

Kevin Vanneste

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10731663/publications.pdf>

Version: 2024-02-01

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 | 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. | 3.8 | 6 |
| 2 | 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, . | 3.0 | 4 |
| 3 | 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, . | 2.0 | 20 |
| 4 | Case Report: Multidrug Resistant <i>Raoultella ornithinolytica</i> in a Septicemic Calf. <i>Frontiers in Veterinary Science</i> , 2021, 8, 631716. | 2.2 | 5 |
| 5 | 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. | 2.4 | 26 |
| 6 | 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. | 3.6 | 4 |
| 7 | 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, . | 2.0 | 16 |
| 8 | A Bioinformatics Whole-Genome Sequencing Workflow for Clinical <i>Mycobacterium tuberculosis</i> Complex Isolate Analysis, Validated Using a Reference Collection Extensively Characterized with Conventional Methods and <i>In Silico</i> Approaches. <i>Journal of Clinical Microbiology</i> , 2021, 59, . | 3.9 | 18 |
| 9 | A shotgun metagenomics approach to detect and characterize unauthorized genetically modified microorganisms in microbial fermentation products. <i>Food Chemistry Molecular Sciences</i> , 2021, 2, 100023. | 2.1 | 5 |
| 10 | Whole Genome Sequencing Provides an Added Value to the Investigation of Staphylococcal Food Poisoning Outbreaks. <i>Frontiers in Microbiology</i> , 2021, 12, 750278. | 3.5 | 7 |
| 11 | Evaluation of WGS performance for bacterial pathogen characterization with the Illumina technology optimized for time-critical situations. <i>Microbial Genomics</i> , 2021, 7, . | 2.0 | 4 |
| 12 | Towards Real-Time and Affordable Strain-Level Metagenomics-Based Foodborne Outbreak Investigations Using Oxford Nanopore Sequencing Technologies. <i>Frontiers in Microbiology</i> , 2021, 12, 738284. | 3.5 | 19 |
| 13 | Whole-Genome Sequencing-Based Antimicrobial Resistance Characterization and Phylogenomic Investigation of 19 Multidrug-Resistant and Extended-Spectrum Beta-Lactamase-Positive <i>Escherichia coli</i> Strains Collected From Hospital Patients in Benin in 2019. <i>Frontiers in Microbiology</i> , 2021, 12, 752883. | 3.5 | 8 |
| 14 | Strategy for the identification of micro-organisms producing food and feed products: Bacteria producing food enzymes as study case. <i>Food Chemistry</i> , 2020, 305, 125431. | 8.2 | 18 |
| 15 | 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. | 4.1 | 23 |
| 16 | Increased viral read counts and metagenomic full genome characterization of porcine astrovirus 4 and Posavirus 1 in sows in a swine farm with unexplained neonatal piglet diarrhea. <i>Virus Genes</i> , 2020, 56, 696-704. | 1.6 | 4 |
| 17 | Identification of an unauthorized genetically modified bacteria in food enzyme through whole-genome sequencing. <i>Scientific Reports</i> , 2020, 10, 7094. | 3.3 | 14 |
| 18 | Screening strategy targeting the presence of food enzyme-producing fungi in food enzyme preparations. <i>Food Control</i> , 2020, 117, 107295. | 5.5 | 6 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Evaluation of a commercial exogenous internal process control for diagnostic RNA virus metagenomics from different animal clinical samples. <i>Journal of Virological Methods</i> , 2020, 283, 113916. | 2.1 | 10 |
| 20 | Isolation of Drug-Resistant <i>Gallibacterium anatis</i> from Calves with Unresponsive Bronchopneumonia, Belgium. <i>Emerging Infectious Diseases</i> , 2020, 26, . | 4.3 | 18 |
| 21 | 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: <i>Neisseria meningitidis</i> as a Proof-of-Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 362. | 3.5 | 51 |
| 22 | 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. | 2.6 | 18 |
| 23 | Revisiting ancestral polyploidy in plants. <i>Science Advances</i> , 2017, 3, e1603195. | 10.3 | 73 |
| 24 | The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016, 530, 331-335. | 27.8 | 460 |
| 25 | Horsetails Are Ancient Polyploids: Evidence from <i>Equisetum giganteum</i> . <i>Plant Cell</i> , 2015, 27, 1567-1578. | 6.6 | 78 |
| 26 | The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015, 47, 65-72. | 21.4 | 413 |
| 27 | Tangled up in two: a burst of genome duplications at the end of the Cretaceous and the consequences for plant evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130353. | 4.0 | 141 |
| 28 | The TPLATE Adaptor Complex Drives Clathrin-Mediated Endocytosis in Plants. <i>Cell</i> , 2014, 156, 691-704. | 28.9 | 238 |
| 29 | The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362. | 27.8 | 725 |
| 30 | Analysis of 41 plant genomes supports a wave of successful genome duplications in association with the Cretaceous–Paleogene boundary. <i>Genome Research</i> , 2014, 24, 1334-1347. | 5.5 | 381 |
| 31 | The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584. | 27.8 | 1,303 |
| 32 | Inference of Genome Duplications from Age Distributions Revisited. <i>Molecular Biology and Evolution</i> , 2013, 30, 177-190. | 8.9 | 145 |
| 33 | Gamma Paleohexaploidy in the Stem Lineage of Core Eudicots: Significance for MADS-Box Gene and Species Diversification. <i>Molecular Biology and Evolution</i> , 2012, 29, 3793-3806. | 8.9 | 127 |
| 34 | A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. <i>F1000Research</i> , 0, 10, 80. | 1.6 | 8 |
| 35 | A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. <i>F1000Research</i> , 0, 10, 80. | 1.6 | 0 |