E Michael Gertz

List of Publications by Year
in descending order

42 papers	5,635 citations	331670 21 h-index	289244 40 g-index
46 all docs	46 docs citations	46 times ranked	11455 citing authors

#	Article	IF	Citations
1	Deconvolving Clinically Relevant Cellular Immune Cross-talk from Bulk Gene Expression Using CODEFACS and LIRICS Stratifies Patients with Melanoma to Antiâ€“PD-1 Therapy. Cancer Discovery, 2022, 12, 1088-1105.	9.4	28
2	Tumor heterogeneity assessed by sequencing and fluorescence in situ hybridization (FISH) data. Bioinformatics, 2021, 37, 4704-4711.	4.1	5
3	Single Cell Genetic Profiling of Tumors of Breast Cancer Patients Aged 50 Years and Older Reveals Enormous Intratumor Heterogeneity Independent of Individual Prognosis. Cancers, 2021, 13, 3366.	3.7	8
4	High Levels of Chromosomal Copy Number Alterations and TP53 Mutations Correlate with Poor Outcome in Younger Breast Cancer Patients. American Journal of Pathology, 2020, 190, 1643-1656.	3.8	10
5	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. Journal of Computational Biology, 2020, 27, 565-598.	1.6	10
6	Single-Cellâ€“Derived Primary Rectal Carcinoma Cell Lines Reflect Intratumor Heterogeneity Associated with Treatment Response. Clinical Cancer Research, 2020, 26, 3468-3480.	7.0	9
7	Aneuploidy, TP53 mutation, and amplification of MYC correlate with increased intratumor heterogeneity and poor prognosis of breast cancer patients. Genes Chromosomes and Cancer, 2018, 57, 165-175.	2.8	27
8	Tumor Copy Number Data Deconvolution Integrating Bulk and Single-cell Sequencing Data. , 2018, , .		0
9	The evolution of single cell-derived colorectal cancer cell lines is dominated by the continued selection of tumor-specific genomic imbalances, despite random chromosomal instability. Carcinogenesis, 2018, 39, 993-1005.	2.8	20
10	Genome-Wide Changes in Protein Translation Efficiency Are Associated with Autism. Genome Biology and Evolution, 2018, 10, 1902-1919.	2.5	15
11	A commonSLC26A4-linked haplotype underlying non-syndromic hearing loss with enlargement of the vestibular aqueduct. Journal of Medical Genetics, 2017, 54, 665-673.	3.2	29
12	Phylogenetic analysis of multiple FISH markers in oral tongue squamous cell carcinoma suggests that a diverse distribution of copy number changes is associated with poor prognosis. International Journal of Cancer, 2016, 138, 98-109.	5.1	16
13	FISHtrees 3.0: Tumor Phylogenetics Using a Ploidy Probe. PLoS ONE, 2016, 11, e0158569.	2.5	13
14	Inferring models of multiscale copy number evolution for single-tumor phylogenetics. Bioinformatics, 2015, 31, i258-i267.	4.1	28
15	Potential non-B DNA regions in the human genome are associated with higher rates of nucleotide mutation and expression variation. Nucleic Acids Research, 2014, 42, 12367-12379.	14.5	45
16	Inherited biallelic CSF3R mutations in severe congenital neutropenia. Blood, 2014, 123, 3811-3817.	1.4	79
17	PSEUDOMARKER 2.0: efficient computation of likelihoods using NOMAD. BMC Bioinformatics, 2014, 15, 47.	2.6	26
18	JAGN1 deficiency causes aberrant myeloid cell homeostasis and congenital neutropenia. Nature Genetics, 2014, 46, 1021-1027.	21.4	119

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19	Accuracy and coverage assessment of Oryctolagus cuniculus (rabbit) genes encoding immunoglobulins in the whole genome sequence assembly (OryCun2.0) and localization of the IGH locus to chromosome 20. Immunogenetics, 2013, 65, 749-762.	2.4	19
20	Linkage analysis of a large African family segregating stuttering suggests polygenic inheritance. Human Genetics, 2013, 132, 385-396.	3.8	35
21	Loss-of-function mutations in the IL-21 receptor gene cause a primary immunodeficiency syndrome. Journal of Experimental Medicine, 2013, 210, 433-443.	8.5	186
22	Deficiency Of JAGN1 Causes Severe Congenital Neutropenia Associated With Defective Secretory Pathway and Aberrant Myeloid Cell Homeostasis. Blood, 2013, 122, 439-439.	1.4	2
23	Inherited Biallelic Loss-Of-Function Mutations In CSF3R Define a Novel Type Of Severe Congenital Neutropenia With Full Myeloid Cell Maturation and Refractoriness To RhG-CSF. Blood, 2013, 122, 1025-1025.	1.4	0
24	The phenotype of human STK4 deficiency. Blood, 2012, 119, 3450-3457.	1.4	286
25	Deleterious Mutations in LRBA Are Associated with a Syndrome of Immune Deficiency and Autoimmunity. American Journal of Human Genetics, 2012, 90, 986-1001.	6.2	452
26	Comparative Analysis of Genome Sequences of the Th2 Cytokine Region of Rabbit (Oryctolagus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4 III.S7236.	1.0	7
27	The Phenotype of Human STK4 Deficiency. Blood, 2011, 118, 692-692.	1.4	2
28	Using an iterative linear solver in an interior-point method for generating support vector machines. Computational Optimization and Applications, 2010, 47, 431-453.	1.6	7
29	Mutations in STAT3 and diagnostic guidelines for hyper-IgE syndrome. Journal of Allergy and Clinical Immunology, 2010, 125, 424-432.e8.	2.9	247
30	PSI-BLAST pseudocounts and the minimum description length principle. Nucleic Acids Research, 2009, 37, 815-824.	14.5	120
31	Evaluating annotations of an Agilent expression chip suggests that many features cannot be interpreted. BMC Genomics, 2009, 10, 566.	2.8	8
32	Inflammatory Bowel Disease and Mutations Affecting the Interleukin-10 Receptor. New England Journal of Medicine, 2009, 361, 2033-2045.	27.0	1,244
33	Relevance of biallelic versus monoallelic TNFRSF13B mutations in distinguishing disease-causing from risk-increasing TNFRSF13B variants in antibody deficiency syndromes. Blood, 2009, 113, 1967-1976.	1.4	254
34	The effectiveness of position- and composition-specific gap costs for protein similarity searches. Bioinformatics, 2008, 24, i15-i23.	4.1	6
35	Composition-based statistics and translated nucleotide searches: Improving the TBLASTN module of BLAST. BMC Biology, 2006, 4, 41.	3.8	420
36	WindowMasker: window-based masker for sequenced genomes. Bioinformatics, 2006, 22, 134-141.	4.1	253

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37	Retrieval accuracy, statistical significance and compositional similarity in protein sequence database searches. Nucleic Acids Research, 2006, 34, 5966-5973.	14.5	53
38	A Fast and Symmetric DUST Implementation to Mask Low-Complexity DNA Sequences. Journal of Computational Biology, 2006, 13, 1028-1040.	1.6	434
39	Protein database searches using compositionally adjusted substitution matrices. FEBS Journal, 2005, 272, 5101-5109.	4.7	881
40	A primal-dual trust region algorithm for nonlinear optimization. Mathematical Programming, 2004, 100, 49.	2.4	14
41	A quasi-Newton trust-region method. Mathematical Programming, 2004, 100, 447.	2.4	27
42	Object-oriented software for quadratic programming. ACM Transactions on Mathematical Software, 2003, 29, 58-81.	2.9	184