

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	Tn-seq: high-throughput parallel sequencing for fitness and genetic interaction studies in microorganisms. <i>Nature Methods</i> , 2009, 6, 767-772.	19.0	802
2	Transposon insertion sequencing: a new tool for systems-level analysis of microorganisms. <i>Nature Reviews Microbiology</i> , 2013, 11, 435-442.	28.6	428
3	A decade of advances in transposon-insertion sequencing. <i>Nature Reviews Genetics</i> , 2020, 21, 526-540.	16.3	228
4	A fine scale phenotypeâ€“genotype virulence map of a bacterial pathogen. <i>Genome Research</i> , 2012, 22, 2541-2551.	5.5	224
5	Control of Virulence by Small RNAs in <i>Streptococcus pneumoniae</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002788.	4.7	137
6	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
7	Strain Dependent Genetic Networks for Antibiotic-Sensitivity in a Bacterial Pathogen with a Large Pan-Genome. <i>PLoS Pathogens</i> , 2016, 12, e1005869.	4.7	66
8	Antibiotics Disrupt Coordination between Transcriptional and Phenotypic Stress Responses in Pathogenic Bacteria. <i>Cell Reports</i> , 2017, 20, 1705-1716.	6.4	65
9	Genomeâ€“Wide Fitness and Genetic Interactions Determined by Tnâ€“seq, a Highâ€“Throughput Massively Parallel Sequencing Method for Microorganisms. <i>Current Protocols in Microbiology</i> , 2010, 19, Unit1E.3.	6.5	63
10	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
11	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
12	Genomic Analyses of Pneumococci from Children with Sickle Cell Disease Expose Host-Specific Bacterial Adaptations and Deficits in Current Interventions. <i>Cell Host and Microbe</i> , 2014, 15, 587-599.	11.0	57
13	Droplet Tn-Seq combines microfluidics with Tn-Seq for identifying complex single-cell phenotypes. <i>Nature Communications</i> , 2019, 10, 5729.	12.8	54
14	Phage Display of Dynamic Covalent Binding Motifs Enables Facile Development of Targeted Antibiotics. <i>Journal of the American Chemical Society</i> , 2018, 140, 6137-6145.	13.7	50
15	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
16	Genomeâ€“Wide Fitness and Genetic Interactions Determined by Tnâ€“seq, a Highâ€“Throughput Massively Parallel Sequencing Method for Microorganisms. <i>Current Protocols in Molecular Biology</i> , 2014, 106, 7.16.1-24.	2.9	49
17	Bacterial Factors Required for Transmission of <i>Streptococcus pneumoniae</i> in Mammalian Hosts. <i>Cell Host and Microbe</i> , 2019, 25, 884-891.e6.	11.0	48
18	Genomeâ€“Wide Fitness and Genetic Interactions Determined by Tnâ€“seq, a Highâ€“Throughput Massively Parallel Sequencing Method for Microorganisms. <i>Current Protocols in Microbiology</i> , 2015, 36, 1E.3.1-1E.3.24.	6.5	44

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19	MAGenTA: a Galaxy implemented tool for complete Tn-Seq analysis and data visualization. <i>Bioinformatics</i> , 2017, 33, 2781-2783.	4.1	38
20	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
21	The Transcriptional landscape of <i>Streptococcus pneumoniae</i> TIGR4 reveals a complex operon architecture and abundant riboregulation critical for growth and virulence. <i>PLoS Pathogens</i> , 2018, 14, e1007461.	4.7	37
22	Genetics of female mate discrimination of heterospecific males in <i>Nasonia</i> (Hymenoptera,). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td</i>	1.9	32
23	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. <i>MBio</i> , 2019, 10, .	4.1	32
24	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
25	Genetic Conflicts over Sex Ratio: Mite-Endosymbiont Interactions. <i>American Naturalist</i> , 2003, 161, 254-266.	2.1	29
26	Transposon Insertion Sequencing, a Global Measure of Gene Function. <i>Annual Review of Genetics</i> , 2020, 54, 337-365.	7.6	25
27	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
28	The host environment drives HIV-1 fitness. <i>Reviews in Medical Virology</i> , 2005, 15, 219-233.	8.3	20
29	Rapid, Multianalyte Detection of Opioid Metabolites in Wastewater. <i>ACS Nano</i> , 2022, 16, 3704-3714.	14.6	19
30	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
31	The Phenylacetic Acid Catabolic Pathway Regulates Antibiotic and Oxidative Stress Responses in <i>Acinetobacter</i> . <i>MBio</i> , 2022, 13, e0186321.	4.1	18
32	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
33	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
34	Adaptation of HIV-1 Depends on the Host-Cell Environment. <i>PLoS ONE</i> , 2007, 2, e271.	2.5	15
35	A genome-wide atlas of antibiotic susceptibility targets and pathways to tolerance. <i>Nature Communications</i> , 2022, 13, .	12.8	12
36	Detection of a multi-disease biomarker in saliva with graphene field effect transistors. <i>Medical Devices & Sensors</i> , 2020, 3, e10121.	2.7	11

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37	ShinyOmics: collaborative exploration of omics-data. BMC Bioinformatics, 2020, 21, 22.	2.6	11
38	Peptide Probes of Colistin Resistance Discovered via Chemically Enhanced Phage Display. ACS Infectious Diseases, 2020, 6, 2410-2418.	3.8	6
39	Dynamic Pneumococcal Genetic Adaptations Support Bacterial Growth and Inflammation during Coinfection with Influenza. Infection and Immunity, 2021, 89, e0002321.	2.2	6
40	A Pangenomic Perspective on the Emergence, Maintenance, and Predictability of Antibiotic Resistance. , 2020, , 169-202.		5
41	Targeted control of pneumolysin production by a mobile genetic element in Streptococcus pneumoniae. Microbial Genomics, 2022, 8, .	2.0	5
42	Host-informed therapies for the treatment of pneumococcal pneumonia. Trends in Molecular Medicine, 2021, 27, 971-989.	6.7	4
43	Topologically correct synthetic reconstruction of pathogen social behavior found during Yersinia growth in deep tissue sites. ELife, 2020, 9, .	6.0	3
44	Yersinia pseudotuberculosis doxycycline tolerance strategies include modulating expression of genes involved in cell permeability and tRNA modifications. PLoS Pathogens, 2022, 18, e1010556.	4.7	1