

Roland KÄŕlliker

List of Publications by Year in descending order

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79
papers

2,571
citations

172207

29
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214527

47
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88
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88
docs citations

88
times ranked

2281
citing authors

#	ARTICLE	IF	CITATIONS
1	Development and characterisation of simple sequence repeat (SSR) markers for perennial ryegrass (<i>Lolium perenne</i> L.). <i>Theoretical and Applied Genetics</i> , 2001, 102, 405-415.	1.8	170
2	Benefits of Condensed Tannins in Forage Legumes Fed to Ruminants: Importance of Structure, Concentration, and Diet Composition. <i>Crop Science</i> , 2019, 59, 861-885.	0.8	154
3	Advanced phenotyping offers opportunities for improved breeding of forage and turf species. <i>Annals of Botany</i> , 2012, 110, 1271-1279.	1.4	113
4	Semi-automated genetic analyses of soil microbial communities: comparison of T-RFLP and RISA based on descriptive and discriminative statistical approaches. <i>Journal of Microbiological Methods</i> , 2005, 61, 349-360.	0.7	98
5	Title is missing!. <i>Euphytica</i> , 2001, 122, 191-201.	0.6	86
6	Title is missing!. <i>Euphytica</i> , 1999, 106, 261-270.	0.6	80
7	Development and characterisation of simple sequence repeat (SSR) markers for white clover (<i>Trifolium repens</i> L.). <i>Theoretical and Applied Genetics</i> , 2001, 102, 416-424.	1.8	79
8	Construction of a consensus linkage map for red clover (<i>Trifolium pratense</i> L.). <i>BMC Plant Biology</i> , 2009, 9, 57.	1.6	68
9	Bulked AFLP analysis for the assessment of genetic diversity in white clover (<i>Trifolium repens</i> L.). <i>Euphytica</i> , 2001, 121, 305-315.	0.6	67
10	Genetic characterisation of seed yield and fertility traits in perennial ryegrass (<i>Lolium perenne</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 117, 781-791.	1.8	67
11	QTL analysis of seed yield components in red clover (<i>Trifolium pratense</i> L.). <i>Theoretical and Applied Genetics</i> , 2006, 112, 536-545.	1.8	63
12	Fertilization and defoliation frequency affect genetic diversity of <i>Festuca pratensis</i> Huds. in permanent grasslands. <i>Molecular Ecology</i> , 1998, 7, 1557-1567.	2.0	59
13	Swiss Mattenkleee landraces, a distinct and diverse genetic resource of red clover (<i>Trifolium pratense</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.8	57
14	Genetic mapping reveals a single major QTL for bacterial wilt resistance in Italian ryegrass (<i>Lolium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.8	50
15	Development and mapping of DArT markers within the <i>Festuca</i> - <i>Lolium</i> complex. <i>BMC Genomics</i> , 2009, 10, 473.	1.2	49
16	Consistent detection of QTLs for crown rust resistance in Italian ryegrass (<i>Lolium multiflorum</i> Lam.) across environments and phenotyping methods. <i>Theoretical and Applied Genetics</i> , 2007, 115, 9-17.	1.8	48
17	The noncanonical type III secretion system of <i>Xanthomonas translucens</i> pv. <i>graminis</i> is essential for forage grass infection. <i>Molecular Plant Pathology</i> , 2013, 14, 576-588.	2.0	48
18	Isolation and characterization of microsatellite markers from the entomopathogenic fungus <i>Metarhizium anisopliae</i> . <i>Molecular Ecology Notes</i> , 2005, 5, 384-386.	1.7	47

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19	Marker assisted polycross breeding to increase diversity and yield in perennial ryegrass (<i>Lolium</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10	0.6	43
20	EST-derived SSR markers used as anchor loci for the construction of a consensus linkage map in ryegrass (<i>Lolium</i> spp.). <i>BMC Plant Biology</i> , 2010, 10, 177.	1.6	42
21	Spatial distribution of <i>Metarhizium</i> clade 1 in agricultural landscapes with arable land and different semi-natural habitats. <i>Applied Soil Ecology</i> , 2012, 52, 20-28.	2.1	42
22	Red Clover. , 2010, , 439-455.		41
23	Optimization of bulked AFLP analysis and its application for exploring diversity of natural and cultivated populations of red clover. <i>Genome</i> , 2005, 48, 474-486.	0.9	40
24	Improving Persistence in Red Clover: Insights from QTL Analysis and Comparative Phenotypic Evaluation. <i>Crop Science</i> , 2008, 48, 269-277.	0.8	39
25	Drought Effects on Proanthocyanidins in Sainfoin (<i>Onobrychis viciifolia</i> Scop.) Are Dependent on the Plant's Ontogenetic Stage. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 9307-9316.	2.4	39
26	Genetic Diversity in Diploid Cultivars of Rhodesgrass Determined on the Basis of Amplified Fragment Length Polymorphism Markers. <i>Crop Science</i> , 2003, 43, 1516-1522.	0.8	36
27	A novel strategy to extract specific phylogenetic sequence information from community T-RFLP. <i>Journal of Microbiological Methods</i> , 2006, 66, 512-520.	0.7	35
28	Intra-specific variability of ozone sensitivity in <i>Centaurea jacea</i> L., a potential bioindicator for elevated ozone concentrations. <i>Environmental Pollution</i> , 2004, 131, 1-12.	3.7	34
29	Genetic diversity and pathogenicity of the grass pathogen <i>Xanthomonas translucens</i> pv. <i>graminis</i> . <i>Systematic and Applied Microbiology</i> , 2006, 29, 109-119.	1.2	34
30	Diurnal Leaf Starch Content: An Orphan Trait in Forage Legumes. <i>Agronomy</i> , 2017, 7, 16.	1.3	32
31	Expressed sequence tag-derived microsatellite markers of perennial ryegrass (<i>Lolium perenne</i> L.). <i>Molecular Breeding</i> , 2008, 21, 533-548.	1.0	31
32	An optimized microsatellite marker set for detection of <i>Metarhizium anisopliae</i> genotype diversity on field and regional scales. <i>Mycological Research</i> , 2009, 113, 1016-1024.	2.5	31
33	Habitat and management affect genetic structure of <i>Festuca pratensis</i> but not <i>Lolium multiflorum</i> ecotype populations. <i>Plant Breeding</i> , 2008, 127, 510-517.	1.0	30
34	Characterization of novel microsatellite loci for red clover (<i>Trifolium pratense</i> L.) from enriched genomic libraries. <i>Molecular Ecology Notes</i> , 2006, 6, 50-53.	1.7	28
35	Genetic diversity of natural orchardgrass (<i>Dactylis glomerata</i> L.) populations in three regions in Europe. <i>BMC Genetics</i> , 2013, 14, 102.	2.7	28
36	Genetic mapping of DArT markers in the <i>Festuca</i> - <i>Lolium</i> complex and their use in freezing tolerance association analysis. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1133-1147.	1.8	27

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37	Dry matter allocation and nitrogen productivity explain growth responses to photoperiod and temperature in forage grasses. <i>Oecologia</i> , 1999, 121, 441-446.	0.9	26
38	Pooled DNA sequencing to identify SNPs associated with a major QTL for bacterial wilt resistance in Italian ryegrass (<i>Lolium multiflorum</i> Lam.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 947-958.	1.8	26
39	Indicators for genetic and phenotypic diversity of <i>Dactylis glomerata</i> in Swiss permanent grassland. <i>Ecological Indicators</i> , 2014, 38, 181-191.	2.6	25
40	Characterization of novel SSR markers in diverse sainfoin (<i>Onobrychis viciifolia</i>) germplasm. <i>BMC Genetics</i> , 2016, 17, 124.	2.7	24
41	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974 ^T (ATCC 19319 ^T). <i>Genome Announcements</i> , 2016, 4, .	0.8	24
42	Comparative genomics of host adaptive traits in <i>Xanthomonas translucens</i> pv. <i>graminis</i> . <i>BMC Genomics</i> , 2017, 18, 35.	1.2	24
43	Phenotyping a Dynamic Trait: Leaf Growth of Perennial Ryegrass Under Water Limiting Conditions. <i>Frontiers in Plant Science</i> , 2019, 10, 344.	1.7	23
44	DNA-Based Assessment of Genetic Diversity in Grassland Plant Species: Challenges, Approaches, and Applications. <i>Agronomy</i> , 2019, 9, 881.	1.3	21
45	First assembly of the gene space of <i>Lolium multiflorum</i> and comparison to other Poaceae genomes. <i>Grassland Science</i> , 2019, 65, 125-134.	0.6	20
46	DNA barcode trnH-psbA is a promising candidate for efficient identification of forage legumes and grasses. <i>BMC Research Notes</i> , 2020, 13, 35.	0.6	20
47	Indicators for the on-farm assessment of crop cultivar and livestock breed diversity: a survey-based participatory approach. <i>Biodiversity and Conservation</i> , 2014, 23, 3051-3071.	1.2	19
48	Complete Genome Assemblies of All <i>Xanthomonas translucens</i> Pathotype Strains Reveal Three Genetically Distinct Clades. <i>Frontiers in Microbiology</i> , 2021, 12, 817815.	1.5	19
49	Value of permanent grassland habitats as reservoirs of <i>Festuca pratensis</i> Huds. and <i>Lolium multiflorum</i> Lam. populations for breeding and conservation. <i>Euphytica</i> , 2008, 164, 239.	0.6	17
50	Improved polycross breeding of tall fescue through marker-based parental selection. <i>Plant Breeding</i> , 2011, 130, 701-707.	1.0	17
51	The Complete Genome Sequence of <i>Xanthomonas theicola</i> , the Causal Agent of Canker on Tea Plants, Reveals Novel Secretion Systems in Clade-1 <i>Xanthomonads</i> . <i>Phytopathology</i> , 2021, 111, 611-616.	1.1	17
52	Expression profiling of Italian ryegrass (<i>Lolium multiflorum</i> Lam.) during infection with the bacterial wilt inducing pathogen <i>Xanthomonas translucens</i> pv. <i>graminis</i> . <i>Plant Breeding</i> , 2006, 125, 43-51.	1.0	14
53	Promising options for improving performance and proanthocyanidins of the forage legume sainfoin (<i>Onobrychis viciifolia</i> Scop.). <i>Euphytica</i> , 2017, 213, 1.	0.6	14
54	Field Performance of Cell Suspension-Derived Tall Fescue Regenerants and Their Half-sib Families. <i>Crop Science</i> , 1999, 39, 375-381.	0.8	13

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55	Effect of season and cutting frequency on root and shoot competition between <i>Festuca pratensis</i> and <i>Dactylis glomerata</i> . <i>Grass and Forage Science</i> , 2002, 57, 247-254.	1.2	13
56	Development of novel microsatellite markers for the grassland species <i>Lolium multiflorum</i> , <i>Lolium perenne</i> and <i>Festuca pratensis</i> . <i>Molecular Ecology Notes</i> , 2006, 6, 1108-1110.	1.7	13
57	Transcriptional responses of Italian ryegrass during interaction with <i>Xanthomonas translucens</i> pv. <i>graminis</i> reveal novel candidate genes for bacterial wilt resistance. <i>Theoretical and Applied Genetics</i> , 2011, 122, 567-579.	1.8	13
58	Evidence and consequences of self-fertilisation in the predominantly outbreeding forage legume <i>Onobrychis viciifolia</i> . <i>BMC Genetics</i> , 2015, 16, 117.	2.7	10
59	Field performance of cell-suspension-derived <i>Lolium perenne</i> L. regenerants and their progenies. <i>Theoretical and Applied Genetics</i> , 1998, 96, 634-639.	1.8	9
60	Marker-trait association analysis for agronomic and compositional traits in sainfoin (<i>Onobrychis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	0.3	9
61	Fertility and growth in the field of <i>Lolium perenne</i> and <i>Festuca rubra</i> plants regenerated from suspension cultured cells and protoplasts. <i>Plant Breeding</i> , 1998, 117, 37-43.	1.0	8
62	Genetic Diversity of Diurnal Carbohydrate Accumulation in White Clover (<i>Trifolium repens</i> L.). <i>Agronomy</i> , 2018, 8, 47.	1.3	8
63	Elevated ozone affects the genetic composition of <i>Plantago lanceolata</i> L. populations. <i>Environmental Pollution</i> , 2008, 152, 380-386.	3.7	7
64	Phenotypic and molecular genetic characterization indicate no major race-specific interactions between <i>Xanthomonas translucens</i> pv. <i>graminis</i> and <i>Lolium multiflorum</i> . <i>Plant Pathology</i> , 2011, 60, 314-324.	1.2	7
65	Marker-assisted Selection in Forage Crops and Turf: A Review. , 2010, , 383-390.		6
66	Draft genome sequences of three <i>Xanthomonas translucens</i> pathovar reference strains (pv.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 T Genomic Sciences, 2016, 11, 50.	1.5	6
67	Characterization and Utilization of Genetic Resources for Improvement and Management of Grassland Species. , 2009, , 55-70.		6
68	A multispecies amplicon sequencing approach for genetic diversity assessments in grassland plant species. <i>Molecular Ecology Resources</i> , 2022, 22, 1725-1745.	2.2	6
69	Development of 16 microsatellite markers for the European cockchafer, <i>Melolontha melolontha</i> . <i>Molecular Ecology Resources</i> , 2008, 8, 158-160.	2.2	5
70	Development and Application of Biotechnological and Molecular Genetic Tools. , 2010, , 89-113.		5
71	A DNA marker assay based on high-resolution melting curve analysis for distinguishing species of the <i>Festuca</i> "Lolium complex. <i>Molecular Breeding</i> , 2014, 34, 421-429.	1.0	5
72	The potential of alternative seed treatments to control anthracnose disease in white lupin. <i>Crop Protection</i> , 2022, 158, 106009.	1.0	5

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73	SNP Genotyping Technologies. , 2013, , 187-210.		3
74	Draft Genome Sequence of the Xanthomonas bromi Type Strain LMG 947. Genome Announcements, 2016, 4, .	0.8	3
75	Enhanced polycross breeding of tall fescue through marker-based paternity identification and estimation of combining ability. Euphytica, 2020, 216, 1.	0.6	2
76	A Non-destructive Method to Quantify Leaf Starch Content in Red Clover. Frontiers in Plant Science, 2020, 11, 569948.	1.7	2
77	DArTFest â€“ A Platform for High-Throughput Genome Profiling Within the Festuca â€“ Lolium Complex. , 2010, , 443-448.		1
78	Intra-specific variability of ozone sensitivity in Centaurea jacea L., a potential bioindicator for elevated ozone concentrations. Environmental Pollution, 2004, 131, 1-1.	3.7	0
79	Identification of Genes Induced in Lolium multiflorum by Bacterial Wilt Infection. , 2010, , 483-487.		0