

Moran Yassour

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

33,726
citations

257101

24
h-index

414034

32
g-index

38
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38
docs citations

38
times ranked

45528
citing authors

#	ARTICLE	IF	CITATIONS
1	The Infant Gut Commensal <i>Bacteroides dorei</i> Presents a Generalized Transcriptional Response to Various Human Milk Oligosaccharides. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 854122.	1.8	14
2	The evolution, evolvability and engineering of gene regulatory DNA. <i>Nature</i> , 2022, 603, 455-463.	13.7	126
3	Amniotic fluid biomarkers predict the severity of congenital cytomegalovirus infection. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	9
4	Preemies going pro: How probiotic treatment matures the microbiome of extreme premature infants. <i>Cell Host and Microbe</i> , 2022, 30, 599-600.	5.1	2
5	Human milk oligosaccharides and the infant gut microbiome from an eco-evolutionary perspective. <i>Current Opinion in Microbiology</i> , 2022, 68, 102156.	2.3	5
6	Lessons learned from the prenatal microbiome controversy. <i>Microbiome</i> , 2021, 9, 8.	4.9	67
7	The compositional development of the microbiome in early life. , 2021, , 177-195.		2
8	Lessons from applied large-scale pooling of 133,816 SARS-CoV-2 RT-PCR tests. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	66
9	Characterization of the Oral Microbiome Among Children With Type 1 Diabetes Compared With Healthy Children. <i>Frontiers in Microbiology</i> , 2021, 12, 756808.	1.5	12
10	Delivery Mode Affects Stability of Early Infant Gut Microbiota. <i>Cell Reports Medicine</i> , 2020, 1, 100156.	3.3	97
11	Genomic variation and strain-specific functional adaptation in the human gut microbiome during early life. <i>Nature Microbiology</i> , 2019, 4, 470-479.	5.9	164
12	Antigen discovery and specification of immunodominance hierarchies for MHCII-restricted epitopes. <i>Nature Medicine</i> , 2018, 24, 1762-1772.	15.2	64
13	SplinctomeR Enables Group Comparisons in Longitudinal Microbiome Studies. <i>Frontiers in Microbiology</i> , 2018, 9, 785.	1.5	48
14	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. <i>Cell Host and Microbe</i> , 2018, 24, 133-145.e5.	5.1	822
15	Strain-Level Analysis of Mother-to-Child Bacterial Transmission during the First Few Months of Life. <i>Cell Host and Microbe</i> , 2018, 24, 146-154.e4.	5.1	311
16	A novel <i>Ruminococcus gnavus</i> clade enriched in inflammatory bowel disease patients. <i>Genome Medicine</i> , 2017, 9, 103.	3.6	478
17	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. <i>Cell</i> , 2016, 165, 842-853.	13.5	968
18	Natural history of the infant gut microbiome and impact of antibiotic treatment on bacterial strain diversity and stability. <i>Science Translational Medicine</i> , 2016, 8, 343ra81.	5.8	763

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19	Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. <i>Genome Medicine</i> , 2016, 8, 17.	3.6	219
20	The Treatment-Naïve Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	5.1	2,582
21	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. <i>Nature Protocols</i> , 2013, 8, 1494-1512.	5.5	7,054
22	High-Resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling. <i>Science</i> , 2012, 335, 552-557.	6.0	496
23	Comparative Functional Genomics of the Fission Yeasts. <i>Science</i> , 2011, 332, 930-936.	6.0	458
24	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	9.4	17,264
25	Comprehensive comparative analysis of strand-specific RNA sequencing methods. <i>Nature Methods</i> , 2010, 7, 709-715.	9.0	662
26	High-resolution nucleosome mapping reveals transcription-dependent promoter packaging. <i>Genome Research</i> , 2010, 20, 90-100.	2.4	332
27	Strand-specific RNA sequencing reveals extensive regulated long antisense transcripts that are conserved across yeast species. <i>Genome Biology</i> , 2010, 11, R87.	13.9	122
28	RNA polymerase mapping during stress responses reveals widespread nonproductive transcription in yeast. <i>Genome Biology</i> , 2010, 11, R75.	13.9	52
29	Development and evaluation of RNA-seq methods. <i>Genome Biology</i> , 2010, 11, P26.	13.9	5
30	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3264-3269.	3.3	201
31	Nucleosome positioning from tiling microarray data. <i>Bioinformatics</i> , 2008, 24, i139-i146.	1.8	19