

Victor Guryev

List of Publications by Year in descending order

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129
papers

11,293
citations

61984

43
h-index

34986

98
g-index

144
all docs

144
docs citations

144
times ranked

20426
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetic Shadowing and Computational Identification of Human microRNA Genes. <i>Cell</i> , 2005, 120, 21-24.	28.9	1,194
2	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	8.8	742
3	Whole-genome sequence variation, population structure and demographic history of the Dutch population. <i>Nature Genetics</i> , 2014, 46, 818-825.	21.4	641
4	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	12.8	636
5	Transcription Factor Achaete Scute-Like 2 Controls Intestinal Stem Cell Fate. <i>Cell</i> , 2009, 136, 903-912.	28.9	615
6	Unmasking Transcriptional Heterogeneity in Senescent Cells. <i>Current Biology</i> , 2017, 27, 2652-2660.e4.	3.9	559
7	Genome-wide patterns and properties of de novo mutations in humans. <i>Nature Genetics</i> , 2015, 47, 822-826.	21.4	384
8	Chromothripsis as a mechanism driving complex de novo structural rearrangements in the germline. <i>Human Molecular Genetics</i> , 2011, 20, 1916-1924.	2.9	268
9	Genome-wide RNA Tomography in the Zebrafish Embryo. <i>Cell</i> , 2014, 159, 662-675.	28.9	248
10	The Genome of the Netherlands: design, and project goals. <i>European Journal of Human Genetics</i> , 2014, 22, 221-227.	2.8	246
11	Many novel mammalian microRNA candidates identified by extensive cloning and RAKE analysis. <i>Genome Research</i> , 2006, 16, 1289-1298.	5.5	242
12	Genome-Wide Pattern of TCF7L2/TCF4 Chromatin Occupancy in Colorectal Cancer Cells. <i>Molecular and Cellular Biology</i> , 2008, 28, 2732-2744.	2.3	208
13	Constitutional Chromothripsis Rearrangements Involve Clustered Double-Stranded DNA Breaks and Nonhomologous Repair Mechanisms. <i>Cell Reports</i> , 2012, 1, 648-655.	6.4	193
14	Distribution and functional impact of DNA copy number variation in the rat. <i>Nature Genetics</i> , 2008, 40, 538-545.	21.4	186
15	Mutagenic Capacity of Endogenous G4 DNA Underlies Genome Instability in FANCD1-Defective <i>C. elegans</i> . <i>Current Biology</i> , 2008, 18, 900-905.	3.9	186
16	Single-cell sequencing reveals karyotype heterogeneity in murine and human malignancies. <i>Genome Biology</i> , 2016, 17, 115.	8.8	178
17	Chromothripsis is a common mechanism driving genomic rearrangements in primary and metastatic colorectal cancer. <i>Genome Biology</i> , 2011, 12, R103.	9.6	177
18	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. <i>Nature Genetics</i> , 2013, 45, 767-775.	21.4	176

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19	Genetic variation in the zebrafish. <i>Genome Research</i> , 2006, 16, 491-497.	5.5	173
20	SNP and haplotype mapping for genetic analysis in the rat. <i>Nature Genetics</i> , 2008, 40, 560-566.	21.4	172
21	Generation of gene knockouts and mutant models in the laboratory rat by ENU-driven target-selected mutagenesis. <i>Pharmacogenetics and Genomics</i> , 2006, 16, 159-169.	1.5	161
22	Genome Sequencing Reveals Loci under Artificial Selection that Underlie Disease Phenotypes in the Laboratory Rat. <i>Cell</i> , 2013, 154, 691-703.	28.9	154
23	Protein biogenesis machinery is a driver of replicative aging in yeast. <i>ELife</i> , 2015, 4, e08527.	6.0	151
24	Single-cell whole genome sequencing reveals no evidence for common aneuploidy in normal and Alzheimer's disease neurons. <i>Genome Biology</i> , 2016, 17, 116.	8.8	118
25	Characteristics of de novo structural changes in the human genome. <i>Genome Research</i> , 2015, 25, 792-801.	5.5	115
26	Quantitative and Qualitative Proteome Characteristics Extracted from In-Depth Integrated Genomics and Proteomics Analysis. <i>Cell Reports</i> , 2013, 5, 1469-1478.	6.4	113
27	Genome-wide profiling of nucleosome sensitivity and chromatin accessibility in <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2016, 44, 1036-1051.	14.5	111
28	Negative selection in humans and fruit flies involves synergistic epistasis. <i>Science</i> , 2017, 356, 539-542.	12.6	103
29	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. <i>Nature Communications</i> , 2016, 7, 12989.	12.8	99
30	Dominant-Negative <i>ALK2</i> Allele Associates With Congenital Heart Defects. <i>Circulation</i> , 2009, 119, 3062-3069.	1.6	97
31	Parental DNA Methylation States Are Associated with Heterosis in Epigenetic Hybrids. <i>Plant Physiology</i> , 2018, 176, 1627-1645.	4.8	93
32	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010, 20, 791-803.	5.5	84
33	Genomic landscape of rat strain and substrain variation. <i>BMC Genomics</i> , 2015, 16, 357.	2.8	84
34	Dense and accurate whole-chromosome haplotyping of individual genomes. <i>Nature Communications</i> , 2017, 8, 1293.	12.8	83
35	BLM helicase suppresses recombination at G-quadruplex motifs in transcribed genes. <i>Nature Communications</i> , 2018, 9, 271.	12.8	83
36	Accurate SNP and mutation detection by targeted custom microarray-based genomic enrichment of short-fragment sequencing libraries. <i>Nucleic Acids Research</i> , 2010, 38, e116-e116.	14.5	79

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37	CONREAL: Conserved Regulatory Elements Anchored Alignment Algorithm for Identification of Transcription Factor Binding Sites by Phylogenetic Footprinting. <i>Genome Research</i> , 2003, 14, 170-178.	5.5	78
38	CONREAL web server: identification and visualization of conserved transcription factor binding sites. <i>Nucleic Acids Research</i> , 2005, 33, W447-W450.	14.5	78
39	Phylogeny of the Genus <i>Chironomus</i> (Diptera) Inferred from DNA Sequences of Mitochondrial Cytochrome b and Cytochrome oxidase I. <i>Molecular Phylogenetics and Evolution</i> , 2001, 19, 9-21.	2.7	67
40	Characterizing polymorphic inversions in human genomes by single-cell sequencing. <i>Genome Research</i> , 2016, 26, 1575-1587.	5.5	67
41	Haplotype Block Structure Is Conserved across Mammals. <i>PLoS Genetics</i> , 2006, 2, e121.	3.5	66
42	Gene expression variability: the other dimension in transcriptome analysis. <i>Physiological Genomics</i> , 2019, 51, 145-158.	2.3	61
43	Efficient transgenesis and annotated genome sequence of the regenerative flatworm model <i>Macrostomum lignano</i> . <i>Nature Communications</i> , 2017, 8, 2120.	12.8	60
44	TGF- β 2 activation impairs fibroblast ability to support adult lung epithelial progenitor cell organoid formation. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2019, 317, L14-L28.	2.9	53
45	Direct chromosome-length haplotyping by single-cell sequencing. <i>Genome Research</i> , 2016, 26, 1565-1574.	5.5	52
46	Single Nucleotide Polymorphisms Associated With Rat Expressed Sequences. <i>Genome Research</i> , 2004, 14, 1438-1443.	5.5	50
47	A genome-wide SNP panel for mapping and association studies in the rat. <i>BMC Genomics</i> , 2008, 9, 95.	2.8	46
48	A p300 and SIRT1 Regulated Acetylation Switch of C/EBP β Controls Mitochondrial Function. <i>Cell Reports</i> , 2018, 22, 497-511.	6.4	45
49	Insights in dynamic kinome reprogramming as a consequence of MEK inhibition in MLL-rearranged AML. <i>Leukemia</i> , 2014, 28, 589-599.	7.2	42
50	Aging as Accelerated Accumulation of Somatic Variants: Whole-Genome Sequencing of Centenarian and Middle-Aged Monozygotic Twin Pairs. <i>Twin Research and Human Genetics</i> , 2013, 16, 1026-1032.	0.6	40
51	Systematic biases in DNA copy number originate from isolation procedures. <i>Genome Biology</i> , 2013, 14, R33.	9.6	39
52	Efficient Double Fragmentation CHIP-seq Provides Nucleotide Resolution Protein-DNA Binding Profiles. <i>PLoS ONE</i> , 2010, 5, e15092.	2.5	39
53	Proteogenomics: From next-generation sequencing (NGS) and mass spectrometry-based proteomics to precision medicine. <i>Clinica Chimica Acta</i> , 2019, 498, 38-46.	1.1	38
54	Sperm DNA damage causes genomic instability in early embryonic development. <i>Science Advances</i> , 2020, 6, eaaz7602.	10.3	37

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55	Lung tissue gene-expression signature for the ageing lung in COPD. <i>Thorax</i> , 2018, 73, 609-617.	5.6	36
56	Improving mammalian genome scaffolding using large insert mate-pair next-generation sequencing. <i>BMC Genomics</i> , 2013, 14, 257.	2.8	35
57	An ENU-Mutagenesis Screen in the Mouse: Identification of Novel Developmental Gene Functions. <i>PLoS ONE</i> , 2011, 6, e19357.	2.5	35
58	Whole-genome sequencing of 1,171 elderly admixed individuals from Brazil. <i>Nature Communications</i> , 2022, 13, 1004.	12.8	35
59	Age-related gene and miRNA expression changes in airways of healthy individuals. <i>Scientific Reports</i> , 2019, 9, 3765.	3.3	34
60	ALK2 mutation in a patient with Down's syndrome and a congenital heart defect. <i>European Journal of Human Genetics</i> , 2011, 19, 389-393.	2.8	33
61	Nasal gene expression differentiates COPD from controls and overlaps bronchial gene expression. <i>Respiratory Research</i> , 2017, 18, 213.	3.6	33
62	Quantification of Aneuploidy in Mammalian Systems. <i>Methods in Molecular Biology</i> , 2019, 1896, 159-190.	0.9	33
63	Genetic basis of transcriptome differences between the founder strains of the rat HXB/BXH recombinant inbred panel. <i>Genome Biology</i> , 2012, 13, r31.	9.6	32
64	Nasal epithelium as a proxy for bronchial epithelium for smoking-induced gene expression and expression Quantitative Trait Loci. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 314-317.e15.	2.9	32
65	breakpointR: an R/Bioconductor package to localize strand state changes in Strand-seq data. <i>Bioinformatics</i> , 2020, 36, 1260-1261.	4.1	32
66	Cigarette smoke exposure decreases CFLAR expression in the bronchial epithelium, augmenting susceptibility for lung epithelial cell death and DAMP release. <i>Scientific Reports</i> , 2018, 8, 12426.	3.3	31
67	Genome-wide mapping of sister chromatid exchange events in single yeast cells using Strand-seq. <i>ELife</i> , 2017, 6, .	6.0	30
68	Comparing genome-wide chromatin profiles using ChIP-chip or ChIP-seq. <i>Bioinformatics</i> , 2010, 26, 1000-1006.	4.1	28
69	Improved generation of rat gene knockouts by target-selected mutagenesis in mismatch repair-deficient animals. <i>BMC Genomics</i> , 2008, 9, 460.	2.8	27
70	Population variability in <i>Chironomus</i> (<i>Camptochironomus</i>) species (Diptera, Nematocera) with a Holarctic distribution: evidence of mitochondrial gene flow. <i>Insect Molecular Biology</i> , 2002, 11, 387-397.	2.0	25
71	Genomes and phenomes of a population of outbred rats and its progenitors. <i>Scientific Data</i> , 2014, 1, 140011.	5.3	25
72	Essential role for cyclic-AMP responsive element binding protein 1 (CREB) in the survival of acute lymphoblastic leukemia. <i>Oncotarget</i> , 2015, 6, 14970-14981.	1.8	25

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73	Identification of a Rat Model for Usher Syndrome Type 1B by N-Ethyl-N-nitrosourea Mutagenesis-Driven Forward Genetics. <i>Genetics</i> , 2005, 170, 1887-1896.	2.9	24
74	Efficient target-selected mutagenesis in <i>Caenorhabditis elegans</i> : Toward a knockout for every gene. <i>Genome Research</i> , 2007, 17, 649-658.	5.5	24
75	Reduced expression of C/EBP β -LIP extends health and lifespan in mice. <i>ELife</i> , 2018, 7, .	6.0	23
76	Insertional polymorphism of a non-LTR mobile element (NLRCh1) in European populations of <i>Chironomus riparius</i> (Diptera, Chironomidae) as detected by transposon insertion display. <i>Genome</i> , 2004, 47, 1154-1163.	2.0	22
77	Resilience to aging in the regeneration-capable flatworm <i>Macrostomum lignano</i> . <i>Aging Cell</i> , 2018, 17, e12739.	6.7	22
78	CASCAD: a database of annotated candidate single nucleotide polymorphisms associated with expressed sequences. <i>BMC Genomics</i> , 2005, 6, 10.	2.8	21
79	AGER expression and alternative splicing in bronchial biopsies of smokers and never smokers. <i>Respiratory Research</i> , 2019, 20, 70.	3.6	21
80	Proteomic alterations in early stage cervical cancer. <i>Oncotarget</i> , 2018, 9, 18128-18147.	1.8	20
81	Identification of Two Protein-Signaling States Delineating Transcriptionally Heterogeneous Human Medulloblastoma. <i>Cell Reports</i> , 2018, 22, 3206-3216.	6.4	19
82	Efficient single nucleotide polymorphism discovery in laboratory rat strains using wild rat-derived SNP candidates. <i>BMC Genomics</i> , 2005, 6, 170.	2.8	17
83	Systematic generation of in vivo G protein-coupled receptor mutants in the rat. <i>Pharmacogenomics Journal</i> , 2011, 11, 326-336.	2.0	17
84	Proteogenomics: Key Driver for Clinical Discovery and Personalized Medicine. <i>Advances in Experimental Medicine and Biology</i> , 2016, 926, 21-47.	1.6	17
85	Title is missing!. <i>Invertebrate Systematics</i> , 2002, 16, 599.	1.3	16
86	Next-generation sequencing approaches in genetic rodent model systems to study functional effects of human genetic variation. <i>FEBS Letters</i> , 2009, 583, 1668-1673.	2.8	16
87	Isolation of deletion alleles by G4 DNA-induced mutagenesis. <i>Nature Methods</i> , 2009, 6, 655-657.	19.0	16
88	Integrated proteogenomic approach identifying a protein signature of COPD and a new splice variant of SORBS1. <i>Thorax</i> , 2020, 75, 180-183.	5.6	16
89	Microalterations of Inherently Unstable Genomic Regions in Rat Mammary Carcinomas as Revealed by Long Oligonucleotide Array-Based Comparative Genomic Hybridization. <i>Cancer Research</i> , 2009, 69, 5159-5167.	0.9	15
90	Identification of an RNA Polymerase III Regulator Linked to Disease-Associated Protein Aggregation. <i>Molecular Cell</i> , 2017, 65, 1096-1108.e6.	9.7	14

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91	Gene network approach reveals co-expression patterns in nasal and bronchial epithelium. <i>Scientific Reports</i> , 2019, 9, 15835.	3.3	14
92	A Novel Role for Bronchial MicroRNAs and Long Noncoding RNAs in Asthma Remission. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 614-618.	5.6	13
93	Kinase activity profiling reveals active signal transduction pathways in pediatric acute lymphoblastic leukemia: A new approach for target discovery. <i>Proteomics</i> , 2015, 15, 1245-1254.	2.2	12
94	VEGFC Antibody Therapy Drives Differentiation of AML. <i>Cancer Research</i> , 2018, 78, 5940-5948.	0.9	12
95	Peptide microarray profiling identifies phospholipase C gamma 1 (PLC- γ 1) as a potential target for t(8;21) AML. <i>Oncotarget</i> , 2017, 8, 67344-67354.	1.8	12
96	Variant calling: Considerations, practices, and developments. <i>Human Mutation</i> , 2022, 43, 976-985.	2.5	11
97	Genetic Etiology of Renal Agenesis: Fine Mapping of Renag1 and Identification of Kit as the Candidate Functional Gene. <i>PLoS ONE</i> , 2015, 10, e0118147.	2.5	10
98	Genomic variability and protein species "Improving sequence coverage for proteogenomics. <i>Journal of Proteomics</i> , 2016, 134, 25-36.	2.4	10
99	Exploring Conservation of Transcription Factor Binding Sites with CONREAL. <i>Methods in Molecular Biology</i> , 2007, 395, 437-448.	0.9	9
100	C/EBP β isoform-specific regulation of migration and invasion in triple-negative breast cancer cells. <i>Npj Breast Cancer</i> , 2022, 8, 11.	5.2	9
101	Exact hypothesis testing for shrinkage-based Gaussian graphical models. <i>Bioinformatics</i> , 2019, 35, 5011-5017.	4.1	8
102	Estimates of gene ensemble noise highlight critical pathways and predict disease severity in H1N1, COVID-19 and mortality in sepsis patients. <i>Scientific Reports</i> , 2021, 11, 10793.	3.3	8
103	Whole genome sequencing of nearly isogenic WMI and WLI inbred rats identifies genes potentially involved in depression and stress reactivity. <i>Scientific Reports</i> , 2021, 11, 14774.	3.3	8
104	The sputum transcriptome better predicts COPD exacerbations after the withdrawal of inhaled corticosteroids than sputum eosinophils. <i>ERJ Open Research</i> , 2021, 7, 00097-2021.	2.6	7
105	A novel mutant allele of Ncx1: a single amino acid substitution leads to cardiac dysfunction. <i>International Journal of Developmental Biology</i> , 2010, 54, 1465-1470.	0.6	7
106	Single Nucleotide Polymorphism (SNP) Panels for Rapid Positional Cloning in Zebrafish. <i>Methods in Cell Biology</i> , 2011, 104, 219-235.	1.1	6
107	Single-nucleotide polymorphism rs2070600 regulates <i>AGER</i> splicing and the sputum levels of the COPD biomarker soluble receptor for advanced glycation end-products. <i>ERJ Open Research</i> , 2021, 7, 00947-2020.	2.6	6
108	Deposition Bias of Chromatin Proteins Inverts under DNA Replication Stress Conditions. <i>ACS Chemical Biology</i> , 2021, 16, 2193-2201.	3.4	6

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109	Construction of Whole Genomes from Scaffolds Using Single Cell Strand-Seq Data. International Journal of Molecular Sciences, 2021, 22, 3617.	4.1	5
110	Peptide microarray of pediatric acute myeloid leukemia is related to relapse and reveals involvement of DNA damage response and repair. Oncotarget, 2019, 10, 4679-4690.	1.8	5
111	Age-specific oncogenic pathways in head and neck squamous cell carcinoma—are elderly a different subcategory?. Cellular Oncology (Dordrecht), 2022, 45, 1-18.	4.4	5
112	Using a priori knowledge to align sequencing reads to their exact genomic position. Nucleic Acids Research, 2012, 40, e125-e125.	14.5	4
113	Nasal gene expression changes with inhaled corticosteroid treatment in asthma. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 191-194.	5.7	4
114	Telomerase subunit Est2 marks internal sites that are prone to accumulate DNA damage. BMC Biology, 2021, 19, 247.	3.8	4
115	InvertypR: Bayesian inversion genotyping with Strand-seq data. BMC Genomics, 2021, 22, 582.	2.8	3
116	Introgressed chromosome 2 quantitative trait loci restores aldosterone regulation and reduces response to salt in the stroke-prone spontaneously hypertensive rat. Journal of Hypertension, 2014, 32, 2013-2021.	0.5	2
117	Effect of IKZF1 deletions on signal transduction pathways in Philadelphia chromosome negative pediatric B-cell precursor acute lymphoblastic leukemia (BCP-ALL). Experimental Hematology and Oncology, 2015, 4, 23.	5.0	2
118	Comparison of genome-wide gene expression profiling by RNA Sequencing versus microarray in bronchial biopsies of COPD patients before and after inhaled corticosteroid treatment: does it provide new insights?. ERJ Open Research, 2021, 7, 00104-2021.	2.6	2
119	The developmental stage of the medulloblastoma cell-of-origin restricts Sonic hedgehog pathway usage and drug sensitivity. Journal of Cell Science, 2022, 135, .	2.0	2
120	Assessment of variant pathogenicity in a highly admixed population. Human Mutation, 2017, 38, 749-749.	2.5	1
121	The Microbiome in Bronchial Biopsies from Smokers and Ex-Smokers with Stable COPD - A Metatranscriptomic Approach. COPD: Journal of Chronic Obstructive Pulmonary Disease, 2022, 19, 81-87.	1.6	1
122	MBRS-36. IDENTIFICATION OF TWO PROTEIN-SIGNALING STATES DELINEATING TRANSCRIPTIONALLY HETEROGENEOUS HUMAN MEDULLOBLASTOMA. Neuro-Oncology, 2018, 20, i136-i136.	1.2	0
123	MEDU-07. THE DEVELOPMENTAL STAGE OF THE MEDULLOBLASTOMA CELL-OF-ORIGIN IS MAINTAINED IN CANCER AND RESTRICTS HEDGEHOG PATHWAY USAGE AND DRUG SENSITIVITY. Neuro-Oncology, 2019, 21, ii104-ii104.	1.2	0
124	The $\hat{\rho}$ -shrunken™ partial correlation in Gaussian graphical models. BMC Bioinformatics, 2021, 22, 424.	2.6	0
125	Effect of IKZF1 Deletions on Signal Transduction Pathways in Philadelphia Chromosome-Negative B-Cell Precursor Acute Lymphoblastic Leukemia (BCP-ALL). Blood, 2014, 124, 3770-3770.	1.4	0
126	Kinomic Profiling of Pediatric Acute Myeloid Leukemia for Detailed Cellular Insights. Blood, 2014, 124, 1046-1046.	1.4	0

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127	Accurate Prediction of Protein Sequences for Proteogenomics Data Integration. <i>Methods in Molecular Biology</i> , 2022, 2420, 233-260.	0.9	0
128	Exploring Conservation of Transcription Factor Binding Sites with CONREAL. , 0, , 437-448.		0
129	Airway Wall Splice-QTL Analysis Reveals Novel Downstream Mechanisms for Well-Known GWAS Asthma-SNPs. , 2022, , .		0