Gabor T Marth

List of Publications by Year
in descending order

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48 papers	75,671 citations	201674 27 h-index	214800 47 g-index
53 all docs	53 docs citations	53 times ranked	115613 citing authors

#	Article	IF	Citations
1	The Sequence Alignment/Map format and SAMtools. Bioinformatics, 2009, 25, 2078-2079.	4.1	49,124
2	The variant call format and VCFtools. Bioinformatics, 2011, 27, 2156-2158.	4.1	11,326
3	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
4	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
5	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
6	BamTools: a C++ API and toolkit for analyzing and managing BAM files. Bioinformatics, 2011, 27, 1691-1692.	4.1	843
7	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
8	SpeedSeq: ultra-fast personal genome analysis and interpretation. Nature Methods, 2015, 12, 966-968.	19.0	515
9	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	12.6	341
10	A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. PLoS Genetics, 2011, 7, e1002236.	3.5	278
11	MYC Drives Temporal Evolution of Small Cell Lung Cancer Subtypes by Reprogramming Neuroendocrine Fate. Cancer Cell, 2020, 38, 60-78.e12.	16.8	262
12	MOSAIK: A Hash-Based Algorithm for Accurate Next-Generation Sequencing Short-Read Mapping. PLoS ONE, 2014, 9, e90581.	2.5	249
13	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. Nature Genetics, 2018, 50, 727-736.	21.4	235
14	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. Science, 2018, 362, .	12.6	234
15	Novel somatic and germline mutations in intracranial germ cell tumours. Nature, 2014, 511, 241-245.	27.8	181
16	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	9.6	173
17	GIGGLE: a search engine for large-scale integrated genome analysis. Nature Methods, 2018, 15, 123-126.	19.0	154
18	Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. Genome Biology, 2016, 17, 111.	8.8	152

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19	Combating subclonal evolution of resistant cancer phenotypes. Nature Communications, 2017, 8, 1231.	12.8	124
20	Genomic analyses implicate noncoding de novo variants in congenital heart disease. Nature Genetics, 2020, 52, 769-777.	21.4	97
21	Whole-genome analysis for effective clinical diagnosis and gene discovery in early infantile epileptic encephalopathy. Npj Genomic Medicine, 2018, 3, 22.	3.8	64
22	Sequence Analysis and Characterization of Active HumanAlusubfamilies Based on the 1000 Genomes Pilot Project. Genome Biology and Evolution, 2015, 7, evv167.	2.5	60
23	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. Genome Biology, 2014, 15, 443.	8.8	59
24	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.	2.5	55
25	Tangram: a comprehensive toolbox for mobile element insertion detection. BMC Genomics, 2014, 15, 795.	2.8	54
26	Somalier: rapid relatedness estimation for cancer and germline studies using efficient genome sketches. Genome Medicine, 2020, 12, 62.	8.2	48
27	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.	4.7	40
28	bam.iobio: a web-based, real-time, sequence alignment file inspector. Nature Methods, 2014, 11, 1189-1189.	19.0	38
29	Copy Number Variation detection from 1000 Genomes project exon capture sequencing data. BMC Bioinformatics, 2012, 13, 305.	2.6	23
30	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.	2.8	19
31	The Extracellular Milieu of Toxoplasma 's Lytic Cycle Drives Lab Adaptation, Primarily by Transcriptional Reprogramming. MSystems, 2021, 6, e0119621.	3.8	17
32	Association ofTMTC2With Human Nonsyndromic Sensorineural Hearing Loss. JAMA Otolaryngology - Head and Neck Surgery, 2016, 142, 866.	2.2	15
33	The distribution and mutagenesis of short coding INDELs from 1,128 whole exomes. BMC Genomics, 2015, 16, 143.	2.8	9
34	Rapid clinical diagnostic variant investigation of genomic patient sequencing data with iobio web tools. Journal of Clinical and Translational Science, 2017, 1, 381-386.	0.6	6
35	The stochastic nature of errors in next-generation sequencing of circulating cell-free DNA. PLoS ONE, 2020, 15, e0229063.	2.5	6
36	Comprehensive variant calling from wholeâ€genome sequencing identifies a complex inversion that disrupts <scp>ZFPM2</scp> in familial congenital diaphragmatic hernia. Molecular Genetics & Genomic Medicine, 2022, 10, e1888.	1.2	6

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37	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.	1.7	5
38	Novel temporal and spatial patterns of metastatic colonization from breast cancer rapid-autopsy tumor biopsies. Genome Medicine, 2021, 13, 170.	8.2	5
39	Toolbox for Mobile-Element Insertion Detection on Cancer Genomes. Cancer Informatics, 2014, 13s4, CIN.S13979.	1.9	4
40	Toolbox for Mobile-Element Insertion Detection on Cancer Genomes. Cancer Informatics, 2015, 14s1, CIN.S24657.	1.9	4
41	Ongoing clonal evolution in chronic myelomonocytic leukemia on hypomethylating agents: a computational perspective. Leukemia, 2018, 32, 2049-2054.	7.2	4
42	Gene.iobio: an interactive web tool for versatile, clinically-driven variant interrogation and prioritization. Scientific Reports, 2021, 11, 20307.	3.3	4
43	Genepanel.iobio - an easy to use web tool for generating disease- and phenotype-associated gene lists. BMC Medical Genomics, 2019, 12, 190.	1.5	3
44	Mobile element insertions and associated structural variants in longitudinal breast cancer samples. Scientific Reports, 2021, 11, 13020.	3.3	3
45	ped_draw: pedigree drawing with ease. BMC Bioinformatics, 2020, 21, 569.	2.6	2
46	Clin.iobio: A Collaborative Diagnostic Workflow to Enable Team-Based Precision Genomics. Journal of Personalized Medicine, 2022, 12, 73.	2.5	1
47	OncoGEMINI: software for investigating tumor variants from multiple biopsies with integrated cancer annotations. Genome Medicine, 2021, 13, 46.	8.2	0
48	COMPUTATIONAL TOOLS FOR NEXT-GENERATION SEQUENCING APPLICATIONS â€“ Session Introduction. , 2007, , .		0