

Andrey Morgun

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

3,470
citations

430874

18
h-index

677142

22
g-index

26
all docs

26
docs citations

26
times ranked

4409
citing authors

#	ARTICLE	IF	CITATIONS
1	Intestinal microbiota signatures of clinical response and immune-related adverse events in melanoma patients treated with anti-PD-1. <i>Nature Medicine</i> , 2022, 28, 545-556.	30.7	167
2	Microbiota and adipocyte mitochondrial damage in type 2 diabetes are linked by <i>Mmp12</i> + macrophages. <i>Journal of Experimental Medicine</i> , 2022, 219, .	8.5	24
3	Transkingdom interactions between <i>Lactobacilli</i> and hepatic mitochondria attenuate western diet-induced diabetes. <i>Nature Communications</i> , 2021, 12, 101.	12.8	86
4	Fecal microbiota transplant overcomes resistance to anti-PD-1 therapy in melanoma patients. <i>Science</i> , 2021, 371, 595-602.	12.6	746
5	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response. <i>Science</i> , 2021, 374, 1632-1640.	12.6	369
6	Role of gut microbiota in type 2 diabetes pathophysiology. <i>EBioMedicine</i> , 2020, 51, 102590.	6.1	954
7	Gut-resident CX3CR1 ^{hi} macrophages induce tertiary lymphoid structures and IgA response in situ. <i>Science Immunology</i> , 2020, 5, .	11.9	63
8	Dietary Indole-3-Carbinol Activates AhR in the Gut, Alters Th17-Microbe Interactions, and Exacerbates Insulinitis in NOD Mice. <i>Frontiers in Immunology</i> , 2020, 11, 606441.	4.8	19
9	Commensal bacteria contribute to insulin resistance in aging by activating innate B1a cells. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	121
10	CVID enteropathy is characterized by exceedingly low mucosal IgA levels and interferon-driven inflammation possibly related to the presence of a pathobiont. <i>Clinical Immunology</i> , 2018, 197, 139-153.	3.2	66
11	Transkingdom Networks: A Systems Biology Approach to Identify Causal Members of Host-Microbiota Interactions. <i>Methods in Molecular Biology</i> , 2018, 1849, 227-242.	0.9	23
12	Transkingdom network reveals bacterial players associated with cervical cancer gene expression program. <i>PeerJ</i> , 2018, 6, e5590.	2.0	24
13	Interplay between viruses and bacterial microbiota in cancer development. <i>Seminars in Immunology</i> , 2017, 32, 14-24.	5.6	35
14	Multi-omics Comparative Analysis Reveals Multiple Layers of Host Signaling Pathway Regulation by the Gut Microbiota. <i>MSystems</i> , 2017, 2, .	3.8	19
15	Antibiotic-Induced Alterations in Gut Microbiota Are Associated with Changes in Glucose Metabolism in Healthy Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 2306.	3.5	103
16	<i>Akkermansia muciniphila</i> mediates negative effects of IFN γ on glucose metabolism. <i>Nature Communications</i> , 2016, 7, 13329.	12.8	232
17	Unexpected links reflect the noise in networks. <i>Biology Direct</i> , 2016, 11, 52.	4.6	35
18	Investigating a holobiont: Microbiota perturbations and transkingdom networks. <i>Gut Microbes</i> , 2016, 7, 126-135.	9.8	38

#	ARTICLE	IF	CITATIONS
19	Differentially correlated genes in co-expression networks control phenotype transitions. F1000Research, 2016, 5, 2740.	1.6	8
20	Reverse enGENEering of Regulatory Networks from Big Data: A Roadmap for Biologists. Bioinformatics and Biology Insights, 2015, 9, BBI.S12467.	2.0	38
21	Uncovering effects of antibiotics on the host and microbiota using transkingdom gene networks. Gut, 2015, 64, 1732-1743.	12.1	261
22	MÃ©nage Ã trois: an evolutionary interplay between human papillomavirus, a tumor, and a woman. Trends in Microbiology, 2014, 22, 345-353.	7.7	36