List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Differences between Tissue-Associated Intestinal Microfloras of Patients with Crohn's Disease and Ulcerative Colitis. Journal of Clinical Microbiology, 2006, 44, 4136-4141.	1.8	480
2	Competitive and cooperative metabolic interactions in bacterial communities. Nature Communications, 2011, 2, 589.	5.8	413
3	Oscillospira : a Central, Enigmatic Component of the Human Gut Microbiota. Trends in Microbiology, 2016, 24, 523-524.	3.5	413
4	<i>Oscillospira</i> and related bacteria – From metagenomic species to metabolic features. Environmental Microbiology, 2017, 19, 835-841.	1.8	320
5	The large-scale organization of the bacterial network of ecological co-occurrence interactions. Nucleic Acids Research, 2010, 38, 3857-3868.	6.5	259
6	Genotype Is a Stronger Determinant than Sex of the Mouse Gut Microbiota. Microbial Ecology, 2011, 61, 423-428.	1.4	201
7	The evolution of modularity in bacterial metabolic networks. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6976-6981.	3.3	197
8	Bacterial type III secretion systems are ancient and evolved by multiple horizontal-transfer events. Gene, 2003, 312, 151-163.	1.0	192
9	Curli Fibers Mediate Internalization ofEscherichia coli by Eukaryotic Cells. Infection and Immunity, 2001, 69, 2659-2665.	1.0	188
10	The Complexity Hypothesis Revisited: Connectivity Rather Than Function Constitutes a Barrier to Horizontal Gene Transfer. Molecular Biology and Evolution, 2011, 28, 1481-1489.	3.5	187
11	Antibiotic resistance: turning evolutionary principles into clinical reality. FEMS Microbiology Reviews, 2020, 44, 171-188.	3.9	154
12	Gastric microbiota is altered in oesophagitis and <scp>B</scp> arrett's oesophagus and further modified by proton pump inhibitors. Environmental Microbiology, 2014, 16, 2905-2914.	1.8	150
13	Interactions between the intestinal microbiota and bile acids in gallstones patients. Environmental Microbiology Reports, 2015, 7, 874-880.	1.0	142
14	Low Species Barriers in Halophilic Archaea and the Formation of Recombinant Hybrids. Current Biology, 2012, 22, 1444-1448.	1.8	123
15	Harnessing the landscape of microbial culture media to predict new organism–media pairings. Nature Communications, 2015, 6, 8493.	5.8	119
16	No evidence of inhibition of horizontal gene transfer by CRISPR–Cas on evolutionary timescales. ISME Journal, 2015, 9, 2021-2027.	4.4	105
17	Association between translation efficiency and horizontal gene transfer within microbial communities. Nucleic Acids Research, 2011, 39, 4743-4755.	6.5	99
18	Archaea in and on the Human Body: Health Implications and Future Directions. PLoS Pathogens, 2015, 11, e1004833.	2.1	98

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19	By their genes ye shall know them: genomic signatures of predatory bacteria. ISME Journal, 2013, 7, 756-769.	4.4	92
20	Metabolic-network-driven analysis of bacterial ecological strategies. Genome Biology, 2009, 10, R61.	13.9	88
21	The Formation of Escherichia coli Curli Amyloid Fibrils is Mediated by Prion-like Peptide Repeats. Journal of Molecular Biology, 2005, 352, 245-252.	2.0	87
22	The origins of eukaryotic-like proteins in Legionella pneumophila. International Journal of Medical Microbiology, 2010, 300, 470-481.	1.5	86
23	Pouch Inflammation Is Associated With a Decrease in Specific Bacterial Taxa. Gastroenterology, 2015, 149, 718-727.	0.6	80
24	DNA as a Phosphate Storage Polymer and the Alternative Advantages of Polyploidy for Growth or Survival. PLoS ONE, 2014, 9, e94819.	1.1	78
25	Fecal microbiome signatures of pancreatic cancer patients. Scientific Reports, 2019, 9, 16801.	1.6	77
26	Virulence factors of septicemic Escherichia coli strains. International Journal of Medical Microbiology, 2005, 295, 455-462.	1.5	75
27	Extensive Gene Diversity in Septicemic Escherichia coli Strains. Journal of Clinical Microbiology, 2005, 43, 66-73.	1.8	74
28	Complexity, connectivity, and duplicability as barriers to lateral gene transfer. Genome Biology, 2007, 8, R156.	13.9	70
29	A systematic assessment of automated ribosomal intergenic spacer analysis (ARISA) as a tool for estimating bacterial richness. Research in Microbiology, 2010, 161, 192-197.	1.0	70
30	Composition and dynamics of the gill microbiota of an invasive Indoâ€Pacific oyster in the eastern Mediterranean Sea. Environmental Microbiology, 2011, 13, 1467-1476.	1.8	70
31	Role of fibronectin in curli-mediated internalization. FEMS Microbiology Letters, 2002, 212, 55-58.	0.7	68
32	CEACAM1 recognition by bacterial pathogens is species-specific. BMC Microbiology, 2010, 10, 117.	1.3	68
33	Matrix-Assisted Refolding of Single-Chain Fv– Cellulose Binding Domain Fusion Proteins. Protein Expression and Purification, 1999, 17, 249-259.	0.6	67
34	Virulence and the heat shock response. International Journal of Medical Microbiology, 2003, 292, 453-461.	1.5	63
35	In and out: an analysis of epibiotic vs periplasmic bacterial predators. ISME Journal, 2014, 8, 625-635.	4.4	63
36	A Degenerate Type III Secretion System from Septicemic Escherichia coli Contributes to Pathogenesis. Journal of Bacteriology, 2005, 187, 8164-8171.	1.0	62

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37	Detecting Horizontal Gene Transfer between Closely Related Taxa. PLoS Computational Biology, 2015, 11, e1004408.	1.5	60
38	In Vivo Analysis of Various Substrates Utilized by Cystathionine Â-Synthase and O-Acetylhomoserine Sulfhydrylase in Methionine Biosynthesis. Molecular Biology and Evolution, 2003, 20, 1513-1520.	3.5	58
39	Phylogenetic- and genome-derived insight into the evolution of N-glycosylation in Archaea. Molecular Phylogenetics and Evolution, 2013, 68, 327-339.	1.2	53
40	Predominantly Antibiotic-resistant Intestinal Microbiome Persists in Patients With Pouchitis Who Respond to Antibiotic Therapy. Gastroenterology, 2020, 158, 610-624.e13.	0.6	53
41	CRISPR loci reveal networks of gene exchange in archaea. Biology Direct, 2011, 6, 65.	1.9	52
42	Eisenbergiella tayi gen. nov., sp. nov., isolated from human blood. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 907-914.	0.8	51
43	Coordinated change at the colony level in fruit bat fur microbiomes through time. Nature Ecology and Evolution, 2019, 3, 116-124.	3.4	51
44	Evolutionary plasticity of methionine biosynthesis. Gene, 2005, 355, 48-57.	1.0	50
45	Multilocus sequence typing (MLST) ofEscherichia coliO78 strains. FEMS Microbiology Letters, 2003, 222, 199-203.	0.7	49
46	Reconstructing ancestral gene content by coevolution. Genome Research, 2010, 20, 122-132.	2.4	49
47	Weighted Genome Trees: Refinements and Applications. Journal of Bacteriology, 2005, 187, 1305-1316.	1.0	47
48	Ancient lateral gene transfer in the evolution of Bdellovibrio bacteriovorus. Trends in Microbiology, 2006, 14, 64-69.	3.5	45
49	Distinct Microbiotas are Associated with lleum-Restricted and Colon-Involving Crohn's Disease. Inflammatory Bowel Diseases, 2016, 22, 293-302.	0.9	45
50	A likelihood framework to analyse phyletic patterns. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 3903-3911.	1.8	44
51	High tolerance to self-targeting of the genome by the endogenous CRISPR-Cas system in an archaeon. Nucleic Acids Research, 2017, 45, 5208-5216.	6.5	44
52	Cell Surface Glycosylation Is Required for Efficient Mating of Haloferax volcanii. Frontiers in Microbiology, 2017, 8, 1253.	1.5	41
53	Antibiotic Cocktail for Pediatric Acute Severe Colitis and the Microbiome: The PRASCO Randomized Controlled Trial. Inflammatory Bowel Diseases, 2020, 26, 1733-1742.	0.9	41
54	Cell fusion and hybrids in Archaea. Bioengineered, 2013, 4, 126-129.	1.4	40

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55	Homing endonucleases residing within inteins: evolutionary puzzles awaiting genetic solutions. Biochemical Society Transactions, 2011, 39, 169-173.	1.6	38
56	The correlation between Clostridium-difficile infection and human gut concentrations of Bacteroidetes phylum and clostridial species. European Journal of Clinical Microbiology and Infectious Diseases, 2014, 33, 377-383.	1.3	38
57	Have archaeal genes contributed to bacterial virulence?. Trends in Microbiology, 2004, 12, 213-219.	3.5	37
58	Extracellular DNA metabolism in Haloferax volcanii. Frontiers in Microbiology, 2014, 5, 57.	1.5	37
59	An Evolutionary Analysis of Lateral Gene Transfer in Thymidylate Synthase Enzymes. Systematic Biology, 2010, 59, 212-225.	2.7	36
60	Carriage of Colibactin-producing Bacteria and Colorectal Cancer Risk. Trends in Microbiology, 2020, 28, 874-876.	3.5	36
61	Glycan Degradation (GlyDeR) Analysis Predicts Mammalian Gut Microbiota Abundance and Host Diet-Specific Adaptations. MBio, 2014, 5, .	1.8	35
62	The gill microbiota of invasive and indigenous <i>Spondylus</i> oysters from the Mediterranean Sea and northern Red Sea. Environmental Microbiology Reports, 2015, 7, 860-867.	1.0	34
63	Impact of a homing intein on recombination frequency and organismal fitness. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4654-61.	3.3	33
64	The Guts of Dietary Habits. Science, 2011, 334, 45-46.	6.0	32
65	Decoupling Environment-Dependent and Independent Genetic Robustness across Bacterial Species. PLoS Computational Biology, 2010, 6, e1000690.	1.5	31
66	Contribution of lateral gene transfer to the gene repertoire of a gut-adapted methanogen. Genomics, 2012, 99, 52-58.	1.3	31
67	A Novel Nutritional Predictor Links Microbial Fastidiousness with Lowered Ubiquity, Growth Rate, and Cooperativeness. PLoS Computational Biology, 2014, 10, e1003726.	1.5	31
68	Pervasive acquisition of CRISPR memory driven by inter-species mating of archaea can limit gene transfer and influence speciation. Nature Microbiology, 2019, 4, 177-186.	5.9	30
69	The nuts and bolts of the <i>Haloferax</i> CRISPR-Cas system I-B. RNA Biology, 2019, 16, 469-480.	1.5	29
70	Alterations of Enteric Microbiota in Patients with a Normal Ileal Pouch Are Predictive of Pouchitis. Journal of Crohn's and Colitis, 2017, 11, 314-320.	0.6	28
71	Native homing endonucleases can target conserved genes in humans and in animal models. Nucleic Acids Research, 2011, 39, 6646-6659.	6.5	27
72	The Escherichia coli Type III Secretion System 2 Has a Global Effect on Cell Surface. MBio, 2018, 9, .	1.8	27

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73	A Genetic Investigation of the KEOPS Complex in Halophilic Archaea. PLoS ONE, 2012, 7, e43013.	1.1	26
74	The operon of invasive. International Journal of Medical Microbiology, 2005, 295, 227-236.	1.5	25
75	The Ubiquitous Conserved Glycopeptidase Gcp Prevents Accumulation of Toxic Glycated Proteins. MBio, 2010, 1, .	1.8	23
76	Menaquinone and Iron Are Essential for Complex Colony Development in Bacillus subtilis. PLoS ONE, 2013, 8, e79488.	1.1	23
77	Competition between social cheater viruses is driven by mechanistically different cheating strategies. Science Advances, 2020, 6, .	4.7	23
78	Effect of Maternal Diet and Milk Lipid Composition on the Infant Gut and Maternal Milk Microbiomes. Nutrients, 2020, 12, 2539.	1.7	23
79	Sequence Features of E. coli mRNAs Affect Their Degradation. PLoS ONE, 2011, 6, e28544.	1.1	22
80	Phylo SI: a new genome-wide approach for prokaryotic phylogeny. Nucleic Acids Research, 2014, 42, 2391-2404.	6.5	22
81	Genomics-based epidemiology of bovine Mycoplasma bovis strains in Israel. BMC Genomics, 2020, 21, 70.	1.2	22
82	A novel ColV plasmid encoding type IV pili. Microbiology (United Kingdom), 2003, 149, 177-184.	0.7	21
83	Neutrality of Foreign Complex Subunits in an Experimental Model of Lateral Gene Transfer. Molecular Biology and Evolution, 2008, 25, 1835-1840.	3.5	21
84	Lateral acquisition of genes is affected by the friendliness of their products. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 343-348.	3.3	21
85	Computational evaluation of cellular metabolic costs successfully predicts genes whose expression is deleterious. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19166-19171.	3.3	21
86	Comparative Analysis of Surface Layer Glycoproteins and Genes Involved in Protein Glycosylation in the Genus Haloferax. Genes, 2018, 9, 172.	1.0	20
87	The Evolutionary Origins of Extreme Halophilic Archaeal Lineages. Genome Biology and Evolution, 2021, 13, .	1.1	20
88	Systems-Wide Prediction of Enzyme Promiscuity Reveals a New Underground Alternative Route for Pyridoxal 5'-Phosphate Production in E. coli. PLoS Computational Biology, 2016, 12, e1004705.	1.5	20
89	A halocin-H4 mutant Haloferax mediterranei strain retains the ability to inhibit growth of other halophilic archaea. Extremophiles, 2013, 17, 973-979.	0.9	19
90	Dysbiosis in Metabolic Genes of the Gut Microbiomes of Patients with an Ileo-anal Pouch Resembles That Observed in Crohn's Disease. MSystems, 2021, 6, .	1.7	19

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91	In Vivo Characterization of the Homing Endonuclease within the polB Gene in the Halophilic Archaeon Haloferax volcanii. PLoS ONE, 2011, 6, e15833.	1.1	18
92	Community structure dynamics during startup in microbial fuel cells – The effect of phosphate concentrations. Bioresource Technology, 2016, 212, 151-159.	4.8	18
93	Direct sequencing of RNA with MinION Nanopore: detecting mutations based on associations. Nucleic Acids Research, 2019, 47, e148.	6.5	18
94	OmpA of a septicemic Escherichia coli O78 – secretion and convergent evolution. International Journal of Medical Microbiology, 2004, 294, 373-381.	1.5	17
95	The contribution of common rpsL mutations in Escherichia coli to sensitivity to ribosome targeting antibiotics. International Journal of Medical Microbiology, 2013, 303, 558-562.	1.5	16
96	Pandemic Bacteremic Escherichia Coli Strains: Evolution and Emergence of Drug-Resistant Pathogens. Current Topics in Microbiology and Immunology, 2018, 416, 163-180.	0.7	16
97	The Effect of Density-Dependent Phase on the Locust Gut Bacterial Composition. Frontiers in Microbiology, 2018, 9, 3020.	1.5	15
98	Locust Bacterial Symbionts: An Update. Insects, 2020, 11, 655.	1.0	15
99	Horizontal Gene Transfer in Archaea—From Mechanisms to Genome Evolution. Annual Review of Microbiology, 2022, 76, 481-502.	2.9	15
100	Complex Histories of Genes Encoding 3-Hydroxy-3-methylglutaryl-CoenzymeA Reductase. Molecular Biology and Evolution, 2006, 23, 168-178.	3.5	14
101	Extensive inter-domain lateral gene transfer in the evolution of the human commensal Methanosphaera stadtmanae. Frontiers in Genetics, 2012, 3, 182.	1.1	14
102	The gut microbiota of tollâ€like receptor 2â€deficient mice exhibits lineageâ€specific modifications. Environmental Microbiology Reports, 2009, 1, 65-70.	1.0	13
103	Finally, Archaea Get Their CRISPR-Cas Toolbox. Trends in Microbiology, 2017, 25, 430-432.	3.5	13
104	Integration of a Foreign Gene into a Native Complex Does Not Impair Fitness in an Experimental Model of Lateral Gene Transfer. Molecular Biology and Evolution, 2010, 27, 2441-2445.	3.5	11
105	The Associations between Diet and Socioeconomic Disparities and the Intestinal Microbiome in Preadolescence. Nutrients, 2021, 13, 2645.	1.7	11
106	Detection of Spatial and Temporal Influences on Bacterial Communities in an Urban Stream by Automated Ribosomal Intergenic Ribosomal Spacer Analysis. Microbes and Environments, 2011, 26, 360-366.	0.7	10
107	Fine-Scale Temporal Dynamics of a Fragmented Lotic Microbial Ecosystem. Scientific Reports, 2012, 2, 207.	1.6	10
108	Alteration in Urease-producing Bacteria in the Gut Microbiomes of Patients with Inflammatory Bowel Diseases. Journal of Crohn's and Colitis, 2021, 15, 2066-2077.	0.6	10

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109	Parity and disparity between two <i>Chama</i> oysters: the reproductive biology of the Indoâ€Pacific <i>C.Âpacifica</i> Broderip, invasive to the Mediterranean Sea; and <i>C.Âsavignyi</i> Lamy, indigenous to the Red Sea. Marine Ecology, 2012, 33, 261-271.	0.4	9
110	Maximal Sum of Metabolic Exchange Fluxes Outperforms Biomass Yield as a Predictor of Growth Rate of Microorganisms. PLoS ONE, 2014, 9, e98372.	1.1	9
111	Escherichia coli isolates from patients with bacteremic urinary tract infection are genetically distinct from those derived from sepsis following prostate transrectal biopsy. International Journal of Medical Microbiology, 2015, 305, 464-468.	1.5	9
112	Starch Consumption May Modify Antiglycan Antibodies and Fecal Fungal Composition in Patients With Ileo-Anal Pouch. Inflammatory Bowel Diseases, 2019, 25, 742-749.	0.9	9
113	Anode Surface Bioaugmentation Enhances Deterministic Biofilm Assembly in Microbial Fuel Cells. MBio, 2021, 12, .	1.8	9
114	Sexually Transmitted Escherichia coli Urethritis and Orchiepididymitis. Sexually Transmitted Diseases, 2012, 39, 16-17.	0.8	8
115	Effect of ribosome-targeting antibiotics on streptomycin-resistant Mycobacterium mutants in the rpsL gene. International Journal of Antimicrobial Agents, 2013, 42, 129-132.	1.1	8
116	Cis-regulatory evolution in prokaryotes revealed by interspecific archaeal hybrids. Scientific Reports, 2017, 7, 3986.	1.6	8
117	Insights into gene expression changes under conditions that facilitate horizontal gene transfer (mating) of a model archaeon. Scientific Reports, 2020, 10, 22297.	1.6	8
118	CRISPR/Cas systems in archaea. Mobile Genetic Elements, 2012, 2, 63-64.	1.8	7
119	Ribosomal mutations affecting the translation of genes that use nonâ€optimal codons. FEBS Journal, 2014, 281, 3701-3718.	2.2	7
120	Socioeconomic disparities and household crowding in association with the fecal microbiome of school-age children. Npj Biofilms and Microbiomes, 2022, 8, 10.	2.9	7
121	Deriving enzymatic and taxonomic signatures of metagenomes from short read data. BMC Bioinformatics, 2010, 11, 390.	1.2	6
122	Adaptation induced by self-targeting in a type I-B CRISPR-Cas system. Journal of Biological Chemistry, 2020, 295, 13502-13515.	1.6	6
123	Dynamics of bacterial composition in the locust reproductive tract are affected by the density-dependent phase. FEMS Microbiology Ecology, 2020, 96, .	1.3	6
124	Long-term Antibiotic Treatment in Pouchitis—Patterns of Use and Safety. Inflammatory Bowel Diseases, 2022, 28, 1027-1033.	0.9	6
125	Analysis of Coevolving Gene Families Using Mutually Exclusive Orthologous Modules. Genome Biology and Evolution, 2011, 3, 413-423.	1.1	5
126	Protein Splicing Activity of the Haloferax volcanii PolB-c Intein Is Sensitive to Homing Endonuclease Domain Mutations. Biochemistry, 2020, 59, 3359-3367.	1.2	5

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127	<i>Escherichia coli</i> Strains from Patients with Inflammatory Bowel Diseases have Disease-specific Genomic Adaptations. Journal of Crohn's and Colitis, 2022, 16, 1584-1597.	0.6	5
128	In situ transplant analysis of free-living bacteria in a lotic ecosystem. Research in Microbiology, 2013, 164, 262-269.	1.0	4
129	Specific Changes in the Mammalian Gut Microbiome as a Biomarker for Oxytocin-Induced Behavioral Changes. Microorganisms, 2021, 9, 1938.	1.6	4
130	The unbearable ease of expression—how avoidance of spurious transcription can shape G+C content in bacterial genomes. FEMS Microbiology Letters, 2018, 365, .	0.7	3
131	Specific Desulfuromonas Strains Can Determine Startup Times of Microbial Fuel Cells. Applied Sciences (Switzerland), 2020, 10, 8570.	1.3	3
132	The maternal foam plug constitutes a reservoir for the desert locust's bacterial symbionts. Environmental Microbiology, 2021, 23, 2461-2472.	1.8	3
133	Repeat modularity as a beneficial property of multiple CRISPR-Cas systems. RNA Biology, 2019, 16, 585-587.	1.5	3
134	The impact of Mediterranean diet on coronary plaque vulnerability, microvascular function, inflammation and microbiome after an acute coronary syndrome: study protocol for the MEDIMACS randomized, controlled, mechanistic clinical trial. Trials, 2021, 22, 795.	0.7	3
135	Microbiomeâ€related aspects of locust densityâ€dependent phase transition. Environmental Microbiology, 2022, 24, 507-516.	1.8	3
136	Can Colonoscopy Aspirates be a Substitute for Fecal Samples in Analyses of the Intestinal Microbiota?. Bioscience of Microbiota, Food and Health, 2012, 31, 71-76.	0.8	2
137	The Complexity Hypothesis and Other Connectivity Barriers to Lateral Gene Transfer. , 2013, , 137-145.		2
138	Complexity Apparently Is Not a Barrier to Lateral Gene Transfers. Microbe Magazine, 2009, 4, 549-553.	0.4	2
139	Lateral Gene Transfer and the Synthesis of Thymidine. , 2013, , 3-14.		1
140	Reply to Antibiotic Use Patterns in the Management of Chronic Pouchitis. Inflammatory Bowel Diseases, 2022, , .	0.9	1
141	Investigating a lotic microbial community following a severe detergent spill. Archives of Microbiology, 2014, 196, 119-124.	1.0	0
142	Reply. Inflammatory Bowel Diseases, 2016, 22, E15-E16.	0.9	0
143	Reply. Gastroenterology, 2020, 159, 401-402.	0.6	0
144	Reviewing the right papers. FEMS Microbiology Letters, 2020, 367, .	0.7	0

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145	Intestinal Microbiota and Intestinal Disease: Inflammatory Bowel Diseases. , 2012, , 223-230.		0