Aleksandar David Kostic

List of Publications by Year in Descending Order

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	Systematically assessing microbiome-disease associations identifies drivers of inconsistency in metagenomic research.. *PLoS Biology*, **2022**, 20, e3001556	9.7	0
50	The human microbiome: A coming of age story.. *Cell Host and Microbe*, **2022**, 30, 449-453	23.4	
49	Using Cartesian Doubt To Build a Sequencing-Based View of Microbiology. *MSystems*, **2021**, 6, e0057421	7.6	0
48	The genomic landscape of Mexican Indigenous populations brings insights into the peopling of the Americas. *Nature Communications*, **2021**, 12, 5942	17.4	2
47	Circulating short and medium chain fatty acids are associated with normoalbuminuria in type 1 diabetes of long duration. *Scientific Reports*, **2021**, 11, 8592	4.9	2
46	Gene-level metagenomic architectures across diseases yield high-resolution microbiome diagnostic indicators. *Nature Communications*, **2021**, 12, 2907	17.4	9
45	Reconstruction of ancient microbial genomes from the human gut. *Nature*, **2021**, 594, 234-239	50.4	39
44	Mechanisms of microbial-neuronal interactions in pain and nociception. *Neurobiology of Pain (Cambridge, Mass.)*, **2021**, 9, 100056	4	8
43	Leveraging vibration of effects analysis for robust discovery in observational biomedical data science. *PLoS Biology*, **2021**, 19, e3001398	9.7	2
42	A systematic machine learning and data type comparison yields metagenomic predictors of infant age, sex, breastfeeding, antibiotic usage, country of origin, and delivery type. *PLoS Computational Biology*, **2020**, 16, e1007895	5	7
41	Reply to "Is physical performance (in mice) increased by Veillonella atypica or decreased by Lactobacillus bulgaricus?". *Journal of Sport and Health Science*, **2020**, 9, 201-202	8.2	0
40	CoproID predicts the source of coprolites and paleofeces using microbiome composition and host DNA content. *PeerJ*, **2020**, 8, e9001	3.1	17
39	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		
38	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		
37	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		
36	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		
35	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		

34	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		
33	Meta-omics analysis of elite athletes identifies a performance-enhancing microbe that functions via lactate metabolism. *Nature Medicine*, **2019**, 25, 1104-1109	50.5	242
32	Bacteroides-Derived Sphingolipids Are Critical for Maintaining Intestinal Homeostasis and Symbiosis. *Cell Host and Microbe*, **2019**, 25, 668-680.e7	23.4	112
31	The Landscape of Genetic Content in the Gut and Oral Human Microbiome. *Cell Host and Microbe*, **2019**, 26, 283-295.e8	23.4	103
30	Predictive metabolomic profiling of microbial communities using amplicon or metagenomic sequences. *Nature Communications*, **2019**, 10, 3136	17.4	89
29	Assessment of the cPAS-based BGISEQ-500 platform for metagenomic sequencing. *GigaScience*, **2018**, 7, 1-8	7.6	82
28	Aether: leveraging linear programming for optimal cloud computing in genomics. *Bioinformatics*, **2018**, 34, 1565-1567	7.2	5
27	in Colorectal Cancer Relates to Immune Response Differentially by Tumor Microsatellite Instability Status. *Cancer Immunology Research*, **2018**, 6, 1327-1336	12.5	78
26	A Microbiome Foundation for the Study of Crohn's Disease. *Cell Host and Microbe*, **2017**, 21, 301-304	23.4	29
25	Gut Microbiota: Small Molecules Modulate Host Cellular Functions. *Current Biology*, **2017**, 27, R307-R310	6.3	3
24	Emerging Concepts and Technologies for the Discovery of Microorganisms Involved in Human Disease. *Annual Review of Pathology: Mechanisms of Disease*, **2017**, 12, 217-244	34	8
23	Intestinal virome changes precede autoimmunity in type I diabetes-susceptible children. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E6166-E6175	11.5	151
22	Association of Dietary Patterns With Risk of Colorectal Cancer Subtypes Classified by Fusobacterium nucleatum in Tumor Tissue. *JAMA Oncology*, **2017**, 3, 921-927	13.4	177
21	Fusobacterium nucleatum in colorectal carcinoma tissue and patient prognosis. *Gut*, **2016**, 65, 1973-1980	19.2	454
20	Fusobacterium nucleatum in Colorectal Carcinoma Tissue According to Tumor Location. *Clinical and Translational Gastroenterology*, **2016**, 7, e200	4.2	156
19	Dysbiosis, inflammation, and response to treatment: a longitudinal study of pediatric subjects with newly diagnosed inflammatory bowel disease. *Genome Medicine*, **2016**, 8, 75	14.4	147
18	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. *Cell*, **2016**, 165, 842-53	56.2	584
17	An integrative view of microbiome-host interactions in inflammatory bowel diseases. *Cell Host and Microbe*, **2015**, 17, 577-91	23.4	178

16	Fusobacterium nucleatum and T Cells in Colorectal Carcinoma. *JAMA Oncology*, **2015**, 1, 653-61	13.4	336
15	The dynamics of the human infant gut microbiome in development and in progression toward type 1 diabetes. *Cell Host and Microbe*, **2015**, 17, 260-73	23.4	639
14	The treatment-naive microbiome in new-onset Crohn's disease. *Cell Host and Microbe*, **2014**, 15, 382-392	23.4	1836
13	Inflammatory bowel disease as a model for translating the microbiome. *Immunity*, **2014**, 40, 843-54	32.3	237
12	Human genome-wide RNAi screen identifies an essential role for inositol pyrophosphates in Type-I interferon response. *PLoS Pathogens*, **2014**, 10, e1003981	7.6	53
11	The microbiome in inflammatory bowel disease: current status and the future ahead. *Gastroenterology*, **2014**, 146, 1489-99	13.3	1055
10	Fusobacterium nucleatum potentiates intestinal tumorigenesis and modulates the tumor-immune microenvironment. *Cell Host and Microbe*, **2013**, 14, 207-15	23.4	1275
9	Microbes and inflammation in colorectal cancer. *Cancer Immunology Research*, **2013**, 1, 150-7	12.5	43
8	Exploring host-microbiota interactions in animal models and humans. *Genes and Development*, **2013**, 27, 701-18	12.6	308
7	Prognostically relevant gene signatures of high-grade serous ovarian carcinoma. *Journal of Clinical Investigation*, **2013**, 123, 517-25	15.9	371
6	Genomic analysis identifies association of Fusobacterium with colorectal carcinoma. *Genome Research*, **2012**, 22, 292-8	9.7	1165
5	Keystone microbiome meeting 2012: a mountain top experience. *EMBO Reports*, **2012**, 13, 478-480	6.5	78
4	PathSeq: software to identify or discover microbes by deep sequencing of human tissue. *Nature Biotechnology*, **2011**, 29, 393-6	44.5	213
3	The mutational landscape of head and neck squamous cell carcinoma. *Science*, **2011**, 333, 1157-60	33.3	1836
2	The TPR-containing domain within Est1 homologs exhibits species-specific roles in telomerase interaction and telomere length homeostasis. *BMC Molecular Biology*, **2011**, 12, 45	4.5	7
1	The predictive power of the microbiome exceeds that of genome-wide association studies in the discrimination of complex human disease		10