

Integrative Genomics Viewer (IGV): high-performance g exploration

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Citation Report

#	ARTICLE	IF	CITATIONS
3	The role of memory for past test in the underconfidence with practice effect.. Journal of Experimental Psychology: Learning Memory and Cognition, 2007, 33, 238-244.	0.7	128
4	VarB: a variation browsing and analysis tool for variants derived from next-generation sequencing data. Bioinformatics, 2012, 28, 2983-2985.	1.8	8
5	Transmembrane Proteins UNC-40/DCC, PTP-3/LAR, and MIG-21 Control Anteriorâ€“Posterior Neuroblast Migration with Leftâ€“Right Functional Asymmetry in <i>Caenorhabditis elegans</i> . Genetics, 2012, 192, 1373-1388.	1.2	30
6	D-peaks: A visual tool to display ChIP-seq peaks along the genome. Transcription, 2012, 3, 255-259.	1.7	2
7	Exome sequencing and complex disease: practical aspects of rare variant association studies. Human Molecular Genetics, 2012, 21, R1-R9.	1.4	114
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12	Multiscale Integration of -Omic, Imaging, and Clinical Data in Biomedical Informatics. IEEE Reviews in Biomedical Engineering, 2012, 5, 74-87.	13.1	48
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20	SeqAnt 2012: Recent Developments in Next-Generation Sequencing Annotation. , 0, , .		0

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21	Unraveling genomic variation from next generation sequencing data. <i>BioData Mining</i> , 2013, 6, 13.	2.2	43
22	Simultaneous and complete genome sequencing of influenza A and B with high coverage by Illumina MiSeq Platform. <i>Journal of Virological Methods</i> , 2013, 193, 394-404.	1.0	55
23	Clinical Validation of a Next-Generation Sequencing Screen for Mutational Hotspots in 46 Cancer-Related Genes. <i>Journal of Molecular Diagnostics</i> , 2013, 15, 607-622.	1.2	314
24	Intraclonal genome diversity of <i>Pseudomonas aeruginosa</i> clones CHA and TB. <i>BMC Genomics</i> , 2013, 14, 416.	1.2	21
25	Genome wide analysis of the complete GlnR nitrogen-response regulon in <i>Mycobacterium smegmatis</i> . <i>BMC Genomics</i> , 2013, 14, 301.	1.2	66
26	Transcriptome analysis of embryo maturation in maize. <i>BMC Plant Biology</i> , 2013, 13, 19.	1.6	38
27	Pervasive genetic hitchhiking and clonal interference in forty evolving yeast populations. <i>Nature</i> , 2013, 500, 571-574.	13.7	523
28	A novel method to predict regulatory regions based on histone mark landscapes in macrophages. <i>Immunobiology</i> , 2013, 218, 1416-1427.	0.8	18
29	A novel rearrangement of occludin causes brain calcification and renal dysfunction. <i>Human Genetics</i> , 2013, 132, 1223-1234.	1.8	24
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31	Technical and implementation issues in using next-generation sequencing of cancers in clinical practice. <i>British Journal of Cancer</i> , 2013, 109, 827-835.	2.9	91
32	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , 2013, 8, 1765-1786.	5.5	1,124
33	Mutations in KARS, Encoding Lysyl-tRNA Synthetase, Cause Autosomal-Recessive Nonsyndromic Hearing Impairment DFNB89. <i>American Journal of Human Genetics</i> , 2013, 93, 132-140.	2.6	90
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35	The NF-Y complex negatively regulates <i>Caenorhabditis elegans</i> <i>tbx-2</i> expression. <i>Developmental Biology</i> , 2013, 382, 38-47.	0.9	13
36	A Mesodermal Factor, T, Specifies Mouse Germ Cell Fate by Directly Activating Germline Determinants. <i>Developmental Cell</i> , 2013, 27, 516-529.	3.1	206
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41	Consed: a graphical editor for next-generation sequencing. <i>Bioinformatics</i> , 2013, 29, 2936-2937.	1.8	260
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43	Next-generation biobanking of metastases to enable multidimensional molecular profiling in personalized medicine. <i>Modern Pathology</i> , 2013, 26, 1413-1424.	2.9	35
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56	Genome sequence and analysis of methylotrophic yeast <i>Hansenula polymorpha</i> DL1. <i>BMC Genomics</i> , 2013, 14, 837.	1.2	81

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76	HIF1A Employs CDK8-Mediator to Stimulate RNAPII Elongation in Response to Hypoxia. <i>Cell</i> , 2013, 153, 1327-1339.	13.5	300
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1965	MicroRNA-532-5p Regulates Pericyte Function by Targeting the Transcription Regulator BACH1 and Angiotensin-1. <i>Molecular Therapy</i> , 2018, 26, 2823-2837.	3.7	30
1966	TIMP3 and TIMP1 are risk genes for bicuspid aortic valve and aortopathy in Turner syndrome. <i>PLoS Genetics</i> , 2018, 14, e1007692.	1.5	61

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1968	Direct-to-consumer DNA testing of 6,000 dogs reveals 98.6-kb duplication associated with blue eyes and heterochromia in Siberian Huskies. <i>PLoS Genetics</i> , 2018, 14, e1007648.	1.5	21
1969	De Novo Sequence and Copy Number Variants Are Strongly Associated with Tourette Disorder and Implicate Cell Polarity in Pathogenesis. <i>Cell Reports</i> , 2018, 24, 3441-3454.e12.	2.9	91
1970	The methylome of the marbled crayfish links gene body methylation to stable expression of poorly accessible genes. <i>Epigenetics and Chromatin</i> , 2018, 11, 57.	1.8	56
1971	The Duality of the MAPK Signaling Pathway in the Control of Metabolic Processes and Cellulose Production in <i>Trichoderma reesei</i> . <i>Scientific Reports</i> , 2018, 8, 14931.	1.6	31
1972	Phenotypic expression of a spectrum of Neurofibromatosis Type 1 (NF1) mutations identified through NGS and MLPA. <i>Journal of the Neurological Sciences</i> , 2018, 395, 95-105.	0.3	29
1973	Opportunities in Functional Genomics: A Primer on Lab and Computational Aspects. <i>Journal of Shellfish Research</i> , 2018, 37, 747-754.	0.3	1
1974	Oligodendrocyte differentiation of induced pluripotent stem cells derived from subjects with schizophrenias implicate abnormalities in development. <i>Translational Psychiatry</i> , 2018, 8, 230.	2.4	39
1975	TransAtlasDB: an integrated database connecting expression data, metadata and variants. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	2
1976	Phytophthora methylomes are modulated by 6mA methyltransferases and associated with adaptive genome regions. <i>Genome Biology</i> , 2018, 19, 181.	3.8	61
1977	Causative Mutations and Mechanism of Androgenetic Hydatidiform Moles. <i>American Journal of Human Genetics</i> , 2018, 103, 740-751.	2.6	69
1978	Reduction of stratum corneum ceramides in Neu-Laxova syndrome caused by phosphoglycerate dehydrogenase deficiency. <i>Journal of Lipid Research</i> , 2018, 59, 2413-2420.	2.0	14
1979	Firefly genomes illuminate parallel origins of bioluminescence in beetles. <i>ELife</i> , 2018, 7, .	2.8	108
1980	Genomic overview of closely related fungi with different Protea host ranges. <i>Fungal Biology</i> , 2018, 122, 1201-1214.	1.1	1
1981	BacCapSeq: a Platform for Diagnosis and Characterization of Bacterial Infections. <i>MBio</i> , 2018, 9, .	1.8	42
1982	STIM1 R304W causes muscle degeneration and impaired platelet activation in mice. <i>Cell Calcium</i> , 2018, 76, 87-100.	1.1	21
1983	Comparison of RNA-seq and microarray platforms for splice event detection using a cross-platform algorithm. <i>BMC Genomics</i> , 2018, 19, 703.	1.2	20
1984	Identification and characterization of novel fusion genes in prostate cancer by targeted RNA capture and next-generation sequencing. <i>Acta Biochimica Et Biophysica Sinica</i> , 2018, 50, 1166-1172.	0.9	10

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1987	Computational Epigenomics and Its Application in Regulatory Genomics. , 2018, , 115-139.		0
1988	Bacillus wiedmannii biovar thuringiensis: a specialized mosquitocidal pathogen with plasmids from diverse origins. Genome Biology and Evolution, 2018, 10, 2823-2833.	1.1	28
1989	Functional Genomics. Advances in Experimental Medicine and Biology, 2018, 1102, 11-30.	0.8	3
1990	N-methyladenine DNA Modification in Glioblastoma. Cell, 2018, 175, 1228-1243.e20.	13.5	236
1991	Exon Junction Complexes Suppress Spurious Splice Sites to Safeguard Transcriptome Integrity. Molecular Cell, 2018, 72, 482-495.e7.	4.5	61
1992	An <i>Anopheles stephensi</i> Promoter-Trap: Augmenting Genome Annotation and Functional Genomics. G3: Genes, Genomes, Genetics, 2018, 8, 3119-3130.	0.8	6
1993	p73 Is Required for Ovarian Follicle Development and Regulates a Gene Network Involved in Cell-to-Cell Adhesion. IScience, 2018, 8, 236-249.	1.9	17
1994	Characterization of phenotypic variation and genome aberrations observed among <i>Phytophthora ramorum</i> isolates from diverse hosts. BMC Genomics, 2018, 19, 320.	1.2	21
1995	Structural Variants and Selective Sweep Foci Contribute to Insecticide Resistance in the <i>Drosophila</i> Genetic Reference Panel. G3: Genes, Genomes, Genetics, 2018, 8, 3489-3497.	0.8	33
1996	Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy and Tools. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	1.9	14
1997	SV-plaudit: A cloud-based framework for manually curating thousands of structural variants. GigaScience, 2018, 7, .	3.3	30
1998	Whole-Genome Sequencing Reveals Elevated Tumor Mutational Burden and Initiating Driver Mutations in African Men with Treatment-Na ⁺ ve, High-Risk Prostate Cancer. Cancer Research, 2018, 78, 6736-6746.	0.4	66
1999	Mutational and copy number asset of primary sporadic neuroendocrine tumors of the small intestine. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2018, 473, 709-717.	1.4	40
2000	New Citrus chloroplast haplotypes revealed by molecular markers using Algerian and Spanish accessions. Genetic Resources and Crop Evolution, 2018, 65, 2199-2214.	0.8	2
2001	Ancient genome-wide analyses infer kinship structure in an Early Medieval Alemannic graveyard. Science Advances, 2018, 4, eaao1262.	4.7	28
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2005	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. <i>Nature Communications</i> , 2018, 9, 3787.	5.8	112
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2007	Genomic and epigenomic immunity in common bean: the unusual features of NB-LRR gene family. <i>DNA Research</i> , 2018, 25, 161-172.	1.5	71
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2009	Homologous recombination is an intrinsic defense against antiviral RNA interference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9211-E9219.	3.3	17
2010	PlaNC-TE: a comprehensive knowledgebase of non-coding RNAs and transposable elements in plants. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-7.	1.4	19
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2012	FNBtools: A Software to Identify Homozygous Lesions in Deletion Mutant Populations. <i>Frontiers in Plant Science</i> , 2018, 9, 976.	1.7	15
2013	The interplay of EIA ^{Ntr} with C ₄ source regulation of the <i>Pu</i> promoter of <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , 2018, 20, 4555-4566.	1.8	3
2014	Pushing the limits of de novo genome assembly for complex prokaryotic genomes harboring very long, near identical repeats. <i>Nucleic Acids Research</i> , 2018, 46, 8953-8965.	6.5	104
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2018	Trans-heterozygosity for mutations enhances the risk of recurrent/chronic pancreatitis in patients with Cystic Fibrosis. <i>Molecular Medicine</i> , 2018, 24, 38.	1.9	23
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2032	Whole-Genome Sequence of Infectious Pancreatic Necrosis Virus Isolated from Farmed Brook Trout (<i>Salvelinus fontinalis</i>) in Pennsylvania. Genome Announcements, 2018, 6, .	0.8	7
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2041	Discovery and expression analysis of novel transcripts of the human SR-related CTD-associated factor 1 (SCAF1) gene in human cancer cells using Next-Generation Sequencing. <i>Gene</i> , 2018, 670, 155-165.	1.0	9
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2050	Naturally occurring a loss of a giant plasmid from <i>Mycobacterium ulcerans</i> subsp. <i>shinshuense</i> makes it non-pathogenic. <i>Scientific Reports</i> , 2018, 8, 8218.	1.6	14
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2061	Homozygosity for CREB3L1 premature stop codon in first case of recessive osteogenesis imperfecta associated with OASIS-deficiency to survive infancy. <i>Bone</i> , 2018, 114, 268-277.	1.4	23
2062	Dynamics of Genome Alterations in Crohn's Disease-Associated Colorectal Carcinogenesis. <i>Clinical Cancer Research</i> , 2018, 24, 4997-5011.	3.2	22
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2065	Global characterization of copy number variants in epilepsy patients from whole genome sequencing. <i>PLoS Genetics</i> , 2018, 14, e1007285.	1.5	50
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2067	Clinical Implementation and Validation of Automated Human Genome Variation Society (HGVS) Nomenclature System for Next-Generation Sequencing-Based Assays for Cancer. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 628-634.	1.2	9
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2072	The cJUN NH2-terminal kinase (JNK) signaling pathway promotes genome stability and prevents tumor initiation. <i>ELife</i> , 2018, 7, .	2.8	28
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2074	Transcriptome Remodeling of Differentiated Cells during Chronological Ageing of Yeast Colonies: New Insights into Metabolic Differentiation. <i>Oxidative Medicine and Cellular Longevity</i> , 2018, 2018, 1-17.	1.9	12
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2088	Comparative studies of <i>Toxoplasma gondii</i> transcriptomes: insights into stage conversion based on gene expression profiling and alternative splicing. <i>Parasites and Vectors</i> , 2018, 11, 402.	1.0	21
2089	Molecular Background of Colorectal Tumors From Patients With Lynch Syndrome Associated With Germline Variants in PMS2. <i>Gastroenterology</i> , 2018, 155, 844-851.	0.6	38
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2098	Requirements for Neurogenin2 during mouse postnatal retinal neurogenesis. <i>Developmental Biology</i> , 2018, 442, 220-235.	0.9	11
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2103	No detectable effect of <i>Wolbachia w</i> Mel on the prevalence and abundance of the RNA virome of <i>Drosophila melanogaster</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181165.	1.2	53
2104	Capturing variation in <i>Lens</i> (Fabaceae): Development and utility of an exome capture array for lentil. <i>Applications in Plant Sciences</i> , 2018, 6, e01165.	0.8	54
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2113	Id Proteins Suppress E2A-Driven Invariant Natural Killer T Cell Development prior to TCR Selection. <i>Frontiers in Immunology</i> , 2018, 9, 42.	2.2	13
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3950	Profiling chromatin accessibility in formalin-fixed paraffin-embedded samples. <i>Genome Research</i> , 2022, 32, 150-161.	2.4	16
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3953	Current gene panels account for nearly all homologous recombination repair-associated multiple-case breast cancer families. <i>Npj Breast Cancer</i> , 2021, 7, 109.	2.3	3
3954	Regional Specific Differentiation of Integumentary Organs: Regulation of Gene Clusters within the Avian Epidermal Differentiation Complex and Impacts of SATB2 Overexpression. <i>Genes</i> , 2021, 12, 1291.	1.0	4
3955	Ancient DNA reveals multiple origins and migration waves of extinct Japanese brown bear lineages. <i>Royal Society Open Science</i> , 2021, 8, 210518.	1.1	8
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3960	Integrative genome-wide analyses reveal the transcriptional aberrations in Japanese esophageal squamous cell carcinoma. <i>Cancer Science</i> , 2021, 112, 4377-4392.	1.7	6
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3963	PATZ1 fusions define a novel molecularly distinct neuroepithelial tumor entity with a broad histological spectrum. <i>Acta Neuropathologica</i> , 2021, 142, 841-857.	3.9	36
3964	A graphical, interactive and GPU-enabled workflow to process long-read sequencing data. <i>BMC Genomics</i> , 2021, 22, 626.	1.2	7
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3981	HBO1-MLL interaction promotes AF4/ENL/P-TEFb-mediated leukemogenesis. <i>ELife</i> , 2021, 10, .	2.8	11
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3995	Two loss-of-function alleles of the <i>glutathione S-transferase</i> (<i>GST</i>) gene cause anthocyanin deficiency in flower and fruit skin of peach (<i>Prunus persica</i>). <i>Plant Journal</i> , 2021, 107, 1320-1331.	2.8	29

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3999	CẢ;ic biáº;n thá»f gene OsTZF1 liÃ³n quan Ä´áº;n kháº;£ nÄfng chá»«u máº-n á»Ý giá»'ng lÃ³a Ä»'c Phá»¥ng báº±ng ph/Æ;ing phÃ;ip giá» Chi Khoa Hoc = <i>Journal of Science</i> , 2021, 57, 159-168.	0.1	8
4000	Identification of TIA1 mRNA targets during human neuronal development. <i>Molecular Biology Reports</i> , 2021, 48, 6349-6361.	1.0	8
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4027	Somatic mutation analysis in <i>Salix suchowensis</i> reveals early segregated cell lineages. <i>Molecular Biology and Evolution</i> , 2021, 38, 5292-5308.	3.5	10
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4116	On Computationally-Enhanced Visual Analysis of Heterogeneous Data and Its Application in Biomedical Informatics. <i>Lecture Notes in Computer Science</i> , 2014, , 117-140.	1.0	37
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4125	Preferential expression of a HPV genotype in invasive cervical carcinomas infected by multiple genotypes. <i>Genomics</i> , 2020, 112, 2942-2948.	1.3	17
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