

Konstantin Krutovsky

List of Publications by Year in descending order

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118
papers

3,028
citations

201385

27
h-index

197535

49
g-index

129
all docs

129
docs citations

129
times ranked

3048
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.0	210
2	Forest tree population genomics and adaptive evolution. <i>New Phytologist</i> , 2006, 170, 227-238.	3.5	206
3	Association Genetics of Coastal Douglas Fir (<i>Pseudotsuga menziesii</i> var. <i>menziesii</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 193	1.2	193
4	Nucleotide Diversity and Linkage Disequilibrium in Cold-Hardiness- and Wood Quality-Related Candidate Genes in Douglas Fir. <i>Genetics</i> , 2005, 171, 2029-2041.	1.2	167
5	Comparative Mapping in the Pinaceae. <i>Genetics</i> , 2004, 168, 447-461.	1.2	117
6	RAPDs and allozymes exhibit similar levels of diversity and differentiation among populations and races of Douglas-fir. <i>Heredity</i> , 1998, 81, 69-78.	1.2	100
7	Evolution of Exon-Intron Structure and Alternative Splicing. <i>PLoS ONE</i> , 2011, 6, e18055.	1.1	94
8	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.) Tj ETQq0 0 0 rgBT /Overlock 10 150 457 T	1.0	150
9	Structure and expression of duplicate AGAMOUS orthologues in poplar. <i>Plant Molecular Biology</i> , 2000, 44, 619-634.	2.0	88
10	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.	1.2	78
11	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.	0.9	78
12	An annotated genetic map of loblolly pine based on microsatellite and cDNA markers. <i>BMC Genetics</i> , 2011, 12, 17.	2.7	60
13	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, 627-640.	2.3	56
14	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.	1.0	53
15	Exome genotyping, linkage disequilibrium and population structure in loblolly pine (<i>Pinus taeda</i> L.). <i>BMC Genomics</i> , 2016, 17, 730.	1.2	53
16	A Reference Genome Sequence for the European Silver Fir (<i>Abies alba</i> Mill.): A Community-Generated Genomic Resource. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2039-2049.	0.8	53
17	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.	1.2	51
18	RAPD Genome maps of Douglas-fir. , 1998, 89, 197-205.		50

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19	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.	1.2	49
20	Highly variable SSR markers in Douglas-fir: Mendelian inheritance and map locations. <i>Theoretical and Applied Genetics</i> , 2004, 108, 873-880.	1.8	47
21	Landscape Genomics: Understanding Relationships Between Environmental Heterogeneity and Genomic Characteristics of Populations. <i>Population Genomics</i> , 2017, , 261-322.	0.2	46
22	Self-citation can inflate h-index. <i>Scientometrics</i> , 2008, 77, 373-375.	1.6	45
23	Relationships among the Spruces (<i>Picea</i> , Pinaceae) of Southwestern North America. <i>Systematic Botany</i> , 2004, 29, 275-295.	0.2	42
24	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.	0.6	40
25	Stepwise large genome assembly approach: a case of Siberian larch (<i>Larix sibirica</i> Ledeb). <i>BMC Bioinformatics</i> , 2019, 20, 37.	1.2	40
26	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.	0.6	39
27	Genetic variation and signatures of natural selection in populations of European beech (<i>Fagus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.6	38
28	Development of Genetic Markers in Eucalyptus Species by Target Enrichment and Exome Sequencing. <i>PLoS ONE</i> , 2015, 10, e0116528.	1.1	29
29	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.	0.6	29
30	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.	2.0	25
31	Detecting the genetic basis of local adaptation in loblolly pine (<i>Pinus taeda</i> L.) using whole exome-wide genotyping and an integrative landscape genomics analysis approach. <i>Ecology and Evolution</i> , 2019, 9, 6798-6809.	0.8	25
32	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.	0.8	24
33	Integrating DNA Barcoding and Traditional Taxonomy for the Identification of Dipterocarps in Remnant Lowland Forests of Sumatra. <i>Plants</i> , 2019, 8, 461.	1.6	24
34	Seed dispersal at alpine treeline: an assessment of seed movement within the alpine treeline ecotone. <i>Ecosphere</i> , 2017, 8, e01649.	1.0	23
35	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.	0.6	23
36	Response of Four Tree Species to Changing Climate in a Moisture-Limited Area of South Siberia. <i>Forests</i> , 2019, 10, 999.	0.9	23

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37	Isolation of a full-length CC–NBS–LRR resistance gene analog candidate from sugar pine showing low nucleotide diversity. <i>Tree Genetics and Genomes</i> , 2006, 2, 76-85.	0.6	22
38	Conserved ortholog sets in forest trees. <i>Tree Genetics and Genomes</i> , 2006, 3, 61-70.	0.6	22
39	Transferability and Polymorphism of SSR Markers Located in Flavonoid Pathway Genes in <i>Fragaria</i> and <i>Rubus</i> Species. <i>Genes</i> , 2020, 11, 11.	1.0	21
40	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.	1.0	18
41	Population Epigenomics: Advancing Understanding of Phenotypic Plasticity, Acclimation, Adaptation and Diseases. <i>Population Genomics</i> , 2018, , 179-260.	0.2	18
42	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.	1.6	16
43	Somaclonal variation of haploid in vitro tissue culture obtained from Siberian larch (<i>Larix sibirica</i>) Tj ETQq1 1 0.784314 rgBT /Overlock II <i>Biology - Plant</i> , 2014, 50, 655-664.	0.9	15
44	Siberian larch (<i>Larix sibirica</i> Ledeb.) chloroplast genome and development of polymorphic chloroplast markers. <i>BMC Bioinformatics</i> , 2019, 20, 38.	1.2	15
45	Gene Flow, Spatial Structure, Local Adaptation, and Assisted Migration in Trees. , 2012, , 71-116.		14
46	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.	1.1	13
47	Saving the world’s ash forests calls for international cooperation now. <i>Nature Ecology and Evolution</i> , 2019, 3, 141-144.	3.4	13
48	Effect of Natural Polysaccharide Matrix-Based Selenium Nanocomposites on <i>Phytophthora cactorum</i> and Rhizospheric Microorganisms. <i>Nanomaterials</i> , 2021, 11, 2274.	1.9	13
49	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.	1.0	12
50	Selenium Nanocomposites in Natural Matrices as Potato Recovery Agent. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4576.	1.8	12
51	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.	1.1	12
52	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.	0.2	11
53	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.	3.2	11
54	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.	0.7	11

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55	Assessment of Genetic Diversity in Differently Colored Raspberry Cultivars Using SSR Markers Located in Flavonoid Biosynthesis Genes. <i>Agronomy</i> , 2019, 9, 518.	1.3	11
56	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.	1.0	11
57	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.	0.8	10
58	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.	0.9	10
59	Exploring the genetic basis of gene transcript abundance and metabolite levels in loblolly pine (<i>Pinus</i>)	2.7	10
60	â€¦ Fell Upas Sits, the Hydra-Tree of Death â€¦, or the Phytotoxicity of Trees. <i>Molecules</i> , 2019, 24, 1636.	1.7	10
61	Novel Nanobiocomposites Based on Natural Polysaccharides as Universal Trophic Low-Dose Micronutrients. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12006.	1.8	10
62	<i>Larix</i> species range dynamics in Siberia since the Last Glacial captured from sedimentary ancient DNA. <i>Communications Biology</i> , 2022, 5, .	2.0	10
63	Allozyme evidence for polyzygotic polyembryony in Siberian stone pine (<i>Pinus sibirica</i> Du Tour). <i>Theoretical and Applied Genetics</i> , 1995, 90, 811-818.	1.8	9
64	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.	0.8	9
65	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.	0.2	9
66	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.	0.8	9
67	Mitochondrial DNA in Siberian conifers indicates multiple postglacial colonization centers. <i>Canadian Journal of Forest Research</i> , 2019, 49, 875-883.	0.8	9
68	Mass spectrometry reveals the presence of specific set of epigenetic DNA modifications in the Norway spruce genome. <i>Scientific Reports</i> , 2019, 9, 19314.	1.6	9
69	From population genetics to population genomics of forest trees: Integrated population genomics approach. <i>Russian Journal of Genetics</i> , 2006, 42, 1088-1100.	0.2	8
70	Plant responses to global change: next generation biogeography. <i>Physical Geography</i> , 2016, 37, 93-119.	0.6	8
71	High Morphological Differentiation in Crown Architecture Contrasts with Low Population Genetic Structure of German Norway Spruce Stands. <i>Forests</i> , 2018, 9, 752.	0.9	8
72	Genetic Variation of European Beech Populations and Their Progeny from Northeast Germany to Southwest Switzerland. <i>Forests</i> , 2018, 9, 469.	0.9	8

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73	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, .	0.6	8
74	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.	0.2	7
75	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.	0.2	7
76	Advancing Biogeography Through Population Genomics. <i>Population Genomics</i> , 2018, , 539-585.	0.2	7
77	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.	0.8	7
78	De novo sequencing, assembly and functional annotation of <i>Armillaria borealis</i> genome. <i>BMC Genomics</i> , 2020, 21, 534.	1.2	7
79	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.	1.1	7
80	Targeted re-sequencing and genome-wide association analysis for wood property traits in breeding population of <i>Eucalyptus tereticornis</i> A— <i>E. grandis</i> . <i>Genomics</i> , 2021, 113, 4276-4292.	1.3	7
81	De novo transcriptome assembly of cold stressed clones of the hexaploid <i>Sequoia sempervirens</i> (D.) Tj ETQq1 1 0.784314 rgBT /Overl 2.4	2.4	6
82	Genetic diversity of common guava in Kenya: an underutilized naturalized fruit species. <i>Fruits</i> , 2019, 74, 236-248.	0.3	6
83	Genetic mechanisms of aging in plants: What can we learn from them?. <i>Ageing Research Reviews</i> , 2022, 77, 101601.	5.0	6
84	Tree Rings Reveal the Impact of Soil Temperature on Larch Growth in the Forest-Steppe of Siberia. <i>Forests</i> , 2021, 12, 1765.	0.9	6
85	Early Detection and Identification of the Main Fungal Pathogens for Resistance Evaluation of New Genotypes of Forest Trees. <i>Forests</i> , 2018, 9, 732.	0.9	5
86	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.	0.4	5
87	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.	1.6	5
88	Development of novel <i>Quercus rubra</i> chloroplast genome CAPS markers for haplotype identification. <i>Silvae Genetica</i> , 2020, 69, 78-85.	0.4	5
89	Species- and Age-Specific Growth Reactions to Extreme Droughts of the Keystone Tree Species across Forest-Steppe and Sub-Taiga Habitats of South Siberia. <i>Forests</i> , 2022, 13, 1027.	0.9	5
90	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.	0.4	4

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91	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.	0.2	4
92	Effect of Phosphinothricin on Transgenic Downy Birch (<i>Betula pubescens</i> Ehrh.) Containing bar or GS1 Genes. <i>Forests</i> , 2019, 10, 1067.	0.9	4
93	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.	0.9	4
94	Genome-Wide Prediction of Transcription Start Sites in Conifers. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1735.	1.8	4
95	Comparative analysis of alignment-free genome clustering and whole genome alignment-based phylogenomic relationship of coronaviruses. <i>PLoS ONE</i> , 2022, 17, e0264640.	1.1	4
96	Comparative Genomics of Seasonal Senescence in Forest Trees. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3761.	1.8	4
97	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.	1.3	4
98	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.	0.8	3
99	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.	0.4	3
100	Hybrid and Environmental Effects on Gene Expression in Poplar Clones in Pure and Mixed with Black Locust Stands. <i>Forests</i> , 2020, 11, 1075.	0.9	3
101	ITS secondary structure reconstruction to resolve taxonomy and phylogeny of the <i>Betula</i> L. genus. <i>PeerJ</i> , 2021, 9, e10889.	0.9	3
102	Structure and Phylogeny of the Curly Birch Chloroplast Genome. <i>Frontiers in Genetics</i> , 2021, 12, 625764.	1.1	3
103	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.	0.1	3
104	Conflicting genomic signals affect phylogenetic inference in four species of North American pines. <i>AoB PLANTS</i> , 2016, 8, .	1.2	2
105	De Novo Assembly and Cluster Analysis of Siberian Larch Transcriptome and Genome. <i>Lecture Notes in Computer Science</i> , 2016, , 455-464.	1.0	2
106	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.	0.7	2
107	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.	0.8	2
108	Geographic Patterns of Genetic Variation among Cacao (<i>Theobroma cacao</i> L.) Populations Based on Chloroplast Markers. <i>Diversity</i> , 2021, 13, 249.	0.7	2

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109	Comparative Genomics Analysis of Repetitive Elements in Ten Gymnosperm Species: “Dark Repeatome” and Its Abundance in Conifer and Gnetum Species. <i>Life</i> , 2021, 11, 1234.	1.1	2
110	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.	1.4	2
111	Genetic diversity and parentage analysis of aspen demes. <i>New Forests</i> , 2016, 47, 143-162.	0.7	1
112	Seven-Cluster Structure of Larch Chloroplast Genome. <i>Journal of Siberian Federal University - Biology</i> , 2015, 8, 268-277.	0.2	1
113	Symmetry of Siberian Larch Transcriptome. <i>Journal of Siberian Federal University - Biology</i> , 2015, 8, 278-286.	0.2	1
114	Phylogenetic Relationships, Pathogenic Traits, and Wood-Destroying Properties of <i>Porodaedalea niemelaei</i> M. Fischer Isolated in the Northern Forest Limit of <i>Larix gmelinii</i> Open Woodlands in the Permafrost Area. <i>Journal of Siberian Federal University - Biology</i> , 0, , 1-19.	0.2	1
115	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.	0.9	1
116	Symmetry in a Four-Cluster Triangle Structure of the Siberian Stone Pine (<i>Pinus sibirica</i> Du Tour) Transcriptome. <i>Proceedings (mdpi)</i> , 2018, 2, 55.	0.2	0
117	Symmetry in the Transcriptome and Genome Sequences of Siberian Larch (<i>Larix sibirica</i> Ledeb.). <i>Proceedings (mdpi)</i> , 2018, 2, .	0.2	0
118	The role of jasmonate signaling pathway in plant’s flowering genes response to ionizing radiation. <i>Visnik Ukrain’s Kogo Tovaristva Genetikiv I Selektioneriv</i> , 2019, 17, 45-50.	0.4	0