

# Alexej Abyzov

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/193873/alexej-abyzov-publications-by-year.pdf>

**Version:** 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Somatic mosaicism reveals clonal distributions of neocortical development.. <i>Nature</i> , <b>2022</b> ,	50.4	1
81	All2: A tool for selecting mosaic mutations from comprehensive multi-cell comparisons.. <i>PLoS Computational Biology</i> , <b>2022</b> , 18, e1009487	5	0
80	CNVpytor: a tool for copy number variation detection and analysis from read depth and allele imbalance in whole-genome sequencing. <i>GigaScience</i> , <b>2021</b> , 10,	7.6	6
79	Landmarks of human embryonic development inscribed in somatic mutations. <i>Science</i> , <b>2021</b> , 371, 1249-1253	35.3	13
78	Comprehensive identification of somatic nucleotide variants in human brain tissue. <i>Genome Biology</i> , <b>2021</b> , 22, 92	18.3	3
77	Early developmental asymmetries in cell lineage trees in living individuals. <i>Science</i> , <b>2021</b> , 371, 1245-1248	33.3	7
76	PsychENCODE and beyond: transcriptomics and epigenomics of brain development and organoids. <i>Neuropsychopharmacology</i> , <b>2021</b> , 46, 70-85	8.7	3
75	LongAGE: defining breakpoints of genomic structural variants through optimal and memory efficient alignments of long reads. <i>Bioinformatics</i> , <b>2021</b> , 37, 1015-1017	7.2	2
74	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. <i>Nature Neuroscience</i> , <b>2021</b> , 24, 186-196	25.5	9
73	Adult diffuse glioma GWAS by molecular subtype identifies variants in D2HGDH and FAM20C. <i>Neuro-Oncology</i> , <b>2020</b> , 22, 1602-1613	1	5
72	Cell Lineage Tracing and Cellular Diversity in Humans. <i>Annual Review of Genomics and Human Genetics</i> , <b>2020</b> , 21, 101-116	9.7	4
71	Induced pluripotent stem cells as models of human neurodevelopmental disorders <b>2020</b> , 99-127		
70	The role of somatic mosaicism in brain disease. <i>Current Opinion in Genetics and Development</i> , <b>2020</b> , 65, 84-90	4.9	7
69	Neurological safety of oxaliplatin in patients with uncommon variants in Charcot-Marie-tooth disease genes. <i>Journal of the Neurological Sciences</i> , <b>2020</b> , 411, 116687	3.2	1
68	Analysis of Cell and Nucleus Genome by Next-Generation Sequencing <b>2020</b> , 35-65		
67	Combining copy number, methylation markers, and mutations as a panel for endometrial cancer detection via intravaginal tampon collection. <i>Gynecologic Oncology</i> , <b>2020</b> , 156, 387-392	4.9	9
66	SCLECTOR: ranking amplification bias in single cells using shallow sequencing. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 521	3.6	1

65	Complex mosaic structural variations in human fetal brains. <i>Genome Research</i> , <b>2020</b> , 30, 1695-1704	9.7	9
64	Haplotype-resolved and integrated genome analysis of the cancer cell line HepG2. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 3846-3861	20.1	25
63	Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562. <i>Genome Research</i> , <b>2019</b> , 29, 472-484	9.7	43
62	Approaches and Methods for Variant Analysis in the Genome of a Single Cell. <i>Healthy Ageing and Longevity</i> , <b>2019</b> , 203-228	0.5	1
61	Chromatin organization modulates the origin of heritable structural variations in human genome. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 2766-2777	20.1	9
60	Molecular signatures of multiple myeloma progression through single cell RNA-Seq. <i>Blood Cancer Journal</i> , <b>2019</b> , 9, 2	7	37
59	Molecular characterization of colorectal adenomas with and without malignancy reveals distinguishing genome, transcriptome and methylome alterations. <i>Scientific Reports</i> , <b>2018</b> , 8, 3161	4.9	23
58	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. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1768, 173-190	1.4	9
57	Inferring modes of evolution from colorectal cancer with residual polyp of origin. <i>Oncotarget</i> , <b>2018</b> , 9, 6780-6792	3.3	2
56	Different mutational rates and mechanisms in human cells at pregastrulation and neurogenesis. <i>Science</i> , <b>2018</b> , 359, 550-555	33.3	139
55	Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , <b>2018</b> , 362,	33.3	142
54	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , <b>2018</b> , 362,	33.3	277
53	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , <b>2018</b> , 362,	33.3	434
52	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , <b>2018</b> , 362,	33.3	319
51	One thousand somatic SNVs per skin fibroblast cell set baseline of mosaic mutational load with patterns that suggest proliferative origin. <i>Genome Research</i> , <b>2017</b> , 27, 512-523	9.7	48
50	Human induced pluripotent stem cells for modelling neurodevelopmental disorders. <i>Nature Reviews Neurology</i> , <b>2017</b> , 13, 265-278	15	96
49	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. <i>Science</i> , <b>2017</b> , 356,	33.3	152
48	Patient-reported (EORTC QLQ-CIPN20) versus physician-reported (CTCAE) quantification of oxaliplatin- and paclitaxel/carboplatin-induced peripheral neuropathy in NCCTG/Alliance clinical trials. <i>Supportive Care in Cancer</i> , <b>2017</b> , 25, 3537-3544	3.9	39

47	Landscape and variation of novel retroduplications in 26 human populations. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005567	5	16
46	Principles and Approaches for Discovery and Validation of Somatic Mosaicism in the Human Brain. <i>Neuromethods</i> , <b>2017</b> , 3-24	0.4	1
45	Comprehensive performance comparison of high-resolution array platforms for genome-wide Copy Number Variation (CNV) analysis in humans. <i>BMC Genomics</i> , <b>2017</b> , 18, 321	4.5	43
44	Colorectal Cancer with Residual Polyp of Origin: A Model of Malignant Transformation. <i>Translational Oncology</i> , <b>2016</b> , 9, 280-6	4.9	7
43	Single-cell analysis of targeted transcriptome predicts drug sensitivity of single cells within human myeloma tumors. <i>Leukemia</i> , <b>2016</b> , 30, 1094-102	10.7	42
42	A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. <i>Nature Communications</i> , <b>2016</b> , 7, 11101	17.4	51
41	Elevated variant density around SV breakpoints in germline lineage lends support to error-prone replication hypothesis. <i>Genome Research</i> , <b>2016</b> , 26, 874-81	9.7	3
40	Testing of candidate single nucleotide variants associated with paclitaxel neuropathy in the trial NCCTG N08C1 (Alliance). <i>Cancer Medicine</i> , <b>2016</b> , 5, 631-9	4.8	38
39	FOXP1-Dependent Dysregulation of GABA/Glutamate Neuron Differentiation in Autism Spectrum Disorders. <i>Cell</i> , <b>2015</b> , 162, 375-390	56.2	671
38	VarSim: a high-fidelity simulation and validation framework for high-throughput genome sequencing with cancer applications. <i>Bioinformatics</i> , <b>2015</b> , 31, 1469-71	7.2	42
37	A global reference for human genetic variation. <i>Nature</i> , <b>2015</b> , 526, 68-74	50.4	8599
36	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , <b>2015</b> , 526, 75-81	50.4	1368
35	The PsychENCODE project. <i>Nature Neuroscience</i> , <b>2015</b> , 18, 1707-12	25.5	226
34	MetaSV: an accurate and integrative structural-variant caller for next generation sequencing. <i>Bioinformatics</i> , <b>2015</b> , 31, 2741-4	7.2	95
33	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. <i>Nature Communications</i> , <b>2015</b> , 6, 7256	17.4	56
32	Integrative annotation of variants from 1092 humans: application to cancer genomics. <i>Science</i> , <b>2013</b> , 342, 1235587	33.3	281
31	Child development and structural variation in the human genome. <i>Child Development</i> , <b>2013</b> , 84, 34-48	4.9	17
30	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. <i>Genome Research</i> , <b>2013</b> , 23, 2042-52	9.7	41

29	Somatic copy number mosaicism in human skin revealed by induced pluripotent stem cells. <i>Nature</i> , <b>2012</b> , 492, 438-42	50.4	299
28	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , <b>2012</b> , 489, 57-74	50.4	11449
27	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , <b>2012</b> , 491, 56-65	50.4	6049
26	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , <b>2012</b> , 489, 91-100	50.4	1104
25	Regulatory element copy number differences shape primate expression profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 12656-61	11.5	27
24	Annual Research Review: The promise of stem cell research for neuropsychiatric disorders. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , <b>2011</b> , 52, 504-16	7.9	26
23	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , <b>2011</b> , 470, 59-65	50.4	833
22	Integration of protein motions with molecular networks reveals different mechanisms for permanent and transient interactions. <i>Protein Science</i> , <b>2011</b> , 20, 1745-54	6.3	24
21	AlleleSeq: analysis of allele-specific expression and binding in a network framework. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 522	12.2	228
20	CNVnator: an approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. <i>Genome Research</i> , <b>2011</b> , 21, 974-84	9.7	944
19	AGE: defining breakpoints of genomic structural variants at single-nucleotide resolution, through optimal alignments with gap excision. <i>Bioinformatics</i> , <b>2011</b> , 27, 595-603	7.2	73
18	Genome-wide mapping of copy number variation in humans: comparative analysis of high resolution array platforms. <i>PLoS ONE</i> , <b>2011</b> , 6, e27859	3.7	51
17	A map of human genome variation from population-scale sequencing. <i>Nature</i> , <b>2010</b> , 467, 1061-73	50.4	6142
16	Analysis of combinatorial regulation: scaling of partnerships between regulators with the number of governed targets. <i>PLoS Computational Biology</i> , <b>2010</b> , 6, e1000755	5	20
15	RigidFinder: a fast and sensitive method to detect rigid blocks in large macromolecular complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2010</b> , 78, 309-24	4.2	26
14	PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. <i>Genome Biology</i> , <b>2009</b> , 10, R23	18.3	201
13	MSB: a mean-shift-based approach for the analysis of structural variation in the genome. <i>Genome Research</i> , <b>2009</b> , 19, 106-17	9.7	29
12	An AP endonuclease 1-DNA polymerase beta complex: theoretical prediction of interacting surfaces. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e1000066	5	14

11	A comprehensive analysis of non-sequential alignments between all protein structures. <i>BMC Structural Biology</i> , <b>2007</b> , 7, 78	2.7	14
10	TOPOFIT-DB, a database of protein structural alignments based on the TOPOFIT method. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D317-21	20.1	13
9	Structure SNP (StSNP): a web server for mapping and modeling nsSNPs on protein structures with linkage to metabolic pathways. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W384-92	20.1	38
8	UmuD and RecA directly modulate the mutagenic potential of the Y family DNA polymerase DinB. <i>Molecular Cell</i> , <b>2007</b> , 28, 1058-70	17.6	87
7	Friend, an integrated analytical front-end application for bioinformatics. <i>Bioinformatics</i> , <b>2005</b> , 21, 3677-87.2		21
6	Active site prediction for comparative model structures with thematics. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2005</b> , 3, 127-43	1	8
5	Structural alignment of proteins by a novel TOPOFIT method, as a superimposition of common volumes at a topomax point. <i>Protein Science</i> , <b>2004</b> , 13, 1865-74	6.3	71
4	Haplotype-resolved and integrated genome analysis of the cancer cell line HepG2		1
3	Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562		1
2	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia		3
1	CNVpytor: a tool for CNV/CNA detection and analysis from read depth and allele imbalance in whole genome sequencing		1