

Olga Karnachuk

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3026449/publications.pdf>

Version: 2024-02-01

75
papers

1,530
citations

304368

22
h-index

360668

35
g-index

78
all docs

78
docs citations

78
times ranked

1655
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeted isolation based on metagenome-assembled genomes reveals a phylogenetically distinct group of thermophilic spirochetes from deep biosphere. <i>Environmental Microbiology</i> , 2021, 23, 3585-3598.	1.8	23
2	<i>Desulfovibrio</i> Isolate from the Microbiome of Children with Autistic Spectrum Disorders Immobilizes Iron in Poorly Soluble Crystalline Sulfides. <i>Microbiology</i> , 2021, 90, 268-271.	0.5	3
3	Thermophilic Chloroflexi Dominate in the Microbial Community Associated with Coal-Fire Gas Vents in the Kuznetsk Coal Basin, Russia. <i>Microorganisms</i> , 2021, 9, 948.	1.6	8
4	Isolation of a Novel Chemolithotrophic Sulfate-Reducing Firmicute from a Tyumen Thermal Borehole. <i>Microbiology</i> , 2021, 90, 397-400.	0.5	1
5	A Novel Medium for Cultivation of <i>Desulforudis audaxviator</i> . <i>Microbiology</i> , 2021, 90, 401-404.	0.5	2
6	Microbial sulfate reduction by <i>Desulfovibrio</i> is an important source of hydrogen sulfide from a large swine finishing facility. <i>Scientific Reports</i> , 2021, 11, 10720.	1.6	18
7	<i>Desulfosporosinus metallidurans</i> sp. nov., an acidophilic, metal-resistant sulfate-reducing bacterium from acid mine drainage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	18
8	The Microbial Community of Poultry Farm Waste and Its Role in Hydrogen Sulfide Production. <i>Microbiology</i> , 2021, 90, 507-511.	0.5	2
9	Metagenomic Analysis of the Microbial Community in the Underground Coal Fire Area (Kemerovo) Tj ETQq1 1 0.784314 rgBT /Overlooked Aquificae, and Firmicutes. <i>Microbiology</i> , 2021, 90, 578-587.	0.5	5
10	Comparative Genome Analysis of the Genus <i>Thiothrix</i> Involving Three Novel Species, <i>Thiothrix subterranea</i> sp. nov. Ku-5, <i>Thiothrix litoralis</i> sp. nov. AS and <i>Candidatus Thiothrix anitrata</i> sp. nov. A52, Revealed the Conservation of the Pathways of Dissimilatory Sulfur Metabolism and Variations in the Genetic Inventory for Nitrogen Metabolism and Autotrophic Carbon Fixation. <i>Frontiers in Microbiology</i> , 2021, 12, 760289.	1.5	22
11	<i>Desulfovibrio desulfuricans</i> AY5 Isolated from a Patient with Autism Spectrum Disorder Binds Iron in Low-Soluble Greigite and Pyrite. <i>Microorganisms</i> , 2021, 9, 2558.	1.6	6
12	Diversity of Eukaryotic Microorganisms in the Drainage Waters of a Coal Open-Cast Mine. <i>Microbiology</i> , 2020, 89, 641-646.	0.5	4
13	Copper Precipitation as Insoluble Oxalates by Thermotolerant <i>Aspergillus</i> spp. from Burning Wastes of Coal Mining. <i>Microbiology</i> , 2020, 89, 498-501.	0.5	4
14	Microbial Life in the Deep Subsurface Aquifer Illuminated by Metagenomics. <i>Frontiers in Microbiology</i> , 2020, 11, 572252.	1.5	48
15	Application of Microbial Mats for the Isolation of Spore-Forming Prokaryotes from Deep Biosphere. <i>Microbiology</i> , 2020, 89, 789-792.	0.5	3
16	Sulfate Reduction in Underground Horizons of a Flooded Coal Mine in Kuzbass. <i>Microbiology</i> , 2020, 89, 542-550.	0.5	4
17	Genome Analysis of a Member of the Uncultured Phylum Riflebacteria Revealed Pathways of Organotrophic Metabolism and Dissimilatory Iron Reduction. <i>Microbiology</i> , 2020, 89, 328-336.	0.5	16
18	Complete Genome of a Member of a New Bacterial Lineage in the Microgenomates Group Reveals an Unusual Nucleotide Composition Disparity Between Two Strands of DNA and Limited Metabolic Potential. <i>Microorganisms</i> , 2020, 8, 320.	1.6	23

#	ARTICLE	IF	CITATIONS
19	Complete Genome Sequence of an Uncultured Bacterium of the Candidate Phylum Bipolaricaulota. <i>Microbiology</i> , 2019, 88, 461-468.	0.5	8
20	Isolation of New Thermophilic Sulfidogens from Microbial Mat Associated with Groundwater Discharge in the Tunkin Valley. <i>Microbiology</i> , 2019, 88, 642-645.	0.5	2
21	Genomes of three bacteriophages from the deep subsurface aquifer. <i>Data in Brief</i> , 2019, 22, 488-491.	0.5	5
22	Genome of a Member of the Candidate Archaeal Phylum Verstraetearchaeota from a Subsurface Thermal Aquifer Revealed Pathways of Methyl-Reducing Methanogenesis and Fermentative Metabolism. <i>Microbiology</i> , 2019, 88, 316-323.	0.5	6
23	Selection of a Microbial Community in the Course of Formation of Acid Mine Drainage. <i>Microbiology</i> , 2019, 88, 292-299.	0.5	10
24	A Novel Bacteriophage of the Order Caudovirales from the Soil Metagenome in the Area of an Underground Coal Seam Fire. <i>Microbiology</i> , 2019, 88, 240-243.	0.5	1
25	Sulfur-Oxidizing Bacteria Dominate in the Water from a Flooded Coal Mine Shaft in Kuzbass. <i>Microbiology</i> , 2019, 88, 120-123.	0.5	8
26	Domestication of previously uncultivated <i>Candidatus</i> <i>Desulforudis audaxviator</i> from a deep aquifer in Siberia sheds light on its physiology and evolution. <i>ISME Journal</i> , 2019, 13, 1947-1959.	4.4	48
27	Isolation, characterization, and genome insights into an anaerobic sulfidogenic <i>Tissierella</i> bacterium from Cu-bearing coins. <i>Anaerobe</i> , 2019, 56, 66-77.	1.0	11
28	Phylogeny and physiology of candidate phylum BRC1 inferred from the first complete metagenome-assembled genome obtained from deep subsurface aquifer. <i>Systematic and Applied Microbiology</i> , 2019, 42, 67-76.	1.2	38
29	Genome of the candidate phylum Aminicenantes bacterium from a deep subsurface thermal aquifer revealed its fermentative saccharolytic lifestyle. <i>Extremophiles</i> , 2019, 23, 189-200.	0.9	74
30	Isolation, Characterization, and Metal Response of Novel, Acid-Tolerant <i>Penicillium</i> spp. from Extremely Metal-Rich Waters at a Mining Site in Transbaikal (Siberia, Russia). <i>Microbial Ecology</i> , 2018, 76, 911-924.	1.4	18
31	A metagenomic window into the 2-km-deep terrestrial subsurface aquifer revealed multiple pathways of organic matter decomposition. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	38
32	Lignite coal burning seam in the remote Altai Mountains harbors a hydrogen-driven thermophilic microbial community. <i>Scientific Reports</i> , 2018, 8, 6730.	1.6	19
33	Genome sequence of the copper resistant and acid-tolerant <i>Desulfosporosinus</i> sp. BG isolated from the tailings of a molybdenum-tungsten mine in the Transbaikal area. <i>Genomics Data</i> , 2017, 11, 106-108.	1.3	8
34	Uncultured bacteria and methanogenic archaea predominate in the microbial community of Western Siberian deep subsurface aquifer. <i>Microbiology</i> , 2017, 86, 412-415.	0.5	15
35	Genome sequence of the acid-tolerant <i>Desulfovibrio</i> sp. DV isolated from the sediments of a Pb-Zn mine tailings dam in the Chita region, Russia. <i>Genomics Data</i> , 2017, 11, 125-127.	1.3	3
36	Sulfate-reducing bacteria in the microbial community of acidic drainage from a gold deposit tailing storage. <i>Microbiology</i> , 2017, 86, 286-288.	0.5	2

#	ARTICLE	IF	CITATIONS
37	Selection for novel, acid-tolerant <i>Desulfovibrio</i> spp. from a closed Transbaikal mine site in a temporal pH-gradient bioreactor. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 1669-1679.	0.7	6
38	Metagenome Sequence of a Microbial Community from the Gold Mine Tailings in the Kuzbass Area, Russia. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
39	Variability of the composition of the microbial community of the deep subsurface thermal aquifer in Western Siberia. <i>Microbiology</i> , 2017, 86, 765-772.	0.5	15
40	Metagenome of the Siberian Underground Water Reservoir. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
41	Characterization and Genome Analysis of the First Facultatively Alkaliphilic <i>Thermodesulfovibrio</i> Isolated from the Deep Terrestrial Subsurface. <i>Frontiers in Microbiology</i> , 2016, 7, 2000.	1.5	62
42	Stable and Variable Parts of Microbial Community in Siberian Deep Subsurface Thermal Aquifer System Revealed in a Long-Term Monitoring Study. <i>Frontiers in Microbiology</i> , 2016, 7, 2101.	1.5	27
43	Components of antioxidant systems in the cells of aerotolerant sulfate-reducing bacteria of the genus <i>Desulfovibrio</i> (strains A2 and TomC) isolated from metal mining waste. <i>Microbiology</i> , 2016, 85, 649-657.	0.5	2
44	The complete mitochondrial genome of the acid-tolerant fungus <i>Penicillium</i> ShG4C. <i>Genomics Data</i> , 2016, 10, 141-143.	1.3	3
45	Effect of metal concentration on the microbial community in acid mine drainage of a polysulfide ore deposit. <i>Microbiology</i> , 2016, 85, 745-751.	0.5	19
46	Genomic insights into a new acidophilic, copper-resistant <i>Desulfosporosinus</i> isolate from the oxidized tailings area of an abandoned gold mine. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw111.	1.3	39
47	A novel uncultured bacterium of the family Gallionellaceae: Description and genome reconstruction based on metagenomic analysis of microbial community in acid mine drainage. <i>Microbiology</i> , 2016, 85, 449-461.	0.5	23
48	<i>Firmicutes</i> is an Important Component of Microbial Communities in Water-Injected and Pristine Oil Reservoirs, Western Siberia, Russia. <i>Geomicrobiology Journal</i> , 2016, 33, 387-400.	1.0	25
49	Effect of Tree Species on Enzyme Secretion by the Shiitake Medicinal Mushroom, <i>Lentinus edodes</i> (Agaricomycetes). <i>International Journal of Medicinal Mushrooms</i> , 2016, 18, 637-644.	0.9	2
50	A Novel Uncultured Bacterium of the Family Gallionellaceae: Description and Genome Reconstruction Based on the Metagenomic Analysis of Microbial Community in Acid Mine Drainage. <i>Mikrobiologija</i> , 2016, 85, 421-435.	0.1	7
51	Active sulfate reduction in acidic sediments of gold mine tailings. <i>Microbiology</i> , 2015, 84, 453-455.	0.5	1
52	Draft genome sequence of the first acid-tolerant sulfate-reducing deltaproteobacterium <i>Desulfovibrio</i> sp. TomC having potential for minewater treatment. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-3.	0.7	16
53	Diversity of copper proteins and copper homeostasis systems in <i>Melioribacter roseus</i> , a facultatively anaerobic thermophilic member of the new phylum Ignavibacteriae. <i>Microbiology</i> , 2015, 84, 135-143.	0.5	4
54	An acidophilic <i>Desulfosporosinus</i> isolated from the oxidized mining wastes in the Transbaikal area. <i>Microbiology</i> , 2015, 84, 677-686.	0.5	10

#	ARTICLE	IF	CITATIONS
55	Increased mycelial biomass production by <i>Lentinula edodes</i> intermittently illuminated by green light emitting diodes. <i>Biotechnology Letters</i> , 2014, 36, 2283-2289.	1.1	7
56	Characteristics of the new plasmid, pMTB1, from the metagenome of the microbial community of underground thermal waters of Western Siberia. <i>Biology Bulletin</i> , 2014, 41, 223-227.	0.1	0
57	Characterization of <i>Melioribacter roseus</i> gen. nov., sp. nov., a novel facultatively anaerobic thermophilic cellulolytic bacterium from the class <i>Ignavibacteria</i> , and a proposal of a novel bacterial phylum <i>Ignavibacteriia</i> . <i>Environmental Microbiology</i> , 2013, 15, 1759-1771.	1.8	228
58	Characterization of precipitates formed by H ₂ S-producing, Cu-resistant Firmicute isolates of <i>Tissierella</i> from human gut and <i>Desulfosporosinus</i> from mine waste. <i>Antonie Van Leeuwenhoek</i> , 2013, 103, 1221-1234.	0.7	35
59	Genome Sequence of <i>Desulfosporosinus</i> sp. OT, an Acidophilic Sulfate-Reducing Bacterium from Copper Mining Waste in Norilsk, Northern Siberia. <i>Journal of Bacteriology</i> , 2011, 193, 6104-6105.	1.0	33
60	Genome Sequence of <i>Desulfovibrio</i> sp. A2, a Highly Copper Resistant, Sulfate-Reducing Bacterium Isolated from Effluents of a Zinc Smelter at the Urals. <i>Journal of Bacteriology</i> , 2011, 193, 6793-6794.	1.0	14
61	The search for sulfate-reducing bacteria in mat samples from the lost city hydrothermal field by molecular cloning. <i>Microbiology</i> , 2010, 79, 96-105.	0.5	16
62	Bacteria of the sulfur cycle in the sediments of gold mine tailings, Kuznetsk Basin, Russia. <i>Microbiology</i> , 2009, 78, 483-491.	0.5	23
63	Precipitation of Cu-Sulfides by Copper-Tolerant <i>Desulfovibrio</i> Isolates. <i>Geomicrobiology Journal</i> , 2008, 25, 219-227.	1.0	26
64	Bacterial oxidation of ferrous iron at low temperatures. <i>Biotechnology and Bioengineering</i> , 2007, 97, 1470-1478.	1.7	56
65	Distribution, diversity, and activity of sulfate-reducing bacteria in the water column in Gek-Gel lake, Azerbaijan. <i>Microbiology</i> , 2006, 75, 82-89.	0.5	28
66	Formation of Covellite (CuS) Under Biological Sulfate-Reducing Conditions. <i>Geomicrobiology Journal</i> , 2006, 23, 613-619.	1.0	42
67	Sulfate Reduction Potential in Sediments in the Norilsk Mining Area, Northern Siberia. <i>Geomicrobiology Journal</i> , 2005, 22, 11-25.	1.0	38
68	The evolution of alkaline, saline ground- and surface waters in the southern Siberian steppes. <i>Applied Geochemistry</i> , 2004, 19, 1905-1926.	1.4	25
69	Microbial Processes of the Carbon and Sulfur Cycles in Lake Shira (Khakasia). <i>Microbiology</i> , 2003, 72, 221-229.	0.5	22
70	Copper resistance in <i>Desulfovibrio</i> strain R2. <i>Antonie Van Leeuwenhoek</i> , 2003, 83, 99-106.	0.7	26
71	Alkaline mine drainage from metal sulphide and coal mines: examples from Svalbard and Siberia. <i>Geological Society Special Publication</i> , 2002, 198, 287-296.	0.8	9
72	Growth of sulfate-reducing bacteria with solid-phase electron acceptors. <i>Applied Microbiology and Biotechnology</i> , 2002, 58, 482-486.	1.7	50

#	ARTICLE	IF	CITATIONS
73	Groundwater Contamination from Rural Pit Latrines: Examples from Siberia and Kosova. Water and Environment Journal, 2002, 16, 147-152.	1.0	41
74	Environmental Protection in the Tomsk Region of the Russian Federation: A Case Study. Environmental Management, 2000, 26, 35-46.	1.2	1
75	Environmental Protection in the Tomsk Region of the Russian Federation: A Case Study. Environmental Management, 2000, 26, 585-585.	1.2	0