Gabor T Marth

List of Publications by Citations

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	The Sequence Alignment/Map format and SAMtools. *Bioinformatics*, **2009**, 25, 2078-9	7.2	30805
47	The variant call format and VCFtools. *Bioinformatics*, **2011**, 27, 2156-8	7.2	6200
46	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
45	An integrated map of structural variation in 2,504 human genomes. *Nature*, **2015**, 526, 75-81	50.4	1368
44	Mapping copy number variation by population-scale genome sequencing. *Nature*, **2011**, 470, 59-65	50.4	833
43	BamTools: a C++ API and toolkit for analyzing and managing BAM files. *Bioinformatics*, **2011**, 27, 1691-2	7.2	447
42	Multi-platform discovery of haplotype-resolved structural variation in human genomes. *Nature Communications*, **2019**, 10, 1784	17.4	346
41	SpeedSeq: ultra-fast personal genome analysis and interpretation. *Nature Methods*, **2015**, 12, 966-8	21.6	301
40	Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science*, **2013**, 342, 1235587	33.3	281
39	A comprehensive map of mobile element insertion polymorphisms in humans. *PLoS Genetics*, **2011**, 7, e1002236	6	218
38	MOSAIK: a hash-based algorithm for accurate next-generation sequencing short-read mapping. *PLoS ONE*, **2014**, 9, e90581	3.7	193
37	The functional spectrum of low-frequency coding variation. *Genome Biology*, **2011**, 12, R84	18.3	161
36	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. *Nature Genetics*, **2018**, 50, 727-736	36.3	156
35	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. *Science*, **2018**, 362,	33.3	134
34	Novel somatic and germline mutations in intracranial germ cell tumours. *Nature*, **2014**, 511, 241-5	50.4	131
33	Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. *Genome Biology*, **2016**, 17, 111	18.3	113
32	MYC Drives Temporal Evolution of Small Cell Lung Cancer Subtypes by Reprogramming Neuroendocrine Fate. *Cancer Cell*, **2020**, 38, 60-78.e12	24.3	92

31	Combating subclonal evolution of resistant cancer phenotypes. *Nature Communications*, **2017**, 8, 1231	17.4	79
30	GIGGLE: a search engine for large-scale integrated genome analysis. *Nature Methods*, **2018**, 15, 123-126	21.6	71
29	Sequence Analysis and Characterization of Active Human Alu Subfamilies Based on the 1000 Genomes Pilot Project. *Genome Biology and Evolution*, **2015**, 7, 2608-22	3.9	47
28	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. *Genome Biology*, **2014**, 15, 443	18.3	47
27	Whole-genome analysis for effective clinical diagnosis and gene discovery in early infantile epileptic encephalopathy. *Npj Genomic Medicine*, **2018**, 3, 22	6.2	42
26	Tangram: a comprehensive toolbox for mobile element insertion detection. *BMC Genomics*, **2014**, 15, 795	4.5	39
25	Automated size selection for short cell-free DNA fragments enriches for circulating tumor DNA and improves error correction during next generation sequencing. *PLoS ONE*, **2018**, 13, e0197333	3.7	36
24	Genomic analyses implicate noncoding de novo variants in congenital heart disease. *Nature Genetics*, **2020**, 52, 769-777	36.3	33
23	Forward genetic screening identifies a small molecule that blocks Toxoplasma gondii growth by inhibiting both host- and parasite-encoded kinases. *PLoS Pathogens*, **2014**, 10, e1004180	7.6	27
22	bam.iobio: a web-based, real-time, sequence alignment file inspector. *Nature Methods*, **2014**, 11, 1189	21.6	27
21	Copy Number Variation detection from 1000 Genomes Project exon capture sequencing data. *BMC Bioinformatics*, **2012**, 13, 305	3.6	22
20	Principles and Recommendations for Standardizing the Use of the Next-Generation Sequencing Variant File in Clinical Settings. *Journal of Molecular Diagnostics*, **2017**, 19, 417-426	5.1	13
19	Association of TMTC2 With Human Nonsyndromic Sensorineural Hearing Loss. *JAMA Otolaryngology - Head and Neck Surgery*, **2016**, 142, 866-72	3.9	11
18	Somalier: rapid relatedness estimation for cancer and germline studies using efficient genome sketches. *Genome Medicine*, **2020**, 12, 62	14.4	10
17	The distribution and mutagenesis of short coding INDELs from 1,128 whole exomes. *BMC Genomics*, **2015**, 16, 143	4.5	8
16	Rapid clinical diagnostic variant investigation of genomic patient sequencing data with web tools. *Journal of Clinical and Translational Science*, **2017**, 1, 381-386	0.4	6
15	The stochastic nature of errors in next-generation sequencing of circulating cell-free DNA. *PLoS ONE*, **2020**, 15, e0229063	3.7	4
14	Deep whole-genome sequencing of multiple proband tissues and parental blood reveals the complex genetic etiology of congenital diaphragmatic hernias. *Human Genetics and Genomics Advances*, **2020**, 1, 100008-100008	0.8	3

13	The Extracellular Milieu of 's Lytic Cycle Drives Lab Adaptation, Primarily by Transcriptional Reprogramming. *MSystems*, **2021**, e0119621	7.6	3
12	Ongoing clonal evolution in chronic myelomonocytic leukemia on hypomethylating agents: a computational perspective. *Leukemia*, **2018**, 32, 2049-2054	10.7	2
11	Toolbox for mobile-element insertion detection on cancer genomes. *Cancer Informatics*, **2015**, 14, 37-44	2.4	2
10	Toolbox for mobile-element insertion detection on cancer genomes. *Cancer Informatics*, **2014**, 13, 45-52	2.4	2
9	genepanel.iobio - an easy to use web tool for generating disease- and phenotype-associated gene lists		2
8	Genepanel.iobio - an easy to use web tool for generating disease- and phenotype-associated gene lists. *BMC Medical Genomics*, **2019**, 12, 190	3.7	2
7	Comprehensive variant calling from whole-genome sequencing identifies a complex inversion that disrupts ZFPM2 in familial congenital diaphragmatic hernia.. *Molecular Genetics & Genomic Medicine*, **2022**, e1888	2.3	1
6	Gene.iobio: an interactive web tool for versatile, clinically-driven variant interrogation and prioritization. *Scientific Reports*, **2021**, 11, 20307	4.9	1
5	Novel temporal and spatial patterns of metastatic colonization from breast cancer rapid-autopsy tumor biopsies. *Genome Medicine*, **2021**, 13, 170	14.4	1
4	The extracellular milieu of Toxoplasma lytic cycle drives lab-adaptation and promotes changes in lipid metabolism primarily driven by transcriptional reprogramming		1
3	Mobile element insertions and associated structural variants in longitudinal breast cancer samples. *Scientific Reports*, **2021**, 11, 13020	4.9	1
2	ped_draw: pedigree drawing with ease. *BMC Bioinformatics*, **2020**, 21, 569	3.6	0
1	OncoGEMINI: software for investigating tumor variants from multiple biopsies with integrated cancer annotations. *Genome Medicine*, **2021**, 13, 46	14.4	