Kevin Vanneste

List of Publications by Year
in descending order

35 papers	4,411 citations	471509 17 h-index	361022 35 g-index
37 all docs	37 docs citations	37 times ranked	7120 citing authors

#	Article	IF	Citations
1	The Norway spruce genome sequence and conifer genome evolution. Nature, 2013, 497, 579-584.	27.8	1,303
2	The genome of Eucalyptus grandis. Nature, 2014, 510, 356-362.	27.8	725
3	The genome of the seagrass Zostera marina reveals angiosperm adaptation to the sea. Nature, 2016, 530, 331-335.	27.8	460
4	The genome sequence of the orchid Phalaenopsis equestris. Nature Genetics, 2015, 47, 65-72.	21.4	413
5	Analysis of 41 plant genomes supports a wave of successful genome duplications in association with the Cretaceous–Paleogene boundary. Genome Research, 2014, 24, 1334-1347.	5.5	381
6	The TPLATE Adaptor Complex Drives Clathrin-Mediated Endocytosis in Plants. Cell, 2014, 156, 691-704.	28.9	238
7	Inference of Genome Duplications from Age Distributions Revisited. Molecular Biology and Evolution, 2013, 30, 177-190.	8.9	145
8	Tangled up in two: a burst of genome duplications at the end of the Cretaceous and the consequences for plant evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130353.	4.0	141
9	Gamma Paleohexaploidy in the Stem Lineage of Core Eudicots: Significance for MADS-Box Gene and Species Diversification. Molecular Biology and Evolution, 2012, 29, 3793-3806.	8.9	127
10	Horsetails Are Ancient Polyploids: Evidence from *Equisetum giganteum*. Plant Cell, 2015, 27, 1567-1578.	6.6	78
11	Revisiting ancestral polyploidy in plants. Science Advances, 2017, 3, e1603195.	10.3	73
12	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. Frontiers in Microbiology, 2019, 10, 362.	3.5	51
13	Deepening of In Silico Evaluation of SARS-CoV-2 Detection RT-qPCR Assays in the Context of New Variants. Genes, 2021, 12, 565.	2.4	26
14	Use of Whole Genome Sequencing Data for a First in Silico Specificity Evaluation of the RT-qPCR Assays Used for SARS-CoV-2 Detection. International Journal of Molecular Sciences, 2020, 21, 5585.	4.1	23
15	Validation strategy of a bioinformatics whole genome sequencing workflow for Shiga toxin-producing Escherichia coli using a reference collection extensively characterized with conventional methods. Microbial Genomics, 2021, 7, .	2.0	20
16	Towards Real-Time and Affordable Strain-Level Metagenomics-Based Foodborne Outbreak Investigations Using Oxford Nanopore Sequencing Technologies. Frontiers in Microbiology, 2021, 12, 738284.	3.5	19
17	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. BMC Bioinformatics, 2018, 19, 312.	2.6	18
18	Strategy for the identification of micro-organisms producing food and feed products: Bacteria producing food enzymes as study case. Food Chemistry, 2020, 305, 125431.	8.2	18

#	Article	IF	Citations
19	Isolation of Drug-Resistant *Gallibacterium anatis* from Calves with Unresponsive Bronchopneumonia, Belgium. Emerging Infectious Diseases, 2020, 26, .	4.3	18
20	A Bioinformatics Whole-Genome Sequencing Workflow for Clinical Mycobacterium tuberculosis Complex Isolate Analysis, Validated Using a Reference Collection Extensively Characterized with Conventional Methods and *In Silico* Approaches. Journal of Clinical Microbiology, 2021, 59, .	3.9	18
21	Application of a strain-level shotgun metagenomics approach on food samples: resolution of the source of a Salmonella food-borne outbreak. Microbial Genomics, 2021, 7, .	2.0	16
22	Identification of an unauthorized genetically modified bacteria in food enzyme through whole-genome sequencing. Scientific Reports, 2020, 10, 7094.	3.3	14
23	Evaluation of a commercial exogenous internal process control for diagnostic RNA virus metagenomics from different animal clinical samples. Journal of Virological Methods, 2020, 283, 113916.	2.1	10
24	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. F1000Research, 0, 10, 80.	1.6	8
25	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.	3.5	8
26	Whole Genome Sequencing Provides an Added Value to the Investigation of Staphylococcal Food Poisoning Outbreaks. Frontiers in Microbiology, 2021, 12, 750278.	3.5	7
27	Screening strategy targeting the presence of food enzyme-producing fungi in food enzyme preparations. Food Control, 2020, 117, 107295.	5.5	6
28	First detection of a plasmid-encoded New-Delhi metallo-beta-lactamase-1 (NDM-1) producing Acinetobacter baumannii using whole genome sequencing, isolated in a clinical setting in Benin. Annals of Clinical Microbiology and Antimicrobials, 2021, 20, 5.	3.8	6
29	Case Report: Multidrug Resistant Raoultella ornithinolytica in a Septicemic Calf. Frontiers in Veterinary Science, 2021, 8, 631716.	2.2	5
30	A shotgun metagenomics approach to detect and characterize unauthorized genetically modified microorganisms in microbial fermentation products. Food Chemistry Molecular Sciences, 2021, 2, 100023.	2.1	5
31	Increased viral read counts and metagenomic full genome characterization of porcine astrovirusÂ4 and Posavirus 1 in sows in a swine farm with unexplained neonatal piglet diarrhea. Virus Genes, 2020, 56, 696-704.	1.6	4
32	Food Enzyme Database (FEDA): a web application gathering information about food enzyme preparations available on the European market. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	4
33	Phylogenomic Investigation of Increasing Fluoroquinolone Resistance among Belgian Cases of Shigellosis between 2013 and 2018 Indicates Both Travel-Related Imports and Domestic Circulation. Microorganisms, 2021, 9, 767.	3.6	4
34	Evaluation of WGS performance for bacterial pathogen characterization with the Illumina technology optimized for time-critical situations. Microbial Genomics, 2021, 7, .	2.0	4
35	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. F1000Research, 0, 10, 80.	1.6	0