Nicholas E Ilott

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6430723/publications.pdf

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25	2,863	516215	642321
papers	citations	16 h-index	23 g-index

27	27	27	6268
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Sequencing depth and coverage: key considerations in genomic analyses. Nature Reviews Genetics, 2014, 15, 121-132.	7.7	1,116
2	The Short Chain Fatty Acid Butyrate Imprints an Antimicrobial Program in Macrophages. Immunity, 2019, 50, 432-445.e7.	6.6	612
3	Long non-coding RNAs and enhancer RNAs regulate the lipopolysaccharide-induced inflammatory response in human monocytes. Nature Communications, 2014, 5, 3979.	5.8	281
4	Predicting long non-coding RNAs using RNA sequencing. Methods, 2013, 63, 50-59.	1.9	117
5	Tuning the Transcriptional Response to Hypoxia by Inhibiting Hypoxia-inducible Factor (HIF) Prolyl and Asparaginyl Hydroxylases. Journal of Biological Chemistry, 2016, 291, 20661-20673.	1.6	91
6	Prenatal Exposure to Nicotine Impairs Performance of the 5-Choice Serial Reaction Time Task in Adult Rats. Neuropsychopharmacology, 2011, 36, 1114-1125.	2.8	88
7	A Large Polysaccharide Produced by Helicobacter hepaticus Induces an Anti-inflammatory Gene Signature in Macrophages. Cell Host and Microbe, 2017, 22, 733-745.e5.	5.1	88
8	CGAT: computational genomics analysis toolkit. Bioinformatics, 2014, 30, 1290-1291.	1.8	65
9	Deconvolution of monocyte responses in inflammatory bowel disease reveals an IL-1 cytokine network that regulates IL-23 in genetic and acquired IL-10 resistance. Gut, 2021, 70, 1023-1036.	6.1	58
10	Foxp3+ T reg cells control psoriasiform inflammation by restraining an IFN-lâ€“driven CD8+ T cell response. Journal of Experimental Medicine, 2018, 215, 1987-1998.	4.2	50
11	Alpha kinase 1 controls intestinal inflammation by suppressing the IL-12/Th1 axis. Nature Communications, 2018, 9, 3797.	5.8	47
12	Defining the microbial transcriptional response to colitis through integrated host and microbiome profiling. ISME Journal, 2016, 10, 2389-2404.	4.4	40
13	Gut microbiota: sculptors of the intestinal stem cell niche in health and inflammatory bowel disease. Gut Microbes, 2021, 13, 1990827.	4.3	32
14	Accurate identification and quantification of commensal microbiota bound by host immunoglobulins. Microbiome, 2021, 9, 33.	4.9	29
15	The bacteriology of pleural infection (TORPIDS): an exploratory metagenomics analysis through next generation sequencing. Lancet Microbe, The, 2022, 3, e294-e302.	3.4	22
16	Momâ€™s diet matters: Maternal prebiotic intake in mice reduces anxiety and alters brain gene expression and the fecal microbiome in offspring. Brain, Behavior, and Immunity, 2021, 91, 230-244.	2.0	20
17	CGAT-core: a python framework for building scalable, reproducible computational biology workflows. F1000Research, 0, 8, 377.	0.8	20
18	Genetic influences on attention deficit hyperactivity disorder symptoms from age 2 to 3: A quantitative and molecular genetic investigation. BMC Psychiatry, 2010, 10, 102.	1.1	17

#	Article	IF	Citations
19	Investigation of the serotonin 2C receptor gene in attention deficit hyperactivity disorder in UK samples. BMC Research Notes, 2009, 2, 71.	0.6	16
20	Testing for the mediating role of endophenotypes using molecular genetic data in a twin study of ADHD traits. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 982-992.	1.1	14
21	Genetic and environmental factors shape the host response to Helicobacter hepaticus: insights into IBD pathogenesis. Current Opinion in Microbiology, 2022, 65, 145-155.	2.3	9
22	Long-Term Effects of Gestational Nicotine Exposure and Food-Restriction on Gene Expression in the Striatum of Adolescent Rats. PLoS ONE, 2014, 9, e88896.	1.1	5
23	Pharmacologically induced weight loss is associated with distinct gut microbiome changes in obese rats. BMC Microbiology, 2022, 22, 91.	1.3	4
24	Tissue-dependent transcriptional and bacterial associations in primary sclerosing cholangitis-associated inflammatory bowel disease. Wellcome Open Research, 0, 6, 199.	0.9	0
25	Streamlined processing and analysis of 16S rRNA amplicon sequencing data with OCMS_16S and OCMSlooksy. Wellcome Open Research, 0, 7, 68.	0.9	0