Menachem Fromer

List of Publications by Year
in descending order

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67 papers	33,210 citations	71061 41 h-index	106281 65 g-index
78 all docs	78 docs citations	78 times ranked	52793 citing authors

#	Article	IF	Citations
1	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	13.7	9,051
2	Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence. New England Journal of Medicine, 2014, 371, 2477-2487.	13.9	2,669
3	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	13.7	2,254
4	Patterns and rates of exonic de novo mutations in autism spectrum disorders. Nature, 2012, 485, 242-245.	13.7	1,597
5	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	13.7	1,510
6	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	13.5	1,422
7	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
8	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	13.7	1,305
9	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
10	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
11	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	7.1	952
12	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
13	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
14	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
15	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
16	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
17	Discovery and Statistical Genotyping of Copy-Number Variation from Whole-Exome Sequencing Depth. American Journal of Human Genetics, 2012, 91, 597-607.	2.6	513
18	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. Nature Neuroscience, 2016, 19, 1433-1441.	7.1	427

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19	The PsychENCODE project. Nature Neuroscience, 2015, 18, 1707-1712.	7.1	371
20	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. Nature Biotechnology, 2016, 34, 531-538.	9.4	273
21	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
22	Rare Complete Knockouts in Humans: Population Distribution and Significant Role in Autism Spectrum Disorders. Neuron, 2013, 77, 235-242.	3.8	242
23	Increased Frequency of De Novo Copy Number Variants in Congenital Heart Disease by Integrative Analysis of Single Nucleotide Polymorphism Array and Exome Sequence Data. Circulation Research, 2014, 115, 884-896.	2.0	229
24	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429.	2.9	225
25	Rates, distribution and implications of postzygotic mosaic mutations in autism spectrum disorder. Nature Neuroscience, 2017, 20, 1217-1224.	7.1	212
26	Viral adaptation to host: a proteomeâ€based analysis of codon usage and amino acid preferences. Molecular Systems Biology, 2009, 5, 311.	3.2	209
27	Patterns of genic intolerance of rare copy number variation in 59,898 human exomes. Nature Genetics, 2016, 48, 1107-1111.	9.4	167
28	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	9.4	154
29	Identification of Small Exonic CNV from Whole-Exome Sequence Data and Application to Autism Spectrum Disorder. American Journal of Human Genetics, 2013, 93, 607-619.	2.6	136
30	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. American Journal of Human Genetics, 2018, 102, 1169-1184.	2.6	128
31	Exome sequencing in schizophrenia-affected parentâ€“offspring trios reveals risk conferred by protein-coding de novo mutations. Nature Neuroscience, 2020, 23, 185-193.	7.1	125
32	Using XHMM Software to Detect Copy Number Variation in Wholeâ€Exome Sequencing Data. Current Protocols in Human Genetics, 2014, 81, 7.23.1-21.	3.5	118
33	Efficient algorithms for accurate hierarchical clustering of huge datasets: tackling the entire protein space. Bioinformatics, 2008, 24, i41-i49.	1.8	100
34	The AURORA Study: a longitudinal, multimodal library of brain biology and function after traumatic stress exposure. Molecular Psychiatry, 2020, 25, 283-296.	4.1	92
35	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	2.6	91
36	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. Genome Medicine, 2017, 9, 114.	3.6	86

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37	Arc Requires PSD95 for Assembly into Postsynaptic Complexes Involved with Neural Dysfunction and Intelligence. Cell Reports, 2017, 21, 679-691.	2.9	79
38	Codon usage is associated with the evolutionary age of genes in metazoan genomes. BMC Evolutionary Biology, 2009, 9, 285.	3.2	60
39	ProtoNet 4.0: A hierarchical classification of one million protein sequences. Nucleic Acids Research, 2004, 33, D216-D218.	6.5	56
40	Tradeoff Between Stability and Multispecificity in the Design of Promiscuous Proteins. PLoS Computational Biology, 2009, 5, e1000627.	1.5	54
41	Vg1 RBP intracellular distribution and evolutionarily conserved expression at multiple stages during development. Mechanisms of Development, 1999, 88, 101-106.	1.7	53
42	Transforming Psychiatry into Data-Driven Medicine with Digital Measurement Tools. Npj Digital Medicine, 2018, 1, 37.	5.7	49
43	Practical Guidelines for High-Resolution Epigenomic Profiling of Nucleosomal Histones in Postmortem Human Brain Tissue. Biological Psychiatry, 2017, 81, 162-170.	0.7	48
44	Dead-end elimination for multistate protein design. Journal of Computational Chemistry, 2007, 28, 2122-2129.	1.5	41
45	Genomic aberrations in cervical adenocarcinomas in Hong Kong Chinese women. International Journal of Cancer, 2015, 137, 776-783.	2.3	39
46	A functional hierarchical organization of the protein sequence space. BMC Bioinformatics, 2004, 5, 196.	1.2	32
47	A framework for the detection of de novo mutations in family-based sequencing data. European Journal of Human Genetics, 2017, 25, 227-233.	1.4	29
48	Toward a Mobile Platform for Real-world Digital Measurement of Depression: User-Centered Design, Data Quality, and Behavioral and Clinical Modeling. JMIR Mental Health, 2021, 8, e27589.	1.7	29
49	Developmental Trajectories of Impaired Community Functioning in Schizophrenia. JAMA Psychiatry, 2016, 73, 48.	6.0	26
50	The leader peptide of MMTV Env precursor localizes to the nucleoli in MMTV-derived T cell lymphomas and interacts with nucleolar protein B23. Virology, 2003, 313, 22-32.	1.1	20
51	A computational framework to empower probabilistic protein design. Bioinformatics, 2008, 24, i214-i222.	1.8	20
52	Accurate prediction for atomicâ€level protein design and its application in diversifying the nearâ€optimal sequence space. Proteins: Structure, Function and Bioinformatics, 2009, 75, 682-705.	1.5	17
53	Design of multispecific protein sequences using probabilistic graphical modeling. Proteins: Structure, Function and Bioinformatics, 2010, 78, 530-547.	1.5	16
54	Genetic Effect of Chemotherapy Exposure in Children of Testicular Cancer Survivors. Clinical Cancer Research, 2016, 22, 2183-2189.	3.2	15

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55	A holistic approach for suppression of COVID-19 spread in workplaces and universities. PLoS ONE, 2021, 16, e0254798.	1.1	13
56	SPRINT: side-chain prediction inference toolbox for multistate protein design. Bioinformatics, 2010, 26, 2466-2467.	1.8	11
57	PANDORA: analysis of protein and peptide sets through the hierarchical integration of annotations. Nucleic Acids Research, 2010, 38, W84-W89.	6.5	11
58	Characterization of Single Gene Copy Number Variants in Schizophrenia. Biological Psychiatry, 2020, 87, 736-744.	0.7	10
59	Recovering key biological constituents through sparse representation of gene expression. Bioinformatics, 2011, 27, 655-661.	1.8	9
60	Expansion of tandem repeats in sea anemone Nematostella vectensis proteome: A source for gene novelty?. BMC Genomics, 2009, 10, 593.	1.2	7
61	Unperturbed expression bias of imprinted genes in schizophrenia. Nature Communications, 2018, 9, 2914.	5.8	6
62	When Less Is More: Improving Classification of Protein Families with a Minimal Set of Global Features. Lecture Notes in Computer Science, 2007, , 12-24.	1.0	5
63	Exposing the co-adaptive potential of proteinâ€“protein interfaces through computational sequence design. Bioinformatics, 2010, 26, 2266-2272.	1.8	4
64	Rare Structural Variants. , 2015, , 45-56.		2
65	Prediction of Low Energy Protein Side Chain Configurations Using Markov Random Fields. Statistics in the Health Sciences, 2012, , 255-284.	0.2	1
66	Search Algorithms. , 2009, , .		0
67	Finding k-best solutions using LP relaxations. , 2010, , .		0