List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4842885/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Multiplex Droplet Digital PCR Protocols for Quantification of GM Maize Events. Methods in Molecular Biology, 2018, 1768, 69-98.	0.9	17
2	Decision Support for the Comparative Evaluation and Selection of Analytical Methods: Detection of Genetically Modified Organisms as an Example. Food Analytical Methods, 2018, 11, 2105-2122.	2.6	2
3	Development and validation of a multi-locus DNA metabarcoding method to identify endangered species in complex samples. GigaScience, 2017, 6, 1-18.	6.4	75
4	Development and inter-laboratory assessment of droplet digital PCR assays for multiplex quantification of 15 genetically modified soybean lines. Scientific Reports, 2017, 7, 8601.	3.3	40
5	High Throughput Sequencing for Detection of Foodborne Pathogens. Frontiers in Microbiology, 2017, 8, 2029.	3.5	88
6	Advances in DNA metabarcoding for food and wildlife forensic species identification. Analytical and Bioanalytical Chemistry, 2016, 408, 4615-4630.	3.7	180
7	DNA enrichment approaches to identify unauthorized genetically modified organisms (GMOs). Analytical and Bioanalytical Chemistry, 2016, 408, 4575-4593.	3.7	29
8	Application of whole genome shotgun sequencing for detection and characterization of genetically modified organisms and derived products. Analytical and Bioanalytical Chemistry, 2016, 408, 4595-4614.	3.7	43
9	Multiplex Quantification of 12 European Union Authorized Genetically Modified Maize Lines with Droplet Digital Polymerase Chain Reaction. Analytical Chemistry, 2015, 87, 8218-8226.	6.5	100
10	Characterization of GM events by insert knowledge adapted re-sequencing approaches. Scientific Reports, 2013, 3, 2839.	3.3	89
11	DNA-Fragments Are Transcytosed across CaCo-2 Cells by Adsorptive Endocytosis and Vesicular Mediated Transport. PLoS ONE, 2013, 8, e56671.	2.5	9
12	Detecting un-authorized genetically modified organisms (GMOs) and derived materials. Biotechnology Advances, 2012, 30, 1318-1335.	11.7	129
13	Monitoring the spore dynamics of Aphanomyces astaci in the ambient water of latent carrier crayfish. Veterinary Microbiology, 2012, 160, 99-107.	1.9	50
14	Detection and quantification of the crayfish plague agent in natural waters: direct monitoring approach for aquatic environments. Diseases of Aquatic Organisms, 2011, 95, 9-17.	1.0	70
15	Quantification of dietary DNA in tissues of Atlantic salmon (Salmo salar L.) fed genetically modified feed ingredients. Aquaculture Nutrition, 2011, 17, e668-e674.	2.7	2
16	Comparison of nine different real-time PCR chemistries for qualitative and quantitative applications in GMO detection. Analytical and Bioanalytical Chemistry, 2010, 396, 2023-2029.	3.7	125
17	Non-prejudiced Detection and Characterization of Genetic Modifications. Food Analytical Methods, 2010, 3, 120-128.	2.6	12
18	Influence of storage temperature on gene expression and virulence potential of Listeria monocytogenes strains grown in a salmon matrix. Food Microbiology, 2010, 27, 795-801.	4.2	46

#	Article	IF	CITATIONS
19	Detection of Food-Derived Damaged Nucleosides with Possible Adverse Effects on Human Health Using a Global Adductomics Approach. Journal of Agricultural and Food Chemistry, 2010, 58, 6370-6375.	5.2	16
20	A quantitative TaqMan® MGB real-time polymerase chain reaction based assay for detection of the causative agent of crayfish plague Aphanomyces astaci. Veterinary Microbiology, 2009, 137, 146-155.	1.9	149
21	Testing for genetically modified organisms (GMOs): Past, present and future perspectives. Biotechnology Advances, 2009, 27, 1071-1082.	11.7	144
22	UniquePrimer — a web utility for design of specific PCR primers and probes. Annals of Microbiology, 2009, 59, 391-393.	2.6	2
23	Improved Sample Preparation for Real-Time PCR Detection of Listeria monocytogenes in Hot-Smoked Salmon using Filtering and Immunomagnetic Separation Techniques. Food Analytical Methods, 2009, 2, 23-29.	2.6	17
24	Characterization of unknown genetic modifications using high throughput sequencing and computational subtraction. BMC Biotechnology, 2009, 9, 87.	3.3	21
25	A statistical approach for evaluation of PCR results to improve the practical limit of quantification (LOQ) of GMO analyses (SIMQUANT). European Food Research and Technology, 2008, 227, 1149-1157.	3.3	31
26	Generation of Reference Material by the Use of Multiple Displacement Amplification (MDA) for the Detection of Genetically Modified Organisms (GMOs). Food Analytical Methods, 2008, 1, 181-189.	2.6	6
27	GMO testing—trade, labeling or safety first?. Nature Biotechnology, 2008, 26, 858-859.	17.5	18
28	Gene stacking in transgenic plants: towards compliance between definitions, terminology, and detection within the EU regulatory framework. Environmental Biosafety Research, 2008, 7, 197-218.	1.1	56
29	Anchored PCR for possible detection and characterisation of foreign integrated DNA at near single molecule level. European Food Research and Technology, 2008, 226, 949-956.	3.3	8
30	Polyphasic re-examination of Yarrowia lipolytica strains and the description of three novel Candida species: Candida oslonensis sp. nov., Candida alimentaria sp. nov. and Candida hollandica sp. nov International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 2426-2435.	1.7	62
31	Microarray-based method for detection of unknown genetic modifications. BMC Biotechnology, 2007, 7, 91.	3.3	38
32	Sampling, detection, identification and quantification of genetically modified organisms (GMOs). , 2007, , 231-268.		21
33	Coherence between Legal Requirements and Approaches for Detection of Genetically Modified Organisms (GMOs) and Their Derived Products. Journal of Agricultural and Food Chemistry, 2006, 54, 2799-2809.	5.2	84
34	Novel Reference Gene, PKABA1, Used in a Duplex Real-Time Polymerase Chain Reaction for Detection and Quantitation of Wheat- and Barley-Derived DNA. Journal of Agricultural and Food Chemistry, 2006, 54, 682-687.	5.2	39
35	Equal Performance of TaqMan, MGB, Molecular Beacon, and SYBR Green-Based Detection Assays in Detection and Quantification of Roundup Ready Soybean. Journal of Agricultural and Food Chemistry, 2006, 54, 9658-9663.	5.2	58
36	DNA microarray to detect and identify trichothecene- and moniliformin-producing Fusarium species. Journal of Applied Microbiology, 2006, 102, 061120055200047-???.	3.1	27

#	Article	IF	CITATIONS
37	Simultaneous detection and identification of trichothecene- and moniliformin-producing Fusarium species based on multiplex SNP analysis. Journal of Applied Microbiology, 2006, 102, 061120055200046-???.	3.1	20
38	Persistence and distribution of intravenously injected DNA in blood and organs of Atlantic salmon (Salmo salar L.). European Food Research and Technology, 2006, 222, 258-265.	3.3	16
39	Morphological, chemical and molecular differentiation of Fusarium equiseti isolated from Norwegian cereals. International Journal of Food Microbiology, 2005, 99, 195-206.	4.7	50
40	Phylogeny and toxigenic potential is correlated in Fusarium species as revealed by partial translation elongation factor 1 alpha gene sequences. Mycological Research, 2005, 109, 173-186.	2.5	163
41	Dietary DNA in blood and organs of Atlantic salmon (Salmo salar L.). European Food Research and Technology, 2005, 221, 1-8.	3.3	40
42	Design of a DNA chip for detection of unknown genetically modified organisms (GMOs). Bioinformatics, 2005, 21, 1917-1926.	4.1	35
43	Differentiation of Important and Closely Related Cereal Plant Species (Poaceae) in Food by Hybridization to an Oligonucleotide Array. Journal of Agricultural and Food Chemistry, 2005, 53, 8874-8880.	5.2	34
44	The Modular Analytical Procedure and Validation Approach and the Units of Measurement for Genetically Modified Materials in Foods and Feeds. Journal of AOAC INTERNATIONAL, 2004, 87, 927-936.	1.5	84
45	On reliability. New Phytologist, 2004, 161, 11-13.	7.3	19
46	A Molecular Genetic Analysis of Eragrostis Tef (Zucc.) Trotter:non-Coding Regions of Chloroplast DNA, 18S rDNA and the Transcription Factor VP1. Hereditas, 2004, 132, 193-202.	1.4	9
47	Phylogenetic analyses of the Fusarium poae, Fusarium sporotrichioides and Fusarium langsethiae species complex based on partial sequences of the translation elongation factor-1 alpha gene. International Journal of Food Microbiology, 2004, 95, 287-295.	4.7	81
48	An integrated taxonomic study of Fusarium langsethiae, Fusarium poae and Fusarium sporotrichioides based on the use of composite datasets. International Journal of Food Microbiology, 2004, 95, 341-349.	4.7	30
49	Characterisation of the 5? integration site and development of an event-specific real-time PCR assay for NK603 maize from a low starting copy number. European Food Research and Technology, 2004, 219, 421.	3.3	41
50	Detection and traceability of genetically modified organisms in the food production chain. Food and Chemical Toxicology, 2004, 42, 1157-1180.	3.6	274
51	Kohninia linnaeicola, a New Genus and Species of the Sclerotiniaceae Pathogenic to Linnaea borealis. Mycologia, 2004, 96, 135.	1.9	7
52	Kohninia linnaeicola, a new genus and species of the Sclerotiniaceae pathogenic to Linnaea borealis. Mycologia, 2004, 96, 135-142.	1.9	13
53	Kohninia linnaeicola, a new genus and species of the Sclerotiniaceae pathogenic to Linnaea borealis. Mycologia, 2004, 96, 135-42.	1.9	6
54	PCR technology for screening and quantification of genetically modified organisms (GMOs). Analytical and Bioanalytical Chemistry, 2003, 375, 985-993.	3.7	313

#	Article	IF	CITATIONS
55	Event specific real-time quantitative PCR for genetically modified Bt11 maize (Zea mays). European Food Research and Technology, 2003, 216, 347-354.	3.3	101
56	The use of AFLP to relate cheese-contaminating Penicillium strains to specific points in the production plants. International Journal of Food Microbiology, 2003, 83, 195-204.	4.7	18
57	Differentiation of Penicillium commune and Penicillium palitans isolates from cheese and indoor environments of cheese factories using M13 fingerprinting. Food Microbiology, 2002, 19, 151-157.	4.2	18
58	Roundup Ready ® soybean event-specific real-time quantitative PCR assay and estimation of the practical detection and quantification limits in GMO analyses. European Food Research and Technology, 2001, 213, 432-438.	3.3	209
59	Phylogenetics of Helotiales and Rhytismatales Based on Partial Small Subunit Nuclear Ribosomal DNA Sequences. Mycologia, 2001, 93, 915.	1.9	43
60	<i>Cortinarius</i> phylogeny and possible taxonomic implications of ITS rDNA sequences. Mycologia, 2000, 92, 694-710.	1.9	55
61	Genomic Origin and Organization of the Hybrid Poa jemtlandica(Poaceae) Verified by Genomic In Situ Hybridization and Chloroplast DNA Sequences. Annals of Botany, 2000, 85, 439-445.	2.9	33
62	Cortinarius Phylogeny and Possible Taxonomic Implications of ITS rDNA Sequences. Mycologia, 2000, 92, 694.	1.9	43
63	Structural characteristics and possible horizontal transfer of group I introns between closely related plant pathogenic fungi. Molecular Biology and Evolution, 1999, 16, 114-126.	8.9	134
64	The postfire discomycete Geopyxis carbonaria (Ascomycota) is a biotrophic root associate with Norway spruce (Picea abies) in nature. Molecular Ecology, 1998, 7, 609-616.	3.9	54
65	Molecular Phylogeny and Evolution of Monilinia (Sclerotiniaceae) based on coding and Noncoding rDNA Sequences. American Journal of Botany, 1997, 84, 686-701.	1.7	78
66	Nuclear rDNA Phylogeny of the Sclerotiniaceae. Mycologia, 1997, 89, 885.	1.9	41
67	Nuclear rDNA phylogeny of the Sclerotiniaceae. Mycologia, 1997, 89, 885-899.	1.9	83
68	A synopsis of the genus Scleromitrula (= Verpatinia) (Ascomycotina: Helotiales: Sclerotiniaceae). Mycoscience, 1997, 38, 55-69.	0.8	16
69	Sclerotiniaceous species on Rubus chamaemorus: morphoanatomical and RFLP studies. Mycological Research, 1994, 98, 923-930.	2.5	9