

Maido Remm

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

97
papers

11,834
citations

30
h-index

108
g-index

108
ext. papers

14,580
ext. citations

7.3
avg, IF

6.29
L-index

#	Paper	IF	Citations
97	Development of a dedicated Golden Gate Assembly Platform (RtGGA) for <i>Rhodotorula toruloides</i> . <i>Metabolic Engineering Communications</i> , 2022 , 15, e00200	6.5	1
96	The new COST Action European Venom Network (EUVEN)-synergy and future perspectives of modern venomics. <i>GigaScience</i> , 2021 , 10,	7.6	1
95	Molecular Characterization of Isolates From Different Sources in Estonia Reveals Potential Transmission of Resistance Genes Among Different Reservoirs. <i>Frontiers in Microbiology</i> , 2021 , 12, 601490	5.7	4
94	KATK: Fast genotyping of rare variants directly from unmapped sequencing reads. <i>Human Mutation</i> , 2021 , 42, 777-786	4.7	
93	Competitiveness for Nodule Colonization in <i>Sinorhizobium meliloti</i> : Combined -Tagged Strain Competition and Genome-Wide Association Analysis. <i>MSystems</i> , 2021 , 6, e0055021	7.6	2
92	Chromosomal toxin-antitoxin systems in <i>Pseudomonas putida</i> are rather selfish than beneficial. <i>Scientific Reports</i> , 2020 , 10, 9230	4.9	9
91	Method for the Identification of Plant DNA in Food Using Alignment-Free Analysis of Sequencing Reads: A Case Study on Lupin. <i>Frontiers in Plant Science</i> , 2020 , 11, 646	6.2	6
90	Characteristics of Extended-Spectrum Beta-Lactamase-Producing Enterobacteriaceae and Contact to Animals in Estonia. <i>Microorganisms</i> , 2020 , 8,	4.9	1
89	A human-specific VNTR in the TRIB3 promoter causes gene expression variation between individuals. <i>PLoS Genetics</i> , 2020 , 16, e1008981	6	6
88	The Arrival of Siberian Ancestry Connecting the Eastern Baltic to Uralic Speakers further East. <i>Current Biology</i> , 2019 , 29, 1701-1711.e16	6.3	33
87	Application of Molecular Methods for Carbapenemase Detection. <i>Frontiers in Microbiology</i> , 2019 , 10, 1755	5.7	3
86	AluMine: alignment-free method for the discovery of polymorphic Alu element insertions. <i>Mobile DNA</i> , 2019 , 10, 31	4.4	6
85	Muropeptides Stimulate Growth Resumption from Stationary Phase in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2019 , 9, 18043	4.9	6
84	Phenotypic and Molecular Epidemiology of ESBL-, AmpC-, and Carbapenemase-Producing in Northern and Eastern Europe. <i>Frontiers in Microbiology</i> , 2019 , 10, 2465	5.7	11
83	Genetic variation in the Estonian population: pharmacogenomics study of adverse drug effects using electronic health records. <i>European Journal of Human Genetics</i> , 2019 , 27, 442-454	5.3	13
82	Endophytic bacterial communities in peels and pulp of five root vegetables. <i>PLoS ONE</i> , 2019 , 14, e0210542	3.7	13
81	Primer3_masker: integrating masking of template sequence with primer design software. <i>Bioinformatics</i> , 2018 , 34, 1937-1938	7.2	107

80	Method for the Identification of Taxon-Specific -mers from Chloroplast Genome: A Case Study on Tomato Plant (). <i>Frontiers in Plant Science</i> , 2018 , 9, 6	6.2	12
79	PlasmidSeeker: identification of known plasmids from bacterial whole genome sequencing reads. <i>PeerJ</i> , 2018 , 6, e4588	3.1	40
78	A k-mer-based method for the identification of phenotype-associated genomic biomarkers and predicting phenotypes of sequenced bacteria. <i>PLoS Computational Biology</i> , 2018 , 14, e1006434	5	22
77	Multidrug resistant <i>Pseudomonas aeruginosa</i> in Estonian hospitals. <i>BMC Infectious Diseases</i> , 2018 , 18, 513	4	12
76	Increased sequencing depth does not increase captured diversity of arbuscular mycorrhizal fungi. <i>Mycorrhiza</i> , 2017 , 27, 761-773	3.9	39
75	FastGT: an alignment-free method for calling common SNVs directly from raw sequencing reads. <i>Scientific Reports</i> , 2017 , 7, 2537	4.9	24
74	StrainSeeker: fast identification of bacterial strains from raw sequencing reads using user-provided guide trees. <i>PeerJ</i> , 2017 , 5, e3353	3.1	30
73	Plasmid with Colistin Resistance Gene <i>mcr-1</i> in Extended-Spectrum-β-Lactamase-Producing <i>Escherichia coli</i> Strains Isolated from Pig Slurry in Estonia. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 6933-6936	5.9	33
72	Natural Variation in <i>Arabidopsis Cvi-0</i> Accession Reveals an Important Role of MPK12 in Guard Cell CO ₂ Signaling. <i>PLoS Biology</i> , 2016 , 14, e2000322	9.7	41
71	Heterozygous STAT1 gain-of-function mutations underlie an unexpectedly broad clinical phenotype. <i>Blood</i> , 2016 , 127, 3154-64	2.2	314
70	Microbial population dynamics in response to <i>Pectobacterium atrosepticum</i> infection in potato tubers. <i>Scientific Reports</i> , 2015 , 5, 11606	4.9	35
69	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , 2015 , 25, 459-66	9.7	235
68	GenomeTester4: a toolkit for performing basic set operations - union, intersection and complement on k-mer lists. <i>GigaScience</i> , 2015 , 4, 58	7.6	22
67	Haplotype phasing and inheritance of copy number variants in nuclear families. <i>PLoS ONE</i> , 2015 , 10, e0132713	3.7	13.6
66	MultiPLX: automatic grouping and evaluation of PCR primers. <i>Methods in Molecular Biology</i> , 2015 , 1275, 127-42	1.4	5
65	Fast masking of repeated primer binding sites in eukaryotic genomes. <i>Methods in Molecular Biology</i> , 2015 , 1275, 1-16	1.4	
64	Development of a multiplex real-time PCR assay for the rapid diagnosis of neonatal late onset sepsis. <i>Journal of Microbiological Methods</i> , 2014 , 106, 8-15	2.8	29
63	Structural genomic variation as risk factor for idiopathic recurrent miscarriage. <i>Human Mutation</i> , 2014 , 35, 972-82	4.7	29

62	Macrolide antibiotics allosterically predispose the ribosome for translation arrest. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 9804-9	11.5	77
61	Limnobacter spp. as newly detected phenol-degraders among Baltic Sea surface water bacteria characterised by comparative analysis of catabolic genes. <i>Systematic and Applied Microbiology</i> , 2013 , 36, 525-32	4.2	42
60	Position-specific scoring matrix and hidden Markov model complement each other for the prediction of conopeptide superfamilies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 717-24	4	10
59	Non-syndromic tooth agenesis associated with a nonsense mutation in ectodysplasin-A (EDA). <i>Journal of Dental Research</i> , 2013 , 92, 507-11	8.1	19
58	Primer Design for Large-Scale Multiplex PCR and Arrayed Primer Extension 2013 , 199-208		
57	High-resolution picture of a venom gland transcriptome: case study with the marine snail <i>Conus consors</i> . <i>Toxicon</i> , 2012 , 59, 34-46	2.8	73
56	Identification and analysis of papillomavirus E2 protein binding sites in the human genome. <i>Journal of Virology</i> , 2012 , 86, 348-57	6.6	20
55	Identification and classification of conopeptides using profile Hidden Markov Models. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012 , 1824, 488-92	4	17
54	Shared and Unique Components of Human Population Structure and Genome-Wide Signals of Positive Selection in South Asia. <i>American Journal of Human Genetics</i> , 2012 , 90, 378-379	11	0
53	Characterization of species-specific repeats in 613 prokaryotic species. <i>DNA Research</i> , 2012 , 19, 219-30	4.5	8
52	Primer3--new capabilities and interfaces. <i>Nucleic Acids Research</i> , 2012 , 40, e115	20.1	5267
51	ConoDictor: a tool for prediction of conopeptide superfamilies. <i>Nucleic Acids Research</i> , 2012 , 40, W238-44	10.1	26
50	No evidence of somatic DNA copy number alterations in eutopic and ectopic endometrial tissue in endometriosis. <i>Human Reproduction</i> , 2012 , 27, 1857-64	5.7	15
49	The mitochondrial genome of the venomous cone snail <i>Conus consors</i> . <i>PLoS ONE</i> , 2012 , 7, e51528	3.7	15
48	A parallel SNP array study of genomic aberrations associated with mental retardation in patients and general population in Estonia. <i>European Journal of Medical Genetics</i> , 2011 , 54, 136-43	2.6	7
47	A computational study of elongation factor G (EFG) duplicated genes: diverged nature underlying the innovation on the same structural template. <i>PLoS ONE</i> , 2011 , 6, e22789	3.7	9
46	Antibiotic-induced ribosomal assembly defects result from changes in the synthesis of ribosomal proteins. <i>Molecular Microbiology</i> , 2011 , 80, 54-67	4.1	25
45	Shared and unique components of human population structure and genome-wide signals of positive selection in South Asia. <i>American Journal of Human Genetics</i> , 2011 , 89, 731-44	11	125

44	Detection of NASBA amplified bacterial tmRNA molecules on SLICSel designed microarray probes. <i>BMC Biotechnology</i> , 2011 , 11, 17	3.5	11
43	Fluoride-cleavable, fluorescently labelled reversible terminators: synthesis and use in primer extension. <i>Chemistry - A European Journal</i> , 2011 , 17, 2903-15	4.8	16
42	Population genetic structure in Indian Austroasiatic speakers: the role of landscape barriers and sex-specific admixture. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1013-24	8.3	107
41	Detection of tmRNA molecules on microarrays at low temperatures using helper oligonucleotides. <i>BMC Biotechnology</i> , 2010 , 10, 34	3.5	5
40	Molecular diagnosis of Down syndrome using quantitative APEX-2 microarrays. <i>Prenatal Diagnosis</i> , 2010 , 30, 1170-7	3.2	1
39	Genetic structure of Europeans: a view from the North-East. <i>PLoS ONE</i> , 2009 , 4, e5472	3.7	237
38	Automatic identification of species-specific repetitive DNA sequences and their utilization for detecting microbial organisms. <i>Bioinformatics</i> , 2009 , 25, 1349-55	7.2	13
37	Fluorescent labeling of NASBA amplified tmRNA molecules for microarray applications. <i>BMC Biotechnology</i> , 2009 , 9, 45	3.5	9
36	Array-MAPH: a methodology for the detection of locus copy-number changes in complex genomes. <i>Nature Protocols</i> , 2008 , 3, 849-65	18.8	6
35	Preferred and avoided codon pairs in three domains of life. <i>BMC Genomics</i> , 2008 , 9, 463	4.5	75
34	Predicting failure rate of PCR in large genomes. <i>Nucleic Acids Research</i> , 2008 , 36, e66	20.1	29
33	Application of two different microarray-based copy-number detection methodologies--array-comparative genomic hybridization and array-multiplex amplifiable probe hybridization--with identical amplifiable target sequences. <i>Clinical Chemistry and Laboratory Medicine</i> , 2008 , 46, 722-4	5.9	1
32	Thiopurine S-methyltransferase (TPMT) pharmacogenetics: three new mutations and haplotype analysis in the Estonian population. <i>Clinical Chemistry and Laboratory Medicine</i> , 2008 , 46, 974-9	5.9	15
31	Development of a single tube 640-plex genotyping method for detection of nucleic acid variations on microarrays. <i>Nucleic Acids Research</i> , 2008 , 36, e75	20.1	29
30	Synthesis of four colors fluorescently labelled 3VO-blocked nucleotides with fluoride cleavable blocking group and linker for array based Sequencing-by-Synthesis applications. <i>Nucleic Acids Symposium Series</i> , 2008 , 345-6		2
29	MultiPLX: automatic grouping and evaluation of PCR primers. <i>Methods in Molecular Biology</i> , 2007 , 402, 287-304	1.4	2
28	Translation initiation region sequence preferences in Escherichia coli. <i>BMC Molecular Biology</i> , 2007 , 8, 100	4.5	72
27	Detection of small genomic imbalances using microarray-based multiplex amplifiable probe hybridization. <i>European Journal of Human Genetics</i> , 2007 , 15, 162-72	5.3	11

26	Haplotypes in the human Foxo1a and Foxo3a genes; impact on disease and mortality at old age. <i>European Journal of Human Genetics</i> , 2007 , 15, 294-301	5.3	91
25	Phylogenetic distribution of translational GTPases in bacteria. <i>BMC Genomics</i> , 2007 , 8, 15	4.5	86
24	Evaluating the performance of commercial whole-genome marker sets for capturing common genetic variation. <i>BMC Genomics</i> , 2007 , 8, 159	4.5	23
23	Enhancements and modifications of primer design program Primer3. <i>Bioinformatics</i> , 2007 , 23, 1289-91	7.2	1713
22	Screening of 20 patients with X-linked mental retardation using chromosome X-specific array-MAPH. <i>European Journal of Medical Genetics</i> , 2007 , 50, 399-410	2.6	7
21	Fast masking of repeated primer binding sites in eukaryotic genomes. <i>Methods in Molecular Biology</i> , 2007 , 402, 201-18	1.4	2
20	GENOMEMASKER package for designing unique genomic PCR primers. <i>BMC Bioinformatics</i> , 2006 , 7, 172	3.6	34
19	Highly expressed proteins have an increased frequency of alanine in the second amino acid position. <i>BMC Genomics</i> , 2006 , 7, 28	4.5	25
18	SNPmasker: automatic masking of SNPs and repeats across eukaryotic genomes. <i>Nucleic Acids Research</i> , 2006 , 34, W651-5	20.1	14
17	An evaluation of the performance of tag SNPs derived from HapMap in a Caucasian population. <i>PLoS Genetics</i> , 2006 , 2, e27	6	81
16	Linkage disequilibrium patterns and tagSNP transferability among European populations. <i>American Journal of Human Genetics</i> , 2005 , 76, 387-98	11	108
15	Inparanoid: a comprehensive database of eukaryotic orthologs. <i>Nucleic Acids Research</i> , 2005 , 33, D476-80	10.1	541
14	THE WHOLE GENOME TAGSNP SELECTION AND TRANSFERABILITY AMONG HAPMAP POPULATIONS 2005 ,		2
13	X-chromosome as a marker for population history: linkage disequilibrium and haplotype study in Eurasian populations. <i>European Journal of Human Genetics</i> , 2005 , 13, 452-62	5.3	30
12	MultiPLX: automatic grouping and evaluation of PCR primers. <i>Bioinformatics</i> , 2005 , 21, 1701-2	7.2	50
11	High-density genotyping and linkage disequilibrium in the human genome using chromosome 22 as a model. <i>Current Opinion in Chemical Biology</i> , 2002 , 6, 24-30	9.7	4
10	A first-generation linkage disequilibrium map of human chromosome 22. <i>Nature</i> , 2002 , 418, 544-8	50.4	342
9	Automatic clustering of orthologs and in-paralogs from pairwise species comparisons. <i>Journal of Molecular Biology</i> , 2001 , 314, 1041-52	6.5	959

8	Classification of transmembrane protein families in the <i>Caenorhabditis elegans</i> genome and identification of human orthologs. <i>Genome Research</i> , 2000 , 10, 1679-89	9.7	26
7	Human papillomavirus type 18 E1 protein is translated from polycistronic mRNA by a discontinuous scanning mechanism. <i>Journal of Virology</i> , 1999 , 73, 3062-70	6.6	58
6	A high capacity assay for inhibitors of human papillomavirus DNA replication. <i>Nature Biotechnology</i> , 1995 , 13, 1210-4	44.5	7
5	The E2 binding sites determine the efficiency of replication for the origin of human papillomavirus type 18. <i>Nucleic Acids Research</i> , 1992 , 20, 6015-21	20.1	65
4	StrainSeeker: fast identification of bacterial strains from unassembled sequencing reads using user-provided guide trees.		3
3	<i>Pseudomonas putida</i> chromosomal toxin-antitoxin systems carry neither clear fitness benefits nor big costs		1
2	Competitiveness prediction for nodule colonization in <i>Sinorhizobium meliloti</i> through combined in vitro tagged strain characterization and genome-wide association analysis		1
1	Gene content of the fish-hunting cone snail <i>Conus consors</i>		8