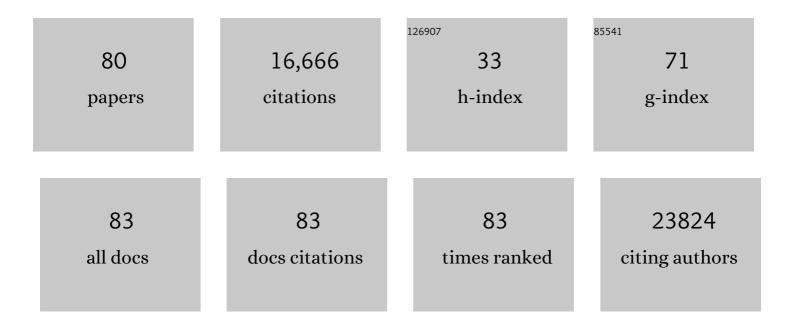
Tatiana A Vishnivetskaya

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	27.8	9,614
2	A framework for human microbiome research. Nature, 2012, 486, 215-221.	27.8	2,249
3	Biogeography of the ecosystems of the healthy human body. Genome Biology, 2013, 14, R1.	9.6	540
4	Calmodulin kinase II inhibition protects against structural heart disease. Nature Medicine, 2005, 11, 409-417.	30.7	526
5	Microbial Populations in Antarctic Permafrost: Biodiversity, State, Age, and Implication for Astrobiology, 2007, 7, 275-311.	3.0	243
6	Host genetic and environmental effects on mouse intestinal microbiota. ISME Journal, 2012, 6, 2033-2044.	9.8	206
7	The Exiguobacterium genus: biodiversity and biogeography. Extremophiles, 2009, 13, 541-555.	2.3	202
8	The deep cold biosphere: facts and hypothesis. FEMS Microbiology Reviews, 1997, 20, 277-290.	8.6	201
9	Psychrobacter cryohalolentis sp. nov. and Psychrobacter arcticus sp. nov., isolated from Siberian permafrost. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 1285-1291.	1.7	169
10	Low-temperature recovery strategies for the isolation of bacteria from ancient permafrost sediments. Extremophiles, 2000, 4, 165-173.	2.3	163
11	Microbes in thawing permafrost: the unknown variable in the climate change equation. ISME Journal, 2012, 6, 709-712.	9.8	153
12	Bacterial Community in Ancient Siberian Permafrost as Characterized by Culture and Culture-Independent Methods. Astrobiology, 2006, 6, 400-414.	3.0	143
13	Mercury and Other Heavy Metals Influence Bacterial Community Structure in Contaminated Tennessee Streams. Applied and Environmental Microbiology, 2011, 77, 302-311.	3.1	137
14	Characterization of Exiguobacterium isolates from the Siberian permafrost. Description of Exiguobacterium sibiricum sp. nov Extremophiles, 2006, 10, 285-294.	2.3	124
15	Improving power production in acetate-fed microbial fuel cells via enrichment of exoelectrogenic organisms in flow-through systems. Biochemical Engineering Journal, 2009, 48, 71-80.	3.6	110
16	The Evolution of AÎ ² Peptide Burden in the APP23 Transgenic Mice: Implications for AÎ ² Deposition in Alzheimer Disease. Molecular Medicine, 2001, 7, 609-618.	4.4	99
17	An active atmospheric methane sink in high Arctic mineral cryosols. ISME Journal, 2015, 9, 1880-1891.	9.8	92
18	<i>Caldicellulosiruptor obsidiansis</i> sp. nov., an Anaerobic, Extremely Thermophilic, Cellulolytic Bacterium Isolated from Obsidian Pool, Yellowstone National Park. Applied and Environmental Microbiology, 2010, 76, 1014-1020.	3.1	91

#	Article	IF	CITATIONS
19	Commercial DNA extraction kits impact observed microbial community composition in permafrost samples. FEMS Microbiology Ecology, 2014, 87, 217-230.	2.7	89
20	Integrating engineering design improvements with exoelectrogen enrichment process to increase power output from microbial fuel cells. Journal of Power Sources, 2009, 191, 520-527.	7.8	86
21	Permafrost microbiology. Permafrost and Periglacial Processes, 1995, 6, 281-291.	3.4	84
22	Controlling accumulation of fermentation inhibitors in biorefinery recycle water using microbial fuel cells. Biotechnology for Biofuels, 2009, 2, 7.	6.2	72
23	Environmental proteomics reveals early microbial community responses to biostimulation at a uranium―and nitrateâ€contaminated site. Proteomics, 2013, 13, 2921-2930.	2.2	71
24	Metagenomic analyses of the late Pleistocene permafrost – additional tools for reconstruction of environmental conditions. Biogeosciences, 2016, 13, 2207-2219.	3.3	59
25	Diversity and genomic insights into the uncultured <scp><i>C</i></scp> <i>hloroflexi</i> from the human microbiota. Environmental Microbiology, 2014, 16, 2635-2643.	3.8	55
26	Bacteria in Permafrost. , 2008, , 83-102.		53
27	Microbial Communities in Subpermafrost Saline Fracture Water at the Lupin Au Mine, Nunavut, Canada. Microbial Ecology, 2009, 58, 786-807.	2.8	52
28	Effect of low temperature and culture media on the growth and freeze-thawing tolerance of Exiguobacterium strains. Cryobiology, 2007, 54, 234-240.	0.7	51
29	Characterization of Archaeal Community in Contaminated and Uncontaminated Surface Stream Sediments. Microbial Ecology, 2010, 60, 784-795.	2.8	51
30	Complete Genome Sequence of the Thermophilic Bacterium Exiguobacterium sp. AT1b. Journal of Bacteriology, 2011, 193, 2880-2881.	2.2	47
31	Putative Transposases Conserved in Exiguobacterium Isolates from Ancient Siberian Permafrost and from Contemporary Surface Habitats. Applied and Environmental Microbiology, 2005, 71, 6954-6962.	3.1	43
32	Enhancement in current density and energy conversion efficiency of 3-dimensional MFC anodes using pre-enriched consortium and continuous supply of electron donors. Bioresource Technology, 2011, 102, 5098-5104.	9.6	40
33	Microbial Community Changes in Response to Ethanol or Methanol Amendments for U(VI) Reduction. Applied and Environmental Microbiology, 2010, 76, 5728-5735.	3.1	38
34	Extended survival of several organisms and amino acids under simulated martian surface conditions. Icarus, 2011, 211, 1162-1178.	2.5	38
35	Microbial community structure with trends in methylation gene diversity and abundance in mercury-contaminated rice paddy soils in Guizhou, China. Environmental Sciences: Processes and Impacts, 2018, 20, 673-685.	3.5	36
36	Microbiome assembly in thawing permafrost and its feedbacks to climate. Global Change Biology, 2022, 28, 5007-5026.	9.5	34

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37	A living bdelloid rotifer from 24,000-year-old Arctic permafrost. Current Biology, 2021, 31, R712-R713.	3.9	33
38	Draft Genome Sequences of 10 Strains of the Genus <i>Exiguobacterium</i> . Genome Announcements, 2014, 2, .	0.8	31
39	The resistance of viable permafrost algae to simulated environmental stresses: implications for astrobiology. International Journal of Astrobiology, 2003, 2, 171-177.	1.6	29
40	Effects of simulated spring thaw of permafrost from mineral cryosol on CO ₂ emissions and atmospheric CH ₄ uptake. Journal of Geophysical Research G: Biogeosciences, 2015, 120, 1764-1784.	3.0	28
41	Donorâ€dependent Extent of Uranium Reduction for Bioremediation of Contaminated Sediment Microcosms. Journal of Environmental Quality, 2009, 38, 53-60.	2.0	26
42	Viable Cyanobacteria and Green Algae from the Permafrost Darkness. Soil Biology, 2009, , 73-84.	0.8	26
43	Characterization of the Deltaproteobacteria in contaminated and uncontaminated stream sediments and identification of potential mercury methylators. Aquatic Microbial Ecology, 2012, 66, 271-282.	1.8	26
44	Improved Yield of High Molecular Weight DNA Coincides with Increased Microbial Diversity Access from Iron Oxide Cemented Sub-Surface Clay Environments. PLoS ONE, 2014, 9, e102826.	2.5	25
45	Predominance of Anaerobic, Spore-Forming Bacteria in Metabolically Active Microbial Communities from Ancient Siberian Permafrost. Applied and Environmental Microbiology, 2019, 85, .	3.1	25
46	Methane in Gas Shows from Boreholes in Epigenetic Permafrost of Siberian Arctic. Geosciences (Switzerland), 2019, 9, 67.	2.2	23
47	Methanogens in the Antarctic Dry Valley permafrost. FEMS Microbiology Ecology, 2018, 94, .	2.7	22
48	Genomic and Expression Analyses of Cold-Adapted Microorganisms. , 0, , 126-155.		22
49	Metagenomes from Thawing Low-Soil-Organic-Carbon Mineral Cryosols and Permafrost of the Canadian High Arctic. Genome Announcements, 2014, 2, .	0.8	20
50	Community Analysis of Plant Biomass-Degrading Microorganisms from Obsidian Pool, Yellowstone National Park. Microbial Ecology, 2015, 69, 333-345.	2.8	20
51	A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. Genetics, 2020, 214, 719-733.	2.9	20
52	The deep cold biosphere: facts and hypothesis. FEMS Microbiology Reviews, 1997, 20, 277-290.	8.6	19
53	Microbial Communities Involved in Biological Ammonium Removal from Coal Combustion Wastewaters. Microbial Ecology, 2013, 66, 49-59.	2.8	17
54	Highâ€Performance Bioanode Development for Fermentable Substrates via Controlled Electroactive Biofilm Growth. ChemElectroChem, 2014, 1, 1940-1947.	3.4	17

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55	Are permafrost microorganisms as old as permafrost?. FEMS Microbiology Ecology, 2021, 97, .	2.7	17
56	Genomic reconstruction of fossil and living microorganisms in ancient Siberian permafrost. Microbiome, 2021, 9, 110.	11.1	17
57	Changes in northern Gulf of Mexico sediment bacterial and archaeal communities exposed to hypoxia. Geobiology, 2015, 13, 478-493.	2.4	16
58	Atmospheric <scp>CH</scp> ₄ oxidation by Arctic permafrost and mineral cryosols as a function of water saturation and temperature. Geobiology, 2017, 15, 94-111.	2.4	14
59	Earth's perennially frozen environments as a model of cryogenic planet ecosystems. Permafrost and Periglacial Processes, 2018, 29, 246-256.	3.4	14
60	Eight Metagenome-Assembled Genomes Provide Evidence for Microbial Adaptation in 20,000- to 1,000,000-Year-Old Siberian Permafrost. Applied and Environmental Microbiology, 2021, 87, e0097221.	3.1	13
61	Anaerobic High-Throughput Cultivation Method for Isolation of Thermophiles Using Biomass-Derived Substrates. , 2012, 908, 153-168.		11
62	Comparative Metagenomics of the Active Layer and Permafrost from Low-Carbon Soil in the Canadian High Arctic. Environmental Science & Technology, 2021, 55, 12683-12693.	10.0	10
63	Metagenome-Assembled Genome of USCα AHI, a Potential High-Affinity Methanotroph from Axel Heiberg Island, Canadian High Arctic. Microbiology Resource Announcements, 2019, 8, .	0.6	8
64	Elucidating Biogeochemical Reduction of Chromate via Carbon Amendments and Soil Sterilization. Geomicrobiology Journal, 2007, 24, 125-132.	2.0	7
65	Microbial Life In Permafrost. , 2004, , 151-169.		7
66	Chapter 10. Viable Phototrophs: Cyanobacteria and Green Algae from the Permafrost Darkness. , 2005, , 140-158.		7
67	Permafrost Active Layer Microbes From Ny Ãlesund, Svalbard (79°N) Show Autotrophic and Heterotrophic Metabolisms With Diverse Carbon-Degrading Enzymes. Frontiers in Microbiology, 2021, 12, 757812.	3.5	7
68	Insights into community of photosynthetic microorganisms from permafrost. FEMS Microbiology Ecology, 2020, 96, .	2.7	6
69	Proteomic Insights: Cryoadaptation of Permafrost Bacteria. Soil Biology, 2009, , 169-181.	0.8	4
70	Free Iron and Iron-Reducing Microorganisms in Permafrost and Permafrost-Affected Soils of Northeastern Siberia. Eurasian Soil Science, 2020, 53, 1455-1468.	1.6	4
71	Surface reflectance degradation by microbial communities. Journal of Building Physics, 2016, 40, 263-277.	2.4	3
72	Draft Genome Sequence of Antarctic Methanogen Enriched from Dry Valley Permafrost. Genome Announcements, 2016, 4, .	0.8	2

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73	Thaumarchaea Genome Sequences from a High Arctic Active Layer. Microbiology Resource Announcements, 2020, 9, .	0.6	2
74	Biogeochemical Characteristics of Earth's Volcanic Permafrost: An Analog of Extraterrestrial Environments. Astrobiology, 2022, 22, 812-828.	3.0	2
75	Microbial Carbon Cycling in Permafrost. , 0, , 181-199.		1
76	Effect of Growth Temperature and Culture Medium on the Cryotolerance of Permafrost Exiguobacterium Sibiricum 255-15 by Proteome-Wide Mass Mapping. The Open Proteomics Journal, 2009, 2, 8-19.	0.4	1
77	Draft Genome Sequence of Microbacterium sp. Gd 4-13, Isolated from Gydanskiy Peninsula Permafrost Sediments of Marine Origin. Microbiology Resource Announcements, 2019, 8, .	0.6	1
78	MICROBIAL DIVERSITY OF SIBERIAN PERMAFROST. , 2018, , .		0
79	Metagenomes from Late Pleistocene Ice Complex Sediments of the Siberian Arctic. Microbiology Resource Announcements, 2019, 8, .	0.6	0
80	Draft Genome Sequences of 10 Pseudomonas sp. Isolates from the Active Layer of Permafrost in Ny	0.6	0

Å...lesund, Svalbard, Norway. Microbiology Resource Announcements, 2022, , e0020122.