

Aleksandar David Kostic

List of Publications by Citations

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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.

51 papers	12,274 citations	29 h-index	60 g-index
60 ext. papers	15,543 ext. citations	16.8 avg, IF	6.01 L-index

#	Paper	IF	Citations
51	The treatment-naive microbiome in new-onset Crohn's disease. <i>Cell Host and Microbe</i> , 2014 , 15, 382-392	23.4	1836
50	The mutational landscape of head and neck squamous cell carcinoma. <i>Science</i> , 2011 , 333, 1157-60	33.3	1836
49	Fusobacterium nucleatum potentiates intestinal tumorigenesis and modulates the tumor-immune microenvironment. <i>Cell Host and Microbe</i> , 2013 , 14, 207-15	23.4	1275
48	Genomic analysis identifies association of Fusobacterium with colorectal carcinoma. <i>Genome Research</i> , 2012 , 22, 292-8	9.7	1165
47	The microbiome in inflammatory bowel disease: current status and the future ahead. <i>Gastroenterology</i> , 2014 , 146, 1489-99	13.3	1055
46	The dynamics of the human infant gut microbiome in development and in progression toward type 1 diabetes. <i>Cell Host and Microbe</i> , 2015 , 17, 260-73	23.4	639
45	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. <i>Cell</i> , 2016 , 165, 842-53	56.2	584
44	Fusobacterium nucleatum in colorectal carcinoma tissue and patient prognosis. <i>Gut</i> , 2016 , 65, 1973-1980	9.2	454
43	Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. <i>Journal of Clinical Investigation</i> , 2013 , 123, 517-25	15.9	371
42	Fusobacterium nucleatum and T Cells in Colorectal Carcinoma. <i>JAMA Oncology</i> , 2015 , 1, 653-61	13.4	336
41	Exploring host-microbiota interactions in animal models and humans. <i>Genes and Development</i> , 2013 , 27, 701-18	12.6	308
40	Meta-omics analysis of elite athletes identifies a performance-enhancing microbe that functions via lactate metabolism. <i>Nature Medicine</i> , 2019 , 25, 1104-1109	50.5	242
39	Inflammatory bowel disease as a model for translating the microbiome. <i>Immunity</i> , 2014 , 40, 843-54	32.3	237
38	PathSeq: software to identify or discover microbes by deep sequencing of human tissue. <i>Nature Biotechnology</i> , 2011 , 29, 393-6	44.5	213
37	An integrative view of microbiome-host interactions in inflammatory bowel diseases. <i>Cell Host and Microbe</i> , 2015 , 17, 577-91	23.4	178
36	Association of Dietary Patterns With Risk of Colorectal Cancer Subtypes Classified by Fusobacterium nucleatum in Tumor Tissue. <i>JAMA Oncology</i> , 2017 , 3, 921-927	13.4	177
35	Fusobacterium nucleatum in Colorectal Carcinoma Tissue According to Tumor Location. <i>Clinical and Translational Gastroenterology</i> , 2016 , 7, e200	4.2	156

34	Intestinal virome changes precede autoimmunity in type I diabetes-susceptible children. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E6166-E6175	11.5	151
33	Dysbiosis, inflammation, and response to treatment: a longitudinal study of pediatric subjects with newly diagnosed inflammatory bowel disease. <i>Genome Medicine</i> , 2016 , 8, 75	14.4	147
32	Bacteroides-Derived Sphingolipids Are Critical for Maintaining Intestinal Homeostasis and Symbiosis. <i>Cell Host and Microbe</i> , 2019 , 25, 668-680.e7	23.4	112
31	The Landscape of Genetic Content in the Gut and Oral Human Microbiome. <i>Cell Host and Microbe</i> , 2019 , 26, 283-295.e8	23.4	103
30	Predictive metabolomic profiling of microbial communities using amplicon or metagenomic sequences. <i>Nature Communications</i> , 2019 , 10, 3136	17.4	89
29	Assessment of the cPAS-based BGISEQ-500 platform for metagenomic sequencing. <i>GigaScience</i> , 2018 , 7, 1-8	7.6	82
28	Keystone microbiome meeting 2012: a mountain top experience. <i>EMBO Reports</i> , 2012 , 13, 478-480	6.5	78
27	in Colorectal Cancer Relates to Immune Response Differentially by Tumor Microsatellite Instability Status. <i>Cancer Immunology Research</i> , 2018 , 6, 1327-1336	12.5	78
26	Human genome-wide RNAi screen identifies an essential role for inositol pyrophosphates in Type-I interferon response. <i>PLoS Pathogens</i> , 2014 , 10, e1003981	7.6	53
25	Microbes and inflammation in colorectal cancer. <i>Cancer Immunology Research</i> , 2013 , 1, 150-7	12.5	43
24	Reconstruction of ancient microbial genomes from the human gut. <i>Nature</i> , 2021 , 594, 234-239	50.4	39
23	A Microbiome Foundation for the Study of Crohn's Disease. <i>Cell Host and Microbe</i> , 2017 , 21, 301-304	23.4	29
22	CopriD predicts the source of coprolites and paleofeces using microbiome composition and host DNA content. <i>PeerJ</i> , 2020 , 8, e9001	3.1	17
21	The predictive power of the microbiome exceeds that of genome-wide association studies in the discrimination of complex human disease		10
20	Gene-level metagenomic architectures across diseases yield high-resolution microbiome diagnostic indicators. <i>Nature Communications</i> , 2021 , 12, 2907	17.4	9
19	Emerging Concepts and Technologies for the Discovery of Microorganisms Involved in Human Disease. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2017 , 12, 217-244	34	8
18	Mechanisms of microbial-neuronal interactions in pain and nociception. <i>Neurobiology of Pain (Cambridge, Mass)</i> , 2021 , 9, 100056	4	8
17	A systematic machine learning and data type comparison yields metagenomic predictors of infant age, sex, breastfeeding, antibiotic usage, country of origin, and delivery type. <i>PLoS Computational Biology</i> , 2020 , 16, e1007895	5	7

16	The TPR-containing domain within Est1 homologs exhibits species-specific roles in telomerase interaction and telomere length homeostasis. <i>BMC Molecular Biology</i> , 2011 , 12, 45	4.5	7
15	Aether: leveraging linear programming for optimal cloud computing in genomics. <i>Bioinformatics</i> , 2018 , 34, 1565-1567	7.2	5
14	Gut Microbiota: Small Molecules Modulate Host Cellular Functions. <i>Current Biology</i> , 2017 , 27, R307-R3106.3		3
13	The genomic landscape of Mexican Indigenous populations brings insights into the peopling of the Americas. <i>Nature Communications</i> , 2021 , 12, 5942	17.4	2
12	Circulating short and medium chain fatty acids are associated with normoalbuminuria in type 1 diabetes of long duration. <i>Scientific Reports</i> , 2021 , 11, 8592	4.9	2
11	Leveraging vibration of effects analysis for robust discovery in observational biomedical data science. <i>PLoS Biology</i> , 2021 , 19, e3001398	9.7	2
10	Reply to "Is physical performance (in mice) increased by <i>Veillonella atypica</i> or decreased by <i>Lactobacillus bulgaricus</i> ?". <i>Journal of Sport and Health Science</i> , 2020 , 9, 201-202	8.2	0
9	Using Cartesian Doubt To Build a Sequencing-Based View of Microbiology. <i>MSystems</i> , 2021 , 6, e00574217.6		0
8	Systematically assessing microbiome-disease associations identifies drivers of inconsistency in metagenomic research.. <i>PLoS Biology</i> , 2022 , 20, e3001556	9.7	0
7	The human microbiome: A coming of age story.. <i>Cell Host and Microbe</i> , 2022 , 30, 449-453	23.4	
6	A systematic machine learning and data type comparison yields metagenomic predictors of infant age, sex, breastfeeding, antibiotic usage, country of origin, and delivery type 2020 , 16, e1007895		
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