Alexej Abyzov

List of Publications by Citations

82 papers	41,273 citations	37 h-index	95 g-index
95 ext. papers	51,387 ext. citations	16.3 avg, IF	8.2 L-index

#	Paper	IF	Citations
82	An integrated encyclopedia of DNA elements in the human genome. *Nature*, **2012**, 489, 57-74	50.4	11449
81	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
80	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
79	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
78	An integrated map of structural variation in 2,504 human genomes. *Nature*, **2015**, 526, 75-81	50.4	1368
77	Architecture of the human regulatory network derived from ENCODE data. *Nature*, **2012**, 489, 91-100	50.4	1104
76	CNVnator: an approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. *Genome Research*, **2011**, 21, 974-84	9.7	944
75	Mapping copy number variation by population-scale genome sequencing. *Nature*, **2011**, 470, 59-65	50.4	833
74	FOXG1-Dependent Dysregulation of GABA/Glutamate Neuron Differentiation in Autism Spectrum Disorders. *Cell*, **2015**, 162, 375-390	56.2	671
73	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. *Science*, **2018**, 362,	33.3	434
72	Comprehensive functional genomic resource and integrative model for the human brain. *Science*, **2018**, 362,	33.3	319
71	Somatic copy number mosaicism in human skin revealed by induced pluripotent stem cells. *Nature*, **2012**, 492, 438-42	50.4	299
70	Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science*, **2013** , 342, 1235587	33.3	281
69	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362,	33.3	277
68	AlleleSeq: analysis of allele-specific expression and binding in a network framework. *Molecular Systems Biology*, **2011**, 7, 522	12.2	228
67	The PsychENCODE project. *Nature Neuroscience*, **2015**, 18, 1707-12	25.5	226
66	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	18.3	201

65	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. *Science*, **2017**, 356,	33.3	152
64	Transcriptome and epigenome landscape of human cortical development modeled in organoids. *Science*, **2018**, 362,	33.3	142
63	Different mutational rates and mechanisms in human cells at pregastrulation and neurogenesis. *Science*, **2018**, 359, 550-555	33.3	139
62	Human induced pluripotent stem cells for modelling neurodevelopmental disorders. *Nature Reviews Neurology*, **2017**, 13, 265-278	15	96
61	MetaSV: an accurate and integrative structural-variant caller for next generation sequencing. *Bioinformatics*, **2015**, 31, 2741-4	7.2	95
60	UmuD and RecA directly modulate the mutagenic potential of the Y family DNA polymerase DinB. *Molecular Cell*, **2007**, 28, 1058-70	17.6	87
59	AGE: defining breakpoints of genomic structural variants at single-nucleotide resolution, through optimal alignments with gap excision. *Bioinformatics*, **2011**, 27, 595-603	7.2	73
58	Structural alignment of proteins by a novel TOPOFIT method, as a superimposition of common volumes at a topomax point. *Protein Science*, **2004**, 13, 1865-74	6.3	71
57	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. *Nature Communications*, **2015**, 6, 7256	17.4	56
56	Genome-wide mapping of copy number variation in humans: comparative analysis of high resolution array platforms. *PLoS ONE*, **2011**, 6, e27859	3.7	51
55	A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. *Nature Communications*, **2016**, 7, 11101	17.4	51
54	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	9.7	48
53	Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562. *Genome Research*, **2019**, 29, 472-484	9.7	43
52	Comprehensive performance comparison of high-resolution array platforms for genome-wide Copy Number Variation (CNV) analysis in humans. *BMC Genomics*, **2017**, 18, 321	4.5	43
51	VarSim: a high-fidelity simulation and validation framework for high-throughput genome sequencing with cancer applications. *Bioinformatics*, **2015**, 31, 1469-71	7.2	42
50	Single-cell analysis of targeted transcriptome predicts drug sensitivity of single cells within human myeloma tumors. *Leukemia*, **2016**, 30, 1094-102	10.7	42
49	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. *Genome Research*, **2013**, 23, 2042-52	9.7	41
48	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	3.9	39

47	Structure SNP (StSNP): a web server for mapping and modeling nsSNPs on protein structures with linkage to metabolic pathways. *Nucleic Acids Research*, **2007**, 35, W384-92	20.1	38
46	Testing of candidate single nucleotide variants associated with paclitaxel neuropathy in the trial NCCTG N08C1 (Alliance). *Cancer Medicine*, **2016**, 5, 631-9	4.8	38
45	Molecular signatures of multiple myeloma progression through single cell RNA-Seq. *Blood Cancer Journal*, **2019**, 9, 2	7	37
44	MSB: a mean-shift-based approach for the analysis of structural variation in the genome. *Genome Research*, **2009**, 19, 106-17	9.7	29
43	Regulatory element copy number differences shape primate expression profiles. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 12656-61	11.5	27
42	Annual Research Review: The promise of stem cell research for neuropsychiatric disorders. *Journal of Child Psychology and Psychiatry and Allied Disciplines*, **2011**, 52, 504-16	7.9	26
41	RigidFinder: a fast and sensitive method to detect rigid blocks in large macromolecular complexes. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 309-24	4.2	26
40	Haplotype-resolved and integrated genome analysis of the cancer cell line HepG2. *Nucleic Acids Research*, **2019**, 47, 3846-3861	20.1	25
39	Integration of protein motions with molecular networks reveals different mechanisms for permanent and transient interactions. *Protein Science*, **2011**, 20, 1745-54	6.3	24
38	Molecular characterization of colorectal adenomas with and without malignancy reveals distinguishing genome, transcriptome and methylome alterations. *Scientific Reports*, **2018**, 8, 3161	4.9	23
37	Friend, an integrated analytical front-end application for bioinformatics. *Bioinformatics*, **2005**, 21, 3677-8	7.2	21
36	Analysis of combinatorial regulation: scaling of partnerships between regulators with the number of governed targets. *PLoS Computational Biology*, **2010**, 6, e1000755	5	20
35	Child development and structural variation in the human genome. *Child Development*, **2013**, 84, 34-48	4.9	17
34	Landscape and variation of novel retroduplications in 26 human populations. *PLoS Computational Biology*, **2017**, 13, e1005567	5	16
33	An AP endonuclease 1-DNA polymerase beta complex: theoretical prediction of interacting surfaces. *PLoS Computational Biology*, **2008**, 4, e1000066	5	14
32	A comprehensive analysis of non-sequential alignments between all protein structures. *BMC Structural Biology*, **2007**, 7, 78	2.7	14
31	TOPOFIT-DB, a database of protein structural alignments based on the TOPOFIT method. *Nucleic Acids Research*, **2007**, 35, D317-21	20.1	13
30	Landmarks of human embryonic development inscribed in somatic mutations. *Science*, **2021**, 371, 1249-1253	3.3	13

29	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	1.4	9
28	Combining copy number, methylation markers, and mutations as a panel for endometrial cancer detection via intravaginal tampon collection. *Gynecologic Oncology*, **2020**, 156, 387-392	4.9	9
27	Complex mosaic structural variations in human fetal brains. *Genome Research*, **2020**, 30, 1695-1704	9.7	9
26	Chromatin organization modulates the origin of heritable structural variations in human genome. *Nucleic Acids Research*, **2019**, 47, 2766-2777	20.1	9
25	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. *Nature Neuroscience*, **2021**, 24, 186-196	25.5	9
24	Active site prediction for comparative model structures with thematics. *Journal of Bioinformatics and Computational Biology*, **2005**, 3, 127-43	1	8
23	The role of somatic mosaicism in brain disease. *Current Opinion in Genetics and Development*, **2020**, 65, 84-90	4.9	7
22	Colorectal Cancer with Residual Polyp of Origin: A Model of Malignant Transformation. *Translational Oncology*, **2016**, 9, 280-6	4.9	7
21	Early developmental asymmetries in cell lineage trees in living individuals. *Science*, **2021**, 371, 1245-1248	33.3	7
20	CNVpytor: a tool for copy number variation detection and analysis from read depth and allele imbalance in whole-genome sequencing. *GigaScience*, **2021**, 10,	7.6	6
19	Adult diffuse glioma GWAS by molecular subtype identifies variants in D2HGDH and FAM20C. *Neuro-Oncology*, **2020**, 22, 1602-1613	1	5
18	Cell Lineage Tracing and Cellular Diversity in Humans. *Annual Review of Genomics and Human Genetics*, **2020**, 21, 101-116	9.7	4
17	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia		3
16	Comprehensive identification of somatic nucleotide variants in human brain tissue. *Genome Biology*, **2021**, 22, 92	18.3	3
15	Elevated variant density around SV breakpoints in germline lineage lends support to error-prone replication hypothesis. *Genome Research*, **2016**, 26, 874-81	9.7	3
14	PsychENCODE and beyond: transcriptomics and epigenomics of brain development and organoids. *Neuropsychopharmacology*, **2021**, 46, 70-85	8.7	3
13	Inferring modes of evolution from colorectal cancer with residual polyp of origin. *Oncotarget*, **2018**, 9, 6780-6792	3.3	2
12	LongAGE: defining breakpoints of genomic structural variants through optimal and memory efficient alignments of long reads. *Bioinformatics*, **2021**, 37, 1015-1017	7.2	2

11	Neurological safety of oxaliplatin in patients with uncommon variants in Charcot-Marie-tooth disease genes. *Journal of the Neurological Sciences*, **2020**, 411, 116687	3.2	1
10	Principles and Approaches for Discovery and Validation of Somatic Mosaicism in the Human Brain. *Neuromethods*, **2017**, 3-24	0.4	1
9	Haplotype-resolved and integrated genome analysis of the cancer cell line HepG2		1
8	Approaches and Methods for Variant Analysis in the Genome of a Single Cell. *Healthy Ageing and Longevity*, **2019**, 203-228	0.5	1
7	Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562		1
6	SCELLECTOR: ranking amplification bias in single cells using shallow sequencing. *BMC Bioinformatics*, **2020**, 21, 521	3.6	1
5	CNVpytor: a tool for CNV/CNA detection and analysis from read depth and allele imbalance in whole genome sequencing		1
4	Somatic mosaicism reveals clonal distributions of neocortical development.. *Nature*, **2022**,	50.4	1
3	All2: A tool for selecting mosaic mutations from comprehensive multi-cell comparisons.. *PLoS Computational Biology*, **2022**, 18, e1009487	5	0
2	Induced pluripotent stem cells as models of human neurodevelopmental disorders **2020**, 99-127		
1	Analysis of Cell and Nucleus Genome by Next-Generation Sequencing **2020**, 35-65		