

# Natalia Shulzhenko

## List of Publications by Year in descending order

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Version: 2024-02-01

28  
papers

2,773  
citations

361296

20  
h-index

501076

28  
g-index

32  
all docs

32  
docs citations

32  
times ranked

4544  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fecal Implants From AppNL <sup>−G</sup> and AppNL <sup>−F/E4</sup> Donor Mice Sufficient to Induce Behavioral Phenotypes in Germ-Free Mice. <i>Frontiers in Behavioral Neuroscience</i> , 2022, 16, 791128.	1.0	14
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, .	4.2	24
3	Transkingdom interactions between Lactobacilli and hepatic mitochondria attenuate western diet-induced diabetes. <i>Nature Communications</i> , 2021, 12, 101.	5.8	86
4	Role of gut microbiota in type 2 diabetes pathophysiology. <i>EBioMedicine</i> , 2020, 51, 102590.	2.7	954
5	Improvements in Metabolic Syndrome by Xanthohumol Derivatives Are Linked to Altered Gut Microbiota and Bile Acid Metabolism. <i>Molecular Nutrition and Food Research</i> , 2020, 64, e1900789.	1.5	32
6	Gut-resident CX3CR1 <sup>+</sup> macrophages induce tertiary lymphoid structures and IgA response in situ. <i>Science Immunology</i> , 2020, 5, .	5.6	63
7	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.	2.2	19
8	Commensal bacteria contribute to insulin resistance in aging by activating innate B1a cells. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	121
9	CVID enteropathy is characterized by exceeding low mucosal IgA levels and interferon-driven inflammation possibly related to the presence of a pathobiont. <i>Clinical Immunology</i> , 2018, 197, 139-153.	1.4	66
10	Transkingdom Networks: A Systems Biology Approach to Identify Causal Members of Host-Microbiota Interactions. <i>Methods in Molecular Biology</i> , 2018, 1849, 227-242.	0.4	23
11	Transkingdom network reveals bacterial players associated with cervical cancer gene expression program. <i>PeerJ</i> , 2018, 6, e5590.	0.9	24
12	Mycobacterium tuberculosis Proteome Response to Antituberculosis Compounds Reveals Metabolic Escape Pathways That Prolong Bacterial Survival. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	22
13	Interplay between viruses and bacterial microbiota in cancer development. <i>Seminars in Immunology</i> , 2017, 32, 14-24.	2.7	35
14	Multi-omics Comparative Analysis Reveals Multiple Layers of Host Signaling Pathway Regulation by the Gut Microbiota. <i>MSystems</i> , 2017, 2, .	1.7	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.	1.5	103
16	Arsenic exposure and intestinal microbiota in children from Sirajdikhan, Bangladesh. <i>PLoS ONE</i> , 2017, 12, e0188487.	1.1	41
17	<i>Akkermansia muciniphila</i> mediates negative effects of IFN $\gamma$ on glucose metabolism. <i>Nature Communications</i> , 2016, 7, 13329.	5.8	232
18	Unexpected links reflect the noise in networks. <i>Biology Direct</i> , 2016, 11, 52.	1.9	35

#	ARTICLE	IF	CITATIONS
19	Investigating a holobiont: Microbiota perturbations and transkingdom networks. <i>Gut Microbes</i> , 2016, 7, 126-135.	4.3	38
20	Differentially correlated genes in co-expression networks control phenotype transitions. <i>F1000Research</i> , 2016, 5, 2740.	0.8	8
21	Reverse enGENEering of Regulatory Networks from Big Data: A Roadmap for Biologists. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S12467.	1.0	38
22	Uncovering effects of antibiotics on the host and microbiota using transkingdom gene networks. <i>Gut</i> , 2015, 64, 1732-1743.	6.1	261
23	MÃ©nage Ã  trois: an evolutionary interplay between human papillomavirus, a tumor, and a woman. <i>Trends in Microbiology</i> , 2014, 22, 345-353.	3.5	36
24	Bridging immunity and lipid metabolism by gut microbiota. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 132, 253-262.	1.5	61
25	Gene network reconstruction reveals cell cycle and antiviral genes as major drivers of cervical cancer. <i>Nature Communications</i> , 2013, 4, 1806.	5.8	65
26	Crosstalk between B lymphocytes, microbiota and the intestinal epithelium governs immunity versus metabolism in the gut. <i>Nature Medicine</i> , 2011, 17, 1585-1593.	15.2	323
27	Selection of control genes for quantitative RT-PCR based on microarray data. <i>Biochemical and Biophysical Research Communications</i> , 2005, 337, 306-312.	1.0	18
28	Specificity of Alternative Splice Form Detection Using RT-PCR with a Primer Spanning the Exon Junction. <i>BioTechniques</i> , 2003, 34, 1244-1249.	0.8	8