Michael E Zwick

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2285550/publications.pdf

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79	7,149	186265	88630
papers	citations	28 h-index	70 g-index

85	85	85	13308
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	27.8	2,254
2	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	28.9	1,422
3	Microarray-based genomic selection for high-throughput resequencing. Nature Methods, 2007, 4, 907-909.	19.0	374
4	High-Throughput Variation Detection and Genotyping Using Microarrays. Genome Research, 2001, 11, 1913-1925.	5.5	258
5	Dysbiosis, inflammation, and response to treatment: a longitudinal study of pediatric subjects with newly diagnosed inflammatory bowel disease. Genome Medicine, 2016, 8, 75.	8.2	211
6	Structure and Complexity of a Bacterial Transcriptome. Journal of Bacteriology, 2009, 191, 3203-3211.	2.2	191
7	Haplotype Inference in Random Population Samples. American Journal of Human Genetics, 2002, 71, 1129-1137.	6.2	176
8	Genomic characterization of the Bacillus cereus sensu lato species: Backdrop to the evolution of Bacillus anthracis. Genome Research, 2012, 22, 1512-1524.	5.5	148
9	Genome-Wide Association Study Identifies African-Specific Susceptibility Loci in African Americans With Inflammatory Bowel Disease. Gastroenterology, 2017, 152, 206-217.e2.	1.3	120
10	Microarray-based mutation detection in thedystrophingene. Human Mutation, 2008, 29, 1091-1099.	2.5	113
11	Identification of novel FMR1 variants by massively parallel sequencing in developmentally delayed males. American Journal of Medical Genetics, Part A, 2010, 152A, 2512-2520.	1.2	108
12	Genomic characterization of the Yersinia genus. Genome Biology, 2010, 11, R1.	9.6	103
13	Genetic Variation in Rates of Nondisjunction: Association of Two Naturally Occurring Polymorphisms in the Chromokinesin nod With Increased Rates of Nondisjunction in Drosophila melanogaster. Genetics, 1999, 152, 1605-1614.	2.9	93
14	Mutations in the human SC4MOL gene encoding a methyl sterol oxidase cause psoriasiform dermatitis, microcephaly, and developmental delay. Journal of Clinical Investigation, 2011, 121, 976-984.	8.2	91
15	Genetic contributors to risk of schizophrenia in the presence of a 22q11.2 deletion. Molecular Psychiatry, 2021, 26, 4496-4510.	7.9	87
16	PATTERNS OFGENETICVARIATION INMENDELIAN ANDCOMPLEXTRAITS. Annual Review of Genomics and Human Genetics, 2000, 1, 387-407.	6.2	78
17	Novel features of 3q29 deletion syndrome: Results from the 3q29 registry. American Journal of Medical Genetics, Part A, 2016, 170, 999-1006.	1.2	73
18	Characterization of Genetic Loci That Affect Susceptibility to Inflammatory Bowel Diseases in African Americans. Gastroenterology, 2015, 149, 1575-1586.	1.3	65

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19	Microarray-based resequencing of multiple Bacillus anthracis isolates. Genome Biology, 2004, 6, R10.	9.6	64
20	Clinical and Genomic Correlates of Neutrophil Reactive Oxygen Species Production in Pediatric Patients With Crohnâ€™s Disease. Gastroenterology, 2018, 154, 2097-2110.	1.3	63
21	Discrepancies in dbSNP confirmation rates and allele frequency distributions from varying genotyping error rates and patterns. Bioinformatics, 2004, 20, 1022-1032.	4.1	52
22	Exome Sequencing Identifies a Novel FOXP3 Mutation in a 2â€Generation Family With Inflammatory Bowel Disease. Journal of Pediatric Gastroenterology and Nutrition, 2014, 58, 561-568.	1.8	47
23	Complete Sequence of the 22q11.2 Allele in 1,053 Subjects with 22q11.2 Deletion Syndrome Reveals Modifiers of Conotruncal Heart Defects. American Journal of Human Genetics, 2020, 106, 26-40.	6.2	42
24	Copy number abnormalities in sporadic canine colorectal cancers. Genome Research, 2010, 20, 341-350.	5.5	40
25	New discoveries in schizophrenia genetics reveal neurobiological pathways: A review of recent findings. European Journal of Medical Genetics, 2015, 58, 704-714.	1.3	39
26	SeqAnt: A web service to rapidly identify and annotate DNA sequence variations. BMC Bioinformatics, 2010, 11, 471.	2.6	38
27	Neuropsychiatric phenotypes and a distinct constellation of ASD features in 3q29 deletion syndrome: results from the 3q29 registry. Molecular Autism, 2019, 10, 30.	4.9	38
28	Inherited genetic susceptibility to acute lymphoblastic leukemia in Down syndrome. Blood, 2019, 134, 1227-1237.	1.4	37
29	Dissecting Allele Architecture of Early Onset IBD Using High-Density Genotyping. PLoS ONE, 2015, 10, e0128074.	2.5	35
30	Excess variants in AFF2 detected by massively parallel sequencing of males with autism spectrum disorder. Human Molecular Genetics, 2012, 21, 4356-4364.	2.9	34
31	PEMapper and PECaller provide a simplified approach to whole-genome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1923-E1932.	7.1	31
32	Brief Report: Susceptibility to Childhoodâ€Onset Rheumatoid Arthritis: Investigation of a Weighted Genetic Risk Score That Integrates Cumulative Effects of Variants at Five Genetic Loci. Arthritis and Rheumatism, 2013, 65, 1663-1667.	6.7	29
33	Bystro: rapid online variant annotation and natural-language filtering at whole-genome scale. Genome Biology, 2018, 19, 14.	8.8	29
34	Genome-Wide Association Study of Down Syndrome-Associated Atrioventricular Septal Defects. G3: Genes, Genomes, Genetics, 2015, 5, 1961-1971.	1.8	28
35	Rapid Identification of Genetic Modifications in Bacillus anthracis Using Whole Genome Draft Sequences Generated by 454 Pyrosequencing. PLoS ONE, 2010, 5, e12397.	2.5	27
36	Array-Based FMR1 Sequencing and Deletion Analysis in Patients with a Fragile X Syndromeâ€“Like Phenotype. PLoS ONE, 2010, 5, e9476.	2.5	26

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37	Multiplex Chromosomal Exome Sequencing Accelerates Identification of ENU-Induced Mutations in the Mouse. G3: Genes, Genomes, Genetics, 2012, 2, 143-150.	1.8	25
38	Contribution of copy-number variation to Down syndromeâ€“associated atrioventricular septal defects. Genetics in Medicine, 2015, 17, 554-560.	2.4	24
39	Enhanced Contribution of HLA in Pediatric Onset Ulcerative Colitis. Inflammatory Bowel Diseases, 2018, 24, 829-838.	1.9	23
40	Targeted sequencing of the human X chromosome exome. Genomics, 2011, 98, 260-265.	2.9	22
41	Identification of rare X-linked neuroligin variants by massively parallel sequencing in males with autism spectrum disorder. Molecular Autism, 2012, 3, 8.	4.9	22
42	Genetic variants and pathways implicated in a pediatric inflammatory bowel disease cohort. Genes and Immunity, 2019, 20, 131-142.	4.1	22
43	Whole-genome sequencing of African Americans implicates differential genetic architecture in inflammatory bowel disease. American Journal of Human Genetics, 2021, 108, 431-445.	6.2	21
44	Classic Weinstein: Tetrad Analysis, Genetic Variation and Achiasmate Segregation in Drosophila and Humans. Genetics, 1999, 152, 1615-1629.	2.9	21
45	Genotyping of Bacillus cereus Strains by Microarray-Based Resequencing. PLoS ONE, 2008, 3, e2513.	2.5	20
46	Common NOD2 risk variants in African Americans with CrohnÊ¼s disease are due exclusively to recent Caucasian admixture. Inflammatory Bowel Diseases, 2012, 18, 2357-2359.	1.9	18
47	Applying Rapid Genome Sequencing Technologies To Characterize Pathogen Genomes. Analytical Chemistry, 2008, 80, 520-528.	6.5	17
48	Disruption of RAB40AL function leads to Martinâ€“Probst syndrome, a rare X-linked multisystem neurodevelopmental human disorder. Journal of Medical Genetics, 2012, 49, 332-340.	3.2	17
49	Combining Microarrayâ€based Genomic Selection (MGS) with the Illumina Genome Analyzer Platform to Sequence Diploid Target Regions. Annals of Human Genetics, 2009, 73, 502-513.	0.8	16
50	Empirical Evaluation of Oligonucleotide Probe Selection for DNA Microarrays. PLoS ONE, 2010, 5, e9921.	2.5	14
51	Evaluating Rare Variants in Complex Disorders Using Next-Generation Sequencing. Current Psychiatry Reports, 2013, 15, 349.	4.5	14
52	Identifying genetic factors that contribute to the increased risk of congenital heart defects in infants with Down syndrome. Scientific Reports, 2020, 10, 18051.	3.3	14
53	New phenotypes associated with 3q29 duplication syndrome: Results from the 3q29 registry. American Journal of Medical Genetics, Part A, 2020, 182, 1152-1166.	1.2	14
54	Site- and Taxa-Specific Disease-Associated Oral Microbial Structures Distinguish Inflammatory Bowel Diseases. Inflammatory Bowel Diseases, 2021, 27, 1889-1900.	1.9	14

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55	Analysis of Copy Number Variants on Chromosome 21 in Down Syndrome-Associated Congenital Heart Defects. G3: Genes, Genomes, Genetics, 2018, 8, 105-111.	1.8	13
56	Technology: A genome sequencing center in every lab. European Journal of Human Genetics, 2005, 13, 1167-1168.	2.8	11
57	Omicseq: a web-based search engine for exploring omics datasets. Nucleic Acids Research, 2017, 45, W445-W452.	14.5	11
58	Genetic and Transcriptomic Variation Linked to Neutrophil Granulocyteâ€“Macrophage Colony-Stimulating Factor Signaling in Pediatric Crohnâ€™s Disease. Inflammatory Bowel Diseases, 2019, 25, 547-560.	1.9	8
59	Genetic variation and linkage disequilibrium in Bacillus anthracis. Scientific Reports, 2011, 1, 169.	3.3	7
60	Variant ATRX Syndrome with Dysfunction ofATRXandMAGT1Genes. Human Mutation, 2014, 35, 58-62.	2.5	7
61	Induced pluripotent stem cells from subjects with Lesch-Nyhan disease. Scientific Reports, 2021, 11, 8523.	3.3	7
62	Organizing core facilities as force multipliers: strategies for research universities. Journal of Biomolecular Techniques, 2021, 32, 36-41.	1.5	7
63	Identification of PSMB5 as a genetic modifier of fragile Xâ€“associated tremor/ataxia syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	7
64	Microarray oligonucleotide probe designer: a Web service. Open Access Bioinformatics, 2010, 2, 145.	0.9	5
65	Identifying susceptibility genes for primary ovarian insufficiency on the high-risk genetic background of a fragile X premutation. Fertility and Sterility, 2021, 116, 843-854.	1.0	5
66	Signatures of somatic mutations and gene expression from p16INK4A positive head and neck squamous cell carcinomas (HNSCC). PLoS ONE, 2020, 15, e0238497.	2.5	5
67	Novel Missense CNTNAP2 Variant Identified in Two Consanguineous Pakistani Families With Developmental Delay, Epilepsy, Intellectual Disability, and Aggressive Behavior. Frontiers in Neurology, 0, 13, .	2.4	5
68	Metabolic Pathway Analysis and Effectiveness of Tamoxifen in Danish Breast Cancer Patients. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 582-590.	2.5	4
69	Neutrophil GM-CSF signaling in inflammatory bowel disease patients is influenced by non-coding genetic variants. Scientific Reports, 2019, 9, 9168.	3.3	3
70	Bayesian Pathway Analysis for Complex Interactions. American Journal of Epidemiology, 2020, 189, 1610-1622.	3.4	3
71	Sex-specific recombination patterns predict parent of origin for recurrent genomic disorders. BMC Medical Genomics, 2021, 14, 154.	1.5	2
72	Reply to PlÃ¼ss et al.: The strength of PEMapper/PECaller lies in unbiased calling using large sample sizes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8323-E8323.	7.1	1

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73	SeqAnt. , 2017, , .		1
74	Organizing core facilities as force multipliers: strategies for research universities. Journal of Biomolecular Techniques, 2021, , jbt.2021-3202-002.	1.5	0
75	Staff Scientist Perspectives on Onboarding and Professional Development: A Case Study. Journal of Biomolecular Techniques, 2021, 32, jbt.21-3204-001.	1.5	0
76	Title is missing!. , 2020, 15, e0238497.		0
77	Title is missing!. , 2020, 15, e0238497.		0
78	Title is missing!. , 2020, 15, e0238497.		0
79	Title is missing!. , 2020, 15, e0238497.		0