Gabor T Marth

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7286935/publications.pdf

Version: 2024-02-01

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	Clin.iobio: A Collaborative Diagnostic Workflow to Enable Team-Based Precision Genomics. Journal of Personalized Medicine, 2022, 12, 73.	2.5	1
2	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
3	OncoGEMINI: software for investigating tumor variants from multiple biopsies with integrated cancer annotations. Genome Medicine, 2021, 13, 46.	8.2	0
4	Mobile element insertions and associated structural variants in longitudinal breast cancer samples. Scientific Reports, 2021, 11, 13020.	3.3	3
5	Gene.iobio: an interactive web tool for versatile, clinically-driven variant interrogation and prioritization. Scientific Reports, 2021, 11, 20307.	3.3	4
6	Novel temporal and spatial patterns of metastatic colonization from breast cancer rapid-autopsy tumor biopsies. Genome Medicine, 2021, 13, 170.	8.2	5
7	The Extracellular Milieu of Toxoplasma 's Lytic Cycle Drives Lab Adaptation, Primarily by Transcriptional Reprogramming. MSystems, 2021, 6, e0119621.	3.8	17
8	Somalier: rapid relatedness estimation for cancer and germline studies using efficient genome sketches. Genome Medicine, 2020, 12, 62.	8.2	48
9	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
10	ped_draw: pedigree drawing with ease. BMC Bioinformatics, 2020, 21, 569.	2.6	2
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	Genomic analyses implicate noncoding de novo variants in congenital heart disease. Nature Genetics, 2020, 52, 769-777.	21.4	97
13	The stochastic nature of errors in next-generation sequencing of circulating cell-free DNA. PLoS ONE, 2020, 15, e0229063.	2.5	6
14	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
15	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
16	GIGGLE: a search engine for large-scale integrated genome analysis. Nature Methods, 2018, 15, 123-126.	19.0	154
17	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
18	Ongoing clonal evolution in chronic myelomonocytic leukemia on hypomethylating agents: a computational perspective. Leukemia, 2018, 32, 2049-2054.	7.2	4

#	Article	IF	Citations
19	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. Science, 2018, 362, .	12.6	234
20	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
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	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
23	Combating subclonal evolution of resistant cancer phenotypes. Nature Communications, 2017, 8, 1231.	12.8	124
24	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
25	Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. Genome Biology, 2016, 17, 111.	8.8	152
26	Association ofTMTC2With Human Nonsyndromic Sensorineural Hearing Loss. JAMA Otolaryngology - Head and Neck Surgery, 2016, 142, 866.	2.2	15
27	Sequence Analysis and Characterization of Active HumanAlusubfamilies Based on the 1000 Genomes Pilot Project. Genome Biology and Evolution, 2015, 7, evv167.	2.5	60
28	Toolbox for Mobile-Element Insertion Detection on Cancer Genomes. Cancer Informatics, 2015, 14s1, CIN.S24657.	1.9	4
29	The distribution and mutagenesis of short coding INDELs from 1,128 whole exomes. BMC Genomics, 2015, 16, 143.	2.8	9
30	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
31	SpeedSeq: ultra-fast personal genome analysis and interpretation. Nature Methods, 2015, 12, 966-968.	19.0	515
32	MOSAIK: A Hash-Based Algorithm for Accurate Next-Generation Sequencing Short-Read Mapping. PLoS ONE, 2014, 9, e90581.	2.5	249
33	Toolbox for Mobile-Element Insertion Detection on Cancer Genomes. Cancer Informatics, 2014, 13s4, CIN.S13979.	1.9	4
34	Tangram: a comprehensive toolbox for mobile element insertion detection. BMC Genomics, 2014, 15, 795.	2.8	54
35	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. Genome Biology, 2014, 15, 443.	8.8	59
36	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

#	Article	IF	Citations
37	bam.iobio: a web-based, real-time, sequence alignment file inspector. Nature Methods, 2014, 11, 1189-1189.	19.0	38
38	Novel somatic and germline mutations in intracranial germ cell tumours. Nature, 2014, 511, 241-245.	27.8	181
39	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	12.6	341
40	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
41	Copy Number Variation detection from 1000 Genomes project exon capture sequencing data. BMC Bioinformatics, 2012, 13, 305.	2.6	23
42	The variant call format and VCFtools. Bioinformatics, 2011, 27, 2156-2158.	4.1	11,326
43	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	9.6	173
44	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
45	BamTools: a C++ API and toolkit for analyzing and managing BAM files. Bioinformatics, 2011, 27, 1691-1692.	4.1	843
46	A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. PLoS Genetics, 2011, 7, e1002236.	3.5	278
47	The Sequence Alignment/Map format and SAMtools. Bioinformatics, 2009, 25, 2078-2079.	4.1	49,124
48	COMPUTATIONAL TOOLS FOR NEXT-GENERATION SEQUENCING APPLICATIONS â€“ Session Introduction. , 2007, , .		0