

Páll K Ingvarsson

List of Publications by Year in descending order

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Version: 2024-02-01

130
papers

8,272
citations

53794

45
h-index

54911

84
g-index

154
all docs

154
docs citations

154
times ranked

8920
citing authors

#	ARTICLE	IF	CITATIONS
1	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	27.8	1,303
2	Association genetics of complex traits in plants. <i>New Phytologist</i> , 2011, 189, 909-922.	7.3	306
3	Local drift load and the heterosis of interconnected populations. <i>Heredity</i> , 2000, 84, 452-457.	2.6	240
4	Nucleotide Polymorphism and Linkage Disequilibrium Within and Among Natural Populations of European Aspen (<i>Populus tremula</i> L., Salicaceae). <i>Genetics</i> , 2005, 169, 945-953.	2.9	236
5	Common features of segregation distortion in plants and animals. <i>Genetica</i> , 2003, 117, 27-35.	1.1	218
6	Restoration of genetic variation lost – the genetic rescue hypothesis. <i>Trends in Ecology and Evolution</i> , 2001, 16, 62-63.	8.7	186
7	Using association mapping to dissect the genetic basis of complex traits in plants. <i>Briefings in Functional Genomics</i> , 2010, 9, 157-165.	2.7	174
8	Multilocus Patterns of Nucleotide Polymorphism and the Demographic History of <i>Populus tremula</i> . <i>Genetics</i> , 2008, 180, 329-340.	2.9	173
9	Insights into Conifer Giga-Genomes. <i>Plant Physiology</i> , 2014, 166, 1724-1732.	4.8	164
10	Contrasting Rates of Molecular Evolution and Patterns of Selection among Gymnosperms and Flowering Plants. <i>Molecular Biology and Evolution</i> , 2017, 34, 1363-1377.	8.9	164
11	ADAPTIVE POPULATION DIFFERENTIATION IN PHENOLOGY ACROSS A LATITUDINAL GRADIENT IN EUROPEAN ASPEN (<i>POPULUS TREMULA</i> , L.): A COMPARISON OF NEUTRAL MARKERS, CANDIDATE GENES AND PHENOTYPIC TRAITS. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 2849-2860.	2.3	161
12	Clinal Variation in phyB2, a Candidate Gene for Day-Length-Induced Growth Cessation and Bud Set, Across a Latitudinal Gradient in European Aspen (<i>Populus tremula</i>). <i>Genetics</i> , 2006, 172, 1845-1853.	2.9	156
13	Nucleotide Polymorphism and Phenotypic Associations Within and Around the <i>phytochrome B2</i> Locus in European Aspen (<i>Populus tremula</i> , Salicaceae). <i>Genetics</i> , 2008, 178, 2217-2226.	2.9	151
14	Molecular Evolution of Insertions and Deletion in the Chloroplast Genome of <i>Silene</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 1737-1740.	8.9	146
15	Natural phenological variation in aspen (<i>Populus tremula</i>): the SwAsp collection. <i>Tree Genetics and Genomes</i> , 2008, 4, 279-292.	1.6	140
16	A single gene underlies the dynamic evolution of poplar sex determination. <i>Nature Plants</i> , 2020, 6, 630-637.	9.3	138
17	Population, quantitative and comparative genomics of adaptation in forest trees. <i>Current Opinion in Plant Biology</i> , 2008, 11, 149-155.	7.1	136
18	A METAPOPOPULATION PERSPECTIVE ON GENETIC DIVERSITY AND DIFFERENTIATION IN PARTIALLY SELF-FERTILIZING PLANTS. <i>Evolution; International Journal of Organic Evolution</i> , 2002, 56, 2368-2373.	2.3	134

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19	Gene Expression and Protein Length Influence Codon Usage and Rates of Sequence Evolution in <i>Populus tremula</i> . <i>Molecular Biology and Evolution</i> , 2006, 24, 836-844.	8.9	121
20	Admixture facilitates adaptation from standing variation in the European aspen (<i>Populus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 T	3.9	108
21	Heterosis increases the effective migration rate. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 1321-1326.	2.6	107
22	Gene co-expression network connectivity is an important determinant of selective constraint. <i>PLoS Genetics</i> , 2017, 13, e1006402.	3.5	106
23	Evaluating the accuracy of genomic prediction of growth and wood traits in two <i>Eucalyptus</i> species and their F1 hybrids. <i>BMC Plant Biology</i> , 2017, 17, 110.	3.6	104
24	GENE FLOW AND SELECTION ON PHENOTYPIC PLASTICITY IN AN ISLAND SYSTEM OF <i>RANA TEMPORARIA</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 684-697.	2.3	95
25	Natural Selection and Recombination Rate Variation Shape Nucleotide Polymorphism Across the Genomes of Three Related <i>Populus</i> Species. <i>Genetics</i> , 2016, 202, 1185-1200.	2.9	93
26	Towards decoding the conifer giga-genome. <i>Plant Molecular Biology</i> , 2012, 80, 555-569.	3.9	91
27	Analysis of conifer <i>FLOWERING LOCUS T</i> / <i>TERMINAL FLOWER1</i> -like genes provides evidence for dramatic biochemical evolution in the angiosperm <i>FT</i> lineage. <i>New Phytologist</i> , 2012, 196, 1260-1273.	7.3	90
28	Genetic Differentiation, Clinal Variation and Phenotypic Associations With Growth Cessation Across the <i>Populus tremula</i> Photoperiodic Pathway. <i>Genetics</i> , 2010, 186, 1033-1044.	2.9	86
29	Functional and evolutionary genomic inferences in <i>Populus</i> through genome and population sequencing of American and European aspen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10970-E10978.	7.1	84
30	Variation in Linked Selection and Recombination Drive Genomic Divergence during Allopatric Speciation of European and American Aspens. <i>Molecular Biology and Evolution</i> , 2016, 33, 1754-1767.	8.9	83
31	Demography and speciation history of the homoploid hybrid pine <i>Pinus densata</i> on the Tibetan Plateau. <i>Molecular Ecology</i> , 2012, 21, 4811-4827.	3.9	82
32	Genome-wide association study of agronomic traits in bread wheat reveals novel putative alleles for future breeding programs. <i>BMC Plant Biology</i> , 2019, 19, 541.	3.6	77
33	Molecular evolution of synonymous codon usage in <i>Populus</i> . <i>BMC Evolutionary Biology</i> , 2008, 8, 307.	3.2	76
34	Natural Selection on Synonymous and Nonsynonymous Mutations Shapes Patterns of Polymorphism in <i>Populus tremula</i> . <i>Molecular Biology and Evolution</i> , 2010, 27, 650-660.	8.9	76
35	A major locus controls local adaptation and adaptive life history variation in a perennial plant. <i>Genome Biology</i> , 2018, 19, 72.	8.8	76
36	Single-Copy Genes as Molecular Markers for Phylogenomic Studies in Seed Plants. <i>Genome Biology and Evolution</i> , 2017, 9, 1130-1147.	2.5	75

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37	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 August 2009â€“30 September 2009. <i>Molecular Ecology Resources</i> , 2010, 10, 232-236.	4.8	71
38	Genetic Variation in Functional Traits Influences Arthropod Community Composition in Aspen (<i>Populus tremula</i> L.). <i>PLoS ONE</i> , 2012, 7, e37679.	2.5	70
39	Floral sex ratios, disease and seed set in dioecious <i>Silene dioica</i> . <i>Journal of Ecology</i> , 1998, 86, 79-91.	4.0	69
40	Geographic structure in metabolome and herbivore community coâ€“occurs with genetic structure in plant defence genes. <i>Ecology Letters</i> , 2013, 16, 791-798.	6.4	63
41	Genome-Wide Analysis Reveals Diverged Patterns of Codon Bias, Gene Expression, and Rates of Sequence Evolution in <i>Picea</i> Gene Families. <i>Genome Biology and Evolution</i> , 2015, 7, 1002-1015.	2.5	63
42	Genomic relationships reveal significant dominance effects for growth in hybrid <i>Eucalyptus</i> . <i>Plant Science</i> , 2018, 267, 84-93.	3.6	60
43	Genealogical evidence for epidemics of selfish genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11265-11269.	7.1	59
44	KIN-STRUCTURED COLONIZATION AND SMALL-SCALE GENETIC DIFFERENTIATION IN <i>SILENE DIOICA</i> . <i>Evolution; International Journal of Organic Evolution</i> , 1999, 53, 605-611.	2.3	53
45	Variation in Mutation Rate and Polymorphism Among Mitochondrial Genes of <i>Silene vulgaris</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 1783-1791.	8.9	51
46	Whole genome duplication in coast redwood (<i>Sequoia sempervirens</i>) and its implications for explaining the rarity of polyploidy in conifers. <i>New Phytologist</i> , 2016, 211, 186-193.	7.3	49
47	Genomeâ€“wide association study identified novel candidate loci affecting wood formation in Norway spruce. <i>Plant Journal</i> , 2019, 100, 83-100.	5.7	49
48	Local Selection Across a Latitudinal Gradient Shapes Nucleotide Diversity in Balsam Poplar, <i>Populus balsamifera</i> L. <i>Genetics</i> , 2011, 188, 941-952.	2.9	47
49	Evolutionary Origins of Pseudogenes and Their Association with Regulatory Sequences in Plants. <i>Plant Cell</i> , 2019, 31, 563-578.	6.6	47
50	Genetic architecture and genomic patterns of gene flow between hybridizing species of <i>Picea</i> . <i>Heredity</i> , 2015, 115, 153-164.	2.6	46
51	Identification of additive, dominant, and epistatic variation conferred by key genes in cellulose biosynthesis pathway in <i>Populus tomentosa</i> . <i>DNA Research</i> , 2015, 22, 53-67.	3.4	46
52	<i>Populus tremula</i> (European aspen) shows no evidence of sexual dimorphism. <i>BMC Plant Biology</i> , 2014, 14, 276.	3.6	45
53	Genomeâ€“wide signatures of environmental adaptation in European aspen (<i>Populus tremula</i>) under current and future climate conditions. <i>Evolutionary Applications</i> , 2020, 13, 132-142.	3.1	43
54	Autumn senescence in aspen is not triggered by day length. <i>Physiologia Plantarum</i> , 2018, 162, 123-134.	5.2	40

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55	The effects of clonal forestry on genetic diversity in wild and domesticated stands of forest trees. <i>Scandinavian Journal of Forest Research</i> , 2019, 34, 370-379.	1.4	39
56	An Ultra-Dense Haploid Genetic Map for Evaluating the Highly Fragmented Genome Assembly of Norway Spruce (<i>Picea abies</i>). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1623-1632.	1.8	39
57	Natural selection on floral traits of female <i>Silene dioica</i> by a sexually transmitted disease. <i>New Phytologist</i> , 2006, 169, 729-739.	7.3	37
58	Population subdivision and the Hudson-Kreitman-Aguade test: testing for deviations from the neutral model in organelle genomes. <i>Genetical Research</i> , 2004, 83, 31-39.	0.9	34
59	Multilocus analysis of nucleotide variation and speciation in three closely related <i>Populus</i> (<i>Salicaceae</i>) species. <i>Molecular Ecology</i> , 2015, 24, 4994-5005.	3.9	33
60	Spatial and temporal variation in disease levels of a floral smut (<i>Anthracoidea heterospora</i>) on <i>Carex nigra</i> . <i>Journal of Ecology</i> , 1998, 86, 53-61.	4.0	32
61	Molecular Population Genetics of Herbivore-induced Protease Inhibitor Genes in European Aspen (<i>Populus tremula</i> L., <i>Salicaceae</i>). <i>Molecular Biology and Evolution</i> , 2005, 22, 1802-1812.	8.9	32
62	EXTINCTION-RECOLONIZATION DYNAMICS IN THE MYCOPHAGOUS BEETLE PHALACRUS SUBSTRIATUS. <i>Evolution; International Journal of Organic Evolution</i> , 1997, 51, 187-195.	2.3	31
63	Evolutionary Quantitative Genomics of <i>Populus trichocarpa</i> . <i>PLoS ONE</i> , 2015, 10, e0142864.	2.5	31
64	Towards integration of population and comparative genomics in forest trees. <i>New Phytologist</i> , 2016, 212, 338-344.	7.3	31
65	Evidence for widespread selection in shaping the genomic landscape during speciation of <i>Populus</i> . <i>Molecular Ecology</i> , 2020, 29, 1120-1136.	3.9	31
66	Demography and Natural Selection Have Shaped Genetic Variation in the Widely Distributed Conifer Norway Spruce (<i>Picea abies</i>). <i>Genome Biology and Evolution</i> , 2020, 12, 3803-3817.	2.5	30
67	Large-scale patterns in genetic variation, gene flow and differentiation in five species of European Coenagrionid damselfly provide mixed support for the central-marginal hypothesis. <i>Ecography</i> , 2013, 36, 744-755.	4.5	29
68	Demographic History and Natural Selection Shape Patterns of Deleterious Mutation Load and Barriers to Introgression across <i>Populus</i> Genome. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	29
69	Linkage disequilibrium vs. pedigree: Genomic selection prediction accuracy in conifer species. <i>PLoS ONE</i> , 2020, 15, e0232201.	2.5	28
70	Patterns of Attack by Insect Herbivores and a Fungus on Saplings in a Tropical Tree Plantation. <i>Environmental Entomology</i> , 1995, 24, 1487-1494.	1.4	26
71	Development of a highly efficient 50K single nucleotide polymorphism genotyping array for the large and complex genome of Norway spruce (<i>Picea abies</i> L. Karst) by whole genome resequencing and its transferability to other spruce species. <i>Molecular Ecology Resources</i> , 2021, 21, 880-896.	4.8	26
72	Adaptive evolution of the <i>Populus tremula</i> photoperiod pathway. <i>Molecular Ecology</i> , 2011, 20, 1463-1474.	3.9	25

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73	Comparative Nucleotide Diversity Across North American and European Populus Species. Journal of Molecular Evolution, 2012, 74, 257-272.	1.8	25
74	Linking plant genes to insect communities: Identifying the genetic bases of plant traits and community composition. Molecular Ecology, 2019, 28, 4404-4421.	3.9	25
75	Inferring the Genomic Landscape of Recombination Rate Variation in European Aspen (<i>Populus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	24
76	Lone wolf to the rescue. Nature, 2002, 420, 472-472.	27.8	23
77	THE EFFECT OF DELAYED POPULATION GROWTH ON THE GENETIC DIFFERENTIATION OF LOCAL POPULATIONS SUBJECT TO FREQUENT EXTINCTIONS AND RECOLONIZATIONS. Evolution; International Journal of Organic Evolution, 1997, 51, 29-35.	2.3	22
78	Population Dynamics of Resource Limited Plants and Their Pollinators. Theoretical Population Biology, 1998, 54, 44-49.	1.1	22
79	Extinction-Recolonization Dynamics in the Mycophagous Beetle Phalacrus substriatus. Evolution; International Journal of Organic Evolution, 1997, 51, 187.	2.3	21
80	Molecular Evolution of a Small Gene Family of Wound Inducible Kunitz Trypsin Inhibitors in Populus. Journal of Molecular Evolution, 2006, 63, 108-119.	1.8	21
81	Pollinator functional response and plant population dynamics: Pollinators as a limiting resource. Evolutionary Ecology, 1995, 9, 421-428.	1.2	20
82	Kin-structured colonization in Phalacrus substriatus. Heredity, 1998, 80, 456-463.	2.6	20
83	Kin-Structured Colonization and Small-Scale Genetic Differentiation in Silene dioica. Evolution; International Journal of Organic Evolution, 1999, 53, 605.	2.3	20
84	Storage lipid accumulation is controlled by photoperiodic signal acting via regulators of growth cessation and dormancy in hybrid aspen. New Phytologist, 2018, 219, 619-630.	7.3	20
85	Molecular Population Genetics of Elicitor-Induced Resistance Genes in European Aspen (Populus) Tj ETQq1 1 0.784314 rgBT /Overlock	2.5	20
86	A METAPOPOPULATION PERSPECTIVE ON GENETIC DIVERSITY AND DIFFERENTIATION IN PARTIALLY SELF-FERTILIZING PLANTS. Evolution; International Journal of Organic Evolution, 2002, 56, 2368.	2.3	19
87	Adaptive Introgression Facilitates Adaptation to High Latitudes in European Aspen (<i>Populus) Tj ETQq1 1 0.784314 rgBT /Overlock	3.9	19
88	BatchMap: A parallel implementation of the OneMap R package for fast computation of F1 linkage maps in outcrossing species. PLoS ONE, 2017, 12, e0189256.	2.5	19
89	Using Norway spruce clones in Swedish forestry: implications of clones for management. Scandinavian Journal of Forest Research, 2019, 34, 390-404.	1.4	17
90	Genetic Status of the Swedish Central collection of heirloom apple cultivars. Scientia Horticulturae, 2020, 272, 109599.	3.6	16

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91	Evolution of strong reproductive isolation in plants: broad-scale patterns and lessons from a perennial model group. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190544.	4.0	16
92	Evolution of the G-matrix in life history traits in the common frog during a recent colonisation of an island system. <i>Evolutionary Ecology</i> , 2012, 26, 863-878.	1.2	15
93	Quantitative genetic architecture of adaptive phenology traits in the deciduous tree, <i>Populus trichocarpa</i> (Torr. and Gray). <i>Heredity</i> , 2020, 125, 449-458.	2.6	15
94	The Effect of Delayed Population Growth on the Genetic Differentiation of Local Populations Subject to Frequent Extinctions and Recolonizations. <i>Evolution; International Journal of Organic Evolution</i> , 1997, 51, 29.	2.3	14
95	Linked selection shapes the landscape of genomic variation in three oak species. <i>New Phytologist</i> , 2022, 233, 555-568.	7.3	14
96	Hierarchical genetic structure and effective population sizes in <i>Phalacrus substriatus</i> . <i>Heredity</i> , 1997, 79, 153-161.	2.6	13
97	Geographical structure and adaptive population differentiation in herbivore defence genes in European aspen (<i>Populus tremula</i> L., Salicaceae). <i>Molecular Ecology</i> , 2012, 21, 2197-2207.	3.9	13
98	Adaptive signals of flowering time pathways in wild barley from Israel over 28 generations. <i>Heredity</i> , 2020, 124, 62-76.	2.6	13
99	Integration of genome wide association studies and co-expression networks reveal roles of <i>PtoWRKY42</i> and <i>PtoUGT76C1</i> in <i>trans</i> -zeatin metabolism and cytokinin sensitivity in poplar. <i>New Phytologist</i> , 2021, 231, 1462-1477.	7.3	13
100	An excess of nonsynonymous polymorphism and extensive haplotype structure at the <i>PtABI1B</i> locus in European aspen (<i>Populus tremula</i>): a case of balancing selection in an obligately outcrossing plant?. <i>Heredity</i> , 2007, 99, 381-388.	2.6	12
101	Increased genetic divergence between two closely related fir species in areas of range overlap. <i>Ecology and Evolution</i> , 2014, 4, 1019-1029.	1.9	12
102	Estimates of structural complexity in clonal plant morphology: comparisons of grazed and ungrazed <i>Acaena magellanica</i> rhizomes. <i>Canadian Journal of Botany</i> , 1999, 77, 869-876.	1.1	12
103	LncRNA PMAT ¹ module represses <i>PtoMATE</i> and <i>PtoARF2</i> promoting Pb ²⁺ uptake and plant growth in poplar. <i>Journal of Hazardous Materials</i> , 2022, 433, 128769.	12.4	12
104	Integrating genome-wide association mapping of additive and dominance genetic effects to improve genomic prediction accuracy in <i>Eucalyptus</i> . <i>Plant Genome</i> , 2022, 15, e20208.	2.8	12
105	Molecular Diversification in the Quorum-Sensing System of <i>Vibrio cholerae</i> : Role of Natural Selection in the Emergence of Pandemic Strains. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3808-3812.	3.1	11
106	Comparative Study of Pine Reference Genomes Reveals Transposable Element Interconnected Gene Networks. <i>Genes</i> , 2020, 11, 1216.	2.4	11
107	The Effect of a Vector-Borne Disease on the Dynamics of Natural Plant Populations: A Model for <i>Ustilago violacea</i> Infection of <i>Lychnis viscaria</i> . <i>Journal of Ecology</i> , 1993, 81, 263.	4.0	10
108	Applying an artificial neural network approach for drought tolerance screening among Iranian wheat landraces and cultivars grown under well-watered and rain-fed conditions. <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	2.1	10

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109	Killing two enemies with one stone? Genomics of resistance to two sympatric pathogens in Norway spruce. <i>Molecular Ecology</i> , 2021, 30, 4433-4447.	3.9	9
110	Cohort-structured tree populations. <i>Heredity</i> , 2010, 105, 331-332.	2.6	7
111	Using Norway spruce clones in Swedish forestry: introduction. <i>Scandinavian Journal of Forest Research</i> , 2019, 34, 333-335.	1.4	6
112	The genetic basis of adaptation in phenology in an introduced population of Black Cottonwood (<i>Populus trichocarpa</i> , Torr. & Gray). <i>BMC Plant Biology</i> , 2021, 21, 317.	3.6	6
113	Genome-Wide Association Mapping of Mixed Linkage (1,3;1,4)- β -Glucan and Starch Contents in Rice Whole Grain. <i>Frontiers in Plant Science</i> , 2021, 12, 665745.	3.6	6
114	Variant Calling Using Whole Genome Resequencing and Sequence Capture for Population and Evolutionary Genomic Inferences in Norway Spruce (<i>Picea Abies</i>). <i>Compendium of Plant Genomes</i> , 2020, , 9-36.	0.5	6
115	Genome-wide association mapping uncovers sex-associated copy number variation markers and female hemizygous regions on the W chromosome in <i>Salix viminalis</i> . <i>BMC Genomics</i> , 2021, 22, 710.	2.8	6
116	Pathway position constrains the evolution of an ecologically important pathway in aspens (<i>Populus tremula</i> L.). <i>Molecular Ecology</i> , 2018, 27, 3317-3330.	3.9	5
117	Characterization of Dynamic Regulatory Gene and Protein Networks in Wheat Roots Upon Perceiving Water Deficit Through Comparative Transcriptomics Survey. <i>Frontiers in Plant Science</i> , 2021, 12, 710867.	3.6	5
118	<i>GIGANTEA</i> influences leaf senescence in trees in two different ways. <i>Plant Physiology</i> , 2021, 187, 2435-2450.	4.8	5
119	Variant Calling Using NGS Data in European Aspen (<i>Populus tremula</i>). , 2015, , 43-61.		5
120	Estimates of structural complexity in clonal plant morphology: comparisons of grazed and ungrazed <i>Acaena magellanica</i> rhizomes. <i>Canadian Journal of Botany</i> , 1999, 77, 869-876.	1.1	4
121	Exploitative competition between two seed parasites on the common sedge, <i>Carex nigra</i> . <i>Oikos</i> , 2000, 91, 362-370.	2.7	4
122	DIFFERENTIAL MIGRATION FROM HIGH FITNESS DEMES IN THE SHINING FUNGUS BEETLE, PHALACRUS SUBSTRIATUS. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 297-301.	2.3	4
123	Cross-species amplification and development of microsatellites for six species of European Coenagrionid damselflies. <i>Conservation Genetics Resources</i> , 2012, 4, 191-196.	0.8	4
124	The ecological consequences of using clones in forestry. <i>Scandinavian Journal of Forest Research</i> , 2019, 34, 380-389.	1.4	4
125	Hierarchical genetic structure and effective population sizes in <i>Phalacrus substriatus</i> . <i>Heredity</i> , 1997, 79, 153-161.	2.6	4
126	Genome-wide association study for lignocellulosic compounds and fermentable sugar in rice straw. <i>Plant Genome</i> , 2022, 15, e20174.	2.8	3

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127	Comparing the Effectiveness of Exome Capture Probes, Genotyping by Sequencing and Whole-Genome Re-Sequencing for Assessing Genetic Diversity in Natural and Managed Stands of <i>Picea abies</i> . <i>Forests</i> , 2020, 11, 1185.	2.1	2
128	DIFFERENTIAL MIGRATION FROM HIGH FITNESS DEMES IN THE SHINING FUNGUS BEETLE, <i>PHALACRUS SUBSTRIATUS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 297.	2.3	1
129	Phenotypic plasticity in <i>Populus trichocarpa</i> clones across environments in the Nordic–Baltic region. <i>Scandinavian Journal of Forest Research</i> , 2022, 37, 1-5.	1.4	1
130	Small- and large-scale heterogeneity in genetic variation across the collard flycatcher genome: implications for estimating genetic diversity in nonmodel organisms. <i>Molecular Ecology Resources</i> , 2017, 17, 583-585.	4.8	0