Nicola Segata

List of Publications by Year
in descending order

164 papers	67,502 citations	8181 76 h-index	4885 168 g-index
199 all docs	199 docs citations	199 times ranked	59480 citing authors

#	Article	IF	Citations
1	Metagenomic biomarker discovery and explanation. Genome Biology, 2011, 12, R60.	9.6	11,192
2	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
3	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	27.8	9,614
4	A framework for human microbiome research. Nature, 2012, 486, 215-221.	27.8	2,249
5	MetaPhlAn2 for enhanced metagenomic taxonomic profiling. Nature Methods, 2015, 12, 902-903.	19.0	1,843
6	Metagenomic microbial community profiling using unique clade-specific marker genes. Nature Methods, 2012, 9, 811-814.	19.0	1,591
7	Expansion of intestinal Prevotella copri correlates with enhanced susceptibility to arthritis. ELife, 2013, 2, e01202.	6.0	1,507
8	Microbial Co-occurrence Relationships in the Human Microbiome. PLoS Computational Biology, 2012, 8, e1002606.	3.2	1,268
9	Shotgun metagenomics, from sampling to analysis. Nature Biotechnology, 2017, 35, 833-844.	17.5	1,196
10	Species-level functional profiling of metagenomes and metatranscriptomes. Nature Methods, 2018, 15, 962-968.	19.0	1,125
11	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. Cell, 2019, 176, 649-662.e20.	28.9	1,087
12	Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. PLoS Computational Biology, 2012, 8, e1002358.	3.2	939
13	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. Cell Host and Microbe, 2018, 24, 133-145.e5.	11.0	822
14	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. ELife, 2021, 10, .	6.0	808
15	Composition of the adult digestive tract bacterial microbiome based on seven mouth surfaces, tonsils, throat and stool samples. Genome Biology, 2012, 13, R42.	9.6	797
16	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. Nature Communications, 2013, 4, 2304.	12.8	797
17	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. Nature Medicine, 2019, 25, 679-689.	30.7	734
18	Compact graphical representation of phylogenetic data and metadata with GraPhlAn. PeerJ, 2015, 3, e1029.	2.0	701

#	ARTICLE	IF	CITATIONS
19	A unified catalog of 204,938 reference genomes from the human gut microbiome. Nature Biotechnology, 2021, 39, 105-114.	17.5	628
20	Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. Nature Medicine, 2019, 25, 667-678.	30.7	602
21	A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy. PLoS ONE, 2012, 7, e36466.	2.5	572
22	Relating the metatranscriptome and metagenome of the human gut. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2329-38.	7.1	552
23	Microbial strain-level population structure and genetic diversity from metagenomes. Genome Research, 2017, 27, 626-638.	5.5	540
24	Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. Nature Medicine, 2021, 27, 321-332.	30.7	477
25	A Guide to Enterotypes across the Human Body: Meta-Analysis of Microbial Community Structures in Human Microbiome Datasets. PLoS Computational Biology, 2013, 9, e1002863.	3.2	446
26	Machine Learning Meta-analysis of Large Metagenomic Datasets: Tools and Biological Insights. PLoS Computational Biology, 2016, 12, e1004977.	3.2	434
27	Human postprandial responses to food and potential for precision nutrition. Nature Medicine, 2020, 26, 964-973.	30.7	418
28	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. Nature Communications, 2020, 11, 2500.	12.8	368
29	Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. ISME Journal, 2014, 8, 1403-1417.	9.8	352
30	Studying Vertical Microbiome Transmission from Mothers to Infants by Strain-Level Metagenomic Profiling. MSystems, 2017, 2, .	3.8	329
31	Strain-level microbial epidemiology and population genomics from shotgun metagenomics. Nature Methods, 2016, 13, 435-438.	19.0	328
32	SARS-CoV-2 from faeces to wastewater treatment: What do we know? A review. Science of the Total Environment, 2020, 743, 140444.	8.0	321
33	Strain-Level Analysis of Mother-to-Child Bacterial Transmission during the First Few Months of Life. Cell Host and Microbe, 2018, 24, 146-154.e4.	11.0	311
34	Accessible, curated metagenomic data through ExperimentHub. Nature Methods, 2017, 14, 1023-1024.	19.0	292
35	The Prevotella copri Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. Cell Host and Microbe, 2019, 26, 666-679.e7.	11.0	274
36	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. Nature Communications, 2020, 11, 6389.	12.8	269

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37	Computational meta'omics for microbial community studies. Molecular Systems Biology, 2013, 9, 666.	7.2	253
38	Endogenous murine microbiota member Faecalibaculum rodentium and its human homologue protect from intestinal tumour growth. Nature Microbiology, 2020, 5, 511-524.	13.3	248
39	Prevotella diversity, niches and interactions with the human host. Nature Reviews Microbiology, 2021, 19, 585-599.	28.6	248
40	Selective maternal seeding and environment shape the human gut microbiome. Genome Research, 2018, 28, 561-568.	5.5	247
41	bioBakery: a metaâ€™omic analysis environment. Bioinformatics, 2018, 34, 1235-1237.	4.1	241
42	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. Microbiome, 2017, 5, 66.	11.1	240
43	High-Specificity Targeted Functional Profiling in Microbial Communities with ShortBRED. PLoS Computational Biology, 2015, 11, e1004557.	3.2	235
44	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. Scientific Reports, 2015, 5, 15782.	3.3	233
45	Distinct Genetic and Functional Traits of Human Intestinal Prevotella copri Strains Are Associated with Different Habitual Diets. Cell Host and Microbe, 2019, 25, 444-453.e3.	11.0	229
46	Intestinal Akkermansia muciniphila predicts clinical response to PD-1 blockade in patients with advanced non-small-cell lung cancer. Nature Medicine, 2022, 28, 315-324.	30.7	225
47	Building essential biodiversity variables (<scp>EBV</scp>s) of species distribution and abundance at a global scale. Biological Reviews, 2018, 93, 600-625.	10.4	218
48	Cross-reactivity between tumor MHC class Iâ€"restricted antigens and an enterococcal bacteriophage. Science, 2020, 369, 936-942.	12.6	217
49	Biodiversity and functional genomics in the human microbiome. Trends in Genetics, 2013, 29, 51-58.	6.7	207
50	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature Communications, 2019, 10, 5477.	12.8	197
51	Gut Bacteria Composition Drives Primary Resistance to Cancer Immunotherapy in Renal Cell Carcinoma Patients. European Urology, 2020, 78, 195-206.	1.9	192
52	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. Applied and Environmental Microbiology, 2015, 81, 7078-7087.	3.1	191
53	Large-scale genome-wide analysis links lactic acid bacteria from food with the gut microbiome. Nature Communications, 2020, 11, 2610.	12.8	190
54	Genomic characterization of Nontuberculous Mycobacteria. Scientific Reports, 2017, 7, 45258.	3.3	176

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55	The Genome of Th17 Cell-Inducing Segmented Filamentous Bacteria Reveals Extensive Auxotrophy and Adaptations to the Intestinal Environment. Cell Host and Microbe, 2011, 10, 260-272.	11.0	175
56	Gut vascular barrier impairment leads to intestinal bacteria dissemination and colorectal cancer metastasis to liver. Cancer Cell, 2021, 39, 708-724.e11.	16.8	175
57	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
58	Gut Microbiome: Westernization and the Disappearance of Intestinal Diversity. Current Biology, 2015, 25, R611-R613.	3.9	169
59	Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis. Npj Biofilms and Microbiomes, 2017, 3, 14.	6.4	159
60	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. Nature Medicine, 2022, 28, 535-544.	30.7	158
61	Metagenomic Sequencing with Strain-Level Resolution Implicates Uropathogenic E.Âcoli in Necrotizing Enterocolitis and Mortality in Preterm Infants. Cell Reports, 2016, 14, 2912-2924.	6.4	143
62	Ketogenic diet and ketone bodies enhance the anticancer effects of PD-1 blockade. JCI Insight, 2021, 6, .	5.0	143
63	Evidence of natural Wolbachia infections in field populations of Anopheles gambiae. Nature Communications, 2014, 5, 3985.	12.8	142
64	Reconstruction of ancient microbial genomes from the human gut. Nature, 2021, 594, 234-239.	27.8	139
65	Large-scale comparative metagenomics of <i>Blastocystis</i>, a common member of the human gut microbiome. ISME Journal, 2017, 11, 2848-2863.	9.8	136
66	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
67	The new phylogeny of the genus Mycobacterium : The old and the news. Infection, Genetics and Evolution, 2017, 56, 19-25.	2.3	128
68	On the Road to Strain-Resolved Comparative Metagenomics. MSystems, 2018, 3, .	3.8	119
69	Microbiota-gut brain axis involvement in neuropsychiatric disorders. Expert Review of Neurotherapeutics, 2019, 19, 1037-1050.	2.8	116
70	Distinct Polysaccharide Utilization Profiles of Human Intestinal Prevotella copri Isolates. Cell Host and Microbe, 2019, 26, 680-690.e5.	11.0	115
71	Neonatal antibiotic exposure impairs child growth during the first six years of life by perturbing intestinal microbial colonization. Nature Communications, 2021, 12, 443.	12.8	113
72	Multiple levels of the unknown in microbiome research. BMC Biology, 2019, 17, 48.	3.8	101

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73	The reproductive tracts of two malaria vectors are populated by a core microbiome and by gender- and swarm-enriched microbial biomarkers. Scientific Reports, 2016, 6, 24207.	3.3	93
74	Microbial community function and biomarker discovery in the human microbiome. Genome Biology, 2011, 12, .	9.6	89
75	MetaMLST: multi-locus strain-level bacterial typing from metagenomic samples. Nucleic Acids Research, 2017, 45, e7-e7.	14.5	88
76	Toward an Efficient Method of Identifying Core Genes for Evolutionary and Functional Microbial Phylogenies. PLoS ONE, 2011, 6, e24704.	2.5	86
77	Blue poo: impact of gut transit time on the gut microbiome using a novel marker. Gut, 2021, 70, 1665-1674.	12.1	84
78	Faecal microbiota transplantation for the treatment of diarrhoea induced by tyrosine-kinase inhibitors in patients with metastatic renal cell carcinoma. Nature Communications, 2020, 11, 4333.	12.8	82
79	Large-Scale Phylogenomics of the <i>Lactobacillus casei</i> Group Highlights Taxonomic Inconsistencies and Reveals Novel Clade-Associated Features. MSystems, 2017, 2, .	3.8	79
80	Effect of Gluten-Free Diet on Gut Microbiota Composition in Patients with Celiac Disease and Non-Celiac Gluten/Wheat Sensitivity. Nutrients, 2020, 12, 1832.	4.1	75
81	Analysis of 1321 Eubacterium rectale genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. Genome Biology, 2020, 21, 138.	8.8	72
82	Intestinal microbiota influences clinical outcome and side effects of early breast cancer treatment. Cell Death and Differentiation, 2021, 28, 2778-2796.	11.2	72
83	Evaluation of bifidobacterial community composition in the human gut by means of a targeted amplicon sequencing (ITS) protocol. FEMS Microbiology Ecology, 2014, 90, n/a-n/a.	2.7	71
84	Large scale genome reconstructions illuminate Wolbachia evolution. Nature Communications, 2020, 11, 5235.	12.8	71
85	Detecting contamination in viromes using ViromeQC. Nature Biotechnology, 2019, 37, 1408-1412.	17.5	69
86	Uncovering oral Neisseria tropism and persistence using metagenomic sequencing. Nature Microbiology, 2016, 1, 16070.	13.3	68
87	Genomic diversity and ecology of human-associated Akkermansia species in the gut microbiome revealed by extensive metagenomic assembly. Genome Biology, 2021, 22, 209.	8.8	65
88	Altered Fecal Small RNA Profiles in Colorectal Cancer Reflect Gut Microbiome Composition in Stool Samples. MSystems, 2019, 4, .	3.8	59
89	Longitudinal survey of microbiome associated with particulate matter in a megacity. Genome Biology, 2020, 21, 55.	8.8	59
90	Microbial genomes from non-human primate gut metagenomes expand the primate-associated bacterial tree of life with over 1000 novel species. Genome Biology, 2019, 20, 299.	8.8	58

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91	Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of Staphylococcus aureus strains in a paediatric hospital. Genome Medicine, 2018, 10, 82.	8.2	54
92	Strong oral plaque microbiome signatures for dental implant diseases identified by strain-resolution metagenomics. Npj Biofilms and Microbiomes, 2020, 6, 47.	6.4	54
93	MetaRef: a pan-genomic database for comparative and community microbial genomics. Nucleic Acids Research, 2014, 42, D617-D624.	14.5	51
94	Noise reduction for instance-based learning with a local maximal margin approach. Journal of Intelligent Information Systems, 2010, 35, 301-331.	3.9	44
95	Cancer Induces a Stress Ileopathy Depending on Î²-Adrenergic Receptors and Promoting Dysbiosis that Contributes to Carcinogenesis. Cancer Discovery, 2022, 12, 1128-1151.	9.4	44
96	Meal-induced inflammation: postprandial insights from the Personalised REsponses to DIetary Composition Trial (PREDICT) study in 1000 participants. American Journal of Clinical Nutrition, 2021, 114, 1028-1038.	4.7	43
97	Genomic and metagenomic insights into the microbial community of a thermal spring. Microbiome, 2019, 7, 8.	11.1	40
98	A Different Microbiome Gene Repertoire in the Airways of Cystic Fibrosis Patients with Severe Lung Disease. International Journal of Molecular Sciences, 2017, 18, 1654.	4.1	39
99	Stool microRNA profiles reflect different dietary and gut microbiome patterns in healthy individuals. Gut, 2022, 71, 1302-1314.	12.1	39
100	Sociodemographic variation in the oral microbiome. Annals of Epidemiology, 2019, 35, 73-80.e2.	1.9	37
101	The short-term impact of probiotic consumption on the oral cavity microbiome. Scientific Reports, 2018, 8, 10476.	3.3	36
102	Enhanced microbial diversity in the saliva microbiome induced by short-term probiotic intake revealed by 16S rRNA sequencing on the IonTorrent PGM platform. Journal of Biotechnology, 2014, 190, 30-39.	3.8	34
103	Experimental metagenomics and ribosomal profiling of the human skin microbiome. Experimental Dermatology, 2017, 26, 211-219.	2.9	34
104	Expression Profiling of Archival Tumors for Long-term Health Studies. Clinical Cancer Research, 2012, 18, 6136-6146.	7.0	32
105	Variation and transmission of the human gut microbiota across multiple familial generations. Nature Microbiology, 2022, 7, 87-96.	13.3	32
106	Two-stage microbial community experimental design. ISME Journal, 2013, 7, 2330-2339.	9.8	31
107	Characterization of 17 strains belonging to the Mycobacterium simiae complex and description of Mycobacterium paraense sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 656-662.	1.7	31
108	HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. American Journal of Epidemiology, 2019, 188, 1023-1026.	3.4	30

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109	High intake of vegetables is linked to lower white blood cell profile and the effect is mediated by the gut microbiome. BMC Medicine, 2021, 19, 37.	5.5	30
110	Sulfoquinovose is a select nutrient of prominent bacteria and a source of hydrogen sulfide in the human gut. ISME Journal, 2021, 15, 2779-2791.	9.8	30
111	Profiling microbial strains in urban environments using metagenomic sequencing data. Biology Direct, 2018, 13, 9.	4.6	29
112	Impact of insufficient sleep on dysregulated blood glucose control under standardised meal conditions. Diabetologia, 2022, 65, 356-365.	6.3	29
113	How inoculation affects the development and the performances of microalgal-bacterial consortia treating real municipal wastewater. Journal of Environmental Management, 2020, 263, 110427.	7.8	28
114	Tobacco exposure associated with oral microbiota oxygen utilization in the New York City Health and Nutrition Examination Study. Annals of Epidemiology, 2019, 34, 18-25.e3.	1.9	27
115	Host and gut microbiota symbiotic factors: lessons from inflammatory bowel disease and successful symbionts. Cellular Microbiology, 2011, 13, 508-517.	2.1	25
116	Profiling instances in noise reduction. Knowledge-Based Systems, 2012, 31, 28-40.	7.1	25
117	Untargeted Metagenomic Investigation of the Airway Microbiome of Cystic Fibrosis Patients with Moderate-Severe Lung Disease. Microorganisms, 2020, 8, 1003.	3.6	23
118	Immune system and intestinal microbiota determine efficacy of androgen deprivation therapy against prostate cancer. , 2022, 10, e004191.		23
119	Methicillin-resistant Staphylococcus aureus eradication in cystic fibrosis patients: A randomized multicenter study. PLoS ONE, 2019, 14, e0213497.	2.5	22
120	Trial watch : the gut microbiota as a tool to boost the clinical efficacy of anticancer immunotherapy. OncoImmunology, 2020, 9, 1774298.	4.6	22
121	Gut microbiome diversity and composition is associated with hypertension in women. Journal of Hypertension, 2021, 39, 1810-1816.	0.5	22
122	Hallstatt miners consumed blue cheese and beer during the Iron Age and retained a non-Westernized gut microbiome until the Baroque period. Current Biology, 2021, 31, 5149-5162.e6.	3.9	22
123	Clinical populations of Pseudomonas aeruginosa isolated from acute infections show a wide virulence range partially correlated with population structure and virulence gene expression. Microbiology (United Kingdom), 2012, 158, 2089-2098.	1.8	21
124	Dental Implants with Anti-Biofilm Properties: A Pilot Study for Developing a New Sericin-Based Coating. Materials, 2019, 12, 2429.	2.9	21
125	Keyphrases Extraction from Scientific Documents: Improving Machine Learning Approaches with Natural Language Processing. Lecture Notes in Computer Science, 2010, , 102-111.	1.3	21
126	Closely related Lak megaphages replicate in the microbiomes of diverse animals. IScience, 2021, 24, 102875.	4.1	20

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127	Fast Local Support Vector Machines for Large Datasets. Lecture Notes in Computer Science, 2009, , 295-310.	1.3	19
128	Simultaneous Quantification of Multiple Bacteria by the BactoChip Microarray Designed to Target Species-Specific Marker Genes. PLoS ONE, 2013, 8, e55764.	2.5	18
129	Multifaceted modes of action of the anticancer probiotic Enterococcus hirae. Cell Death and Differentiation, 2021, 28, 2276-2295.	11.2	18
130	Metagenomic analysis of ancient dental calculus reveals unexplored diversity of oral archaeal Methanobrevibacter. Microbiome, 2021, 9, 197.	11.1	18
131	Considerations for the design and conduct of human gut microbiota intervention studies relating to foods. European Journal of Nutrition, 2020, 59, 3347-3368.	3.9	17
132	Metagenomic and metabolomic remodeling in nonagenarians and centenarians and its association with genetic and socioeconomic factors. Nature Aging, 2022, 2, 438-452.	11.6	17
133	Shed Light in the DaRk LineagES of the Fungal Tree of Life—STRES. Life, 2020, 10, 362.	2.4	16
134	Phylogenomics of Opsin Genes in Diptera Reveals Lineage-Specific Events and Contrasting Evolutionary Dynamics in <i>Anopheles</i> and <i>Drosophila</i>. Genome Biology and Evolution, 2021, 13, .	2.5	16
135	Consumer Safety Considerations of Skin and Oral Microbiome Perturbation. Clinical Microbiology Reviews, 2019, 32, .	13.6	15
136	The Microbe Directory: An annotated, searchable inventory of microbes' characteristics. Gates Open Research, 2018, 2, 3.	1.1	15
137	No bacteria found in healthy placentas. Nature, 2019, 572, 317-318.	27.8	13
138	Initial exploration of in utero microbial colonization. Nature Medicine, 2020, 26, 469-470.	30.7	12
139	Microbiome as Mediator of Diet on Colorectal Cancer Risk: The Role of Vitamin D, Markers of Inflammation and Adipokines. Nutrients, 2021, 13, 363.	4.1	11
140	Next steps after 15 stimulating years of human gut microbiome research. Microbial Biotechnology, 2022, 15, 164-175.	4.2	11
141	Local SVM approaches for fast and accurate classification of remote-sensing images. International Journal of Remote Sensing, 2012, 33, 6186-6201.	2.9	10
142	Long-adapter single-strand oligonucleotide probes for the massively multiplexed cloning of kilobase genome regions. Nature Biomedical Engineering, 2017, 1, .	22.5	10
143	Over-celling fetal microbial exposure. Cell, 2021, 184, 5839-5841.	28.9	10
144	Commensal Bifidobacterium Strains Enhance the Efficacy of Neo-Epitope Based Cancer Vaccines. Vaccines, 2021, 9, 1356.	4.4	10

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145	A Scalable Noise Reduction Technique for Large Case-Based Systems. Lecture Notes in Computer Science, 2009, , 328-342.	1.3	9
146	Recent genetic exchanges and admixture shape the genome and population structure of the zoonotic pathogen <i>Cryptosporidium parvum</i>. Molecular Ecology, 2023, 32, 2633-2645.	3.9	9
147	Outer Membrane Vesicles From The Gut Microbiome Contribute to Tumor Immunity by Eliciting Cross-Reactive T Cells. Frontiers in Oncology, 0, 12, .	2.8	8
148	Genes Encoding Microbial Acyl Coenzyme A Binding Protein/Diazepam-Binding Inhibitor Orthologs Are Rare in the Human Gut Microbiome and Show No Links to Obesity. Applied and Environmental Microbiology, 2021, 87, e0047121.	3.1	7
149	Lung and Gut Microbiota Changes Associated with Pseudomonas aeruginosa Infection in Mouse Models of Cystic Fibrosis. International Journal of Molecular Sciences, 2021, 22, 12169.	4.1	7
150	Operators for transforming kernels into quasi-local kernels that improve SVM accuracy. Journal of Intelligent Information Systems, 2011, 37, 155-186.	3.9	6
151	Genome Sequence of Pseudomonas aeruginosa PA45, a Highly Virulent Strain Isolated from a Patient with Bloodstream Infection. Genome Announcements, 2013, 1, .	0.8	6
152	Draft Genome Sequence of the Planktic Cyanobacterium Tychonema bourrellyi, Isolated from Alpine Lentic Freshwater. Genome Announcements, 2017, 5, .	0.8	6
153	Computational Tools for Taxonomic Microbiome Profiling of Shotgun Metagenomes. , 2015, , 67-80.		5
154	Draft Genome Sequence of the Cadmium-Resistant Strain JJU2, Belonging to the Family Hapalosiphonaceae of the Cyanobacteria. Microbiology Resource Announcements, 2018, 7, .	0.6	5
155	Draft Genome Sequences of Novel <i>Pseudomonas</i> , <i>Flavobacterium</i> , and <i>Sediminibacterium</i> Species Strains from a Freshwater Ecosystem. Genome Announcements, 2018, 6, .	0.8	4
156	Personal metabolic responses to food predicted using multi-omics machine learning in 1,100 twins and singletons: The PREDICT I Study.. Proceedings of the Nutrition Society, 2020, 79, .	1.0	2
157	The Signal and the Noise: Characteristics of Antisense RNA in Complex Microbial Communities. MSystems, 2020, 5, .	3.8	2
158	228-OR: Decoding Human Postprandial Responses to Food and Their Potential for Precision Nutrition: The PREDICT 1 Study. Diabetes, 2020, 69, .	0.6	2
159	When to suspect contamination rather than colonization â€" lessons from a putative fetal sheep microbiome. Gut Microbes, 2022, 14, 2005751.	9.8	2
160	Postprandial lipemia and CVD; does the magnitude, peak concentration or duration impact intermediary cardiometabolic risk factors differentially? PREDICT I Study.. Proceedings of the Nutrition Society, 2020, 79, .	1.0	1
161	On the Origin and Propagation of the COVID-19 Outbreak in the Italian Province of Trento, a Tourist Region of Northern Italy. Viruses, 2022, 14, 580.	3.3	1
162	Towards the integration of computational systems biology and high-throughput data: supporting differential analysis of microarray gene expression data. Journal of Integrative Bioinformatics, 2008, 5, .	1.5	1

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163	Waldron et al. Reply to â€œCommentary on the HMP16SData Bioconductor Packageâ€• American Journal of Epidemiology, 2019, 188, 1031-1032.	3.4	0
164	Abstract 257: Whole miRNome profiling in fecal and plasma exosome samples for the diagnosis of colorectal cancer. , 2020, , .		0