

Nicola Segata

List of Publications by Year in descending order

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Version: 2024-02-01

164
papers

67,502
citations

8181

76
h-index

4885

168
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all docs

199
docs citations

199
times ranked

59480
citing authors

#	ARTICLE	IF	CITATIONS
1	Recent genetic exchanges and admixture shape the genome and population structure of the zoonotic pathogen <i>Cryptosporidium parvum</i> . <i>Molecular Ecology</i> , 2023, 32, 2633-2645.	3.9	9
2	Stool microRNA profiles reflect different dietary and gut microbiome patterns in healthy individuals. <i>Gut</i> , 2022, 71, 1302-1314.	12.1	39
3	Next steps after 15 stimulating years of human gut microbiome research. <i>Microbial Biotechnology</i> , 2022, 15, 164-175.	4.2	11
4	Impact of insufficient sleep on dysregulated blood glucose control under standardised meal conditions. <i>Diabetologia</i> , 2022, 65, 356-365.	6.3	29
5	Intestinal <i>Akkermansia muciniphila</i> predicts clinical response to PD-1 blockade in patients with advanced non-small-cell lung cancer. <i>Nature Medicine</i> , 2022, 28, 315-324.	30.7	225
6	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. <i>Nature Medicine</i> , 2022, 28, 535-544.	30.7	158
7	Immune system and intestinal microbiota determine efficacy of androgen deprivation therapy against prostate cancer. <i>Prostate Cancer</i> , 2022, 10, e004191.		23
8	On the Origin and Propagation of the COVID-19 Outbreak in the Italian Province of Trento, a Tourist Region of Northern Italy. <i>Viruses</i> , 2022, 14, 580.	3.3	1
9	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
10	Cancer Induces a Stress Ileopathy Depending on β -Adrenergic Receptors and Promoting Dysbiosis that Contributes to Carcinogenesis. <i>Cancer Discovery</i> , 2022, 12, 1128-1151.	9.4	44
11	Variation and transmission of the human gut microbiota across multiple familial generations. <i>Nature Microbiology</i> , 2022, 7, 87-96.	13.3	32
12	When to suspect contamination rather than colonization – lessons from a putative fetal sheep microbiome. <i>Gut Microbes</i> , 2022, 14, 2005751.	9.8	2
13	Metagenomic and metabolomic remodeling in nonagenarians and centenarians and its association with genetic and socioeconomic factors. <i>Nature Aging</i> , 2022, 2, 438-452.	11.6	17
14	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021, 39, 105-114.	17.5	628
15	Microbiome as Mediator of Diet on Colorectal Cancer Risk: The Role of Vitamin D, Markers of Inflammation and Adipokines. <i>Nutrients</i> , 2021, 13, 363.	4.1	11
16	Ketogenic diet and ketone bodies enhance the anticancer effects of PD-1 blockade. <i>JCI Insight</i> , 2021, 6, .	5.0	143
17	High intake of vegetables is linked to lower white blood cell profile and the effect is mediated by the gut microbiome. <i>BMC Medicine</i> , 2021, 19, 37.	5.5	30
18	Sulfoquinovose is a select nutrient of prominent bacteria and a source of hydrogen sulfide in the human gut. <i>ISME Journal</i> , 2021, 15, 2779-2791.	9.8	30

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19	Blue poo: impact of gut transit time on the gut microbiome using a novel marker. <i>Gut</i> , 2021, 70, 1665-1674.	12.1	84
20	Gut microbiome diversity and composition is associated with hypertension in women. <i>Journal of Hypertension</i> , 2021, 39, 1810-1816.	0.5	22
21	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. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0047121.	3.1	7
22	Intestinal microbiota influences clinical outcome and side effects of early breast cancer treatment. <i>Cell Death and Differentiation</i> , 2021, 28, 2778-2796.	11.2	72
23	Reconstruction of ancient microbial genomes from the human gut. <i>Nature</i> , 2021, 594, 234-239.	27.8	139
24	Gut vascular barrier impairment leads to intestinal bacteria dissemination and colorectal cancer metastasis to liver. <i>Cancer Cell</i> , 2021, 39, 708-724.e11.	16.8	175
25	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	6.0	808
26	Prevotella diversity, niches and interactions with the human host. <i>Nature Reviews Microbiology</i> , 2021, 19, 585-599.	28.6	248
27	Multifaceted modes of action of the anticancer probiotic <i>Enterococcus hirae</i> . <i>Cell Death and Differentiation</i> , 2021, 28, 2276-2295.	11.2	18
28	Meal-induced inflammation: postprandial insights from the Personalised REsponses to Dietary Composition Trial (PREDICT) study in 1000 participants. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 1028-1038.	4.7	43
29	Phylogenomics of Opsin Genes in Diptera Reveals Lineage-Specific Events and Contrasting Evolutionary Dynamics in <i>Anopheles</i> and <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	16
30	Genomic diversity and ecology of human-associated <i>Akkermansia</i> species in the gut microbiome revealed by extensive metagenomic assembly. <i>Genome Biology</i> , 2021, 22, 209.	8.8	65
31	Closely related Lak megaphages replicate in the microbiomes of diverse animals. <i>IScience</i> , 2021, 24, 102875.	4.1	20
32	Metagenomic analysis of ancient dental calculus reveals unexplored diversity of oral archaeal <i>Methanobrevibacter</i> . <i>Microbiome</i> , 2021, 9, 197.	11.1	18
33	Neonatal antibiotic exposure impairs child growth during the first six years of life by perturbing intestinal microbial colonization. <i>Nature Communications</i> , 2021, 12, 443.	12.8	113
34	Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. <i>Nature Medicine</i> , 2021, 27, 321-332.	30.7	477
35	Hallstatt miners consumed blue cheese and beer during the Iron Age and retained a non-Westernized gut microbiome until the Baroque period. <i>Current Biology</i> , 2021, 31, 5149-5162.e6.	3.9	22
36	Over-celling fetal microbial exposure. <i>Cell</i> , 2021, 184, 5839-5841.	28.9	10

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37	Commensal Bifidobacterium Strains Enhance the Efficacy of Neo-Epitope Based Cancer Vaccines. <i>Vaccines</i> , 2021, 9, 1356.	4.4	10
38	Lung and Gut Microbiota Changes Associated with <i>Pseudomonas aeruginosa</i> Infection in Mouse Models of Cystic Fibrosis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12169.	4.1	7
39	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	30.7	170
40	Large scale genome reconstructions illuminate <i>Wolbachia</i> evolution. <i>Nature Communications</i> , 2020, 11, 5235.	12.8	71
41	Untargeted Metagenomic Investigation of the Airway Microbiome of Cystic Fibrosis Patients with Moderate-Severe Lung Disease. <i>Microorganisms</i> , 2020, 8, 1003.	3.6	23
42	Strong oral plaque microbiome signatures for dental implant diseases identified by strain-resolution metagenomics. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 47.	6.4	54
43	Faecal microbiota transplantation for the treatment of diarrhoea induced by tyrosine-kinase inhibitors in patients with metastatic renal cell carcinoma. <i>Nature Communications</i> , 2020, 11, 4333.	12.8	82
44	Cross-reactivity between tumor MHC class Iâ€restricted antigens and an enterococcal bacteriophage. <i>Science</i> , 2020, 369, 936-942.	12.6	217
45	Shed Light in the DaRk LineagES of the Fungal Tree of Lifeâ€STRES. <i>Life</i> , 2020, 10, 362.	2.4	16
46	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. <i>Nature Communications</i> , 2020, 11, 6389.	12.8	269
47	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	12.8	368
48	Gut Bacteria Composition Drives Primary Resistance to Cancer Immunotherapy in Renal Cell Carcinoma Patients. <i>European Urology</i> , 2020, 78, 195-206.	1.9	192
49	Large-scale genome-wide analysis links lactic acid bacteria from food with the gut microbiome. <i>Nature Communications</i> , 2020, 11, 2610.	12.8	190
50	Human postprandial responses to food and potential for precision nutrition. <i>Nature Medicine</i> , 2020, 26, 964-973.	30.7	418
51	Postprandial lipemia and CVD; does the magnitude, peak concentration or duration impact intermediary cardiometabolic risk factors differentially? PREDICT I Study.. <i>Proceedings of the Nutrition Society</i> , 2020, 79, .	1.0	1
52	Personal metabolic responses to food predicted using multi-omics machine learning in 1,100 twins and singletons: The PREDICT I Study.. <i>Proceedings of the Nutrition Society</i> , 2020, 79, .	1.0	2
53	Trial watch : the gut microbiota as a tool to boost the clinical efficacy of anticancer immunotherapy. <i>Oncolmmunology</i> , 2020, 9, 1774298.	4.6	22
54	Effect of Gluten-Free Diet on Gut Microbiota Composition in Patients with Celiac Disease and Non-Celiac Gluten/Wheat Sensitivity. <i>Nutrients</i> , 2020, 12, 1832.	4.1	75

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55	Analysis of 1321 <i>Eubacterium rectale</i> genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. <i>Genome Biology</i> , 2020, 21, 138.	8.8	72
56	How inoculation affects the development and the performances of microalgal-bacterial consortia treating real municipal wastewater. <i>Journal of Environmental Management</i> , 2020, 263, 110427.	7.8	28
57	Initial exploration of in utero microbial colonization. <i>Nature Medicine</i> , 2020, 26, 469-470.	30.7	12
58	Longitudinal survey of microbiome associated with particulate matter in a megacity. <i>Genome Biology</i> , 2020, 21, 55.	8.8	59
59	SARS-CoV-2 from faeces to wastewater treatment: What do we know? A review. <i>Science of the Total Environment</i> , 2020, 743, 140444.	8.0	321
60	Endogenous murine microbiota member <i>Faecalibaculum rodentium</i> and its human homologue protect from intestinal tumour growth. <i>Nature Microbiology</i> , 2020, 5, 511-524.	13.3	248
61	The Signal and the Noise: Characteristics of Antisense RNA in Complex Microbial Communities. <i>MSystems</i> , 2020, 5, .	3.8	2
62	Considerations for the design and conduct of human gut microbiota intervention studies relating to foods. <i>European Journal of Nutrition</i> , 2020, 59, 3347-3368.	3.9	17
63	228-OR: Decoding Human Postprandial Responses to Food and Their Potential for Precision Nutrition: The PREDICT 1 Study. <i>Diabetes</i> , 2020, 69, .	0.6	2
64	Abstract 257: Whole miRNome profiling in fecal and plasma exosome samples for the diagnosis of colorectal cancer. , 2020, , .		0
65	Dental Implants with Anti-Biofilm Properties: A Pilot Study for Developing a New Sericin-Based Coating. <i>Materials</i> , 2019, 12, 2429.	2.9	21
66	Consumer Safety Considerations of Skin and Oral Microbiome Perturbation. <i>Clinical Microbiology Reviews</i> , 2019, 32, .	13.6	15
67	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	17.5	11,167
68	Microbiota-gut brain axis involvement in neuropsychiatric disorders. <i>Expert Review of Neurotherapeutics</i> , 2019, 19, 1037-1050.	2.8	116
69	The <i>Prevotella copri</i> Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. <i>Cell Host and Microbe</i> , 2019, 26, 666-679.e7.	11.0	274
70	Distinct Polysaccharide Utilization Profiles of Human Intestinal <i>Prevotella copri</i> Isolates. <i>Cell Host and Microbe</i> , 2019, 26, 680-690.e5.	11.0	115
71	Altered Fecal Small RNA Profiles in Colorectal Cancer Reflect Gut Microbiome Composition in Stool Samples. <i>MSystems</i> , 2019, 4, .	3.8	59
72	No bacteria found in healthy placentas. <i>Nature</i> , 2019, 572, 317-318.	27.8	13

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73	Waldron et al. Reply to "Commentary on the HMP16SData Bioconductor Package". American Journal of Epidemiology, 2019, 188, 1031-1032.	3.4	0
74	Genomic and metagenomic insights into the microbial community of a thermal spring. Microbiome, 2019, 7, 8.	11.1	40
75	Sociodemographic variation in the oral microbiome. Annals of Epidemiology, 2019, 35, 73-80.e2.	1.9	37
76	Multiple levels of the unknown in microbiome research. BMC Biology, 2019, 17, 48.	3.8	101
77	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
78	Methicillin-resistant Staphylococcus aureus eradication in cystic fibrosis patients: A randomized multicenter study. PLoS ONE, 2019, 14, e0213497.	2.5	22
79	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
80	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
81	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. Nature Medicine, 2019, 25, 679-689.	30.7	734
82	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature Communications, 2019, 10, 5477.	12.8	197
83	Detecting contamination in viromes using ViromeQC. Nature Biotechnology, 2019, 37, 1408-1412.	17.5	69
84	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
85	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
86	HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. American Journal of Epidemiology, 2019, 188, 1023-1026.	3.4	30
87	Selective maternal seeding and environment shape the human gut microbiome. Genome Research, 2018, 28, 561-568.	5.5	247
88	bioBakery: a meta-omic analysis environment. Bioinformatics, 2018, 34, 1235-1237.	4.1	241
89	On the Road to Strain-Resolved Comparative Metagenomics. MSystems, 2018, 3, .	3.8	119
90	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

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91	Building essential biodiversity variables (<sc>EBV</sc>s) of species distribution and abundance at a global scale. <i>Biological Reviews</i> , 2018, 93, 600-625.	10.4	218
92	Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of <i>Staphylococcus aureus</i> strains in a paediatric hospital. <i>Genome Medicine</i> , 2018, 10, 82.	8.2	54
93	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	19.0	1,125
94	Draft Genome Sequence of the Cadmium-Resistant Strain JJU2, Belonging to the Family Hapalosiphonaceae of the Cyanobacteria. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	5
95	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. <i>Cell Host and Microbe</i> , 2018, 24, 133-145.e5.	11.0	822
96	Strain-Level Analysis of Mother-to-Child Bacterial Transmission during the First Few Months of Life. <i>Cell Host and Microbe</i> , 2018, 24, 146-154.e4.	11.0	311
97	The short-term impact of probiotic consumption on the oral cavity microbiome. <i>Scientific Reports</i> , 2018, 8, 10476.	3.3	36
98	Profiling microbial strains in urban environments using metagenomic sequencing data. <i>Biology Direct</i> , 2018, 13, 9.	4.6	29
99	The Microbe Directory: An annotated, searchable inventory of microbesâ€™ characteristics. <i>Gates Open Research</i> , 2018, 2, 3.	1.1	15
100	Studying Vertical Microbiome Transmission from Mothers to Infants by Strain-Level Metagenomic Profiling. <i>MSystems</i> , 2017, 2, .	3.8	329
101	Microbial strain-level population structure and genetic diversity from metagenomes. <i>Genome Research</i> , 2017, 27, 626-638.	5.5	540
102	Genomic characterization of Nontuberculous Mycobacteria. <i>Scientific Reports</i> , 2017, 7, 45258.	3.3	176
103	Accessible, curated metagenomic data through ExperimentHub. <i>Nature Methods</i> , 2017, 14, 1023-1024.	19.0	292
104	The new phylogeny of the genus <i>Mycobacterium</i> : The old and the news. <i>Infection, Genetics and Evolution</i> , 2017, 56, 19-25.	2.3	128
105	Large-scale comparative metagenomics of <i>Blastocystis</i> , a common member of the human gut microbiome. <i>ISME Journal</i> , 2017, 11, 2848-2863.	9.8	136
106	Large-Scale Phylogenomics of the <i>Lactobacillus casei</i> Group Highlights Taxonomic Inconsistencies and Reveals Novel Clade-Associated Features. <i>MSystems</i> , 2017, 2, .	3.8	79
107	Shotgun metagenomics, from sampling to analysis. <i>Nature Biotechnology</i> , 2017, 35, 833-844.	17.5	1,196
108	Long-adaptor single-strand oligonucleotide probes for the massively multiplexed cloning of kilobase genome regions. <i>Nature Biomedical Engineering</i> , 2017, 1, .	22.5	10

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109	Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 14.	6.4	159
110	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , 2017, 5, 66.	11.1	240
111	Experimental metagenomics and ribosomal profiling of the human skin microbiome. <i>Experimental Dermatology</i> , 2017, 26, 211-219.	2.9	34
112	MetaMLST: multi-locus strain-level bacterial typing from metagenomic samples. <i>Nucleic Acids Research</i> , 2017, 45, e7-e7.	14.5	88
113	Draft Genome Sequence of the Planktic Cyanobacterium <i>Tychonema bourrellyi</i> , Isolated from Alpine Lentic Freshwater. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
114	A Different Microbiome Gene Repertoire in the Airways of Cystic Fibrosis Patients with Severe Lung Disease. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1654.	4.1	39
115	Machine Learning Meta-analysis of Large Metagenomic Datasets: Tools and Biological Insights. <i>PLoS Computational Biology</i> , 2016, 12, e1004977.	3.2	434
116	Uncovering oral <i>Neisseria tropism</i> and persistence using metagenomic sequencing. <i>Nature Microbiology</i> , 2016, 1, 16070.	13.3	68
117	The reproductive tracts of two malaria vectors are populated by a core microbiome and by gender- and swarm-enriched microbial biomarkers. <i>Scientific Reports</i> , 2016, 6, 24207.	3.3	93
118	Metagenomic Sequencing with Strain-Level Resolution Implicates Uropathogenic <i>E.Âcoli</i> in Necrotizing Enterocolitis and Mortality in Preterm Infants. <i>Cell Reports</i> , 2016, 14, 2912-2924.	6.4	143
119	Strain-level microbial epidemiology and population genomics from shotgun metagenomics. <i>Nature Methods</i> , 2016, 13, 435-438.	19.0	328
120	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. <i>Scientific Reports</i> , 2015, 5, 15782.	3.3	233
121	Computational Tools for Taxonomic Microbiome Profiling of Shotgun Metagenomes. , 2015, , 67-80.		5
122	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7078-7087.	3.1	191
123	Gut Microbiome: Westernization and the Disappearance of Intestinal Diversity. <i>Current Biology</i> , 2015, 25, R611-R613.	3.9	169
124	MetaPhlan2 for enhanced metagenomic taxonomic profiling. <i>Nature Methods</i> , 2015, 12, 902-903.	19.0	1,843
125	Characterization of 17 strains belonging to the <i>Mycobacterium simiae</i> complex and description of <i>Mycobacterium paraense</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 656-662.	1.7	31
126	High-Specificity Targeted Functional Profiling in Microbial Communities with ShortBRED. <i>PLoS Computational Biology</i> , 2015, 11, e1004557.	3.2	235

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127	Compact graphical representation of phylogenetic data and metadata with GraPhlAn. PeerJ, 2015, 3, e1029.	2.0	701
128	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
129	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
130	Evidence of natural Wolbachia infections in field populations of Anopheles gambiae. Nature Communications, 2014, 5, 3985.	12.8	142
131	Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. ISME Journal, 2014, 8, 1403-1417.	9.8	352
132	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
133	MetaRef: a pan-genomic database for comparative and community microbial genomics. Nucleic Acids Research, 2014, 42, D617-D624.	14.5	51
134	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. Nature Communications, 2013, 4, 2304.	12.8	797
135	Two-stage microbial community experimental design. ISME Journal, 2013, 7, 2330-2339.	9.8	31
136	Biodiversity and functional genomics in the human microbiome. Trends in Genetics, 2013, 29, 51-58.	6.7	207
137	Computational meta'omics for microbial community studies. Molecular Systems Biology, 2013, 9, 666.	7.2	253
138	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
139	Genome Sequence of Pseudomonas aeruginosa PA45, a Highly Virulent Strain Isolated from a Patient with Bloodstream Infection. Genome Announcements, 2013, 1, .	0.8	6
140	Simultaneous Quantification of Multiple Bacteria by the BactoChip Microarray Designed to Target Species-Specific Marker Genes. PLoS ONE, 2013, 8, e55764.	2.5	18
141	Expansion of intestinal Prevotella copri correlates with enhanced susceptibility to arthritis. ELife, 2013, 2, e01202.	6.0	1,507
142	Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. PLoS Computational Biology, 2012, 8, e1002358.	3.2	939
143	Microbial Co-occurrence Relationships in the Human Microbiome. PLoS Computational Biology, 2012, 8, e1002606.	3.2	1,268
144	Expression Profiling of Archival Tumors for Long-term Health Studies. Clinical Cancer Research, 2012, 18, 6136-6146.	7.0	32

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145	Composition of the adult digestive tract bacterial microbiome based on seven mouth surfaces, tonsils, throat and stool samples. <i>Genome Biology</i> , 2012, 13, R42.	9.6	797
146	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	27.8	9,614
147	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	27.8	2,249
148	Local SVM approaches for fast and accurate classification of remote-sensing images. <i>International Journal of Remote Sensing</i> , 2012, 33, 6186-6201.	2.9	10
149	Metagenomic microbial community profiling using unique clade-specific marker genes. <i>Nature Methods</i> , 2012, 9, 811-814.	19.0	1,591
150	Clinical populations of <i>Pseudomonas aeruginosa</i> isolated from acute infections show a wide virulence range partially correlated with population structure and virulence gene expression. <i>Microbiology (United Kingdom)</i> , 2012, 158, 2089-2098.	1.8	21
151	Profiling instances in noise reduction. <i>Knowledge-Based Systems</i> , 2012, 31, 28-40.	7.1	25
152	A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy. <i>PLoS ONE</i> , 2012, 7, e36466.	2.5	572
153	Metagenomic biomarker discovery and explanation. <i>Genome Biology</i> , 2011, 12, R60.	9.6	11,192
154	Microbial community function and biomarker discovery in the human microbiome. <i>Genome Biology</i> , 2011, 12, .	9.6	89
155	The Genome of Th17 Cell-Inducing Segmented Filamentous Bacteria Reveals Extensive Auxotrophy and Adaptations to the Intestinal Environment. <i>Cell Host and Microbe</i> , 2011, 10, 260-272.	11.0	175
156	Toward an Efficient Method of Identifying Core Genes for Evolutionary and Functional Microbial Phylogenies. <i>PLoS ONE</i> , 2011, 6, e24704.	2.5	86
157	Host and gut microbiota symbiotic factors: lessons from inflammatory bowel disease and successful symbionts. <i>Cellular Microbiology</i> , 2011, 13, 508-517.	2.1	25
158	Operators for transforming kernels into quasi-local kernels that improve SVM accuracy. <i>Journal of Intelligent Information Systems</i> , 2011, 37, 155-186.	3.9	6
159	Noise reduction for instance-based learning with a local maximal margin approach. <i>Journal of Intelligent Information Systems</i> , 2010, 35, 301-331.	3.9	44
160	Keyphrases Extraction from Scientific Documents: Improving Machine Learning Approaches with Natural Language Processing. <i>Lecture Notes in Computer Science</i> , 2010, , 102-111.	1.3	21
161	A Scalable Noise Reduction Technique for Large Case-Based Systems. <i>Lecture Notes in Computer Science</i> , 2009, , 328-342.	1.3	9
162	Fast Local Support Vector Machines for Large Datasets. <i>Lecture Notes in Computer Science</i> , 2009, , 295-310.	1.3	19

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163	Towards the integration of computational systems biology and high-throughput data: supporting differential analysis of microarray gene expression data. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.5	1
164	Outer Membrane Vesicles From The Gut Microbiome Contribute to Tumor Immunity by Eliciting Cross-Reactive T Cells. <i>Frontiers in Oncology</i> , 0, 12, .	2.8	8