Aitor Blanco-Mguez

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

826 26 28 11 h-index g-index citations papers 10.7 1,493 31 4.3 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
26	Intestinal Akkermansia muciniphila predicts clinical response to PD-1 blockade in patients with advanced non-small-cell lung cancer <i>Nature Medicine</i> , 2022 ,	50.5	23
25	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma <i>Nature Medicine</i> , 2022 ,	50.5	14
24	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	6.3	3
23	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021 , 10,	8.9	114
22	Precision modification of the human gut microbiota targeting surface-associated proteins. <i>Scientific Reports</i> , 2021 , 11, 1270	4.9	1
21	Genomic diversity and ecology of human-associated Akkermansia species in the gut microbiome revealed by extensive metagenomic assembly. <i>Genome Biology</i> , 2021 , 22, 209	18.3	14
20	In silico and functional analyses of immunomodulatory peptides encrypted in the human gut metaproteome. <i>Journal of Functional Foods</i> , 2020 , 70, 103969	5.1	2
19	The extracellular proteins of Lactobacillus acidophilus DSM 20079T display anti-inflammatory effect in both in piglets, healthy human donors and Crohn Disease patients. <i>Journal of Functional Foods</i> , 2020 , 64, 103660	5.1	2
18	Cell wall hydrolase as a surface-associated protein target for the specific detection of Lactobacillus rhamnosus using flow cytometry. <i>Innovative Food Science and Emerging Technologies</i> , 2020 , 59, 102240	6.8	2
17	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	17.4	31
16	In silico prediction reveals the existence of potential bioactive neuropeptides produced by the human gut microbiota. <i>Food Research International</i> , 2019 , 119, 221-226	7	6
15	DEWE: A novel tool for executing differential expression RNA-Seq workflows in biomedical research. <i>Computers in Biology and Medicine</i> , 2019 , 107, 197-205	7	6
14	Computational prediction of the bioactivity potential of proteomes based on expert knowledge. <i>Journal of Biomedical Informatics</i> , 2019 , 91, 103121	10.2	1
13	Next generation community assessment of biomedical entity recognition web servers: metrics, performance, interoperability aspects of BeCalm. <i>Journal of Cheminformatics</i> , 2019 , 11, 42	8.6	4
12	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1032-1056	13.4	8
11	BlasterJS: A novel interactive JavaScript visualisation component for BLAST alignment results. <i>PLoS ONE</i> , 2018 , 13, e0205286	3.7	8
10	MAHMI database: a comprehensive MetaHit-based resource for the study of the mechanism of action of the human microbiota. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	24

LIST OF PUBLICATIONS

9 P4P: a peptidome-based strain-level genome comparison web tool. *Nucleic Acids Research*, **2017**, 45, W2659.W269

8	Probiotics, gut microbiota, and their influence on host health and disease. <i>Molecular Nutrition and Food Research</i> , 2017 , 61, 1600240	5.9	442
7	Screening of the Human Gut Metaproteome Identifies Th17-Promoting Peptides Encrypted in Proteins of Commensal Bacteria. <i>Frontiers in Microbiology</i> , 2017 , 8, 1726	5.7	14
6	A peptidome-based phylogeny pipeline reveals differential peptides at the strain level within Bifidobacterium animalis subsp. lactis. <i>Food Microbiology</i> , 2016 , 60, 137-41	6	3
5	Tackling probiotic and gut microbiota functionality through proteomics. <i>Journal of Proteomics</i> , 2016 , 147, 28-39	3.9	33
4	Improving Phylogeny Reconstruction at the Strain Level Using Peptidome Datasets. <i>PLoS Computational Biology</i> , 2016 , 12, e1005271	5	3
3	From amino acid sequence to bioactivity: The biomedical potential of antitumor peptides. <i>Protein Science</i> , 2016 , 25, 1084-95	6.3	42
2	Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps		2
1	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3		22