Alexej Abyzov

List of Publications by Year in descending order

80 papers	56,896 citations	93792 39 h-index	73587 79 g-index
95 all docs	95 docs citations	95 times ranked	90645 citing authors

#	Article	IF	Citations
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
2	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
3	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
4	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
5	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
6	CNVnator: An approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. Genome Research, 2011, 21, 974-984.	2.4	1,387
7	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	13.7	1,384
8	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991
9	FOXG1-Dependent Dysregulation of GABA/Glutamate Neuron Differentiation in Autism Spectrum Disorders. Cell, 2015, 162, 375-390.	13.5	894
10	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805
11	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	6.0	618
12	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
13	The PsychENCODE project. Nature Neuroscience, 2015, 18, 1707-1712.	7.1	371
14	Somatic copy number mosaicism in human skin revealed by induced pluripotent stem cells. Nature, 2012, 492, 438-442.	13.7	355
15	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
16	AlleleSeq: analysis of alleleâ€specific expression and binding in a network framework. Molecular Systems Biology, 2011, 7, 522.	3.2	284
17	PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. Genome Biology, 2009, 10, R23.	13.9	223
18	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	6.0	220

#	Article	IF	Citations
19	Different mutational rates and mechanisms in human cells at pregastrulation and neurogenesis. Science, 2018, 359, 550-555.	6.0	216
20	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. Science, 2017, 356, .	6.0	206
21	Human induced pluripotent stem cells for modelling neurodevelopmental disorders. Nature Reviews Neurology, 2017, 13, 265-278.	4.9	135
22	MetaSV: an accurate and integrative structural-variant caller for next generation sequencing. Bioinformatics, 2015, 31, 2741-2744.	1.8	131
23	UmuD and RecA Directly Modulate the Mutagenic Potential of the Y Family DNA Polymerase DinB. Molecular Cell, 2007, 28, 1058-1070.	4.5	99
24	AGE: defining breakpoints of genomic structural variants at single-nucleotide resolution, through optimal alignments with gap excision. Bioinformatics, 2011, 27, 595-603.	1.8	84
25	Structural alignment of proteins by a novel TOPOFIT method, as a superimposition of common volumes at a topomax point. Protein Science, 2004, 13, 1865-1874.	3.1	81
26	A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. Nature Communications, 2016, 7, 11101.	5.8	78
27	Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562. Genome Research, 2019, 29, 472-484.	2.4	78
28	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. Nature Communications, 2015, 6, 7256.	5.8	77
29	Molecular signatures of multiple myeloma progression through single cell RNA-Seq. Blood Cancer Journal, 2019, 9, 2.	2.8	74
30	Landmarks of human embryonic development inscribed in somatic mutations. Science, 2021, 371, 1249-1253.	6.0	65
31	Single-cell analysis of targeted transcriptome predicts drug sensitivity of single cells within human myeloma tumors. Leukemia, 2016, 30, 1094-1102.	3.3	64
32	One thousand somatic SNVs per skin fibroblast cell set baseline of mosaic mutational load with patterns that suggest proliferative origin. Genome Research, 2017, 27, 512-523.	2.4	64
33	Comprehensive performance comparison of high-resolution array platforms for genome-wide Copy Number Variation (CNV) analysis in humans. BMC Genomics, 2017, 18, 321.	1.2	60
34	VarSim: a high-fidelity simulation and validation framework for high-throughput genome sequencing with cancer applications. Bioinformatics, 2015, 31, 1469-1471.	1.8	59
35	Genome-Wide Mapping of Copy Number Variation in Humans: Comparative Analysis of High Resolution Array Platforms. PLoS ONE, 2011, 6, e27859.	1.1	59
36	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. Genome Research, 2013, 23, 2042-2052.	2.4	52

#	Article	IF	Citations
37	Patient-reported (EORTC QLQ-CIPN20) versus physician-reported (CTCAE) quantification of oxaliplatin- and paclitaxel/carboplatin-induced peripheral neuropathy in NCCTG/Alliance clinical trials. Supportive Care in Cancer, 2017, 25, 3537-3544.	1.0	52
38	Testing of candidate single nucleotide variants associated with paclitaxel neuropathy in the trial <scp>NCCTG</scp> N08C1 (Alliance). Cancer Medicine, 2016, 5, 631-639.	1.3	48
39	Haplotype-resolved and integrated genome analysis of the cancer cell line HepG2. Nucleic Acids Research, 2019, 47, 3846-3861.	6.5	45
40	Structure SNP (StSNP): a web server for mapping and modeling nsSNPs on protein structures with linkage to metabolic pathways. Nucleic Acids Research, 2007, 35, W384-W392.	6.5	43
41	Early developmental asymmetries in cell lineage trees in living individuals. Science, 2021, 371, 1245-1248.	6.0	39
42	CNVpytor: a tool for copy number variation detection and analysis from read depth and allele imbalance in whole-genome sequencing. GigaScience, 2021, 10, .	3.3	38
43	Integration of protein motions with molecular networks reveals different mechanisms for permanent and transient interactions. Protein Science, 2011, 20, 1745-1754.	3.1	37
44	Regulatory element copy number differences shape primate expression profiles. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12656-12661.	3.3	37
45	Molecular characterization of colorectal adenomas with and without malignancy reveals distinguishing genome, transcriptome and methylome alterations. Scientific Reports, 2018, 8, 3161.	1.6	35
46	MSB: A mean-shift-based approach for the analysis of structural variation in the genome. Genome Research, 2009, 19, 106-117.	2.4	33
47	Annual Research Review: The promise of stem cell research for neuropsychiatric disorders. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2011, 52, 504-516.	3.1	33
48	Landscape and variation of novel retroduplications in 26 human populations. PLoS Computational Biology, 2017, 13, e1005567.	1.5	30
49	RigidFinder: A fast and sensitive method to detect rigid blocks in large macromolecular complexes. Proteins: Structure, Function and Bioinformatics, 2010, 78, 309-324.	1.5	29
50	Comprehensive identification of somatic nucleotide variants in human brain tissue. Genome Biology, 2021, 22, 92.	3.8	26
51	Somatic mosaicism reveals clonal distributions of neocortical development. Nature, 2022, 604, 689-696.	13.7	26
52	Child Development and Structural Variation in the Human Genome. Child Development, 2013, 84, 34-48.	1.7	23
53	Combining copy number, methylation markers, and mutations as a panel for endometrial cancer detection via intravaginal tampon collection. Gynecologic Oncology, 2020, 156, 387-392.	0.6	22
54	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. Nature Neuroscience, 2021, 24, 186-196.	7.1	22

#	Article	IF	Citations
55	Friend, an integrated analytical front-end application for bioinformatics. Bioinformatics, 2005, 21, 3677-3678.	1.8	21
56	Analysis of Combinatorial Regulation: Scaling of Partnerships between Regulators with the Number of Governed Targets. PLoS Computational Biology, 2010, 6, e1000755.	1.5	21
57	Complex mosaic structural variations in human fetal brains. Genome Research, 2020, 30, 1695-1704.	2.4	21
58	The role of somatic mosaicism in brain disease. Current Opinion in Genetics and Development, 2020, 65, 84-90.	1.5	20
59	A comprehensive analysis of non-sequential alignments between all protein structures. BMC Structural Biology, 2007, 7, 78.	2.3	19
60	Adult diffuse glioma GWAS by molecular subtype identifies variants inD2HGDHandFAM20C. Neuro-Oncology, 2020, 22, 1602-1613.	0.6	19
61	An AP Endonuclease 1â€“DNA Polymerase Î² Complex: Theoretical Prediction of Interacting Surfaces. PLoS Computational Biology, 2008, 4, e1000066.	1.5	17
62	Detection and Quantification of Mosaic Genomic DNA Variation in Primary Somatic Tissues Using ddPCR: Analysis of Mosaic Transposable-Element Insertions, Copy-Number Variants, and Single-Nucleotide Variants. Methods in Molecular Biology, 2018, 1768, 173-190.	0.4	17
63	TOPOFIT-DB, a database of protein structural alignments based on the TOPOFIT method. Nucleic Acids Research, 2007, 35, D317-D321.	6.5	15
64	PsychENCODE and beyond: transcriptomics and epigenomics of brain development and organoids. Neuropsychopharmacology, 2021, 46, 70-85.	2.8	15
65	Chromatin organization modulates the origin of heritable structural variations in human genome. Nucleic Acids Research, 2019, 47, 2766-2777.	6.5	12
66	ACTIVE SITE PREDICTION FOR COMPARATIVE MODEL STRUCTURES WITH THEMATICS. Journal of Bioinformatics and Computational Biology, 2005, 03, 127-143.	0.3	10
67	Cell Lineage Tracing and Cellular Diversity in Humans. Annual Review of Genomics and Human Genetics, 2020, 21, 101-116.	2.5	10
68	Colorectal Cancer with Residual Polyp of Origin: A Model of Malignant Transformation. Translational Oncology, 2016, 9, 280-286.	1.7	9
69	Elevated variant density around SV breakpoints in germline lineage lends support to error-prone replication hypothesis. Genome Research, 2016, 26, 874-881.	2.4	7
70	Understanding genome structural variations. Oncotarget, 2016, 7, 7370-7371.	0.8	6
71	SCELLECTOR: ranking amplification bias in single cells using shallow sequencing. BMC Bioinformatics, 2020, 21, 521.	1.2	3
72	Neurological safety of oxaliplatin in patients with uncommon variants in Charcot-Marie-tooth disease genes. Journal of the Neurological Sciences, 2020, 411, 116687.	0.3	3

#	Article	IF	Citations
73	Inferring modes of evolution from colorectal cancer with residual polyp of origin. Oncotarget, 2018, 9, 6780-6792.	0.8	3
74	Postmortem Human Dura Mater Cells Exhibit Phenotypic, Transcriptomic and Genetic Abnormalities that Impact their Use for Disease Modeling. Stem Cell Reviews and Reports, 2022, 18, 3050-3065.	1.7	3
75	LongAGE: defining breakpoints of genomic structural variants through optimal and memory efficient alignments of long reads. Bioinformatics, 2021, 37, 1015-1017.	1.8	2
76	All2: A tool for selecting mosaic mutations from comprehensive multi-cell comparisons. PLoS Computational Biology, 2022, 18, e1009487.	1.5	2
77	Principles and Approaches for Discovery and Validation of Somatic Mosaicism in the Human Brain. Neuromethods, 2017, , 3-24.	0.2	1
78	Approaches and Methods for Variant Analysis in the Genome of a Single Cell. Healthy Ageing and Longevity, 2019, , 203-228.	0.2	1
79	Induced pluripotent stem cells as models of human neurodevelopmental disorders. , 2020, , 99-127.		0
80	Analysis of Cell and Nucleus Genome byÂNext-Generation Sequencing. , 2020, , 35-65.		0