

Roland KÄŕlliker

List of Publications by Year in descending order

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79
papers

2,571
citations

172207

29
h-index

214527

47
g-index

88
all docs

88
docs citations

88
times ranked

2281
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	The potential of alternative seed treatments to control anthracnose disease in white lupin. <i>Crop Protection</i> , 2022, 158, 106009.	1.0	5
3	The Complete Genome Sequence of <i>Xanthomonas theicola</i> , the Causal Agent of Canker on Tea Plants, Reveals Novel Secretion Systems in Clade-1 Xanthomonads. <i>Phytopathology</i> , 2021, 111, 611-616.	1.1	17
4	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
5	Enhanced polycross breeding of tall fescue through marker-based paternity identification and estimation of combining ability. <i>Euphytica</i> , 2020, 216, 1.	0.6	2
6	A Non-destructive Method to Quantify Leaf Starch Content in Red Clover. <i>Frontiers in Plant Science</i> , 2020, 11, 569948.	1.7	2
7	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
8	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
9	DNA-Based Assessment of Genetic Diversity in Grassland Plant Species: Challenges, Approaches, and Applications. <i>Agronomy</i> , 2019, 9, 881.	1.3	21
10	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
11	First assembly of the genome of <i>Lolium multiflorum</i> and comparison to other Poaceae genomes. <i>Grassland Science</i> , 2019, 65, 125-134.	0.6	20
12	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
13	Genetic Diversity of Diurnal Carbohydrate Accumulation in White Clover (<i>Trifolium repens</i> L.). <i>Agronomy</i> , 2018, 8, 47.	1.3	8
14	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
15	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
16	Diurnal Leaf Starch Content: An Orphan Trait in Forage Legumes. <i>Agronomy</i> , 2017, 7, 16.	1.3	32
17	Marker-trait association analysis for agronomic and compositional traits in sainfoin (<i>Onobrychis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 11 0.3 9	0.3	9
18	Draft genome sequences of three <i>Xanthomonas translucens</i> pathovar reference strains (pv.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 67 To Genomic Sciences, 2016, 11, 50.	1.5	6

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19	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
20	Characterization of novel SSR markers in diverse sainfoin (<i>Onobrychis viciifolia</i>) germplasm. <i>BMC Genetics</i> , 2016, 17, 124.	2.7	24
21	Draft Genome Sequence of the <i>Xanthomonas bromi</i> Type Strain LMG 947. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
22	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974 (ATCC 19319). <i>Genome Announcements</i> , 2016, 4, .	0.8	24
23	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
24	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
25	A DNA marker assay based on high-resolution melting curve analysis for distinguishing species of the <i>Festuca</i> - <i>Lolium</i> complex. <i>Molecular Breeding</i> , 2014, 34, 421-429.	1.0	5
26	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
27	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
28	SNP Genotyping Technologies. , 2013, , 187-210.		3
29	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
30	Advanced phenotyping offers opportunities for improved breeding of forage and turf species. <i>Annals of Botany</i> , 2012, 110, 1271-1279.	1.4	113
31	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
32	Improved polycross breeding of tall fescue through marker-based parental selection. <i>Plant Breeding</i> , 2011, 130, 701-707.	1.0	17
33	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
34	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
35	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
36	Marker-assisted Selection in Forage Crops and Turf: A Review. , 2010, , 383-390.		6

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37	DArTFest – A Platform for High-Throughput Genome Profiling Within the Festuca – Lolium Complex. , 2010, , 443-448.		1
38	Identification of Genes Induced in Lolium multiflorum by Bacterial Wilt Infection. , 2010, , 483-487.		0
39	EST-derived SSR markers used as anchor loci for the construction of a consensus linkage map in ryegrass (Lolium spp.). BMC Plant Biology, 2010, 10, 177.	1.6	42
40	Development and Application of Biotechnological and Molecular Genetic Tools. , 2010, , 89-113.		5
41	Red Clover. , 2010, , 439-455.		41
42	An optimized microsatellite marker set for detection of Metarhizium anisopliae genotype diversity on field and regional scales. Mycological Research, 2009, 113, 1016-1024.	2.5	31
43	Development and mapping of DArT markers within the Festuca - Lolium complex. BMC Genomics, 2009, 10, 473.	1.2	49
44	Construction of a consensus linkage map for red clover (Trifolium pratense L.). BMC Plant Biology, 2009, 9, 57.	1.6	68
45	Characterization and Utilization of Genetic Resources for Improvement and Management of Grassland Species. , 2009, , 55-70.		6
46	Expressed sequence tag-derived microsatellite markers of perennial ryegrass (Lolium perenne L.). Molecular Breeding, 2008, 21, 533-548.	1.0	31
47	Value of permanent grassland habitats as reservoirs of Festuca pratensis Huds. and Lolium multiflorum Lam. populations for breeding and conservation. Euphytica, 2008, 164, 239.	0.6	17
48	Genetic characterisation of seed yield and fertility traits in perennial ryegrass (Lolium perenne L.). Theoretical and Applied Genetics, 2008, 117, 781-791.	1.8	67
49	Development of 16 microsatellite markers for the European cockchafer, <i>Melolontha melolontha</i> . Molecular Ecology Resources, 2008, 8, 158-160.	2.2	5
50	Habitat and management affect genetic structure of <i>Festuca pratensis</i> but not <i>Lolium multiflorum</i> ecotype populations. Plant Breeding, 2008, 127, 510-517.	1.0	30
51	Elevated ozone affects the genetic composition of <i>Plantago lanceolata</i> L. populations. Environmental Pollution, 2008, 152, 380-386.	3.7	7
52	Improving Persistence in Red Clover: Insights from QTL Analysis and Comparative Phenotypic Evaluation. Crop Science, 2008, 48, 269-277.	0.8	39
53	Consistent detection of QTLs for crown rust resistance in Italian ryegrass (<i>Lolium multiflorum</i> Lam.) across environments and phenotyping methods. Theoretical and Applied Genetics, 2007, 115, 9-17.	1.8	48
54	A novel strategy to extract specific phylogenetic sequence information from community T-RFLP. Journal of Microbiological Methods, 2006, 66, 512-520.	0.7	35

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55	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
56	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
57	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
58	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
59	Genetic mapping reveals a single major QTL for bacterial wilt resistance in Italian ryegrass (<i>Lolium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	50
60	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
61	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
62	Marker assisted polycross breeding to increase diversity and yield in perennial ryegrass (<i>Lolium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 46	0.6	48
63	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
64	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
65	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, 1-1.	3.7	0
66	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
67	Swiss Mattenklee landraces, a distinct and diverse genetic resource of red clover (<i>Trifolium pratense</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	57
68	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
69	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
70	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
71	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
72	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

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73	Title is missing!. Euphytica, 2001, 122, 191-201.	0.6	86
74	Field Performance of Cell Suspensionâ€Derived Tall Fescue Regenerants and Their Halfâ€sib Families. Crop Science, 1999, 39, 375-381.	0.8	13
75	Title is missing!. Euphytica, 1999, 106, 261-270.	0.6	80
76	Dry matter allocation and nitrogen productivity explain growth responses to photoperiod and temperature in forage grasses. Oecologia, 1999, 121, 441-446.	0.9	26
77	Fertility and growth in the field ofLolium perenneandFestuca rubraplants regenerated from suspension cultured cells and protoplasts. Plant Breeding, 1998, 117, 37-43.	1.0	8
78	Field performance of cell-suspension-derived Lolium perenne L. regenerants and their progenies. Theoretical and Applied Genetics, 1998, 96, 634-639.	1.8	9
79	Fertilization and defoliation frequency affect genetic diversity ofFestuca pratensisHuds. in permanent grasslands. Molecular Ecology, 1998, 7, 1557-1567.	2.0	59