Michael E Zwick

List of Publications by Year
in descending order

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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	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
2	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
3	Induced pluripotent stem cells from subjects with Lesch-Nyhan disease. Scientific Reports, 2021, 11, 8523.	3.3	7
4	Organizing core facilities as force multipliers: strategies for research universities. Journal of Biomolecular Techniques, 2021, 32, 36-41.	1.5	7
5	Site- and Taxa-Specific Disease-Associated Oral Microbial Structures Distinguish Inflammatory Bowel Diseases. Inflammatory Bowel Diseases, 2021, 27, 1889-1900.	1.9	14
6	Sex-specific recombination patterns predict parent of origin for recurrent genomic disorders. BMC Medical Genomics, 2021, 14, 154.	1.5	2
7	Organizing core facilities as force multipliers: strategies for research universities. Journal of Biomolecular Techniques, 2021, , jbt.2021-3202-002.	1.5	0
8	Staff Scientist Perspectives on Onboarding and Professional Development: A Case Study. Journal of Biomolecular Techniques, 2021, 32, jbt.21-3204-001.	1.5	0
9	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
10	Genetic contributors to risk of schizophrenia in the presence of a 22q11.2 deletion. Molecular Psychiatry, 2021, 26, 4496-4510.	7.9	87
11	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
12	Bayesian Pathway Analysis for Complex Interactions. American Journal of Epidemiology, 2020, 189, 1610-1622.	3.4	3
13	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
14	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
15	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
16	Metabolic Pathway Analysis and Effectiveness of Tamoxifen in Danish Breast Cancer Patients. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 582-590.	2.5	4
17	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
18	Title is missing!. , 2020, 15, e0238497.		0

#	Article	IF	Citations
19	Title is missing!. , 2020, 15, e0238497.		0
20	Title is missing!. , 2020, 15, e0238497.		0
21	Title is missing!. , 2020, 15, e0238497.		0
22	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
23	Inherited genetic susceptibility to acute lymphoblastic leukemia in Down syndrome. Blood, 2019, 134, 1227-1237.	1.4	37
24	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
25	Neutrophil GM-CSF signaling in inflammatory bowel disease patients is influenced by non-coding genetic variants. Scientific Reports, 2019, 9, 9168.	3.3	3
26	Genetic variants and pathways implicated in a pediatric inflammatory bowel disease cohort. Genes and Immunity, 2019, 20, 131-142.	4.1	22
27	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
28	Enhanced Contribution of HLA in Pediatric Onset Ulcerative Colitis. Inflammatory Bowel Diseases, 2018, 24, 829-838.	1.9	23
29	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
30	Bystro: rapid online variant annotation and natural-language filtering at whole-genome scale. Genome Biology, 2018, 19, 14.	8.8	29
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	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
33	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
34	SeqAnt. , 2017, , .		1
35	Omicseq: a web-based search engine for exploring omics datasets. Nucleic Acids Research, 2017, 45, W445-W452.	14.5	11
36	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

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37	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
38	Genome-Wide Association Study of Down Syndrome-Associated Atrioventricular Septal Defects. G3: Genes, Genomes, Genetics, 2015, 5, 1961-1971.	1.8	28
39	Dissecting Allele Architecture of Early Onset IBD Using High-Density Genotyping. PLoS ONE, 2015, 10, e0128074.	2.5	35
40	Contribution of copy-number variation to Down syndromeâ€“associated atrioventricular septal defects. Genetics in Medicine, 2015, 17, 554-560.	2.4	24
41	Characterization of Genetic Loci That Affect Susceptibility to Inflammatory Bowel Diseases in African Americans. Gastroenterology, 2015, 149, 1575-1586.	1.3	65
42	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
43	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
44	Variant ATRX Syndrome with Dysfunction ofATRXandMAGT1Genes. Human Mutation, 2014, 35, 58-62.	2.5	7
45	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	27.8	2,254
46	Evaluating Rare Variants in Complex Disorders Using Next-Generation Sequencing. Current Psychiatry Reports, 2013, 15, 349.	4.5	14
47	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
48	Multiplex Chromosomal Exome Sequencing Accelerates Identification of ENU-Induced Mutations in the Mouse. G3: Genes, Genomes, Genetics, 2012, 2, 143-150.	1.8	25
49	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
50	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
51	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
52	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
53	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
54	Targeted sequencing of the human X chromosome exome. Genomics, 2011, 98, 260-265.	2.9	22

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55	Genetic variation and linkage disequilibrium in Bacillus anthracis. Scientific Reports, 2011, 1, 169.	3.3	7
56	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
57	SeqAnt: A web service to rapidly identify and annotate DNA sequence variations. BMC Bioinformatics, 2010, 11, 471.	2.6	38
58	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
59	Array-Based FMR1 Sequencing and Deletion Analysis in Patients with a Fragile X Syndromeâ€“Like Phenotype. PLoS ONE, 2010, 5, e9476.	2.5	26
60	Microarray oligonucleotide probe designer: a Web service. Open Access Bioinformatics, 2010, 2, 145.	0.9	5
61	Copy number abnormalities in sporadic canine colorectal cancers. Genome Research, 2010, 20, 341-350.	5.5	40
62	Empirical Evaluation of Oligonucleotide Probe Selection for DNA Microarrays. PLoS ONE, 2010, 5, e9921.	2.5	14
63	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
64	Genomic characterization of the Yersinia genus. Genome Biology, 2010, 11, R1.	9.6	103
65	Structure and Complexity of a Bacterial Transcriptome. Journal of Bacteriology, 2009, 191, 3203-3211.	2.2	191
66	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
67	Microarray-based mutation detection in thedystrophingene. Human Mutation, 2008, 29, 1091-1099.	2.5	113
68	Applying Rapid Genome Sequencing Technologies To Characterize Pathogen Genomes. Analytical Chemistry, 2008, 80, 520-528.	6.5	17
69	Genotyping of Bacillus cereus Strains by Microarray-Based Resequencing. PLoS ONE, 2008, 3, e2513.	2.5	20
70	Microarray-based genomic selection for high-throughput resequencing. Nature Methods, 2007, 4, 907-909.	19.0	374
71	Technology: A genome sequencing center in every lab. European Journal of Human Genetics, 2005, 13, 1167-1168.	2.8	11
72	Discrepancies in dbSNP confirmation rates and allele frequency distributions from varying genotyping error rates and patterns. Bioinformatics, 2004, 20, 1022-1032.	4.1	52

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73	Microarray-based resequencing of multiple Bacillus anthracis isolates. Genome Biology, 2004, 6, R10.	9.6	64
74	Haplotype Inference in Random Population Samples. American Journal of Human Genetics, 2002, 71, 1129-1137.	6.2	176
75	High-Throughput Variation Detection and Genotyping Using Microarrays. Genome Research, 2001, 11, 1913-1925.	5.5	258
76	PATTERNS OFGENETICVARIATION INMENDELIAN ANDCOMPLEXTRAITS. Annual Review of Genomics and Human Genetics, 2000, 1, 387-407.	6.2	78
77	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
78	Classic Weinstein: Tetrad Analysis, Genetic Variation and Achiasmate Segregation in Drosophila and Humans. Genetics, 1999, 152, 1615-1629.	2.9	21
79	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