10, 1067	2.8	2
20	Complete mitochondrial genome of a woolly mammoth (<i>Mammuthus primigenius</i>) from Maly Lyakhovsky Island (New Siberian Islands, Russia) and its phylogenetic assessment. <i>Mitochondrial DNA Part B: Resources</i> , 2018 , 3, 596-598	0.5	2
19	Hybrid and Environmental Effects on Gene Expression in Poplar Clones in Pure and Mixed with Black Locust Stands. <i>Forests</i> , 2020 , 11, 1075	2.8	1
18	Genetic diversity and parentage analysis of aspen demes. <i>New Forests</i> , 2016 , 47, 143-162	2.6	1
17	Mechanical stress effects on transcriptional regulation of genes encoding microtubule- and actin-associated proteins.. <i>Physiology and Molecular Biology of Plants</i> , 2022 , 28, 17-30	2.8	1
16	Genetic mechanisms of aging in plants: What can we learn from them?. <i>Ageing Research Reviews</i> , 2022 , 101601	12	1
15	Tree Rings Reveal the Impact of Soil Temperature on Larch Growth in the Forest-Steppe of Siberia. <i>Forests</i> , 2021 , 12, 1765	2.8	1
14	Effect of Selenium Nanocomposites Based on Natural Polymer Matrices on the Biomass and Storage of Potato Tubers in a Field Experiment. <i>Agronomy</i> , 2022 , 12, 1281	3.6	1
13	Development of Nuclear Microsatellite Markers with Long (Tri-, Tetra-, Penta-, and Hexanucleotide) Motifs for Three Larch Species Based on the de novo Whole Genome Sequencing of Siberian Larch (<i>Larix sibirica</i> Ledeb.). <i>Russian Journal of Genetics</i> , 2019 , 55, 444-450	0.6	0
12	Response of Poplar Leaf Transcriptome to Changed Management and Environmental Conditions in Pure and Mixed with Black Locust Stands. <i>Forests</i> , 2022 , 13, 147	2.8	0
11	Postgenomic technologies in practical forestry: development of genome-wide markers for timber origin identification and other applications. <i>Forestry Engineering Journal</i> , 2019 , 9, 9-16	0.3	0
10	Chloroplast Haplotypes of Northern Red Oak (<i>Quercus rubra</i> L.) Stands in Germany Suggest Their Origin from Northeastern Canada. <i>Forests</i> , 2020 , 11, 1025	2.8	0
9	Mating System in a Native Norway Spruce (<i>Picea abies</i> [L.] KARST.) Stand-Relatedness and Effective Pollen Population Size Show an Association with the Germination Percentage of Single Tree Progenies. <i>Diversity</i> , 2020 , 12, 266	2.5	0
8	ITS secondary structure reconstruction to resolve taxonomy and phylogeny of the <i>L.</i> genus. <i>PeerJ</i> , 2021 , 9, e10889	3.1	0
7	Geographic Patterns of Genetic Variation among Cacao (<i>Theobroma cacao</i> L.) Populations Based on Chloroplast Markers. <i>Diversity</i> , 2021 , 13, 249	2.5	0
6	Genetic diversity and differentiation of <i>Olea europaea</i> subsp. <i>cuspidata</i> (Wall. & G.Don) Cif. in the Hajar Mountains of Oman. <i>Genetic Resources and Crop Evolution</i> , 2021 , 68, 865-883	2	0

- 5 Comparative analysis of alignment-free genome clustering and whole genome alignment-based phylogenomic relationship of coronaviruses.. *PLoS ONE*, **2022**, 17, e0264640 3.7 0
- 4 Symmetry in a Four-Cluster Triangle Structure of the Siberian Stone Pine (*Pinus sibirica* Du Tour) Transcriptome. *Proceedings (mdpi)*, **2018**, 2, 55 0.3
- 3 Symmetry in the Transcriptome and Genome Sequences of Siberian Larch (*Larix sibirica* Ledeb.). *Proceedings (mdpi)*, **2018**, 2, 56 0.3
- 2 Structure and Phylogeny of the Curly Birch Chloroplast Genome. *Frontiers in Genetics*, **2021**, 12, 625764 4.5
- 1 The role of jasmonate signaling pathway in plant's flowering genes response to ionizing radiation. *Visnik Ukrain's Kogo Tovaristva Genetikiv I Selektioneriv*, **2019**, 17, 45-50 0.3