

# Bruno Fosso

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8293598/publications.pdf>

Version: 2024-02-01

40  
papers

1,572  
citations

394421

19  
h-index

330143

37  
g-index

44  
all docs

44  
docs citations

44  
times ranked

3347  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbiome composition indicate dysbiosis and lower richness in tumor breast tissues compared to healthy adjacent paired tissue, within the same women. BMC Cancer, 2022, 22, 30.	2.6	23
2	Morphological, molecular, and biochemical study of cyanobacteria from a eutrophic Algerian reservoir (Cheffia). Environmental Science and Pollution Research, 2022, 29, 27624.	5.3	1
3	Comparative Fecal Microbiota Analysis of Infants With Acute Bronchiolitis Caused or Not Caused by Respiratory Syncytial Virus. Frontiers in Cellular and Infection Microbiology, 2022, 12, 815715.	3.9	2
4	Analysis of microbiome in gastrointestinal stromal tumors: Looking for different players in tumorigenesis and novel therapeutic options. Cancer Science, 2022, 113, 2590-2599.	3.9	4
5	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
6	A primer on machine learning techniques for genomic applications. Computational and Structural Biotechnology Journal, 2021, 19, 4345-4359.	4.1	8
7	Stem Cell Impairment at the Host-Microbiota Interface in Colorectal Cancer. Cancers, 2021, 13, 996.	3.7	22
8	ITSoneWB: profiling global taxonomic diversity of eukaryotic communities on Galaxy. Bioinformatics, 2021, 37, 4253-4254.	4.1	1
9	Evaluating the Efficiency of DNA Metabarcoding to Analyze the Diet of Hippocampus guttulatus (Teleostea: Syngnathidae). Life, 2021, 11, 998.	2.4	9
10	Accurate detection and quantification of SARS-CoV-2 genomic and subgenomic mRNAs by ddPCR and meta-transcriptomics analysis. Communications Biology, 2021, 4, 1215.	4.4	10
11	Evaluating DNA metabarcoding to analyze diet composition of wild long-snouted seahorse Hippocampus guttulatus. , 2021, , .		1
12	The Microbial Community Associated with Rhizostoma pulmo: Ecological Significance and Potential Consequences for Marine Organisms and Human Health. Marine Drugs, 2020, 18, 437.	4.6	16
13	Gastric Adenocarcinomas and Signet-Ring Cell Carcinoma: Unraveling Gastric Cancer Complexity through Microbiome Analysis – Deepening Heterogeneity for a Personalized Therapy. International Journal of Molecular Sciences, 2020, 21, 9735.	4.1	25
14	A Differential Metabarcoding Approach to Describe Taxonomy Profiles of Bacteria and Archaea in the Saltern of Margherita di Savoia (Italy). Microorganisms, 2020, 8, 936.	3.6	21
15	Endogenous murine microbiota member Faecalibaculum rodentium and its human homologue protect from intestinal tumour growth. Nature Microbiology, 2020, 5, 511-524.	13.3	248
16	Accurate quantification of bacterial abundance in metagenomic DNAs accounting for variable DNA integrity levels. Microbial Genomics, 2020, 6, .	2.0	8
17	Jellyfish summer outbreaks as bacterial vectors and potential hazards for marine animals and humans health? The case of Rhizostoma pulmo (Scyphozoa, Cnidaria). Science of the Total Environment, 2019, 692, 305-318.	8.0	27
18	Enrichment of intestinal Lactobacillus by enhanced secretory IgA coating alters glucose homeostasis in P2rx7 <sup>+/+</sup> mice. Scientific Reports, 2019, 9, 9315.	3.3	18

#	ARTICLE	IF	CITATIONS
19	Dynamic inosinome profiles reveal novel patient stratification and gender-specific differences in glioblastoma. <i>Genome Biology</i> , 2019, 20, 33.	8.8	49
20	No metagenomic evidence of tumorigenic viruses in cancers from a selected cohort of immunosuppressed subjects. <i>Scientific Reports</i> , 2019, 9, 19815.	3.3	3
21	Human Endometrial Microbiota at Term of Normal Pregnancies. <i>Genes</i> , 2019, 10, 971.	2.4	38
22	Management at the service of research: ReOmicS, a quality management system for omics sciences. <i>Palgrave Communications</i> , 2019, 5, .	4.7	2
23	Microbiota composition, gene pool and its expression in Gir cattle ( <i>Bos indicus</i> ) rumen under different forage diets using metagenomic and metatranscriptomic approaches. <i>Systematic and Applied Microbiology</i> , 2018, 41, 374-385.	2.8	29
24	Whole transcriptome profiling of Late-Onset Alzheimer's Disease patients provides insights into the molecular changes involved in the disease. <i>Scientific Reports</i> , 2018, 8, 4282.	3.3	102
25	ITSoneDB: a comprehensive collection of eukaryotic ribosomal RNA Internal Transcribed Spacer 1 (ITS1) sequences. <i>Nucleic Acids Research</i> , 2018, 46, D127-D132.	14.5	31
26	Unbiased Taxonomic Annotation of Metagenomic Samples. <i>Journal of Computational Biology</i> , 2018, 25, 348-360.	1.6	12
27	T Follicular Helper Cells Promote a Beneficial Gut Ecosystem for Host Metabolic Homeostasis by Sensing Microbiota-Derived Extracellular ATP. <i>Cell Reports</i> , 2017, 18, 2566-2575.	6.4	87
28	The metagenomic data life-cycle: standards and best practices. <i>GigaScience</i> , 2017, 6, 1-11.	6.4	42
29	MetaShot: an accurate workflow for taxon classification of host-associated microbiome from shotgun metagenomic data. <i>Bioinformatics</i> , 2017, 33, 1730-1732.	4.1	21
30	Unbiased Taxonomic Annotation of Metagenomic Samples. <i>Lecture Notes in Computer Science</i> , 2017, , 162-173.	1.3	0
31	BioVeL: a virtual laboratory for data analysis and modelling in biodiversity science and ecology. <i>BMC Ecology</i> , 2016, 16, 49.	3.0	45
32	Intestinal microbiota sustains inflammation and autoimmunity induced by hypomorphic <i>RAG</i> defects. <i>Journal of Experimental Medicine</i> , 2016, 213, 355-375.	8.5	61
33	Complexity and Dynamics of the Winemaking Bacterial Communities in Berries, Musts, and Wines from Apulian Grape Cultivars through Time and Space. <i>PLoS ONE</i> , 2016, 11, e0157383.	2.5	60
34	Functional Integration of mRNA Translational Control Programs. <i>Biomolecules</i> , 2015, 5, 1580-1599.	4.0	9
35	The influence of invasive jellyfish blooms on the aquatic microbiome in a coastal lagoon (Varano, SE Tj ETQq1 1 0.784314 rgBT /Over	2.4	58
36	BioMaS: a modular pipeline for Bioinformatic analysis of Metagenomic AmpliconS. <i>BMC Bioinformatics</i> , 2015, 16, 203.	2.6	49

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37	BALB/c and C57BL/6 Mice Differ in Polyreactive IgA Abundance, which Impacts the Generation of Antigen-Specific IgA and Microbiota Diversity. <i>Immunity</i> , 2015, 43, 527-540.	14.3	247
38	e-DNA Meta-Barcoding: From NGS Raw Data to Taxonomic Profiling. <i>Methods in Molecular Biology</i> , 2015, 1269, 257-278.	0.9	4
39	Lactobacillus rossiae, a Vitamin B12 Producer, Represents a Metabolically Versatile Species within the Genus Lactobacillus. <i>PLoS ONE</i> , 2014, 9, e107232.	2.5	74
40	Reference databases for taxonomic assignment in metagenomics. <i>Briefings in Bioinformatics</i> , 2012, 13, 682-695.	6.5	82