Tao Long

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5771190/publications.pdf

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12 papers	2,350 citations	933447 10 h-index	1199594 12 g-index
15 all docs	15 docs citations	15 times ranked	5291 citing authors

#	Article	IF	CITATIONS
1	Nontargeted mass spectrometry of dried blood spots for interrogation of the human circulating metabolome. Journal of Mass Spectrometry, 2021, 56, e4772.	1.6	10
2	Prebiotic-Induced Anti-tumor Immunity Attenuates Tumor Growth. Cell Reports, 2020, 30, 1753-1766.e6.	6.4	105
3	Gut microbiota dependent anti-tumor immunity restricts melanoma growth in Rnf5 \hat{a} ° \hat{a} ° mice. Nature Communications, 2019, 10, 1492.	12.8	114
4	Membralin deficiency dysregulates astrocytic glutamate homeostasis, leading to ALS-like impairment. Journal of Clinical Investigation, 2019, 129, 3103-3120.	8.2	27
5	DDIS-05. PATIENT DERIVED NEUROSPHERE CULTURES IDENTIFY NOVEL CHEMOVULNERABILITIES IN GLIOBLASTOMA. Neuro-Oncology, 2018, 20, vi70-vi70.	1.2	0
6	Somatic APP gene recombination in Alzheimer's disease and normal neurons. Nature, 2018, 563, 639-645.	27.8	179
7	The fecal metabolome as a functional readout of the gut microbiome. Nature Genetics, 2018, 50, 790-795.	21.4	482
8	Whole-genome sequencing identifies common-to-rare variants associated with human blood metabolites. Nature Genetics, 2017, 49, 568-578.	21.4	341
9	Gut Microbiome-Based Metagenomic Signature for Non-invasive Detection of Advanced Fibrosis in Human Nonalcoholic Fatty Liver Disease. Cell Metabolism, 2017, 25, 1054-1062.e5.	16.2	748
10	Omega-3 fatty acids correlate with gut microbiome diversity and production of N-carbamylglutamate in middle aged and elderly women. Scientific Reports, 2017, 7, 11079.	3.3	174
11	Fast and accurate HLA typing from short-read next-generation sequence data with xHLA. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8059-8064.	7.1	118
12	Establishing the involvement of the novel gene <i>AGBL5</i> in retinitis pigmentosa by whole genome sequencing. Physiological Genomics, 2016, 48, 922-927.	2.3	29