

# Vera van Noort

## List of Publications by Citations

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77  
papers

4,465  
citations

34  
h-index

66  
g-index

85  
ext. papers

5,548  
ext. citations

9.6  
avg. IF

5.11  
L-index

#	Paper	IF	Citations
77	Repeatability of published microarray gene expression analyses. <i>Nature Genetics</i> , <b>2009</b> , 41, 149-55	36.3	398
76	Proteome organization in a genome-reduced bacterium. <i>Science</i> , <b>2009</b> , 326, 1235-40	33.3	383
75	Transcriptome complexity in a genome-reduced bacterium. <i>Science</i> , <b>2009</b> , 326, 1268-71	33.3	341
74	Impact of genome reduction on bacterial metabolism and its regulation. <i>Science</i> , <b>2009</b> , 326, 1263-8	33.3	229
73	Evolution and functional cross-talk of protein post-translational modifications. <i>Molecular Systems Biology</i> , <b>2013</b> , 9, 714	12.2	214
72	Insight into structure and assembly of the nuclear pore complex by utilizing the genome of a eukaryotic thermophile. <i>Cell</i> , <b>2011</b> , 146, 277-89	56.2	198
71	The yeast coexpression network has a small-world, scale-free architecture and can be explained by a simple model. <i>EMBO Reports</i> , <b>2004</b> , 5, 280-4	6.5	186
70	Deciphering a global network of functionally associated post-translational modifications. <i>Molecular Systems Biology</i> , <b>2012</b> , 8, 599	12.2	171
69	Proteomic profiling of Plasmodium sporozoite maturation identifies new proteins essential for parasite development and infectivity. <i>PLoS Pathogens</i> , <b>2008</b> , 4, e1000195	7.6	164
68	Predicting gene function by conserved co-expression. <i>Trends in Genetics</i> , <b>2003</b> , 19, 238-42	8.5	156
67	Prediction of drug combinations by integrating molecular and pharmacological data. <i>PLoS Computational Biology</i> , <b>2011</b> , 7, e1002323	5	145
66	Cross-talk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , <b>2012</b> , 8, 571	12.2	144
65	Adaptation to High Ethanol Reveals Complex Evolutionary Pathways. <i>PLoS Genetics</i> , <b>2015</b> , 11, e10056356		105
64	Drug-induced regulation of target expression. <i>PLoS Computational Biology</i> , <b>2010</b> , 6, e1000925	5	100
63	Orthology prediction at scalable resolution by phylogenetic tree analysis. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 83	3.6	97
62	Defining a minimal cell: essentiality of small ORFs and ncRNAs in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 780	12.2	90
61	Characterization of drug-induced transcriptional modules: towards drug repositioning and functional understanding. <i>Molecular Systems Biology</i> , <b>2013</b> , 9, 662	12.2	86

60	Novel drug candidates for the treatment of metastatic colorectal cancer through global inverse gene-expression profiling. <i>Cancer Research</i> , <b>2014</b> , 74, 5690-9	10.1	84
59	Practical and theoretical advances in predicting the function of a protein by its phylogenetic distribution. <i>Journal of the Royal Society Interface</i> , <b>2008</b> , 5, 151-70	4.1	80
58	Network neighbors of drug targets contribute to drug side-effect similarity. <i>PLoS ONE</i> , <b>2011</b> , 6, e22187	3.7	75
57	Drug discovery in the age of systems biology: the rise of computational approaches for data integration. <i>Current Opinion in Biotechnology</i> , <b>2012</b> , 23, 609-16	11.4	71
56	A quantitative liposome microarray to systematically characterize protein-lipid interactions. <i>Nature Methods</i> , <b>2014</b> , 11, 47-50	21.6	66
55	Assessment of phylogenomic and orthology approaches for phylogenetic inference. <i>Bioinformatics</i> , <b>2007</b> , 23, 815-24	7.2	63
54	Gene co-regulation is highly conserved in the evolution of eukaryotes and prokaryotes. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 4725-31	20.1	51
53	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , <b>2013</b> , 13, 7	3	47
52	Annotation of the M. tuberculosis hypothetical orfeome: adding functional information to more than half of the uncharacterized proteins. <i>PLoS ONE</i> , <b>2012</b> , 7, e34302	3.7	47
51	Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. <i>Cell Reports</i> , <b>2015</b> , 12, 1519-30	10.6	44
50	Combinatorial gene regulation in Plasmodium falciparum. <i>Trends in Genetics</i> , <b>2006</b> , 22, 73-8	8.5	43
49	Strand misalignments lead to quasipalindrome correction. <i>Trends in Genetics</i> , <b>2003</b> , 19, 365-9	8.5	42
48	An integrated approach for genome annotation of the eukaryotic thermophile Chaetomium thermophilum. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 13525-33	20.1	40
47	UV crosslinked mRNA-binding proteins captured from leaf mesophyll protoplasts. <i>Plant Methods</i> , <b>2016</b> , 12, 42	5.8	39
46	Bioinformatic analysis of functional differences between the immunoproteasome and the constitutive proteasome. <i>Immunogenetics</i> , <b>2003</b> , 55, 437-49	3.2	37
45	Comparative genomics of the Rab protein family in Apicomplexan parasites. <i>Microbes and Infection</i> , <b>2008</b> , 10, 462-70	9.3	36
44	A VersaTile-driven platform for rapid hit-to-lead development of engineered lysins. <i>Science Advances</i> , <b>2020</b> , 6, eaaz1136	14.3	35
43	Human monogenic disease genes have frequently functionally redundant paralogs. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003073	5	34

42	A Genome-Based Species Taxonomy of the Genus Complex. <i>MSystems</i> , <b>2019</b> , 4,	7.6	27
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> , <b>2016</b> , 44, 1192-202	20.1	25
40	ARA-PEPs: a repository of putative sORF-encoded peptides in <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 37	3.6	23
39	New Bacteriophages against Emerging Lineages ST23 and ST258 of and Efficacy Assessment in Larvae. <i>Viruses</i> , <b>2019</b> , 11,	6.2	20
38	Integrative omics analysis of <i>Pseudomonas aeruginosa</i> virus PA5oct highlights the molecular complexity of jumbo phages. <i>Environmental Microbiology</i> , <b>2020</b> , 22, 2165-2181	5.2	20
37	Comparative genomics for reliable protein-function prediction from genomic data. <i>Trends in Genetics</i> , <b>2004</b> , 20, 340-4	8.5	19
36	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> , <b>2014</b> , 14, 1107-15	4.8	11
35	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> , <b>2019</b> , 59, 2666-2673	11.5	11
34	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> , <b>2018</b> , 20, 85-96	5.2	11
33	A suppressor of axillary meristem maturation promotes longevity in flowering plants. <i>Nature Plants</i> , <b>2020</b> , 6, 368-376	11.5	10
32	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> , <b>2018</b> , 365,	2.9	10
31	Combining sequencing approaches to fully resolve a carbapenemase-encoding megaplasmid in a clinical strain. <i>Emerging Microbes and Infections</i> , <b>2019</b> , 8, 1186-1194	18.9	10
30	Effects of Acetylation and Phosphorylation on Subunit Interactions in Three Large Eukaryotic Complexes. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 2387-2401	7.6	10
29	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> , <b>2022</b> , 13, 302	17.4	9
28	Resurrected Protein Interaction Networks Reveal the Innovation Potential of Ancient Whole-Genome Duplication. <i>Plant Cell</i> , <b>2018</b> , 30, 2741-2760	11.6	9
27	The Ever-Expanding Genus: Description of 43 New Species and Partition of the Group. <i>Microorganisms</i> , <b>2021</b> , 9,	4.9	9
26	Completed Genomic Sequence of HER1410 Reveals a -Containing Chromosome, Two Megaplasms, and an Integrative Plasmidial Prophage. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 2927-2939	3.2	8
25	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> , <b>2018</b> , 102, 7963-7979	5.7	7

24	Integrated Multi-Omics Analysis of Mechanisms Underlying Yeast Ethanol Tolerance. <i>Journal of Proteome Research</i> , <b>2021</b> , 20, 3840-3852	5.6	6
23	Large-scale docking predicts that sORF-encoded peptides may function through protein-peptide interactions in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , <b>2018</b> , 13, e0205179	3.7	6
22	Genome-driven elucidation of phage-host interplay and impact of phage resistance evolution on bacterial fitness. <i>ISME Journal</i> , <b>2021</b> ,	11.9	6
21	Host Range Expansion of Pseudomonas Virus LUZ7 Is Driven by a Conserved Tail Fiber Mutation. <i>Phage</i> , <b>2020</b> , 1, 87-90	1.8	5
20	CART-a chemical annotation retrieval toolkit. <i>Bioinformatics</i> , <b>2016</b> , 32, 2869-71	7.2	5
19	Canonical germinant receptor is dispensable for spore germination in Clostridium botulinum group II strain NCTC 11219. <i>Scientific Reports</i> , <b>2017</b> , 7, 15426	4.9	5
18	Genomics of an endemic cystic fibrosis Burkholderia multivorans strain reveals low within-patient evolution but high between-patient diversity. <i>PLoS Pathogens</i> , <b>2021</b> , 17, e1009418	7.6	5
17	Bacteriophage Therapy for Difficult-to-Treat Infections: The Implementation of a Multidisciplinary Phage Task Force (). <i>Viruses</i> , <b>2021</b> , 13,	6.2	5
16	Discovery and validation of the antimetastatic activity of citalopram in colorectal cancer. <i>Molecular and Cellular Oncology</i> , <b>2015</b> , 2, e975080	1.2	4
15	Molecular dynamics shows complex interplay and long-range effects of post-translational modifications in yeast protein interactions. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1008988	5	4
14	Exploration of the omics evidence landscape: adding qualitative labels to predicted protein-protein interactions. <i>Genome Biology</i> , <b>2007</b> , 8, R197	18.3	3
13	Digital phagograms: predicting phage infectivity through a multilayer machine learning approach.. <i>Current Opinion in Virology</i> , <b>2021</b> , 52, 174-181	7.5	3
12	Reliable Identification of Environmental Isolates Using the Gene. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	3
11	Correlated duplications and losses in the evolution of palmitoylation writer and eraser families. <i>BMC Evolutionary Biology</i> , <b>2017</b> , 17, 83	3	2
10	Evolutionary conservation of Ebola virus proteins predicts important functions at residue level. <i>Bioinformatics</i> , <b>2017</b> , 33, 151-154	7.2	2
9	Shopping for phages? Unpacking design rules for therapeutic phage cocktails.. <i>Current Opinion in Virology</i> , <b>2021</b> , 52, 236-243	7.5	2
8	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. <i>Current Microbiology</i> , <b>2020</b> , 77, 136-145	2.4	2
7	The complete genome of 2,6-dichlorobenzamide (BAM) degrader Aminobacter sp. MSH1 suggests a polyploid chromosome, phylogenetic reassignment, and functions of plasmids. <i>Scientific Reports</i> , <b>2021</b> , 11, 18943	4.9	2

6	yMap: an automated method to map yeast variants to protein modifications and functional regions. <i>Bioinformatics</i> , <b>2017</b> , 33, 571-573	7.2	1
5	Comments on "Human dominant disease genes are enriched in paralogs originating from whole genome duplication". <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003758	5	1
4	A genome-based species taxonomy of the Lactobacillus Genus Complex		1
3	Integrative omics analysis of Pseudomonas aeruginosavirus PA5oct highlights the molecular complexity of jumbo phages		1
2	Quality control and statistical evaluation of combinatorial DNA libraries using nanopore sequencing. <i>BioTechniques</i> , <b>2020</b> , 69, 379-383	2.5	1
1	Towards a reporting guideline for developmental and reproductive toxicology testing in and other nematodes.. <i>Toxicology Research</i> , <b>2021</b> , 10, 1202-1210	2.6	0