

Joerg Overmann

List of Publications by Year in descending order

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Version: 2024-02-01

147
papers

10,556
citations

34076

52
h-index

39638

94
g-index

162
all docs

162
docs citations

162
times ranked

12616
citing authors

#	ARTICLE	IF	CITATIONS
1	BacDive in 2022: the knowledge base for standardized bacterial and archaeal data. <i>Nucleic Acids Research</i> , 2022, 50, D741-D746.	6.5	71
2	Molecular basis of a bacterial-amphibian symbiosis revealed by comparative genomics, modeling, and functional testing. <i>ISME Journal</i> , 2022, 16, 788-800.	4.4	15
3	Sandacrabins – Structurally Unique Antiviral RNA Polymerase Inhibitors from a Rare <i>Myxobacterium</i> . <i>Chemistry - A European Journal</i> , 2022, 28, e202104484.	1.7	10
4	The Evolution of Ecological Diversity in Acidobacteria. <i>Frontiers in Microbiology</i> , 2022, 13, 715637.	1.5	15
5	Differential Response of Acidobacteria to Water Content, Soil Type, and Land Use During an Extended Drought in African Savannah Soils. <i>Frontiers in Microbiology</i> , 2022, 13, 750456.	1.5	9
6	Multilateral benefit-sharing from digital sequence information will support both science and biodiversity conservation. <i>Nature Communications</i> , 2022, 13, 1086.	5.8	34
7	Beyond the ABCs – Discovery of Three New Plasmid Types in Rhodobacterales (RepQ, RepY, RepW). <i>Microorganisms</i> , 2022, 10, 738.	1.6	0
8	Biological Soil Crust From Mesic Forests Promote a Specific Bacteria Community. <i>Frontiers in Microbiology</i> , 2022, 13, 769767.	1.5	8
9	Anaerobic single-cell dispensing facilitates the cultivation of human gut bacteria. <i>Environmental Microbiology</i> , 2022, 24, 3861-3881.	1.8	15
10	Metadata harmonization – Standards are the key for a better usage of omics data for integrative microbiome analysis. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	13
11	<i>Usitatibacter rugosus</i> gen. nov., sp. nov. and <i>Usitatibacter palustris</i> sp. nov., novel members of Usitatibacteraceae fam. nov. within the order Nitrosomonadales isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	47
12	<i>Dinoroseobacter shibae</i> Outer Membrane Vesicles Are Enriched for the Chromosome Dimer Resolution Site. <i>MSystems</i> , 2021, 6, .	1.7	7
13	The mineralosphere – interactive zone of microbial colonization and carbon use in grassland soils. <i>Biology and Fertility of Soils</i> , 2021, 57, 587-601.	2.3	11
14	Recent advances in culture-based gut microbiome research. <i>International Journal of Medical Microbiology</i> , 2021, 311, 151485.	1.5	15
15	Early-Life Immune System Maturation in Chickens Using a Synthetic Community of Cultured Gut Bacteria. <i>MSystems</i> , 2021, 6, .	1.7	68
16	Genomic and proteomic profiles of biofilms on microplastics are decoupled from artificial surface properties. <i>Environmental Microbiology</i> , 2021, 23, 3099-3115.	1.8	43
17	Automated analysis of genomic sequences facilitates high-throughput and comprehensive description of bacteria. <i>ISME Communications</i> , 2021, 1, .	1.7	228
18	Contrasting responses of above- and belowground diversity to multiple components of land-use intensity. <i>Nature Communications</i> , 2021, 12, 3918.	5.8	81

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19	Among stand heterogeneity is key for biodiversity in managed beech forests but does not question the value of unmanaged forests: Response to Bruun and Heilmann&Clausen (2021). Journal of Applied Ecology, 2021, 58, 1817-1826.	1.9	8
20	Microbial occurrence in liquid nitrogen storage tanks: a challenge for cryobanking?. Applied Microbiology and Biotechnology, 2021, 105, 7635-7650.	1.7	5
21	Genome and Methylome analysis of a phylogenetic novel Campylobacter coli cluster with C. jejuni introgression. Microbial Genomics, 2021, 7, .	1.0	0
22	Bacterial colonization of minerals in grassland soils is selective and highly dynamic. Environmental Microbiology, 2020, 22, 917-933.	1.8	23
23	100&year&old enigma solved: identification, genomic characterization and biogeography of the yet uncultured <i>Planctomyces bekefi</i>. Environmental Microbiology, 2020, 22, 198-211.	1.8	25
24	Drivers of the composition of active rhizosphere bacterial communities in temperate grasslands. ISME Journal, 2020, 14, 463-475.	4.4	141
25	Factors determining microbial colonization of liquid nitrogen storage tanks used for archiving biological samples. Applied Microbiology and Biotechnology, 2020, 104, 131-144.	1.7	11
26	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. Nature Microbiology, 2020, 5, 126-140.	5.9	164
27	Cryo-EM structure of a Ca ²⁺ -bound photosynthetic LH1-RC complex containing multiple β -polypeptides. Nature Communications, 2020, 11, 4955.	5.8	35
28	Stochastic Dispersal Rather Than Deterministic Selection Explains the Spatio-Temporal Distribution of Soil Bacteria in a Temperate Grassland. Frontiers in Microbiology, 2020, 11, 1391.	1.5	36
29	Bacterial mock communities as standards for reproducible cytometric microbiome analysis. Nature Protocols, 2020, 15, 2788-2812.	5.5	26
30	Blind spots in global soil biodiversity and ecosystem function research. Nature Communications, 2020, 11, 3870.	5.8	192
31	<i>In Vivo</i> Genome and Methylome Adaptation of <i>cag</i>-Negative Helicobacter pylori during Experimental Human Infection. MBio, 2020, 11, .	1.8	14
32	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. Nature Communications, 2020, 11, 6389.	5.8	269
33	2-Hydroxysorangadenosine: Structure and Biosynthesis of a Myxobacterial Sesquiterpene&Nucleoside. Molecules, 2020, 25, 2676.	1.7	9
34	New ECCO model documents for Material Deposit and Transfer Agreements in compliance with the Nagoya Protocol. FEMS Microbiology Letters, 2020, 367, .	0.7	4
35	Can multi&taxa diversity in European beech forest landscapes be increased by combining different management systems?. Journal of Applied Ecology, 2020, 57, 1363-1375.	1.9	38
36	Terricaulis silvestris gen. nov., sp. nov., a novel prosthecate, budding member of the family Caulobacteraceae isolated from forest soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4966-4977.	0.8	14

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37	A publicly accessible database for <i>Clostridioides difficile</i> genome sequences supports tracing of transmission chains and epidemics. <i>Microbial Genomics</i> , 2020, 6, .	1.0	22
38	<i>Hypericibacter terrae</i> gen. nov., sp. nov. and <i>Hypericibacter adhaerens</i> sp. nov., two new members of the family Rhodospirillaceae isolated from the rhizosphere of <i>Hypericum perforatum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1850-1860.	0.8	14
39	Discovery pipelines for marine resources: an ocean of opportunity for biotechnology?. <i>World Journal of Microbiology and Biotechnology</i> , 2019, 35, 107.	1.7	10
40	Amphibian skin-associated Pigmentiphaga: Genome sequence and occurrence across geography and hosts. <i>PLoS ONE</i> , 2019, 14, e0223747.	1.1	8
41	Trophic networks improve the performance of microbial anodes treating wastewater. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 27.	2.9	23
42	A Dual Role for Ca ²⁺ in Expanding the Spectral Diversity and Stability of Light-Harvesting 1 Reaction Center Photocomplexes of Purple Phototrophic Bacteria. <i>Biochemistry</i> , 2019, 58, 2844-2852.	1.2	23
43	Within-host evolution of <i>Helicobacter pylori</i> shaped by niche-specific adaptation, intragastric migrations and selective sweeps. <i>Nature Communications</i> , 2019, 10, 2273.	5.8	94
44	The use of genomic DNA sequences as type material for valid publication of bacterial species names will have severe implications for clinical microbiology and related disciplines. <i>Diagnostic Microbiology and Infectious Disease</i> , 2019, 95, 102-103.	0.8	15
45	Sequence and cultivation study of Muribaculaceae reveals novel species, host preference, and functional potential of this yet undescribed family. <i>Microbiome</i> , 2019, 7, 28.	4.9	481
46	Relevance of phenotypic information for the taxonomy of not-yet-cultured microorganisms. <i>Systematic and Applied Microbiology</i> , 2019, 42, 22-29.	1.2	34
47	BacDive in 2019: bacterial phenotypic data for High-throughput biodiversity analysis. <i>Nucleic Acids Research</i> , 2019, 47, D631-D636.	6.5	154
48	Isoprenoid Quinones Resolve the Stratification of Redox Processes in a Biogeochemical Continuum from the Photic Zone to Deep Anoxic Sediments of the Black Sea. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	19
49	Genome and Methyloome Variation in <i>Helicobacter pylori</i> With a <i>cag</i> Pathogenicity Island During Early Stages of Human Infection. <i>Gastroenterology</i> , 2018, 154, 612-623.e7.	0.6	40
50	The impact of even-aged and uneven-aged forest management on regional biodiversity of multiple taxa in European beech forests. <i>Journal of Applied Ecology</i> , 2018, 55, 267-278.	1.9	188
51	ATP Content and Cell Viability as Indicators for Cryostress Across the Diversity of Life. <i>Frontiers in Physiology</i> , 2018, 9, 921.	1.3	35
52	Convergent Loss of ABC Transporter Genes From <i>Clostridioides difficile</i> Genomes Is Associated With Impaired Tyrosine Uptake and p-Cresol Production. <i>Frontiers in Microbiology</i> , 2018, 9, 901.	1.5	30
53	Long-read DNA metabarcoding of ribosomal RNA in the analysis of fungi from aquatic environments. <i>Molecular Ecology Resources</i> , 2018, 18, 1500-1514.	2.2	103
54	An overview of the occurrence of ether- and ester-linked iso-diabolic acid membrane lipids in microbial cultures of the Acidobacteria: Implications for brGDGT paleoproxies for temperature and pH. <i>Organic Geochemistry</i> , 2018, 124, 63-76.	0.9	117

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55	Synchronous termination of replication of the two chromosomes is an evolutionary selected feature in Vibrionaceae. <i>PLoS Genetics</i> , 2018, 14, e1007251.	1.5	36
56	<i>Roseisolibacter agri</i> gen. nov., sp. nov., a novel slow-growing member of the under-represented phylum Gemmatimonadetes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1028-1036.	0.8	38
57	Vicinamibacteraceae fam. nov., the first described family within the subdivision 6 Acidobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2331-2334.	0.8	51
58	Cultured microbes represent a substantial fraction of the human and mouse gut microbiota. <i>Gut Microbes</i> , 2017, 8, 493-503.	4.3	79
59	Mobilization and integration of bacterial phenotypic data—Enabling next generation biodiversity analysis through the Bac Dive metadatabase. <i>Journal of Biotechnology</i> , 2017, 261, 187-193.	1.9	8
60	Function of bacterial community dynamics in the formation of cadaveric semiochemicals during <i>in situ</i> carcass decomposition. <i>Environmental Microbiology</i> , 2017, 19, 3310-3322.	1.8	26
61	Microbial Resource Centers Contribute to Bioprospecting of Bacteria and Filamentous Microfungi. <i>Topics in Biodiversity and Conservation</i> , 2017, , 51-79.	0.3	10
62	Successive Conditioning in Complex Artificial Wastewater Increases the Performance of Electrochemically Active Biofilms Treating Real Wastewater. <i>ChemElectroChem</i> , 2017, 4, 3081-3090.	1.7	20
63	Present and Future of Culturing Bacteria. <i>Annual Review of Microbiology</i> , 2017, 71, 711-730.	2.9	192
64	Microbiological Research Under the Nagoya Protocol: Facts and Fiction. <i>Trends in Microbiology</i> , 2017, 25, 85-88.	3.5	50
65	Trajectories and Drivers of Genome Evolution in Surface-Associated Marine <i>Phaeobacter</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 3297-3311.	1.1	13
66	The Composite 259-kb Plasmid of <i>Marteella mediterranea</i> DSM 17316—A Natural Replicon with Functional RepABC Modules from Rhodobacteraceae and Rhizobiaceae. <i>Frontiers in Microbiology</i> , 2017, 8, 1787.	1.5	18
67	Defining the taxonomic status of described subdivision 3 Acidobacteria: proposal of Bryobacteraceae fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 498-501.	0.8	59
68	<i>Luteitalea pratensis</i> gen. nov., sp. nov. a new member of subdivision 6 Acidobacteria isolated from temperate grassland soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1408-1414.	0.8	47
69	<i>Flaviaesturariibacter luteus</i> sp. nov., isolated from an agricultural floodplain soil, and emended description of the genus <i>Flaviaesturariibacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1727-1734.	0.8	14
70	<i>Aridibacter nitratreducens</i> sp. nov., a member of the family Blastocatellaceae, class Blastocatellia, isolated from an African soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4487-4493.	0.8	44
71	Inferring interactions in complex microbial communities from nucleotide sequence data and environmental parameters. <i>PLoS ONE</i> , 2017, 12, e0173765.	1.1	15
72	<i>Fuerstia marisgermanicae</i> gen. nov., sp. nov., an Unusual Member of the Phylum Planctomycetes from the German Wadden Sea. <i>Frontiers in Microbiology</i> , 2016, 7, 2079.	1.5	49

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73	First Complete Genome Sequence of a Subdivision 6 <i>Acidobacterium</i> Strain. <i>Genome Announcements</i> , 2016, 4, .	0.8	14
74	Land-use intensification causes multitrophic homogenization of grassland communities. <i>Nature</i> , 2016, 540, 266-269.	13.7	404
75	Genome Sequence of <i>Prosthecochloris</i> sp. Strain CIB 2401 of the Phylum Chlorobi. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
76	Biodiversity at multiple trophic levels is needed for ecosystem multifunctionality. <i>Nature</i> , 2016, 536, 456-459.	13.7	526
77	The Mouse Intestinal Bacterial Collection (miBC) provides host-specific insight into cultured diversity and functional potential of the gut microbiota. <i>Nature Microbiology</i> , 2016, 1, 16131.	5.9	465
78	Marine Bacteria and Archaea: Diversity, Adaptations, and Culturability. , 2016, , 21-55.		15
79	Genome Analysis of the Fruiting Body-Forming <i>Myxobacterium Chondromyces crocatus</i> Reveals High Potential for Natural Product Biosynthesis. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1945-1957.	1.4	37
80	Estimates of Soil Bacterial Ribosome Content and Diversity Are Significantly Affected by the Nucleic Acid Extraction Method Employed. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2595-2607.	1.4	28
81	BacDive – The Bacterial Diversity Metadatabase in 2016. <i>Nucleic Acids Research</i> , 2016, 44, D581-D585.	6.5	51
82	<i>Occallatibacter riparius</i> gen. nov., sp. nov. and <i>Occallatibacter savannae</i> sp. nov., acidobacteria isolated from Namibian soils, and emended description of the family Acidobacteriaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 219-229.	0.8	46
83	<i>Parviterribacter kavangonensis</i> gen. nov., sp. nov. and <i>Parviterribacter multiflagellatus</i> sp. nov., novel members of Parviterribacteraceae fam. nov. within the order Solirubrobacterales, and emended descriptions of the classes Thermoleophilia and Rubrobacteria and their orders and families. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 652-665.	0.8	56
84	The first representative of the globally widespread subdivision 6 Acidobacteria, <i>Vicinamibacter silvestris</i> gen. nov., sp. nov., isolated from subtropical savannah soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2971-2979.	0.8	59
85	<i>Brevitalea aridisoli</i> , <i>B. deliciosa</i> and <i>Arenimicrobium luteum</i> , three novel species of Acidobacteria subdivision 4 (class Blastocatellia) isolated from savanna soil and description of the novel family Pyrinomonadaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 3355-3366.	0.8	58
86	Life under extreme energy limitation: a synthesis of laboratory- and field-based investigations. <i>FEMS Microbiology Reviews</i> , 2015, 39, 688-728.	3.9	288
87	Significance and future role of microbial resource centers. <i>Systematic and Applied Microbiology</i> , 2015, 38, 258-265.	1.2	44
88	Novel isolates double the number of chemotrophic species and allow the first description of higher taxa in Acidobacteria subdivision 4. <i>Systematic and Applied Microbiology</i> , 2015, 38, 534-544.	1.2	121
89	<i>Terriglobus albidus</i> sp. nov., a member of the family Acidobacteriaceae isolated from Namibian semiarid savannah soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 3297-3304.	0.8	18
90	BacDive – the Bacterial Diversity Metadatabase. <i>Nucleic Acids Research</i> , 2014, 42, D592-D599.	6.5	35

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91	The complex methylome of the human gastric pathogen <i>Helicobacter pylori</i> . Nucleic Acids Research, 2014, 42, 2415-2432.	6.5	132
92	Determinants of <i>Acidobacteria</i> activity inferred from the relative abundances of 16S rRNA transcripts in German grassland and forest soils. Environmental Microbiology, 2014, 16, 658-675.	1.8	103
93	Seasonal controls on grassland microbial biogeography: Are they governed by plants, abiotic properties or both?. Soil Biology and Biochemistry, 2014, 71, 21-30.	4.2	79
94	<i>Aridibacter famidurans</i> gen. nov., sp. nov. and <i>Aridibacter kavangonensis</i> sp. nov., two novel members of subdivision 4 of the Acidobacteria isolated from semiarid savannah soil. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 1866-1875.	0.8	68
95	Ether- and Ester-Bound Iso-Diabolic Acid and Other Lipids in Members of Acidobacteria Subdivision 4. Applied and Environmental Microbiology, 2014, 80, 5207-5218.	1.4	112
96	Genomic analysis reveals key aspects of prokaryotic symbiosis in the phototrophic consortium <i>Chlorochromatium aggregatum</i> . Genome Biology, 2013, 14, R127.	13.9	40
97	<i>Blastocatella fastidiosa</i> gen. nov., sp. nov., isolated from semiarid savanna soil – The first described species of Acidobacteria subdivision 4. Systematic and Applied Microbiology, 2013, 36, 82-89.	1.2	150
98	Principles of Enrichment, Isolation, Cultivation, and Preservation of Prokaryotes. , 2013, , 149-207.		31
99	The Phototrophic Way of Life. , 2013, , 203-257.		39
100	Environmental Factors Affect Acidobacterial Communities below the Subgroup Level in Grassland and Forest Soils. Applied and Environmental Microbiology, 2012, 78, 7398-7406.	1.4	272
101	Enrichment of previously uncultured bacteria from natural complex communities by adhesion to solid surfaces. Environmental Microbiology, 2012, 14, 2984-2997.	1.8	22
102	General Relationships between Abiotic Soil Properties and Soil Biota across Spatial Scales and Different Land-Use Types. PLoS ONE, 2012, 7, e43292.	1.1	142
103	Comparative and Functional Genomics of Anoxygenic Green Bacteria from the Taxa Chlorobi, Chloroflexi, and Acidobacteria. Advances in Photosynthesis and Respiration, 2012, , 47-102.	1.0	145
104	Puf operon sequences and inferred structures of light-harvesting complexes of three closely related Chromatiaceae exhibiting different absorption characteristics. Archives of Microbiology, 2012, 194, 123-134.	1.0	14
105	Close Interspecies Interactions between Prokaryotes from Sulfurous Environments. Frontiers in Microbiology, 2011, 2, 146.	1.5	23
106	Identification and Targeted Cultivation of Abundant Novel Freshwater Sphingomonads and Analysis of Their Population Substructure. Applied and Environmental Microbiology, 2011, 77, 7355-7364.	1.4	22
107	<i>Thalassospira</i> sp. Isolated from the Oligotrophic Eastern Mediterranean Sea Exhibits Chemotaxis toward Inorganic Phosphate during Starvation. Applied and Environmental Microbiology, 2011, 77, 4412-4421.	1.4	41
108	Large-scale distribution and activity patterns of an extremely low-light-adapted population of green sulfur bacteria in the Black Sea. Environmental Microbiology, 2010, 12, 1348-1362.	1.8	87

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109	Expression-based identification of genetic determinants of the bacterial symbiosis of <i>Chlorochromatium aggregatum</i> ™. <i>Environmental Microbiology</i> , 2010, 12, 2259-2276.	1.8	11
110	The Phototrophic Consortium of <i>Chlorochromatium aggregatum</i> ™: A Model for Bacterial Heterologous Multicellularity. <i>Advances in Experimental Medicine and Biology</i> , 2010, 675, 15-29.	0.8	24
111	Ultrastructure, tactic behaviour and potential for sulfate reduction of a novel multicellular magnetotactic prokaryote from North Sea sediments. <i>Environmental Microbiology</i> , 2009, 11, 1493-1505.	1.8	91
112	Identification and analysis of four candidate symbiosis genes from <i>Chlorochromatium aggregatum</i> ™, a highly developed bacterial symbiosis. <i>Environmental Microbiology</i> , 2008, 10, 2842-2856.	1.8	15
113	<i>Edaphobacter modestus</i> gen. nov., sp. nov., and <i>Edaphobacter aggregans</i> sp. nov., acidobacteria isolated from alpine and forest soils. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 1114-1122.	0.8	123
114	Subfossil 16S rRNA Gene Sequences of Green Sulfur Bacteria in the Black Sea and Their Implications for Past Photic Zone Anoxia. <i>Applied and Environmental Microbiology</i> , 2008, 74, 624-632.	1.4	23
115	Ultrastructural Characterization of the Prokaryotic Symbiosis in <i>Chlorochromatium aggregatum</i> ™. <i>Journal of Bacteriology</i> , 2008, 190, 3721-3730.	1.0	61
116	Effects of Plant Biomass, Plant Diversity, and Water Content on Bacterial Communities in Soil Lysimeters: Implications for the Determinants of Bacterial Diversity. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6916-6929.	1.4	61
117	217 000-year-old DNA sequences of green sulfur bacteria in Mediterranean sapropels and their implications for the reconstruction of the paleoenvironment. <i>Environmental Microbiology</i> , 2007, 9, 238-249.	1.8	91
118	Heterotrophic symbionts of phototrophic consortia: members of a novel diverse cluster of <i>Betaproteobacteria</i> characterized by a tandem operon structure. <i>Environmental Microbiology</i> , 2007, 9, 2782-2794.	1.8	16
119	<i>Chlorobium chlorochromatii</i> sp. nov., a symbiotic green sulfur bacterium isolated from the phototrophic consortium of <i>Chlorochromatium aggregatum</i> ™. <i>Archives of Microbiology</i> , 2006, 185, 363-372.	1.0	45
120	<i>Sandarakinorhabdus limnophila</i> gen. nov., sp. nov., a novel bacteriochlorophyll a-containing, obligately aerobic bacterium isolated from freshwater lakes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 847-854.	0.8	72
121	The <i>puf</i> operon of the purple sulfur bacterium <i>Amoebobacter purpureus</i> : structure, transcription and phylogenetic analysis. <i>Archives of Microbiology</i> , 2005, 183, 431-443.	1.0	9
122	Molecular Characterization of the Nonphotosynthetic Partner Bacterium in the Consortium of <i>Chlorochromatium aggregatum</i> ™. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7434-7441.	1.4	36
123	An obligately photosynthetic bacterial anaerobe from a deep-sea hydrothermal vent. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 9306-9310.	3.3	298
124	Specific Detection, Isolation, and Characterization of Selected, Previously Uncultured Members of the Freshwater Bacterioplankton Community. <i>Applied and Environmental Microbiology</i> , 2005, 71, 5908-5919.	1.4	90
125	Physiology and Phylogeny of Green Sulfur Bacteria Forming a Monospecific Phototrophic Assemblage at a Depth of 100 Meters in the Black Sea. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8049-8060.	1.4	216
126	Biogeography, Evolution, and Diversity of Epibionts in Phototrophic Consortia. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4821-4830.	1.4	37

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127	Photosynthesis Genes and LH1 Proteins of <i>Roseospirillum Parvum</i> 9301, a Purple Non-Sulfur Bacterium with Unusual Spectral Properties. <i>Photosynthesis Research</i> , 2004, 81, 181-199.	1.6	15
128	A new purple sulfur bacterium isolated from a littoral microbial mat, <i>Thiorhodococcus drewsii</i> sp. nov.. <i>Archives of Microbiology</i> , 2003, 179, 174-183.	1.0	37
129	A novel approach for high throughput cultivation assays and the isolation of planktonic bacteria. <i>FEMS Microbiology Ecology</i> , 2003, 45, 161-171.	1.3	60
130	The significance of organic carbon compounds for in situ metabolism and chemotaxis of phototrophic consortia. <i>Environmental Microbiology</i> , 2003, 5, 1053-1063.	1.8	25
131	Effect of Signal Compounds and Incubation Conditions on the Culturability of Freshwater Bacterioplankton. <i>Applied and Environmental Microbiology</i> , 2003, 69, 1980-1989.	1.4	104
132	Characterization and In Situ Carbon Metabolism of Phototrophic Consortia. <i>Applied and Environmental Microbiology</i> , 2003, 69, 3739-3750.	1.4	43
133	Cyclic AMP and Acyl Homoserine Lactones Increase the Cultivation Efficiency of Heterotrophic Bacteria from the Central Baltic Sea. <i>Applied and Environmental Microbiology</i> , 2002, 68, 3978-3987.	1.4	218
134	Phototrophic consortia: model systems for symbiotic interrelations between prokaryotes. <i>Archives of Microbiology</i> , 2002, 177, 201-208.	1.0	80
135	Novel bacteriochlorophyll <i>e</i> structures and species-specific variability of pigment composition in green sulfur bacteria. <i>Archives of Microbiology</i> , 2002, 177, 475-485.	1.0	39
136	A Bacteriochlorophyll <i>a</i> Antenna Complex from Purple Bacteria Absorbing at 963 nm. <i>Biochemistry</i> , 2001, 40, 5573-5578.	1.2	53
137	Detection of abundant sulphate-reducing bacteria in marine oxic sediment layers by a combined cultivation and molecular approach. <i>Environmental Microbiology</i> , 2000, 2, 417-427.	1.8	63
138	Phylogenetic affiliation of the bacteria that constitute phototrophic consortia. <i>Archives of Microbiology</i> , 2000, 174, 50-58.	1.0	38
139	Functional Exoenzymes as Indicators of Metabolically Active Bacteria in 124,000-Year-Old Sapropel Layers of the Eastern Mediterranean Sea. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2589-2598.	1.4	75
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141	Specific detection of green sulfur bacteria by in situ hybridization with a fluorescently labeled oligonucleotide probe. <i>Archives of Microbiology</i> , 1999, 171, 265-272.	1.0	41
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144	The ecological niche of the consortium " <i>Pelochromatium roseum</i> ". <i>Archives of Microbiology</i> , 1998, 169, 120-128.	1.0	46

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145	Physiology and tactic response of the phototrophic consortium " Chlorochromatium aggregatum ". Archives of Microbiology, 1998, 169, 129-135.	1.0	67
146	Phylogeny and molecular fingerprinting of green sulfur bacteria. Archives of Microbiology, 1997, 167, 302-309.	1.0	100
147	An extremely low light adapted phototrophic sulfur bacterium from the Black Sea. Limnology and Oceanography, 1992, 37, 150-155.	1.6	275