

Gabor T Marth

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

48 papers	48,374 citations	27 h-index	53 g-index
53 ext. papers	66,493 ext. citations	14 avg, IF	6.93 L-index

#	Paper	IF	Citations
48	Comprehensive variant calling from whole-genome sequencing identifies a complex inversion that disrupts ZFPM2 in familial congenital diaphragmatic hernia.. <i>Molecular Genetics & Genomic Medicine</i> , 2022 , e1888	2.3	1
47	Gene.iobio: an interactive web tool for versatile, clinically-driven variant interrogation and prioritization. <i>Scientific Reports</i> , 2021 , 11, 20307	4.9	1
46	Novel temporal and spatial patterns of metastatic colonization from breast cancer rapid-autopsy tumor biopsies. <i>Genome Medicine</i> , 2021 , 13, 170	14.4	1
45	OncoGEMINI: software for investigating tumor variants from multiple biopsies with integrated cancer annotations. <i>Genome Medicine</i> , 2021 , 13, 46	14.4	
44	Mobile element insertions and associated structural variants in longitudinal breast cancer samples. <i>Scientific Reports</i> , 2021 , 11, 13020	4.9	1
43	The Extracellular Milieu of 's Lytic Cycle Drives Lab Adaptation, Primarily by Transcriptional Reprogramming. <i>MSystems</i> , 2021 , e0119621	7.6	3
42	MYC Drives Temporal Evolution of Small Cell Lung Cancer Subtypes by Reprogramming Neuroendocrine Fate. <i>Cancer Cell</i> , 2020 , 38, 60-78.e12	24.3	92
41	Genomic analyses implicate noncoding de novo variants in congenital heart disease. <i>Nature Genetics</i> , 2020 , 52, 769-777	36.3	33
40	The stochastic nature of errors in next-generation sequencing of circulating cell-free DNA. <i>PLoS ONE</i> , 2020 , 15, e0229063	3.7	4
39	Somalier: rapid relatedness estimation for cancer and germline studies using efficient genome sketches. <i>Genome Medicine</i> , 2020 , 12, 62	14.4	10
38	Deep whole-genome sequencing of multiple proband tissues and parental blood reveals the complex genetic etiology of congenital diaphragmatic hernias. <i>Human Genetics and Genomics Advances</i> , 2020 , 1, 100008-100008	0.8	3
37	ped_draw: pedigree drawing with ease. <i>BMC Bioinformatics</i> , 2020 , 21, 569	3.6	0
36	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019 , 10, 1784	17.4	346
35	Genepanel.iobio - an easy to use web tool for generating disease- and phenotype-associated gene lists. <i>BMC Medical Genomics</i> , 2019 , 12, 190	3.7	2
34	GIGGLE: a search engine for large-scale integrated genome analysis. <i>Nature Methods</i> , 2018 , 15, 123-126	21.6	71
33	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. <i>Nature Genetics</i> , 2018 , 50, 727-736	36.3	156
32	Ongoing clonal evolution in chronic myelomonocytic leukemia on hypomethylating agents: a computational perspective. <i>Leukemia</i> , 2018 , 32, 2049-2054	10.7	2

31	Automated size selection for short cell-free DNA fragments enriches for circulating tumor DNA and improves error correction during next generation sequencing. <i>PLoS ONE</i> , 2018 , 13, e0197333	3.7	36
30	Whole-genome analysis for effective clinical diagnosis and gene discovery in early infantile epileptic encephalopathy. <i>Npj Genomic Medicine</i> , 2018 , 3, 22	6.2	42
29	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. <i>Science</i> , 2018 , 362,	33.3	134
28	Principles and Recommendations for Standardizing the Use of the Next-Generation Sequencing Variant File in Clinical Settings. <i>Journal of Molecular Diagnostics</i> , 2017 , 19, 417-426	5.1	13
27	Combating subclonal evolution of resistant cancer phenotypes. <i>Nature Communications</i> , 2017 , 8, 1231	17.4	79
26	Rapid clinical diagnostic variant investigation of genomic patient sequencing data with web tools. <i>Journal of Clinical and Translational Science</i> , 2017 , 1, 381-386	0.4	6
25	Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. <i>Genome Biology</i> , 2016 , 17, 111	18.3	113
24	Association of TMTC2 With Human Nonsyndromic Sensorineural Hearing Loss. <i>JAMA Otolaryngology - Head and Neck Surgery</i> , 2016 , 142, 866-72	3.9	11
23	The distribution and mutagenesis of short coding INDELs from 1,128 whole exomes. <i>BMC Genomics</i> , 2015 , 16, 143	4.5	8
22	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015 , 526, 75-81	50.4	1368
21	SpeedSeq: ultra-fast personal genome analysis and interpretation. <i>Nature Methods</i> , 2015 , 12, 966-8	21.6	301
20	Sequence Analysis and Characterization of Active Human Alu Subfamilies Based on the 1000 Genomes Pilot Project. <i>Genome Biology and Evolution</i> , 2015 , 7, 2608-22	3.9	47
19	Toolbox for mobile-element insertion detection on cancer genomes. <i>Cancer Informatics</i> , 2015 , 14, 37-44	2.4	2
18	Novel somatic and germline mutations in intracranial germ cell tumours. <i>Nature</i> , 2014 , 511, 241-5	50.4	131
17	MOSAİK: a hash-based algorithm for accurate next-generation sequencing short-read mapping. <i>PLoS ONE</i> , 2014 , 9, e90581	3.7	193
16	Toolbox for mobile-element insertion detection on cancer genomes. <i>Cancer Informatics</i> , 2014 , 13, 45-52	2.4	2
15	Tangram: a comprehensive toolbox for mobile element insertion detection. <i>BMC Genomics</i> , 2014 , 15, 795	4.5	39
14	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. <i>Genome Biology</i> , 2014 , 15, 443	18.3	47

13	Forward genetic screening identifies a small molecule that blocks <i>Toxoplasma gondii</i> growth by inhibiting both host- and parasite-encoded kinases. <i>PLoS Pathogens</i> , 2014 , 10, e1004180	7.6	27
12	bam.iobio: a web-based, real-time, sequence alignment file inspector. <i>Nature Methods</i> , 2014 , 11, 1189	21.6	27
11	Integrative annotation of variants from 1092 humans: application to cancer genomics. <i>Science</i> , 2013 , 342, 1235587	33.3	281
10	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049
9	Copy Number Variation detection from 1000 Genomes Project exon capture sequencing data. <i>BMC Bioinformatics</i> , 2012 , 13, 305	3.6	22
8	The functional spectrum of low-frequency coding variation. <i>Genome Biology</i> , 2011 , 12, R84	18.3	161
7	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011 , 470, 59-65	50.4	833
6	The variant call format and VCFtools. <i>Bioinformatics</i> , 2011 , 27, 2156-8	7.2	6200
5	BamTools: a C++ API and toolkit for analyzing and managing BAM files. <i>Bioinformatics</i> , 2011 , 27, 1691-2	7.2	447
4	A comprehensive map of mobile element insertion polymorphisms in humans. <i>PLoS Genetics</i> , 2011 , 7, e1002236	6	218
3	The Sequence Alignment/Map format and SAMtools. <i>Bioinformatics</i> , 2009 , 25, 2078-9	7.2	30805
2	genepanel.iobio - an easy to use web tool for generating disease- and phenotype-associated gene lists		2
1	The extracellular milieu of <i>Toxoplasma</i> lytic cycle drives lab-adaptation and promotes changes in lipid metabolism primarily driven by transcriptional reprogramming		1