

Nancy H C J Roosens

List of Publications by Year in descending order

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128
papers

3,604
citations

168829

31
h-index

190340

53
g-index

129
all docs

129
docs citations

129
times ranked

4284
citing authors

#	ARTICLE	IF	CITATIONS
1	Retrospective evaluation of routine whole genome sequencing of <i>Mycobacterium tuberculosis</i> at the Belgian National Reference Center, 2019. <i>Acta Clinica Belgica</i> , 2022, 77, 853-860.	0.5	5
2	First monitoring for unauthorized genetically modified bacteria in food enzymes from the food market. <i>Food Control</i> , 2022, 135, 108665.	2.8	6
3	Population Analysis of O26 Shiga Toxin-Producing <i>Escherichia coli</i> Causing Hemolytic Uremic Syndrome in Italy, 1989–2020, Through Whole Genome Sequencing. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 842508.	1.8	4
4	Development of a Taxon-Specific Real-Time PCR Method Targeting the <i>Bacillus subtilis</i> Group to Strengthen the Control of Genetically Modified Bacteria in Fermentation Products. <i>Fermentation</i> , 2022, 8, 78.	1.4	3
5	Optimization and Application of a Multiplex Digital PCR Assay for the Detection of SARS-CoV-2 Variants of Concern in Belgian Influent Wastewater. <i>Viruses</i> , 2022, 14, 610.	1.5	12
6	Detection and identification of authorized and unauthorized GMOs using high-throughput sequencing with the support of a sequence-based GMO database. <i>Food Chemistry Molecular Sciences</i> , 2022, 4, 100096.	0.9	2
7	ddPCR strategy to detect a gene-edited plant carrying a single variation point: Technical feasibility and interpretation issues. <i>Food Control</i> , 2022, 137, 108904.	2.8	7
8	Urinary CC16, a potential indicator of lung integrity and inflammation, increases in children after short-term exposure to PM2.5/PM10 and is driven by the CC16 38GG genotype. <i>Environmental Research</i> , 2022, 212, 113272.	3.7	5
9	Assessment of the Feasibility of a Future Integrated Larger-Scale Epidemiological Study to Evaluate Health Risks of Air Pollution Episodes in Children. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 8531.	1.2	1
10	Retrospective survey of unauthorized genetically modified bacteria harbouring antimicrobial resistance genes in feed additive vitamin B2 commercialized in Belgium: Challenges and solutions. <i>Food Control</i> , 2021, 119, 107476.	2.8	10
11	DNA walking strategy to identify unauthorized genetically modified bacteria in microbial fermentation products. <i>International Journal of Food Microbiology</i> , 2021, 337, 108913.	2.1	18
12	First detection of a plasmid-encoded New-Delhi metallo-beta-lactamase-1 (NDM-1) producing <i>Acinetobacter baumannii</i> using whole genome sequencing, isolated in a clinical setting in Benin. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2021, 20, 5.	1.7	6
13	Food Enzyme Database (FEDA): a web application gathering information about food enzyme preparations available on the European market. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	4
14	Validation strategy of a bioinformatics whole genome sequencing workflow for Shiga toxin-producing <i>Escherichia coli</i> using a reference collection extensively characterized with conventional methods. <i>Microbial Genomics</i> , 2021, 7, .	1.0	20
15	Case Report: Multidrug Resistant <i>Raoultella ornithinolytica</i> in a Septicemic Calf. <i>Frontiers in Veterinary Science</i> , 2021, 8, 631716.	0.9	5
16	Deepening of In Silico Evaluation of SARS-CoV-2 Detection RT-qPCR Assays in the Context of New Variants. <i>Genes</i> , 2021, 12, 565.	1.0	26
17	Phylogenomic Investigation of Increasing Fluoroquinolone Resistance among Belgian Cases of Shigellosis between 2013 and 2018 Indicates Both Travel-Related Imports and Domestic Circulation. <i>Microorganisms</i> , 2021, 9, 767.	1.6	4
18	Application of a strain-level shotgun metagenomics approach on food samples: resolution of the source of a <i>Salmonella</i> food-borne outbreak. <i>Microbial Genomics</i> , 2021, 7, .	1.0	16

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19	A Bioinformatics Whole-Genome Sequencing Workflow for Clinical Mycobacterium tuberculosis Complex Isolate Analysis, Validated Using a Reference Collection Extensively Characterized with Conventional Methods and <i>In Silico</i> Approaches. Journal of Clinical Microbiology, 2021, 59, .	1.8	18
20	Development of a Real-time PCR Method Targeting an Unauthorized Genetically Modified Microorganism Producing Alpha-Amylase. Food Analytical Methods, 2021, 14, 2211-2220.	1.3	9
21	Development of a multiplex mass spectrometry method for simultaneous quantification of urinary proteins related to respiratory health. Scientific Reports, 2021, 11, 10107.	1.6	7
22	Non-Invasive versus Invasive Samples for Zika Virus Surveillance: A Comparative Study in New Caledonia and French Guiana in 2015–2016. Microorganisms, 2021, 9, 1312.	1.6	4
23	A shotgun metagenomics approach to detect and characterize unauthorized genetically modified microorganisms in microbial fermentation products. Food Chemistry Molecular Sciences, 2021, 2, 100023.	0.9	5
24	Coverage of the national surveillance system for human Salmonella infections, Belgium, 2016-2020. PLoS ONE, 2021, 16, e0256820.	1.1	4
25	Evaluation of the added value of viral genomic information for predicting severity of influenza infection. BMC Infectious Diseases, 2021, 21, 785.	1.3	3
26	Whole-genome-based phylogenomic analysis of the Belgian 2016–2017 influenza A(H3N2) outbreak season allows improved surveillance. Microbial Genomics, 2021, 7, .	1.0	6
27	Development of a real-time PCR marker targeting a new unauthorized genetically modified microorganism producing protease identified by DNA walking. International Journal of Food Microbiology, 2021, 354, 109330.	2.1	7
28	Large diversity of linezolid-resistant isolates discovered in food-producing animals through linezolid selective monitoring in Belgium in 2019. Journal of Antimicrobial Chemotherapy, 2021, 77, 49-57.	1.3	29
29	Characterization of Genetically Modified Microorganisms Using Short- and Long-Read Whole-Genome Sequencing Reveals Contaminations of Related Origin in Multiple Commercial Food Enzyme Products. Foods, 2021, 10, 2637.	1.9	4
30	Whole Genome Sequencing Provides an Added Value to the Investigation of Staphylococcal Food Poisoning Outbreaks. Frontiers in Microbiology, 2021, 12, 750278.	1.5	7
31	Strategy to Develop and Evaluate a Multiplex RT-ddPCR in Response to SARS-CoV-2 Genomic Evolution. Current Issues in Molecular Biology, 2021, 43, 1937-1949.	1.0	9
32	Evaluation of WGS performance for bacterial pathogen characterization with the Illumina technology optimized for time-critical situations. Microbial Genomics, 2021, 7, .	1.0	4
33	Towards Real-Time and Affordable Strain-Level Metagenomics-Based Foodborne Outbreak Investigations Using Oxford Nanopore Sequencing Technologies. Frontiers in Microbiology, 2021, 12, 738284.	1.5	19
34	Whole-Genome Sequencing-Based Antimicrobial Resistance Characterization and Phylogenomic Investigation of 19 Multidrug-Resistant and Extended-Spectrum Beta-Lactamase-Positive Escherichia coli Strains Collected From Hospital Patients in Benin in 2019. Frontiers in Microbiology, 2021, 12, 752883.	1.5	8
35	Detection strategy targeting a chloramphenicol resistance gene from genetically modified bacteria in food and feed products. Food Control, 2020, 108, 106873.	2.8	23
36	Strategy for the identification of micro-organisms producing food and feed products: Bacteria producing food enzymes as study case. Food Chemistry, 2020, 305, 125431.	4.2	18

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37	A new multiplex RT-qPCR method for the simultaneous detection and discrimination of Zika and chikungunya viruses. <i>International Journal of Infectious Diseases</i> , 2020, 92, 160-170.	1.5	7
38	Targeting the 16S rRNA Gene for Bacterial Identification in Complex Mixed Samples: Comparative Evaluation of Second (Illumina) and Third (Oxford Nanopore Technologies) Generation Sequencing Technologies. <i>International Journal of Molecular Sciences</i> , 2020, 21, 298.	1.8	117
39	Next-Generation Sequencing: An Eye-Opener for the Surveillance of Antiviral Resistance in Influenza. <i>Trends in Biotechnology</i> , 2020, 38, 360-367.	4.9	37
40	A multiplex oligonucleotide ligation-PCR method for the genoserotyping of common <i>Salmonella</i> using a liquid bead suspension assay. <i>Food Microbiology</i> , 2020, 87, 103394.	2.1	6
41	The Benefits of Whole Genome Sequencing for Foodborne Outbreak Investigation from the Perspective of a National Reference Laboratory in a Smaller Country. <i>Foods</i> , 2020, 9, 1030.	1.9	23
42	Use of Whole Genome Sequencing Data for a First in Silico Specificity Evaluation of the RT-qPCR Assays Used for SARS-CoV-2 Detection. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5585.	1.8	23
43	Development of an NGS-Based Workflow for Improved Monitoring of Circulating Plasmids in Support of Risk Assessment of Antimicrobial Resistance Gene Dissemination. <i>Antibiotics</i> , 2020, 9, 503.	1.5	13
44	Strategy to Detect Genetically Modified Bacteria Carrying Tetracycline Resistance Gene in Fermentation Products. <i>Food Analytical Methods</i> , 2020, 13, 1929-1937.	1.3	11
45	Strain-Level Metagenomic Data Analysis of Enriched In Vitro and In Silico Spiked Food Samples: Paving the Way towards a Culture-Free Foodborne Outbreak Investigation Using STEC as a Case Study. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5688.	1.8	14
46	Gender-dependent association between exhaled nitric oxide and the CC16 38AA genotype in young school children. <i>Immunity, Inflammation and Disease</i> , 2020, 8, 497-505.	1.3	5
47	A Practical Method to Implement Strain-Level Metagenomics-Based Foodborne Outbreak Investigation and Source Tracking in Routine. <i>Microorganisms</i> , 2020, 8, 1191.	1.6	14
48	Impact of DNA extraction on whole genome sequencing analysis for characterization and relatedness of Shiga toxin-producing <i>Escherichia coli</i> isolates. <i>Scientific Reports</i> , 2020, 10, 14649.	1.6	32
49	NGS for (Hemato-) Oncology in Belgium: Evaluation of Laboratory Performance and Feasibility of a National External Quality Assessment Program. <i>Cancers</i> , 2020, 12, 3180.	1.7	3
50	Identification of an unauthorized genetically modified bacteria in food enzyme through whole-genome sequencing. <i>Scientific Reports</i> , 2020, 10, 7094.	1.6	14
51	Screening strategy targeting the presence of food enzyme-producing fungi in food enzyme preparations. <i>Food Control</i> , 2020, 117, 107295.	2.8	6
52	A genoserotyping system for a fast and objective identification of <i>Salmonella</i> serotypes commonly isolated from poultry and pork food sectors in Belgium. <i>Food Microbiology</i> , 2020, 91, 103534.	2.1	12
53	Isolation of Drug-Resistant <i>Gallibacterium anatis</i> from Calves with Unresponsive Bronchopneumonia, Belgium. <i>Emerging Infectious Diseases</i> , 2020, 26, .	2.0	18
54	Combining short and long read sequencing to characterize antimicrobial resistance genes on plasmids applied to an unauthorized genetically modified <i>Bacillus</i> . <i>Scientific Reports</i> , 2020, 10, 4310.	1.6	57

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55	Genetically Modified Micro-Organisms for Industrial Food Enzyme Production: An Overview. <i>Foods</i> , 2020, 9, 326.	1.9	65
56	Are antimicrobial resistance genes key targets to detect genetically modified microorganisms in fermentation products?. <i>International Journal of Food Microbiology</i> , 2020, 331, 108749.	2.1	17
57	First detection of a plasmid located carbapenem resistant blaVIM-1 gene in E. coli isolated from meat products at retail in Belgium in 2015. <i>International Journal of Food Microbiology</i> , 2020, 324, 108624.	2.1	16
58	Selection of a Noninvasive Source of Human DNA Envisaging Genotyping Assays in Epidemiological Studies: Urine or Saliva?. <i>Journal of Biomolecular Techniques</i> , 2020, 31, 27-35.	0.8	4
59	Status and potential of bacterial genomics for public health practice: a scoping review. <i>Implementation Science</i> , 2019, 14, 79.	2.5	28
60	MinION sequencing technology to characterize unauthorized GM petunia plants circulating on the European Union market. <i>Scientific Reports</i> , 2019, 9, 7141.	1.6	18
61	Development of a real-time PCR method for the genosertotyping of Salmonella Paratyphi B variant Java. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 4987-4996.	1.7	7
62	Validation of a Bioinformatics Workflow for Routine Analysis of Whole-Genome Sequencing Data and Related Challenges for Pathogen Typing in a European National Reference Center: Neisseria meningitidis as a Proof-of-Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 362.	1.5	51
63	Shifting national surveillance of Shigella infections toward genosertotyping by the development of a tailored Luminex assay and NGS workflow. <i>MicrobiologyOpen</i> , 2019, 8, e00807.	1.2	8
64	Detailed Evaluation of Data Analysis Tools for Subtyping of Bacterial Isolates Based on Whole Genome Sequencing: Neisseria meningitidis as a Proof of Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 2897.	1.5	8
65	Exploiting the Advantages of Molecular Tools for the Monitoring of Fungal Indoor Air Contamination: First Detection of Exophiala jeanselmei in Indoor Air of Air-Conditioned Offices. <i>Microorganisms</i> , 2019, 7, 674.	1.6	5
66	CHAPTER 8. GMO Detection and Identification Using Next-generation Sequencing. <i>Food Chemistry, Function and Analysis</i> , 2019, , 96-106.	0.1	3
67	A novel genotoxin-specific qPCR array based on the metabolically competent human HepaRG cell line as a rapid and reliable tool for improved in vitro hazard assessment. <i>Archives of Toxicology</i> , 2018, 92, 1593-1608.	1.9	17
68	Detection and discrimination of five E. coli pathotypes using a combinatory SYBR® Green qPCR screening system. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3267-3285.	1.7	17
69	Detection of Plasmid-Mediated Colistin Resistance, <i>mcr-1</i> and <i>mcr-2</i> Genes, in <i>Salmonella</i> spp. Isolated from Food at Retail in Belgium from 2012 to 2015. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 114-117.	0.8	50
70	Inter-laboratory analysis of selected genetically modified plant reference materials with digital PCR. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 211-221.	1.9	11
71	Isolation of <i>Burkholderia pseudomallei</i> from a Pet Green Iguana, Belgium. <i>Emerging Infectious Diseases</i> , 2018, 24, 2331-2333.	2.0	7
72	Application of whole genome data for in silico evaluation of primers and probes routinely employed for the detection of viral species by RT-qPCR using dengue virus as a case study. <i>BMC Bioinformatics</i> , 2018, 19, 312.	1.2	18

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73	Nanopore sequencing technology: a new route for the fast detection of unauthorized GMO. <i>Scientific Reports</i> , 2018, 8, 7903.	1.6	26
74	Development and validation of an integrated DNA walking strategy to detect GMO expressing cry genes. <i>BMC Biotechnology</i> , 2018, 18, 40.	1.7	8
75	The genetic structure of the Belgian population. <i>Human Genomics</i> , 2018, 12, 6.	1.4	7
76	Comparison of SNP-based subtyping workflows for bacterial isolates using WGS data, applied to <i>Salmonella enterica</i> serotype Typhimurium and serotype 1,4,[5],12:i:-. <i>PLoS ONE</i> , 2018, 13, e0192504.	1.1	29
77	Molecular Subtyping of <i>Salmonella</i> Typhimurium with Multiplex Oligonucleotide Ligation-PCR (MOL-PCR). <i>Methods in Molecular Biology</i> , 2017, 1616, 39-69.	0.4	1
78	An integrated strategy combining DNA walking and NGS to detect GMOs. <i>Food Chemistry</i> , 2017, 232, 351-358.	4.2	33
79	How Can We Better Detect Unauthorized GMOs in Food and Feed Chains?. <i>Trends in Biotechnology</i> , 2017, 35, 508-517.	4.9	41
80	Discrimination of three genetically close <i>Aspergillus</i> species by using high resolution melting analysis applied to indoor air as case study. <i>BMC Microbiology</i> , 2017, 17, 84.	1.3	11
81	Model-Based Classification for Digital PCR: Your Umbrella for Rain. <i>Analytical Chemistry</i> , 2017, 89, 4461-4467.	3.2	35
82	Development and performance assessment of a luminex xMAP® direct hybridization assay for the detection and identification of indoor air fungal contamination. <i>PLoS ONE</i> , 2017, 12, e0173390.	1.1	5
83	Biotech rice: Current developments and future detection challenges in food and feed chain. <i>Trends in Food Science and Technology</i> , 2016, 52, 66-79.	7.8	30
84	Optimized MOL-PCR for Characterization of Microbial Pathogens. <i>Current Protocols in Cytometry</i> , 2016, 75, 13.15.1-13.15.15.	3.7	0
85	Statistical framework for detection of genetically modified organisms based on Next Generation Sequencing. <i>Food Chemistry</i> , 2016, 192, 788-798.	4.2	47
86	Use of next generation sequencing data to develop a qPCR method for specific detection of EU-unauthorized genetically modified <i>Bacillus subtilis</i> overproducing riboflavin. <i>BMC Biotechnology</i> , 2015, 15, 103.	1.7	25
87	Guidelines for Optimisation of a Multiplex Oligonucleotide Ligation-PCR for Characterisation of Microbial Pathogens in a Microsphere Suspension Array. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	15
88	Current and New Approaches in GMO Detection: Challenges and Solutions. <i>BioMed Research International</i> , 2015, 2015, 1-22.	0.9	98
89	Genome Sequence of EU-Unauthorized Genetically Modified <i>Bacillus subtilis</i> Strain 2014-3557 Overproducing Riboflavin, Isolated from a Vitamin B2 80% Feed Additive. <i>Genome Announcements</i> , 2015, 3, .	0.8	25
90	Fast and discriminative CoSYPS detection system of viable <i>Salmonella</i> spp. and <i>Listeria</i> spp. in carcass swab samples. <i>International Journal of Food Microbiology</i> , 2015, 192, 103-110.	2.1	6

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91	Next-generation sequencing as a tool for the molecular characterisation and risk assessment of genetically modified plants: Added value or not?. Trends in Food Science and Technology, 2015, 45, 319-326.	7.8	55
92	Overexpression of a novel feedback-desensitized Δ^1 -pyrroline-5-carboxylate synthetase increases proline accumulation and confers salt tolerance in transgenic <i>Nicotiana plumbaginifolia</i> . Plant Cell, Tissue and Organ Culture, 2015, 122, 383-393.	1.2	11
93	Validation of a sensitive DNA walking strategy to characterise unauthorised GMOs using model food matrices mimicking common rice products. Food Chemistry, 2015, 173, 1259-1265.	4.2	31
94	A multiplex oligonucleotide ligation-PCR as a complementary tool for subtyping of <i>Salmonella</i> Typhimurium. Applied Microbiology and Biotechnology, 2015, 99, 8137-8149.	1.7	12
95	Integrated DNA walking system to characterize a broad spectrum of GMOs in food/feed matrices. BMC Biotechnology, 2015, 15, 76.	1.7	20
96	Whole Genome Sequence Analysis of <i>Salmonella</i> Enteritidis PT4 Outbreaks from a National Reference Laboratory's Viewpoint. PLOS Currents, 2015, 7, .	1.4	29
97	Comparative Study of Seven Commercial Kits for Human DNA Extraction from Urine Samples Suitable for DNA Biomarker-Based Public Health Studies. Journal of Biomolecular Techniques, 2014, 25, jbt.14-2504-002.	0.8	54
98	Genome Sequence of the <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Namur Strain 05-2929, Lacking the <i>Salmonella</i> Atypical Fimbrial Operon. Genome Announcements, 2014, 2, .	0.8	2
99	An innovative and integrated approach based on DNA walking to identify unauthorised GMOs. Food Chemistry, 2014, 147, 60-69.	4.2	38
100	Evaluation of viability-qPCR detection system on viable and dead <i>Salmonella</i> serovar Enteritidis. Journal of Microbiological Methods, 2014, 103, 131-137.	0.7	65
101	Inter-laboratory Testing of GMO Detection by Combinatory SYBR®Green PCR Screening (CoSYPS). Food Analytical Methods, 2014, 7, 1719.	1.3	17
102	Development and validation of qualitative SYBR®Green Real-Time PCR for detection and discrimination of <i>Listeria</i> spp. and <i>Listeria monocytogenes</i> . Applied Microbiology and Biotechnology, 2013, 97, 4021-4037.	1.7	44
103	SYBR®Green qPCR <i>Salmonella</i> detection system allowing discrimination at the genus, species and subspecies levels. Applied Microbiology and Biotechnology, 2013, 97, 9811-9824.	1.7	29
104	The GMOseek matrix: a decision support tool for optimizing the detection of genetically modified plants. BMC Bioinformatics, 2013, 14, 256.	1.2	39
105	MLVA as a Tool for Public Health Surveillance of Human <i>Salmonella</i> Typhimurium: Prospective Study in Belgium and Evaluation of MLVA Loci Stability. PLoS ONE, 2013, 8, e84055.	1.1	40
106	How to Deal with the Upcoming Challenges in GMO Detection in Food and Feed. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-11.	3.0	61
107	Metal binding properties and structure of a type III metallothionein from the metal hyperaccumulator plant <i>Noccaea caerulescens</i> . Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 1016-1023.	1.1	17
108	Variation in HMA4 gene copy number and expression among <i>Noccaea caerulescens</i> populations presenting different levels of Cd tolerance and accumulation. Journal of Experimental Botany, 2012, 63, 4179-4189.	2.4	105

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109	Four new SYBR®Green qPCR screening methods for the detection of Roundup Ready®, LibertyLink®, and CryIAb traits in genetically modified products. <i>European Food Research and Technology</i> , 2012, 234, 13-23.	1.6	27
110	SYBR®Green qPCR methods for detection of endogenous reference genes in commodity crops: a step ahead in combinatory screening of genetically modified crops in food and feed products. <i>European Food Research and Technology</i> , 2011, 232, 485-496.	1.6	28
111	A theoretical introduction to "Combinatory SYBR®Green qPCR Screening", a matrix-based approach for the detection of materials derived from genetically modified plants. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 396, 2113-2123.	1.9	57
112	SYBR®Green qPCR screening methods for the presence of "35S promoter" and "NOS terminator" elements in food and feed products. <i>European Food Research and Technology</i> , 2010, 230, 383-393.	1.6	52
113	The Five AhMTP1 Zinc Transporters Undergo Different Evolutionary Fates towards Adaptive Evolution to Zinc Tolerance in <i>Arabidopsis halleri</i> . <i>PLoS Genetics</i> , 2010, 6, e1000911.	1.5	106
114	The use of comparative genome analysis and syntenic relationships allows extrapolating the position of Zn tolerance QTL regions from <i>Arabidopsis halleri</i> into <i>Arabidopsis thaliana</i> . <i>Plant and Soil</i> , 2008, 306, 105-116.	1.8	31
115	Merging methods in molecular and ecological genetics to study the adaptation of plants to anthropogenic metal-polluted sites: implications for phytoremediation. <i>Molecular Ecology</i> , 2008, 17, 108-119.	2.0	43
116	When population genetics serves genomics: putting adaptation back in a spatial and historical context. <i>Current Opinion in Plant Biology</i> , 2008, 11, 129-134.	3.5	19
117	Using <i>Arabidopsis</i> to explore zinc tolerance and hyperaccumulation. <i>Trends in Plant Science</i> , 2008, 13, 208-215.	4.3	89
118	A Major Quantitative Trait Locus for Cadmium Tolerance in <i>Arabidopsis halleri</i> Colocalizes with HMA4, a Gene Encoding a Heavy Metal ATPase. <i>Plant Physiology</i> , 2007, 144, 1052-1065.	2.3	288
119	Adaptative Evolution of Metallothionein 3 in the Cd/Zn Hyperaccumulator <i>Thlaspi caerulescens</i> . <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 2005, 60, 224-228.	0.6	6
120	Variations in plant metallothioneins: the heavy metal hyperaccumulator <i>Thlaspi caerulescens</i> as a study case. <i>Planta</i> , 2005, 222, 716-729.	1.6	89
121	Growth and mineral element composition in two ecotypes of <i>Thlaspi caerulescens</i> on Cd contaminated soil. <i>Plant and Soil</i> , 2005, 273, 327-335.	1.8	36
122	A novel CPx-ATPase from the cadmium hyperaccumulator <i>Thlaspi caerulescens</i> . <i>FEBS Letters</i> , 2004, 569, 140-148.	1.3	165
123	Evidence for copper homeostasis function of metallothionein (MT3) in the hyperaccumulator <i>Thlaspi caerulescens</i> . <i>FEBS Letters</i> , 2004, 577, 9-16.	1.3	108
124	Sequence analysis, transcriptional and posttranscriptional regulation of the rice vdac family. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2003, 1625, 43-51.	2.4	55
125	Expression of the rice vdac isoform2: histochemical localization and expression level. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2002, 1579, 133-141.	2.4	12
126	Title is missing!. <i>Molecular Breeding</i> , 2002, 9, 73-80.	1.0	121

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127	Proline Metabolism in the Wild-Type and in a Salt-Tolerant Mutant of <i>Nicotiana plumbaginifolia</i> Studied by ¹³ C-Nuclear Magnetic Resonance Imaging. <i>Plant Physiology</i> , 1999, 121, 1281-1290.	2.3	54
128	Development of a Molecular Platform for GMO Detection in Food and Feed on the Basis of a Combinatory qPCR Technology. , 0, , .		7