Vera van Noort

List of Publications by Year
in descending order

77 papers	6,100 citations	87888 38 h-index	74163 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. ISME Journal, 2022, 16, 533-542.	9.8	32
2	Digital phagograms: predicting phage infectivity through a multilayer machine learning approach. Current Opinion in Virology, 2022, 52, 174-181.	5.4	21
3	Shopping for phages? Unpacking design rules for therapeutic phage cocktails. Current Opinion in Virology, 2022, 52, 236-243.	5.4	15
4	Combination of pre-adapted bacteriophage therapy and antibiotics for treatment of fracture-related infection due to pandrug-resistant Klebsiella pneumoniae. Nature Communications, 2022, 13, 302.	12.8	97
5	SASpector: analysis of missing genomic regions in draft genomes of prokaryotes. Bioinformatics, 2022, , .	4.1	0
6	Genomics of an endemic cystic fibrosis Burkholderia multivorans strain reveals low within-patient evolution but high between-patient diversity. PLoS Pathogens, 2021, 17, e1009418.	4.7	11
7	Molecular dynamics shows complex interplay and long-range effects of post-translational modifications in yeast protein interactions. PLoS Computational Biology, 2021, 17, e1008988.	3.2	12
8	Integrated Multi-Omics Analysis of Mechanisms Underlying Yeast Ethanol Tolerance. Journal of Proteome Research, 2021, 20, 3840-3852.	3.7	17
9	The Ever-Expanding Pseudomonas Genus: Description of 43 New Species and Partition of the Pseudomonas putida Group. Microorganisms, 2021, 9, 1766.	3.6	206
10	Bacteriophage Therapy for Difficult-to-Treat Infections: The Implementation of a Multidisciplinary Phage Task Force (The PHAGEFORCE Study Protocol). Viruses, 2021, 13, 1543.	3.3	21
11	The complete genome of 2,6-dichlorobenzamide (BAM) degrader Aminobacter sp. MSH1 suggests a polyploid chromosome, phylogenetic reassignment, and functions of plasmids. Scientific Reports, 2021, 11, 18943.	3.3	5
12	Unraveling Protein Interactions between the Temperate Virus Bam35 and Its Bacillus Host Using an Integrative Yeast Two Hybrid–High Throughput Sequencing Approach. International Journal of Molecular Sciences, 2021, 22, 11105.	4.1	0
13	OUP accepted manuscript. Toxicology Research, 2021, 10, 1202-1210.	2.1	2
14	The Genome of the Plant-Associated Lactic Acid Bacterium Lactococcus lactis KF147 Harbors a Hybrid NRPS-PKS System Conserved in Strains of the Dental Cariogenic Streptococcus mutans. Current Microbiology, 2020, 77, 136-145.	2.2	5
15	Quality control and statistical evaluation of combinatorial DNA libraries using nanopore sequencing. BioTechniques, 2020, 69, 379-383.	1.8	2
16	Completed Genomic Sequence of *Bacillus thuringiensis* HER1410 Reveals a *Cry*-Containing Chromosome, Two Megaplasmids, and an Integrative Plasmidial Prophage. G3: Genes, Genomes, Genetics, 2020, 10, 2927-2939.	1.8	20
17	Reliable Identification of Environmental Pseudomonas Isolates Using the rpoD Gene. Microorganisms, 2020, 8, 1166.	3.6	18
18	Host Range Expansion of *Pseudomonas* Virus LUZ7 Is Driven by a Conserved Tail Fiber Mutation. Phage, 2020, 1, 87-90.	1.7	17

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19	A VersaTile-driven platform for rapid hit-to-lead development of engineered lysins. Science Advances, 2020, 6, eaaz1136.	10.3	75
20	Integrative omics analysis of <scp><i>Pseudomonas aeruginosa</i></scp> virus PA5oct highlights the molecular complexity of jumbo phages. Environmental Microbiology, 2020, 22, 2165-2181.	3.8	32
21	A suppressor of axillary meristem maturation promotes longevity in flowering plants. Nature Plants, 2020, 6, 368-376.	9.3	32
22	Combining sequencing approaches to fully resolve a carbapenemase-encoding megaplasmid in a <i>Pseudomonas shirazica</i> clinical strain. Emerging Microbes and Infections, 2019, 8, 1186-1194.	6.5	16
23	A Genome-Based Species Taxonomy of the <i>Lactobacillus</i> Genus Complex. MSystems, 2019, 4, .	3.8	50
24	New Bacteriophages against Emerging Lineages ST23 and ST258 of Klebsiella pneumoniae and Efficacy Assessment in Galleria mellonella Larvae. Viruses, 2019, 11, 411.	3.3	36
25	Dietary intervention and health in patients with systemic lupus erythematosus: A systematic review of the evidence. Critical Reviews in Food Science and Nutrition, 2019, 59, 2666-2673.	10.3	24
26	Community-led comparative genomic and phenotypic analysis of the aquaculture pathogen Pseudomonas baetica a390T sequenced by Ion semiconductor and Nanopore technologies. FEMS Microbiology Letters, 2018, 365, .	1.8	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. Environmental Microbiology, 2018, 20, 85-96.	3.8	19
28	Large-scale docking predicts that sORF-encoded peptides may function through protein-peptide interactions in Arabidopsis thaliana. PLoS ONE, 2018, 13, e0205179.	2.5	10
29	Resurrected Protein Interaction Networks Reveal the Innovation Potential of Ancient Whole-Genome Duplication. Plant Cell, 2018, 30, 2741-2760.	6.6	13
30	Effects of Acetylation and Phosphorylation on Subunit Interactions in Three Large Eukaryotic Complexes. Molecular and Cellular Proteomics, 2018, 17, 2387-2401.	3.8	14
31	Catabolism of the groundwater micropollutant 2,6-dichlorobenzamide beyond 2,6-dichlorobenzoate is plasmid encoded in Aminobacter sp. MSH1. Applied Microbiology and Biotechnology, 2018, 102, 7963-7979.	3.6	15
32	yMap: an automated method to map yeast variants to protein modifications and functional regions. Bioinformatics, 2017, 33, 571-573.	4.1	2
33	ARA-PEPs: a repository of putative sORF-encoded peptides in Arabidopsis thaliana. BMC Bioinformatics, 2017, 18, 37.	2.6	44
34	Canonical germinant receptor is dispensable for spore germination in Clostridium botulinum group II strain NCTC 11219. Scientific Reports, 2017, 7, 15426.	3.3	9
35	Correlated duplications and losses in the evolution of palmitoylation writer and eraser families. BMC Evolutionary Biology, 2017, 17, 83.	3.2	4
36	Evolutionary conservation of Ebola virus proteins predicts important functions at residue level. Bioinformatics, 2017, 33, 151-154.	4.1	2

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37	UV crosslinked mRNA-binding proteins captured from leaf mesophyll protoplasts. Plant Methods, 2016, 12, 42.	4.3	53
38	Integration of multi-omics data of a genome-reduced bacterium: Prevalence of post-transcriptional regulation and its correlation with protein abundances. Nucleic Acids Research, 2016, 44, 1192-1202.	14.5	35
39	CARTâ€"a chemical annotation retrieval toolkit. Bioinformatics, 2016, 32, 2869-2871.	4.1	10
40	Adaptation to High Ethanol Reveals Complex Evolutionary Pathways. PLoS Genetics, 2015, 11, e1005635.	3.5	173
41	Discovery and validation of the antimetastatic activity of citalopram in colorectal cancer. Molecular and Cellular Oncology, 2015, 2, e975080.	0.7	6
42	Defining a minimal cell: essentiality of small <scp>ORF</scp> s and nc <scp>RNA</scp> s in a genomeâ€reduced bacterium. Molecular Systems Biology, 2015, 11, 780.	7.2	133
43	Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. Cell Reports, 2015, 12, 1519-1530.	6.4	59
44	Comments on "Human Dominant Disease Genes Are Enriched in Paralogs Originating from Whole Genome Duplication". PLoS Computational Biology, 2014, 10, e1003758.	3.2	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. Proteomics, 2014, 14, 1107-1115.	2.2	13
46	An integrated approach for genome annotation of the eukaryotic thermophile Chaetomium thermophilum. Nucleic Acids Research, 2014, 42, 13525-13533.	14.5	55
47	A quantitative liposome microarray to systematically characterize protein-lipid interactions. Nature Methods, 2014, 11, 47-50.	19.0	77
48	Novel Drug Candidates for the Treatment of Metastatic Colorectal Cancer through Global Inverse Gene-Expression Profiling. Cancer Research, 2014, 74, 5690-5699.	0.9	142
49	Characterization of drugâ€induced transcriptional modules: towards drug repositioning and functional understanding. Molecular Systems Biology, 2013, 9, 662.	7.2	110
50	Consistent mutational paths predict eukaryotic thermostability. BMC Evolutionary Biology, 2013, 13, 7.	3.2	60
51	Human Monogenic Disease Genes Have Frequently Functionally Redundant Paralogs. PLoS Computational Biology, 2013, 9, e1003073.	3.2	49
52	Evolution and functional crossâ€talk of protein postâ€translational modifications. Molecular Systems Biology, 2013, 9, 714.	7.2	294
53	Deciphering a global network of functionally associated postâ€translational modifications. Molecular Systems Biology, 2012, 8, 599.	7.2	216
54	Crossâ€talk between phosphorylation and lysine acetylation in a genomeâ€reduced bacterium. Molecular Systems Biology, 2012, 8, 571.	7.2	169

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55	Drug discovery in the age of systems biology: the rise of computational approaches for data integration. Current Opinion in Biotechnology, 2012, 23, 609-616.	6.6	86
56	Annotation of the M. tuberculosis Hypothetical Orfeome: Adding Functional Information to More than Half of the Uncharacterized Proteins. PLoS ONE, 2012, 7, e34302.	2.5	58
57	Insight into Structure and Assembly of the Nuclear Pore Complex by Utilizing the Genome of a Eukaryotic Thermophile. Cell, 2011, 146, 277-289.	28.9	232
58	Prediction of Drug Combinations by Integrating Molecular and Pharmacological Data. PLoS Computational Biology, 2011, 7, e1002323.	3.2	173
59	Network Neighbors of Drug Targets Contribute to Drug Side-Effect Similarity. PLoS ONE, 2011, 6, e22187.	2.5	86
60	Drug-Induced Regulation of Target Expression. PLoS Computational Biology, 2010, 6, e1000925.	3.2	120
61	Repeatability of published microarray gene expression analyses. Nature Genetics, 2009, 41, 149-155.	21.4	477
62	Impact of Genome Reduction on Bacterial Metabolism and Its Regulation. Science, 2009, 326, 1263-1268.	12.6	267
63	Proteome Organization in a Genome-Reduced Bacterium. Science, 2009, 326, 1235-1240.	12.6	440
64	Transcriptome Complexity in a Genome-Reduced Bacterium. Science, 2009, 326, 1268-1271.	12.6	394
65	Comparative genomics of the Rab protein family in Apicomplexan parasites. Microbes and Infection, 2008, 10, 462-470.	1.9	42
66	Practical and theoretical advances in predicting the function of a protein by its phylogenetic distribution. Journal of the Royal Society Interface, 2008, 5, 151-170.	3.4	97
67	Proteomic Profiling of Plasmodium Sporozoite Maturation Identifies New Proteins Essential for Parasite Development and Infectivity. PLoS Pathogens, 2008, 4, e1000195.	4.7	191
68	Assessment of phylogenomic and orthology approaches for phylogenetic inference. Bioinformatics, 2007, 23, 815-824.	4.1	87
69	Exploration of the omics evidence landscape: adding qualitative labels to predicted protein-protein interactions. Genome Biology, 2007, 8, R197.	9.6	3
70	Orthology prediction at scalable resolution by phylogenetic tree analysis. BMC Bioinformatics, 2007, 8, 83.	2.6	117
71	Combinatorial gene regulation in Plasmodium falciparum. Trends in Genetics, 2006, 22, 73-78.	6.7	48
72	Gene co-regulation is highly conserved in the evolution of eukaryotes and prokaryotes. Nucleic Acids Research, 2004, 32, 4725-4731.	14.5	99

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73	The yeast coexpression network has a small‑world, scale‑free architecture and can be explained by a simple model. EMBO Reports, 2004, 5, 280-284.	4.5	228
74	Comparative genomics for reliable protein-function prediction from genomic data. Trends in Genetics, 2004, 20, 340-344.	6.7	20
75	Bioinformatic analysis of functional differences between the immunoproteasome and the constitutive proteasome. Immunogenetics, 2003, 55, 437-449.	2.4	39
76	Predicting gene function by conserved co-expression. Trends in Genetics, 2003, 19, 238-242.	6.7	175
77	Strand misalignments lead to quasipalindrome correction. Trends in Genetics, 2003, 19, 365-369.	6.7	47