

Tim van Opijnen

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

3,063
citations

279798

23
h-index

243625

44
g-index

62
all docs

62
docs citations

62
times ranked

3624
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid, Multianalyte Detection of Opioid Metabolites in Wastewater. <i>ACS Nano</i> , 2022, 16, 3704-3714.	14.6	19
2	Targeted control of pneumolysin production by a mobile genetic element in <i>Streptococcus pneumoniae</i> . <i>Microbial Genomics</i> , 2022, 8, .	2.0	5
3	The Phenylacetic Acid Catabolic Pathway Regulates Antibiotic and Oxidative Stress Responses in <i>Acinetobacter</i> . <i>MBio</i> , 2022, 13, e0186321.	4.1	18
4	<i>Yersinia pseudotuberculosis</i> doxycycline tolerance strategies include modulating expression of genes involved in cell permeability and tRNA modifications. <i>PLoS Pathogens</i> , 2022, 18, e1010556.	4.7	1
5	Immunosuppression broadens evolutionary pathways to drug resistance and treatment failure during <i>Acinetobacter baumannii</i> pneumonia in mice. <i>Nature Microbiology</i> , 2022, 7, 796-809.	13.3	17
6	A genome-wide atlas of antibiotic susceptibility targets and pathways to tolerance. <i>Nature Communications</i> , 2022, 13, .	12.8	12
7	Essential Gene Analysis in <i>Acinetobacter baumannii</i> by High-Density Transposon Mutagenesis and CRISPR Interference. <i>Journal of Bacteriology</i> , 2021, 203, e0056520.	2.2	25
8	Dynamic Pneumococcal Genetic Adaptations Support Bacterial Growth and Inflammation during Coinfection with Influenza. <i>Infection and Immunity</i> , 2021, 89, e0002321.	2.2	6
9	Host-informed therapies for the treatment of pneumococcal pneumonia. <i>Trends in Molecular Medicine</i> , 2021, 27, 971-989.	6.7	4
10	Peptide Probes of Colistin Resistance Discovered via Chemically Enhanced Phage Display. <i>ACS Infectious Diseases</i> , 2020, 6, 2410-2418.	3.8	6
11	Transposon Insertion Sequencing, a Global Measure of Gene Function. <i>Annual Review of Genetics</i> , 2020, 54, 337-365.	7.6	25
12	Detection of a multi-disease biomarker in saliva with graphene field effect transistors. <i>Medical Devices & Sensors</i> , 2020, 3, e10121.	2.7	11
13	Entropy of a bacterial stress response is a generalizable predictor for fitness and antibiotic sensitivity. <i>Nature Communications</i> , 2020, 11, 4365.	12.8	30
14	Antibiotic susceptibility signatures identify potential antimicrobial targets in the <i>Acinetobacter baumannii</i> cell envelope. <i>Nature Communications</i> , 2020, 11, 4522.	12.8	62
15	A decade of advances in transposon-insertion sequencing. <i>Nature Reviews Genetics</i> , 2020, 21, 526-540.	16.3	228
16	Dielectrophoresis assisted rapid, selective and single cell detection of antibiotic resistant bacteria with G-FETs. <i>Biosensors and Bioelectronics</i> , 2020, 156, 112123.	10.1	62
17	ShinyOmics: collaborative exploration of omics-data. <i>BMC Bioinformatics</i> , 2020, 21, 22.	2.6	11
18	Topologically correct synthetic reconstruction of pathogen social behavior found during <i>Yersinia</i> growth in deep tissue sites. <i>ELife</i> , 2020, 9, .	6.0	3

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19	A Pangenomic Perspective on the Emergence, Maintenance, and Predictability of Antibiotic Resistance. , 2020, , 169-202.		5
20	The Landscape of Phenotypic and Transcriptional Responses to Ciprofloxacin in <i>Acinetobacter baumannii</i> : Acquired Resistance Alleles Modulate Drug-Induced SOS Response and Prophage Replication. MBio, 2019, 10, .	4.1	32
21	Bacterial Factors Required for Transmission of <i>Streptococcus pneumoniae</i> in Mammalian Hosts. Cell Host and Microbe, 2019, 25, 884-891.e6.	11.0	48
22	Droplet Tn-Seq combines microfluidics with Tn-Seq for identifying complex single-cell phenotypes. Nature Communications, 2019, 10, 5729.	12.8	54
23	Phage Display of Dynamic Covalent Binding Motifs Enables Facile Development of Targeted Antibiotics. Journal of the American Chemical Society, 2018, 140, 6137-6145.	13.7	50
24	The Transcriptional landscape of <i>Streptococcus pneumoniae</i> TIGR4 reveals a complex operon architecture and abundant riboregulation critical for growth and virulence. PLoS Pathogens, 2018, 14, e1007461.	4.7	37
25	MAGenTA: a Galaxy implemented tool for complete Tn-Seq analysis and data visualization. Bioinformatics, 2017, 33, 2781-2783.	4.1	38
26	Antibiotics Disrupt Coordination between Transcriptional and Phenotypic Stress Responses in Pathogenic Bacteria. Cell Reports, 2017, 20, 1705-1716.	6.4	65
27	Strain Dependent Genetic Networks for Antibiotic-Sensitivity in a Bacterial Pathogen with a Large Pan-Genome. PLoS Pathogens, 2016, 12, e1005869.	4.7	66
28	Genome-Wide Fitness and Genetic Interactions Determined by Tn-seq, a High-Throughput Massively Parallel Sequencing Method for Microorganisms. Current Protocols in Microbiology, 2015, 36, 1E.3.1-1E.3.24.	6.5	44
29	Genome-Wide Fitness and Genetic Interactions Determined by Tn-seq, a High-Throughput Massively Parallel Sequencing Method for Microorganisms. Current Protocols in Molecular Biology, 2014, 106, 7.16.1-24.	2.9	49
30	Genomic Analyses of Pneumococci from Children with Sickle Cell Disease Expose Host-Specific Bacterial Adaptations and Deficits in Current Interventions. Cell Host and Microbe, 2014, 15, 587-599.	11.0	57
31	Transposon insertion sequencing: a new tool for systems-level analysis of microorganisms. Nature Reviews Microbiology, 2013, 11, 435-442.	28.6	428
32	Control of Virulence by Small RNAs in <i>Streptococcus pneumoniae</i> . PLoS Pathogens, 2012, 8, e1002788.	4.7	137
33	A fine scale phenotype-genotype virulence map of a bacterial pathogen. Genome Research, 2012, 22, 2541-2551.	5.5	224
34	Genome-Wide Fitness and Genetic Interactions Determined by Tn-seq, a High-Throughput Massively Parallel Sequencing Method for Microorganisms. Current Protocols in Microbiology, 2010, 19, Unit1E.3.	6.5	63
35	Tn-seq: high-throughput parallel sequencing for fitness and genetic interaction studies in microorganisms. Nature Methods, 2009, 6, 767-772.	19.0	802
36	Adaptation of HIV-1 Depends on the Host-Cell Environment. PLoS ONE, 2007, 2, e271.	2.5	15

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37	Effects of Random Mutations in the Human Immunodeficiency Virus Type 1 Transcriptional Promoter on Viral Fitness in Different Host Cell Environments. <i>Journal of Virology</i> , 2006, 80, 6678-6685.	3.4	37
38	Genetic variability in the three genomes of <i>Nasonia</i> : nuclear, mitochondrial and <i>Wolbachia</i> . <i>Insect Molecular Biology</i> , 2005, 14, 653-663.	2.0	16
39	Genetics of female mate discrimination of heterospecific males in <i>Nasonia</i> (Hymenoptera). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf</i>	1.9	32
40	The host environment drives HIV-1 fitness. <i>Reviews in Medical Virology</i> , 2005, 15, 219-233.	8.3	20
41	Human Immunodeficiency Virus Type 1 Subtypes Have a Distinct Long Terminal Repeat That Determines the Replication Rate in a Host-Cell-Specific Manner. <i>Journal of Virology</i> , 2004, 78, 3675-3683.	3.4	82
42	T-cell Activation Leads to Poor Activation of the HIV-1 Clade E Long Terminal Repeat and Weak Association of Nuclear Factor- κ B and NFAT with Its Enhancer Region. <i>Journal of Biological Chemistry</i> , 2004, 279, 52949-52960.	3.4	18
43	The Human Immunodeficiency Virus Type 1 Promoter Contains a CATA Box Instead of a TATA Box for Optimal Transcription and Replication. <i>Journal of Virology</i> , 2004, 78, 6883-6890.	3.4	49
44	Genetic Conflicts over Sex Ratio: Mite-Endosymbiont Interactions. <i>American Naturalist</i> , 2003, 161, 254-266.	2.1	29