Michael Wainberg

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/507644/publications.pdf

Version: 2024-02-01

30 papers 2,698 citations

15 h-index 677027 22 g-index

32 all docs $\begin{array}{c} 32 \\ \text{docs citations} \end{array}$

times ranked

32

5921 citing authors

#	Article	IF	CITATIONS
1	Deletion of Loss-of-Function–Intolerant Genes and Risk of 5 Psychiatric Disorders. JAMA Psychiatry, 2022, 79, 78.	6.0	8
2	Neurobiological, familial and genetic risk factors for dimensional psychopathology in the Adolescent Brain Cognitive Development study. Molecular Psychiatry, 2022, 27, 2731-2741.	4.1	14
3	Predicting causal genes from psychiatric genome-wide association studies using high-level etiological knowledge. Molecular Psychiatry, 2022, 27, 3095-3106.	4.1	4
4	Multiscale neural signatures of major depressive, anxiety, and stress-related disorders. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119 , .	3.3	5
5	Genetics of 35 blood and urine biomarkers in the UK Biobank. Nature Genetics, 2021, 53, 185-194.	9.4	377
6	Cannabis, schizophrenia genetic risk, and psychotic experiences: a cross-sectional study of 109,308 participants from the UK Biobank. Translational Psychiatry, 2021, 11, 211.	2.4	35
7	A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. Nature Genetics, 2021, 53, 638-649.	9.4	86
8	Symptom dimensions of major depression in a large community-based cohort. Psychological Medicine, 2021, , 1-8.	2.7	3
9	Clinical laboratory tests and five-year incidence of major depressive disorder: a prospective cohort study of 433,890 participants from the UK Biobank. Translational Psychiatry, 2021, 11, 380.	2.4	12
10	Association of accelerometer-derived sleep measures with lifetime psychiatric diagnoses: A cross-sectional study of 89,205 participants from the UK Biobank. PLoS Medicine, 2021, 18, e1003782.	3.9	28
11	Multiomic blood correlates of genetic risk identify presymptomatic disease alterations. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21813-21820.	3 . 3	22
12	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. PLoS Genetics, 2020, 16, e1008682.	1.5	31
13	CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities. Nature, 2020, 580, 136-141.	13.7	203
14	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
15	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		O
16	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		0
17	Rare protein-altering variants in ANGPTL7 lower intraocular pressure and protect against glaucoma. , 2020, 16, e1008682.		О
18	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. Nature Communications, 2019, 10, 4063.	5. 8	104

#	Article	IF	Citations
19	Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599.	9.4	592
20	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study. PLoS Medicine, 2019, 16, e1002982.	3.9	34
21	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
22	Title is missing!. , 2019, 16, e1002982.		0
23	Title is missing!. , 2019, 16, e1002982.		0
24	Title is missing!. , 2019, 16, e1002982.		0
25	Title is missing!. , 2019, 16, e1002982.		0
26	Title is missing!. , 2019, 16, e1002982.		0
27	Deep learning in biomedicine. Nature Biotechnology, 2018, 36, 829-838.	9.4	409
28	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	1.1	39
29	Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. Nature Communications, 2017, 8, 15178.	5.8	284
30	High-Throughput Characterization of Cascade type I-E CRISPR Guide Efficacy Reveals Unexpected PAM Diversity and Target Sequence Preferences. Genetics, 2017, 206, 1727-1738.	1.2	23