Vera van Noort

List of Publications by Year in Descending Order

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	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	17.4	9
76	Digital phagograms: predicting phage infectivity through a multilayer machine learning approach.. *Current Opinion in Virology*, **2021**, 52, 174-181	7.5	3
75	Shopping for phages? Unpacking design rules for therapeutic phage cocktails.. *Current Opinion in Virology*, **2021**, 52, 236-243	7.5	2
74	Towards a reporting guideline for developmental and reproductive toxicology testing in and other nematodes.. *Toxicology Research*, **2021**, 10, 1202-1210	2.6	0
73	Genomics of an endemic cystic fibrosis Burkholderia multivorans strain reveals low within-patient evolution but high between-patient diversity. *PLoS Pathogens*, **2021**, 17, e1009418	7.6	5
72	Molecular dynamics shows complex interplay and long-range effects of post-translational modifications in yeast protein interactions. *PLoS Computational Biology*, **2021**, 17, e1008988	5	4
71	Integrated Multi-Omics Analysis of Mechanisms Underlying Yeast Ethanol Tolerance. *Journal of Proteome Research*, **2021**, 20, 3840-3852	5.6	6
70	The Ever-Expanding Genus: Description of 43 New Species and Partition of the Group. *Microorganisms*, **2021**, 9,	4.9	9
69	Genome-driven elucidation of phage-host interplay and impact of phage resistance evolution on bacterial fitness. *ISME Journal*, **2021**,	11.9	6
68	Bacteriophage Therapy for Difficult-to-Treat Infections: The Implementation of a Multidisciplinary Phage Task Force (). *Viruses*, **2021**, 13,	6.2	5
67	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	4.9	2
66	Host Range Expansion of Pseudomonas Virus LUZ7 Is Driven by a Conserved Tail Fiber Mutation. *Phage*, **2020**, 1, 87-90	1.8	5
65	A VersaTile-driven platform for rapid hit-to-lead development of engineered lysins. *Science Advances*, **2020**, 6, eaaz1136	14.3	35
64	Integrative omics analysis of Pseudomonas aeruginosa virus PA5oct highlights the molecular complexity of jumbo phages. *Environmental Microbiology*, **2020**, 22, 2165-2181	5.2	20
63	A suppressor of axillary meristem maturation promotes longevity in flowering plants. *Nature Plants*, **2020**, 6, 368-376	11.5	10
62	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	2.4	2
61	Quality control and statistical evaluation of combinatorial DNA libraries using nanopore sequencing. *BioTechniques*, **2020**, 69, 379-383	2.5	1

60 — Completed Genomic Sequence of HER1410 Reveals a -Containing Chromosome, Two Megaplasmids, and an Integrative Plasmidial Prophage. *G3: Genes, Genomes, Genetics*, **2020**, 10, 2927-2939 — 3.2 — 8

59 — Reliable Identification of Environmental Isolates Using the Gene. *Microorganisms*, **2020**, 8, — 4.9 — 3

58 — A Genome-Based Species Taxonomy of the Genus Complex. *MSystems*, **2019**, 4, — 7.6 — 27

57 — New Bacteriophages against Emerging Lineages ST23 and ST258 of and Efficacy Assessment in Larvae. *Viruses*, **2019**, 11, — 6.2 — 20

56 — Combining sequencing approaches to fully resolve a carbapenemase-encoding megaplasmid in a clinical strain. *Emerging Microbes and Infections*, **2019**, 8, 1186-1194 — 18.9 — 10

55 — 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 — 11.5 — 11

54 — 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, — 2.9 — 10

53 — 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 — 5.7 — 7

52 — 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 — 5.2 — 11

51 — Large-scale docking predicts that sORF-encoded peptides may function through protein-peptide interactions in Arabidopsis thaliana. *PLoS ONE*, **2018**, 13, e0205179 — 3.7 — 6

50 — Resurrected Protein Interaction Networks Reveal the Innovation Potential of Ancient Whole-Genome Duplication. *Plant Cell*, **2018**, 30, 2741-2760 — 11.6 — 9

49 — Effects of Acetylation and Phosphorylation on Subunit Interactions in Three Large Eukaryotic Complexes. *Molecular and Cellular Proteomics*, **2018**, 17, 2387-2401 — 7.6 — 10

48 — ARA-PEPs: a repository of putative sORF-encoded peptides in Arabidopsis thaliana. *BMC Bioinformatics*, **2017**, 18, 37 — 3.6 — 23

47 — yMap: an automated method to map yeast variants to protein modifications and functional regions. *Bioinformatics*, **2017**, 33, 571-573 — 7.2 — 1

46 — Canonical germinant receptor is dispensable for spore germination in Clostridium botulinum group II strain NCTC 11219. *Scientific Reports*, **2017**, 7, 15426 — 4.9 — 5

45 — Correlated duplications and losses in the evolution of palmitoylation writer and eraser families. *BMC Evolutionary Biology*, **2017**, 17, 83 — 3 — 2

44 — Evolutionary conservation of Ebola virus proteins predicts important functions at residue level. *Bioinformatics*, **2017**, 33, 151-154 — 7.2 — 2

43 — CART-a chemical annotation retrieval toolkit. *Bioinformatics*, **2016**, 32, 2869-71 — 7.2 — 5

42 UV crosslinked mRNA-binding proteins captured from leaf mesophyll protoplasts. *Plant Methods*, **2016**, 12, 42 — 5.8 — 39

41 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, 1192-202 — 20.1 — 25

40 Defining a minimal cell: essentiality of small ORFs and ncRNAs in a genome-reduced bacterium. *Molecular Systems Biology*, **2015**, 11, 780 — 12.2 — 90

39 Lipid Cooperativity as a General Membrane-Recruitment Principle for PH Domains. *Cell Reports*, **2015**, 12, 1519-30 — 10.6 — 44

38 Adaptation to High Ethanol Reveals Complex Evolutionary Pathways. *PLoS Genetics*, **2015**, 11, e10056356 — 105

37 Discovery and validation of the antimetastatic activity of citalopram in colorectal cancer. *Molecular and Cellular Oncology*, **2015**, 2, e975080 — 1.2 — 4

36 A quantitative liposome microarray to systematically characterize protein-lipid interactions. *Nature Methods*, **2014**, 11, 47-50 — 21.6 — 66

35 Novel drug candidates for the treatment of metastatic colorectal cancer through global inverse gene-expression profiling. *Cancer Research*, **2014**, 74, 5690-9 — 10.1 — 84

34 Comments on "Human dominant disease genes are enriched in paralogs originating from whole genome duplication". *PLoS Computational Biology*, **2014**, 10, e1003758 — 5 — 1

33 Spike-in SILAC proteomic approach reveals the vitronectin as an early molecular signature of liver fibrosis in hepatitis C infections with hepatic iron overload. *Proteomics*, **2014**, 14, 1107-15 — 4.8 — 11

32 An integrated approach for genome annotation of the eukaryotic thermophile Chaetomium thermophilum. *Nucleic Acids Research*, **2014**, 42, 13525-33 — 20.1 — 40

31 Characterization of drug-induced transcriptional modules: towards drug repositioning and functional understanding. *Molecular Systems Biology*, **2013**, 9, 662 — 12.2 — 86

30 Consistent mutational paths predict eukaryotic thermostability. *BMC Evolutionary Biology*, **2013**, 13, 7 — 3 — 47

29 Human monogenic disease genes have frequently functionally redundant paralogs. *PLoS Computational Biology*, **2013**, 9, e1003073 — 5 — 34

28 Evolution and functional cross-talk of protein post-translational modifications. *Molecular Systems Biology*, **2013**, 9, 714 — 12.2 — 214

27 Drug discovery in the age of systems biology: the rise of computational approaches for data integration. *Current Opinion in Biotechnology*, **2012**, 23, 609-16 — 11.4 — 71

26 Annotation of the M. tuberculosis hypothetical orfeome: adding functional information to more than half of the uncharacterized proteins. *PLoS ONE*, **2012**, 7, e34302 — 3.7 — 47

25 Deciphering a global network of functionally associated post-translational modifications. *Molecular Systems Biology*, **2012**, 8, 599 — 12.2 — 171

24	Cross-talk between phosphorylation and lysine acetylation in a genome-reduced bacterium. *Molecular Systems Biology*, **2012**, 8, 571	12.2	144
23	Insight into structure and assembly of the nuclear pore complex by utilizing the genome of a eukaryotic thermophile. *Cell*, **2011**, 146, 277-89	56.2	198
22	Prediction of drug combinations by integrating molecular and pharmacological data. *PLoS Computational Biology*, **2011**, 7, e1002323	5	145
21	Network neighbors of drug targets contribute to drug side-effect similarity. *PLoS ONE*, **2011**, 6, e22187	3.7	75
20	Drug-induced regulation of target expression. *PLoS Computational Biology*, **2010**, 6, e1000925	5	100
19	Repeatability of published microarray gene expression analyses. *Nature Genetics*, **2009**, 41, 149-55	36.3	398
18	Impact of genome reduction on bacterial metabolism and its regulation. *Science*, **2009**, 326, 1263-8	33.3	229
17	Proteome organization in a genome-reduced bacterium. *Science*, **2009**, 326, 1235-40	33.3	383
16	Transcriptome complexity in a genome-reduced bacterium. *Science*, **2009**, 326, 1268-71	33.3	341
15	Practical and theoretical advances in predicting the function of a protein by its phylogenetic distribution. *Journal of the Royal Society Interface*, **2008**, 5, 151-70	4.1	80
14	Proteomic profiling of Plasmodium sporozoite maturation identifies new proteins essential for parasite development and infectivity. *PLoS Pathogens*, **2008**, 4, e1000195	7.6	164
13	Comparative genomics of the Rab protein family in Apicomplexan parasites. *Microbes and Infection*, **2008**, 10, 462-70	9.3	36
12	Orthology prediction at scalable resolution by phylogenetic tree analysis. *BMC Bioinformatics*, **2007**, 8, 83	3.6	97
11	Assessment of phylogenomic and orthology approaches for phylogenetic inference. *Bioinformatics*, **2007**, 23, 815-24	7.2	63
10	Exploration of the omics evidence landscape: adding qualitative labels to predicted protein-protein interactions. *Genome Biology*, **2007**, 8, R197	18.3	3
9	Combinatorial gene regulation in Plasmodium falciparum. *Trends in Genetics*, **2006**, 22, 73-8	8.5	43
8	Gene co-regulation is highly conserved in the evolution of eukaryotes and prokaryotes. *Nucleic Acids Research*, **2004**, 32, 4725-31	20.1	51
7	The yeast coexpression network has a small-world, scale-free architecture and can be explained by a simple model. *EMBO Reports*, **2004**, 5, 280-4	6.5	186

6	Comparative genomics for reliable protein-function prediction from genomic data. *Trends in Genetics*, **2004**, 20, 340-4	8.5	19
5	Bioinformatic analysis of functional differences between the immunoproteasome and the constitutive proteasome. *Immunogenetics*, **2003**, 55, 437-49	3.2	37
4	Predicting gene function by conserved co-expression. *Trends in Genetics*, **2003**, 19, 238-42	8.5	156
3	Strand misalignments lead to quasipalindrome correction. *Trends in Genetics*, **2003**, 19, 365-9	8.5	42
2	A genome-based species taxonomy of the Lactobacillus Genus Complex		1
1	Integrative omics analysis ofPseudomonas aeruginosavirus PA5oct highlights the molecular complexity of jumbo phages		1