

# Gisle Vestergaard

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8397900/publications.pdf>

Version: 2024-02-01

53  
papers

2,720  
citations

159358

30  
h-index

189595

50  
g-index

59  
all docs

59  
docs citations

59  
times ranked

3345  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of soil microbial communities based on amplicon sequencing of marker genes. <i>Biology and Fertility of Soils</i> , 2017, 53, 485-489.	2.3	197
2	Transitory microbial habitat in the hyperarid Atacama Desert. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2670-2675.	3.3	172
3	Independent virus development outside a host. <i>Nature</i> , 2005, 436, 1101-1102.	13.7	169
4	Making big data smart—how to use metagenomics to understand soil quality. <i>Biology and Fertility of Soils</i> , 2017, 53, 479-484.	2.3	160
5	CRISPR adaptive immune systems of Archaea. <i>RNA Biology</i> , 2014, 11, 156-167.	1.5	129
6	Structural and Genomic Properties of the Hyperthermophilic Archaeal Virus ATV with an Extracellular Stage of the Reproductive Cycle. <i>Journal of Molecular Biology</i> , 2006, 359, 1203-1216.	2.0	110
7	Oral administration of antibiotics increased the potential mobility of bacterial resistance genes in the gut of the fish <i>Piaractus mesopotamicus</i> . <i>Microbiome</i> , 2019, 7, 24.	4.9	98
8	Archaeal CRISPR-based immune systems: exchangeable functional modules. <i>Trends in Microbiology</i> , 2011, 19, 549-556.	3.5	96
9	Delivery mode and gut microbial changes correlate with an increased risk of childhood asthma. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	92
10	Novel oligonucleotide primers reveal a high diversity of microbes which drive phosphorous turnover in soil. <i>Journal of Microbiological Methods</i> , 2016, 125, 91-97.	0.7	80
11	Amplicon sequencing provides more accurate microbiome information in healthy children compared to culturing. <i>Communications Biology</i> , 2019, 2, 291.	2.0	77
12	Pollution from azithromycin-manufacturing promotes macrolide-resistance gene propagation and induces spatial and seasonal bacterial community shifts in receiving river sediments. <i>Environment International</i> , 2019, 123, 501-511.	4.8	74
13	The Microbiome of Endophytic, Wood Colonizing Bacteria from Pine Trees as Affected by Pine Wilt Disease. <i>Scientific Reports</i> , 2017, 7, 4205.	1.6	69
14	CRISPR-based immune systems of the Sulfolobales: complexity and diversity. <i>Biochemical Society Transactions</i> , 2011, 39, 51-57.	1.6	64
15	A novel rudivirus, ARV1, of the hyperthermophilic archaeal genus <i>Acidianus</i> . <i>Virology</i> , 2005, 336, 83-92.	1.1	61
16	Stygiolobus Rod-Shaped Virus and the Interplay of Crenarchaeal Rudiviruses with the CRISPR Antiviral System. <i>Journal of Bacteriology</i> , 2008, 190, 6837-6845.	1.0	58
17	The Influence of Land Use Intensity on the Plant-Associated Microbiome of <i>Dactylis glomerata</i> L.. <i>Frontiers in Plant Science</i> , 2017, 8, 930.	1.7	57
18	Changes induced by heavy metals in the plant-associated microbiome of <i>Miscanthus x giganteus</i> . <i>Science of the Total Environment</i> , 2020, 711, 134433.	3.9	56

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19	A long-term field experiment demonstrates the influence of tillage on the bacterial potential to produce soil structure-stabilizing agents such as exopolysaccharides and lipopolysaccharides. <i>Environmental Microbiomes</i> , 2019, 14, 1.	2.2	54
20	Urbanized microbiota in infants, immune constitution, and later risk of atopic diseases. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 234-243.	1.5	54
21	Structure and Genome Organization of AFV2, a Novel Archaeal Lipothrixvirus with Unusual Terminal and Core Structures. <i>Journal of Bacteriology</i> , 2005, 187, 3855-3858.	1.0	51
22	Structure of the <i>Acidianus</i> Filamentous Virus 3 and Comparative Genomics of Related Archaeal Lipothrixviruses. <i>Journal of Virology</i> , 2008, 82, 371-381.	1.5	49
23	Bacterial potentials for uptake, solubilization and mineralization of extracellular phosphorus in agricultural soils are highly stable under different fertilization regimes. <i>Environmental Microbiology Reports</i> , 2018, 10, 320-327.	1.0	49
24	CRISPR-Cas type I-A Cascade complex couples viral infection surveillance to host transcriptional regulation in the dependence of Csa3b. <i>Nucleic Acids Research</i> , 2017, 45, gkw1265.	6.5	48
25	Biological Soil Crusts from Different Soil Substrates Harbor Distinct Bacterial Groups with the Potential to Produce Exopolysaccharides and Lipopolysaccharides. <i>Microbial Ecology</i> , 2020, 79, 326-341.	1.4	43
26	Metagenomic evidence for co-occurrence of antibiotic, biocide and metal resistance genes in pigs. <i>Environment International</i> , 2022, 158, 106899.	4.8	40
27	CRISPR-Cas Adaptive Immune Systems of the Sulfolobales: Unravelling Their Complexity and Diversity. <i>Life</i> , 2015, 5, 783-817.	1.1	39
28	Discovery of numerous novel small genes in the intergenic regions of the <i>Escherichia coli</i> O157:H7 Sakai genome. <i>PLoS ONE</i> , 2017, 12, e0184119.	1.1	38
29	Getting the best out of long-wavelength X-rays: <i>de novo</i> chlorine/sulfur SAD phasing of a structural protein from ATV. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 304-308.	2.5	37
30	Development of a Stable Lung Microbiome in Healthy Neonatal Mice. <i>Microbial Ecology</i> , 2018, 75, 529-542.	1.4	36
31	More than 2500 years of oil exposure shape sediment microbiomes with the potential for syntrophic degradation of hydrocarbons linked to methanogenesis. <i>Microbiome</i> , 2017, 5, 118.	4.9	31
32	Enrichment of endophytic Actinobacteria in roots and rhizomes of <i>Miscanthus Ã— giganteus</i> plants exposed to diclofenac and sulfamethoxazole. <i>Environmental Science and Pollution Research</i> , 2020, 27, 11892-11904.	2.7	27
33	Prenatal dietary supplements influence the infant airway microbiota in a randomized factorial clinical trial. <i>Nature Communications</i> , 2020, 11, 426.	5.8	25
34	Soil Bacterial Diversity Is Positively Correlated with Decomposition Rates during Early Phases of Maize Litter Decomposition. <i>Microorganisms</i> , 2021, 9, 357.	1.6	25
35	An intriguing relationship between the cyclic diguanylate signaling system and horizontal gene transfer. <i>ISME Journal</i> , 2018, 12, 2330-2334.	4.4	24
36	Effects of industrial effluents containing moderate levels of antibiotic mixtures on the abundance of antibiotic resistance genes and bacterial community composition in exposed creek sediments. <i>Science of the Total Environment</i> , 2020, 706, 136001.	3.9	24

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37	Reduced microbial potential for the degradation of phenolic compounds in the rhizosphere of apple plantlets grown in soils affected by replant disease. <i>Environmental Microbiomes</i> , 2019, 14, 8.	2.2	22
38	Transcriptome-Stable Isotope Probing Provides Targeted Functional and Taxonomic Insights Into Microaerobic Pollutant-Degrading Aquifer Microbiota. <i>Frontiers in Microbiology</i> , 2018, 9, 2696.	1.5	20
39	Microbial Hotspots in Lithic Microhabitats Inferred from DNA Fractionation and Metagenomics in the Atacama Desert. <i>Microorganisms</i> , 2021, 9, 1038.	1.6	19
40	The Impact of the Diurnal Cycle on the Microbial Transcriptome in the Rhizosphere of Barley. <i>Microbial Ecology</i> , 2018, 75, 830-833.	1.4	18
41	Site-Specific Conditions Change the Response of Bacterial Producers of Soil Structure-Stabilizing Agents Such as Exopolysaccharides and Lipopolysaccharides to Tillage Intensity. <i>Frontiers in Microbiology</i> , 2020, 11, 568.	1.5	18
42	Effect of the Nursing Mother on the Gut Microbiome of the Offspring During Early Mouse Development. <i>Microbial Ecology</i> , 2019, 78, 517-527.	1.4	17
43	Microbial Key Players Involved in P Turnover Differ in Artificial Soil Mixtures Depending on Clay Mineral Composition. <i>Microbial Ecology</i> , 2021, 81, 897-907.	1.4	14
44	Response of Barley Plants to Drought Might Be Associated with the Recruiting of Soil-Borne Endophytes. <i>Microorganisms</i> , 2020, 8, 1414.	1.6	11
45	Predicted highly derived class 1 CRISPR-Cas system in Haloarchaea containing diverged Cas5 and Cas7 homologs but no CRISPR array. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	10
46	Definition of Core Bacterial Taxa in Different Root Compartments of <i>Dactylis glomerata</i> , Grown in Soil under Different Levels of Land Use Intensity. <i>Diversity</i> , 2020, 12, 392.	0.7	7
47	Crystal Structure of ATVORF273, a New Fold for a Thermo- and Acido-Stable Protein from the Acidianus Two-Tailed Virus. <i>PLoS ONE</i> , 2012, 7, e45847.	1.1	7
48	Functional Traits Co-Occurring with Mobile Genetic Elements in the Microbiome of the Atacama Desert. <i>Diversity</i> , 2019, 11, 205.	0.7	5
49	The microbiome of captive hamadryas baboons. <i>Animal Microbiome</i> , 2020, 2, 25.	1.5	5
50	Sulfate Alters the Competition Among Microbiome Members of Sediments Chronically Exposed to Asphalt. <i>Frontiers in Microbiology</i> , 2020, 11, 556793.	1.5	5
51	Correction to: Reduced microbial potential for the degradation of phenolic compounds in the rhizosphere of apple plantlets grown in soils affected by replant disease. <i>Environmental Microbiomes</i> , 2019, 14, .	2.2	3
52	Reconstruction of Transformation Processes Catalyzed by the Soil Microbiome Using Metagenomic Approaches. <i>Methods in Molecular Biology</i> , 2016, 1399, 197-206.	0.4	2
53	CRISPR/Cas and CRISPR/Cmr Immune Systems of Archaea. , 2012, , 163-181.		2