

# Vera van Noort

## List of Publications by Year in descending order

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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	Repeatability of published microarray gene expression analyses. <i>Nature Genetics</i> , 2009, 41, 149-155.	21.4	477
2	Proteome Organization in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1235-1240.	12.6	440
3	Transcriptome Complexity in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1268-1271.	12.6	394
4	Evolution and functional cross-talk of protein post-translational modifications. <i>Molecular Systems Biology</i> , 2013, 9, 714.	7.2	294
5	Impact of Genome Reduction on Bacterial Metabolism and Its Regulation. <i>Science</i> , 2009, 326, 1263-1268.	12.6	267
6	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.	28.9	232
7	The yeast coexpression network has a small-world, scale-free architecture and can be explained by a simple model. <i>EMBO Reports</i> , 2004, 5, 280-284.	4.5	228
8	Deciphering a global network of functionally associated post-translational modifications. <i>Molecular Systems Biology</i> , 2012, 8, 599.	7.2	216
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.	3.6	206
10	Proteomic Profiling of Plasmodium Sporozoite Maturation Identifies New Proteins Essential for Parasite Development and Infectivity. <i>PLoS Pathogens</i> , 2008, 4, e1000195.	4.7	191
11	Predicting gene function by conserved co-expression. <i>Trends in Genetics</i> , 2003, 19, 238-242.	6.7	175
12	Prediction of Drug Combinations by Integrating Molecular and Pharmacological Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002323.	3.2	173
13	Adaptation to High Ethanol Reveals Complex Evolutionary Pathways. <i>PLoS Genetics</i> , 2015, 11, e1005635.	3.5	173
14	Cross-talk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2012, 8, 571.	7.2	169
15	Novel Drug Candidates for the Treatment of Metastatic Colorectal Cancer through Global Inverse Gene-Expression Profiling. <i>Cancer Research</i> , 2014, 74, 5690-5699.	0.9	142
16	Defining a minimal cell: essentiality of small ORFs and ncRNAs in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2015, 11, 780.	7.2	133
17	Drug-Induced Regulation of Target Expression. <i>PLoS Computational Biology</i> , 2010, 6, e1000925.	3.2	120
18	Orthology prediction at scalable resolution by phylogenetic tree analysis. <i>BMC Bioinformatics</i> , 2007, 8, 83.	2.6	117

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19	Characterization of drug-induced transcriptional modules: towards drug repositioning and functional understanding. <i>Molecular Systems Biology</i> , 2013, 9, 662.	7.2	110
20	Gene co-regulation is highly conserved in the evolution of eukaryotes and prokaryotes. <i>Nucleic Acids Research</i> , 2004, 32, 4725-4731.	14.5	99
21	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.	3.4	97
22	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.	12.8	97
23	Assessment of phylogenomic and orthology approaches for phylogenetic inference. <i>Bioinformatics</i> , 2007, 23, 815-824.	4.1	87
24	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.	6.6	86
25	Network Neighbors of Drug Targets Contribute to Drug Side-Effect Similarity. <i>PLoS ONE</i> , 2011, 6, e22187.	2.5	86
26	A quantitative liposome microarray to systematically characterize protein-lipid interactions. <i>Nature Methods</i> , 2014, 11, 47-50.	19.0	77
27	A VersaTile-driven platform for rapid hit-to-lead development of engineered lysins. <i>Science Advances</i> , 2020, 6, eaaz1136.	10.3	75
28	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013, 13, 7.	3.2	60
29	Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. <i>Cell Reports</i> , 2015, 12, 1519-1530.	6.4	59
30	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.	2.5	58
31	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <i>Nucleic Acids Research</i> , 2014, 42, 13525-13533.	14.5	55
32	UV crosslinked mRNA-binding proteins captured from leaf mesophyll protoplasts. <i>Plant Methods</i> , 2016, 12, 42.	4.3	53
33	A Genome-Based Species Taxonomy of the <i>Lactobacillus</i> Genus Complex. <i>MSystems</i> , 2019, 4, .	3.8	50
34	Human Monogenic Disease Genes Have Frequently Functionally Redundant Paralogs. <i>PLoS Computational Biology</i> , 2013, 9, e1003073.	3.2	49
35	Combinatorial gene regulation in <i>Plasmodium falciparum</i> . <i>Trends in Genetics</i> , 2006, 22, 73-78.	6.7	48
36	Strand misalignments lead to quasipalindrome correction. <i>Trends in Genetics</i> , 2003, 19, 365-369.	6.7	47

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37	ARA-PEPs: a repository of putative sORF-encoded peptides in <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2017, 18, 37.	2.6	44
38	Comparative genomics of the Rab protein family in Apicomplexan parasites. <i>Microbes and Infection</i> , 2008, 10, 462-470.	1.9	42
39	Bioinformatic analysis of functional differences between the immunoproteasome and the constitutive proteasome. <i>Immunogenetics</i> , 2003, 55, 437-449.	2.4	39
40	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.	3.3	36
41	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.	14.5	35
42	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.	3.8	32
43	A suppressor of axillary meristem maturation promotes longevity in flowering plants. <i>Nature Plants</i> , 2020, 6, 368-376.	9.3	32
44	Genome-driven elucidation of phage-host interplay and impact of phage resistance evolution on bacterial fitness. <i>ISME Journal</i> , 2022, 16, 533-542.	9.8	32
45	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.	10.3	24
46	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.	3.3	21
47	Digital phagograms: predicting phage infectivity through a multilayer machine learning approach. <i>Current Opinion in Virology</i> , 2022, 52, 174-181.	5.4	21
48	Comparative genomics for reliable protein-function prediction from genomic data. <i>Trends in Genetics</i> , 2004, 20, 340-344.	6.7	20
49	Completed Genomic Sequence of <i>Bacillus thuringiensis</i> HER1410 Reveals a Cry-Containing Chromosome, Two Megaplasmids, and an Integrative Plasmidial Prophage. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2927-2939.	1.8	20
50	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.	3.8	19
51	Reliable Identification of Environmental <i>Pseudomonas</i> Isolates Using the <i>rpoD</i> Gene. <i>Microorganisms</i> , 2020, 8, 1166.	3.6	18
52	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, .	1.8	17
53	Host Range Expansion of <i>Pseudomonas</i> Virus LUZ7 Is Driven by a Conserved Tail Fiber Mutation. <i>Phage</i> , 2020, 1, 87-90.	1.7	17
54	Integrated Multi-Omics Analysis of Mechanisms Underlying Yeast Ethanol Tolerance. <i>Journal of Proteome Research</i> , 2021, 20, 3840-3852.	3.7	17

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55	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.	6.5	16
56	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.	3.6	15
57	Shopping for phages? Unpacking design rules for therapeutic phage cocktails. <i>Current Opinion in Virology</i> , 2022, 52, 236-243.	5.4	15
58	Effects of Acetylation and Phosphorylation on Subunit Interactions in Three Large Eukaryotic Complexes. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2387-2401.	3.8	14
59	Spike-in SILAC proteomic approach reveals the vitronectin as an early molecular signature of liver fibrosis in hepatitis C infections with hepatic iron overload. <i>Proteomics</i> , 2014, 14, 1107-1115.	2.2	13
60	Resurrected Protein Interaction Networks Reveal the Innovation Potential of Ancient Whole-Genome Duplication. <i>Plant Cell</i> , 2018, 30, 2741-2760.	6.6	13
61	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.	3.2	12
62	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.	4.7	11
63	CART—a chemical annotation retrieval toolkit. <i>Bioinformatics</i> , 2016, 32, 2869-2871.	4.1	10
64	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.	2.5	10
65	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.	3.3	9
66	Discovery and validation of the antimetastatic activity of citalopram in colorectal cancer. <i>Molecular and Cellular Oncology</i> , 2015, 2, e975080.	0.7	6
67	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.	2.2	5
68	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.	3.3	5
69	Correlated duplications and losses in the evolution of palmitoylation writer and eraser families. <i>BMC Evolutionary Biology</i> , 2017, 17, 83.	3.2	4
70	Exploration of the omics evidence landscape: adding qualitative labels to predicted protein-protein interactions. <i>Genome Biology</i> , 2007, 8, R197.	9.6	3
71	yMap: an automated method to map yeast variants to protein modifications and functional regions. <i>Bioinformatics</i> , 2017, 33, 571-573.	4.1	2
72	Evolutionary conservation of Ebola virus proteins predicts important functions at residue level. <i>Bioinformatics</i> , 2017, 33, 151-154.	4.1	2

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73	Quality control and statistical evaluation of combinatorial DNA libraries using nanopore sequencing. <i>BioTechniques</i> , 2020, 69, 379-383.	1.8	2
74	OUP accepted manuscript. <i>Toxicology Research</i> , 2021, 10, 1202-1210.	2.1	2
75	Comments on "Human Dominant Disease Genes Are Enriched in Paralogs Originating from Whole Genome Duplication". <i>PLoS Computational Biology</i> , 2014, 10, e1003758.	3.2	1
76	Unraveling Protein Interactions between the Temperate Virus Bam35 and Its Bacillus Host Using an Integrative Yeast Two Hybridâ€“High Throughput Sequencing Approach. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11105.	4.1	0
77	SASpector: analysis of missing genomic regions in draft genomes of prokaryotes. <i>Bioinformatics</i> , 2022, , .	4.1	0