

Vera van Noort

List of Publications by Year in descending order

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Version: 2024-02-01

77
papers

6,100
citations

87723

38
h-index

74018

75
g-index

85
all docs

85
docs citations

85
times ranked

9475
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-driven elucidation of phage-host interplay and impact of phage resistance evolution on bacterial fitness. <i>ISME Journal</i> , 2022, 16, 533-542.	4.4	32
2	Digital phagograms: predicting phage infectivity through a multilayer machine learning approach. <i>Current Opinion in Virology</i> , 2022, 52, 174-181.	2.6	21
3	Shopping for phages? Unpacking design rules for therapeutic phage cocktails. <i>Current Opinion in Virology</i> , 2022, 52, 236-243.	2.6	15
4	Combination of pre-adapted bacteriophage therapy and antibiotics for treatment of fracture-related infection due to pandrug-resistant <i>Klebsiella pneumoniae</i> . <i>Nature Communications</i> , 2022, 13, 302.	5.8	97
5	SASpector: analysis of missing genomic regions in draft genomes of prokaryotes. <i>Bioinformatics</i> , 2022, , .	1.8	0
6	Genomics of an endemic cystic fibrosis <i>Burkholderia multivorans</i> strain reveals low within-patient evolution but high between-patient diversity. <i>PLoS Pathogens</i> , 2021, 17, e1009418.	2.1	11
7	Molecular dynamics shows complex interplay and long-range effects of post-translational modifications in yeast protein interactions. <i>PLoS Computational Biology</i> , 2021, 17, e1008988.	1.5	12
8	Integrated Multi-Omics Analysis of Mechanisms Underlying Yeast Ethanol Tolerance. <i>Journal of Proteome Research</i> , 2021, 20, 3840-3852.	1.8	17
9	The Ever-Expanding <i>Pseudomonas</i> Genus: Description of 43 New Species and Partition of the <i>Pseudomonas putida</i> Group. <i>Microorganisms</i> , 2021, 9, 1766.	1.6	206
10	Bacteriophage Therapy for Difficult-to-Treat Infections: The Implementation of a Multidisciplinary Phage Task Force (The PHAGEFORCE Study Protocol). <i>Viruses</i> , 2021, 13, 1543.	1.5	21
11	The complete genome of 2,6-dichlorobenzamide (BAM) degrader <i>Aminobacter</i> sp. MSH1 suggests a polyploid chromosome, phylogenetic reassignment, and functions of plasmids. <i>Scientific Reports</i> , 2021, 11, 18943.	1.6	5
12	Unraveling Protein Interactions between the Temperate Virus Bam35 and Its <i>Bacillus</i> Host Using an Integrative Yeast Two Hybrid-High Throughput Sequencing Approach. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11105.	1.8	0
13	OUP accepted manuscript. <i>Toxicology Research</i> , 2021, 10, 1202-1210.	0.9	2
14	The Genome of the Plant-Associated Lactic Acid Bacterium <i>Lactococcus lactis</i> KF147 Harbors a Hybrid NRPS-PKS System Conserved in Strains of the Dental Cariogenic <i>Streptococcus mutans</i> . <i>Current Microbiology</i> , 2020, 77, 136-145.	1.0	5
15	Quality control and statistical evaluation of combinatorial DNA libraries using nanopore sequencing. <i>BioTechniques</i> , 2020, 69, 379-383.	0.8	2
16	Completed Genomic Sequence of <i>Bacillus thuringiensis</i> HER1410 Reveals a <i>Cry</i> -Containing Chromosome, Two Megaplasmids, and an Integrative Plasmidial Prophage. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2927-2939.	0.8	20
17	Reliable Identification of Environmental <i>Pseudomonas</i> Isolates Using the <i>rpoD</i> Gene. <i>Microorganisms</i> , 2020, 8, 1166.	1.6	18
18	Host Range Expansion of <i>Pseudomonas</i> Virus LUZ7 Is Driven by a Conserved Tail Fiber Mutation. <i>Phage</i> , 2020, 1, 87-90.	0.8	17

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19	A VersaTile-driven platform for rapid hit-to-lead development of engineered lysins. <i>Science Advances</i> , 2020, 6, eaaz1136.	4.7	75
20	Integrative omics analysis of <i>Pseudomonas aeruginosa</i> virus PA5oct highlights the molecular complexity of jumbo phages. <i>Environmental Microbiology</i> , 2020, 22, 2165-2181.	1.8	32
21	A suppressor of axillary meristem maturation promotes longevity in flowering plants. <i>Nature Plants</i> , 2020, 6, 368-376.	4.7	32
22	Combining sequencing approaches to fully resolve a carbapenemase-encoding megaplasmid in a <i>Pseudomonas shirazica</i> clinical strain. <i>Emerging Microbes and Infections</i> , 2019, 8, 1186-1194.	3.0	16
23	A Genome-Based Species Taxonomy of the <i>Lactobacillus</i> Genus Complex. <i>MSystems</i> , 2019, 4, .	1.7	50
24	New Bacteriophages against Emerging Lineages ST23 and ST258 of <i>Klebsiella pneumoniae</i> and Efficacy Assessment in <i>Galleria mellonella</i> Larvae. <i>Viruses</i> , 2019, 11, 411.	1.5	36
25	Dietary intervention and health in patients with systemic lupus erythematosus: A systematic review of the evidence. <i>Critical Reviews in Food Science and Nutrition</i> , 2019, 59, 2666-2673.	5.4	24
26	Community-led comparative genomic and phenotypic analysis of the aquaculture pathogen <i>Pseudomonas baetica</i> a390T sequenced by Ion semiconductor and Nanopore technologies. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	17
27	Catabolic task division between two near-isogenic subpopulations co-existing in a herbicide-degrading bacterial consortium: consequences for the interspecies consortium metabolic model. <i>Environmental Microbiology</i> , 2018, 20, 85-96.	1.8	19
28	Large-scale docking predicts that sORF-encoded peptides may function through protein-peptide interactions in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2018, 13, e0205179.	1.1	10
29	Resurrected Protein Interaction Networks Reveal the Innovation Potential of Ancient Whole-Genome Duplication. <i>Plant Cell</i> , 2018, 30, 2741-2760.	3.1	13
30	Effects of Acetylation and Phosphorylation on Subunit Interactions in Three Large Eukaryotic Complexes. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2387-2401.	2.5	14
31	Catabolism of the groundwater micropollutant 2,6-dichlorobenzamide beyond 2,6-dichlorobenzoate is plasmid encoded in <i>Aminobacter</i> sp. MSH1. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 7963-7979.	1.7	15
32	yMap: an automated method to map yeast variants to protein modifications and functional regions. <i>Bioinformatics</i> , 2017, 33, 571-573.	1.8	2
33	ARA-PEPs: a repository of putative sORF-encoded peptides in <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2017, 18, 37.	1.2	44
34	Canonical germinant receptor is dispensable for spore germination in <i>Clostridium botulinum</i> group II strain NCTC 11219. <i>Scientific Reports</i> , 2017, 7, 15426.	1.6	9
35	Correlated duplications and losses in the evolution of palmitoylation writer and eraser families. <i>BMC Evolutionary Biology</i> , 2017, 17, 83.	3.2	4
36	Evolutionary conservation of Ebola virus proteins predicts important functions at residue level. <i>Bioinformatics</i> , 2017, 33, 151-154.	1.8	2

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37	UV crosslinked mRNA-binding proteins captured from leaf mesophyll protoplasts. <i>Plant Methods</i> , 2016, 12, 42.	1.9	53
38	Integration of multi-omics data of a genome-reduced bacterium: Prevalence of post-transcriptional regulation and its correlation with protein abundances. <i>Nucleic Acids Research</i> , 2016, 44, 1192-1202.	6.5	35
39	CARTâ€”a chemical annotation retrieval toolkit. <i>Bioinformatics</i> , 2016, 32, 2869-2871.	1.8	10
40	Adaptation to High Ethanol Reveals Complex Evolutionary Pathways. <i>PLoS Genetics</i> , 2015, 11, e1005635.	1.5	173
41	Discovery and validation of the antimetastatic activity of citalopram in colorectal cancer. <i>Molecular and Cellular Oncology</i> , 2015, 2, e975080.	0.3	6
42	Defining a minimal cell: essentiality of small <scp>ORF</scp> s and nc <scp>RNA</scp> s in a genomeâ€”reduced bacterium. <i>Molecular Systems Biology</i> , 2015, 11, 780.	3.2	133
43	Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. <i>Cell Reports</i> , 2015, 12, 1519-1530.	2.9	59
44	Comments on "Human Dominant Disease Genes Are Enriched in Paralogs Originating from Whole Genome Duplication". <i>PLoS Computational Biology</i> , 2014, 10, e1003758.	1.5	1
45	Spikeâ€”in <scp>SILAC</scp> proteomic approach reveals the vitronectin as an early molecular signature of liver fibrosis in hepatitis <scp>C</scp> infections with hepatic iron overload. <i>Proteomics</i> , 2014, 14, 1107-1115.	1.3	13
46	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <i>Nucleic Acids Research</i> , 2014, 42, 13525-13533.	6.5	55
47	A quantitative liposome microarray to systematically characterize protein-lipid interactions. <i>Nature Methods</i> , 2014, 11, 47-50.	9.0	77
48	Novel Drug Candidates for the Treatment of Metastatic Colorectal Cancer through Global Inverse Gene-Expression Profiling. <i>Cancer Research</i> , 2014, 74, 5690-5699.	0.4	142
49	Characterization of drugâ€”induced transcriptional modules: towards drug repositioning and functional understanding. <i>Molecular Systems Biology</i> , 2013, 9, 662.	3.2	110
50	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013, 13, 7.	3.2	60
51	Human Monogenic Disease Genes Have Frequently Functionally Redundant Paralogs. <i>PLoS Computational Biology</i> , 2013, 9, e1003073.	1.5	49
52	Evolution and functional crossâ€”talk of protein postâ€”translational modifications. <i>Molecular Systems Biology</i> , 2013, 9, 714.	3.2	294
53	Deciphering a global network of functionally associated postâ€”translational modifications. <i>Molecular Systems Biology</i> , 2012, 8, 599.	3.2	216
54	Crossâ€”talk between phosphorylation and lysine acetylation in a genomeâ€”reduced bacterium. <i>Molecular Systems Biology</i> , 2012, 8, 571.	3.2	169

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55	Drug discovery in the age of systems biology: the rise of computational approaches for data integration. <i>Current Opinion in Biotechnology</i> , 2012, 23, 609-616.	3.3	86
56	Annotation of the <i>M. tuberculosis</i> Hypothetical Orfeome: Adding Functional Information to More than Half of the Uncharacterized Proteins. <i>PLoS ONE</i> , 2012, 7, e34302.	1.1	58
57	Insight into Structure and Assembly of the Nuclear Pore Complex by Utilizing the Genome of a Eukaryotic Thermophile. <i>Cell</i> , 2011, 146, 277-289.	13.5	232
58	Prediction of Drug Combinations by Integrating Molecular and Pharmacological Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002323.	1.5	173
59	Network Neighbors of Drug Targets Contribute to Drug Side-Effect Similarity. <i>PLoS ONE</i> , 2011, 6, e22187.	1.1	86
60	Drug-Induced Regulation of Target Expression. <i>PLoS Computational Biology</i> , 2010, 6, e1000925.	1.5	120
61	Repeatability of published microarray gene expression analyses. <i>Nature Genetics</i> , 2009, 41, 149-155.	9.4	477
62	Impact of Genome Reduction on Bacterial Metabolism and Its Regulation. <i>Science</i> , 2009, 326, 1263-1268.	6.0	267
63	Proteome Organization in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1235-1240.	6.0	440
64	Transcriptome Complexity in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1268-1271.	6.0	394
65	Comparative genomics of the Rab protein family in Apicomplexan parasites. <i>Microbes and Infection</i> , 2008, 10, 462-470.	1.0	42
66	Practical and theoretical advances in predicting the function of a protein by its phylogenetic distribution. <i>Journal of the Royal Society Interface</i> , 2008, 5, 151-170.	1.5	97
67	Proteomic Profiling of Plasmodium Sporozoite Maturation Identifies New Proteins Essential for Parasite Development and Infectivity. <i>PLoS Pathogens</i> , 2008, 4, e1000195.	2.1	191
68	Assessment of phylogenomic and orthology approaches for phylogenetic inference. <i>Bioinformatics</i> , 2007, 23, 815-824.	1.8	87
69	Exploration of the omics evidence landscape: adding qualitative labels to predicted protein-protein interactions. <i>Genome Biology</i> , 2007, 8, R197.	13.9	3
70	Orthology prediction at scalable resolution by phylogenetic tree analysis. <i>BMC Bioinformatics</i> , 2007, 8, 83.	1.2	117
71	Combinatorial gene regulation in <i>Plasmodium falciparum</i> . <i>Trends in Genetics</i> , 2006, 22, 73-78.	2.9	48
72	Gene co-regulation is highly conserved in the evolution of eukaryotes and prokaryotes. <i>Nucleic Acids Research</i> , 2004, 32, 4725-4731.	6.5	99

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73	The yeast coexpression network has a smallâ€world, scaleâ€free architecture and can be explained by a simple model. EMBO Reports, 2004, 5, 280-284.	2.0	228
74	Comparative genomics for reliable protein-function prediction from genomic data. Trends in Genetics, 2004, 20, 340-344.	2.9	20
75	Bioinformatic analysis of functional differences between the immunoproteasome and the constitutive proteasome. Immunogenetics, 2003, 55, 437-449.	1.2	39
76	Predicting gene function by conserved co-expression. Trends in Genetics, 2003, 19, 238-242.	2.9	175
77	Strand misalignments lead to quasipalindrome correction. Trends in Genetics, 2003, 19, 365-369.	2.9	47