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	C/EBPÎ² isoform-specific regulation of migration and invasion in triple-negative breast cancer cells. Npj Breast Cancer, 2022, 8, 11.	5.2	9
2	Age-specific oncogenic pathways in head and neck squamous cell carcinomaÂ-Âare elderly a different subcategory?. Cellular Oncology (Dordrecht), 2022, 45, 1-18.	4.4	5
3	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
4	Whole-genome sequencing of 1,171 elderly admixed individuals from Brazil. Nature Communications, 2022, 13, 1004.	12.8	35
5	Accurate Prediction of Protein Sequences for Proteogenomics Data Integration. Methods in Molecular Biology, 2022, 2420, 233-260.	0.9	0
6	Variant calling: Considerations, practices, and developments. Human Mutation, 2022, 43, 976-985.	2.5	11
7	Airway Wall Splice-QTL Analysis Reveals Novel Downstream Mechanisms for Well-Known GWAS Asthma-SNPs. , 2022, , .		0
8	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
9	Construction of Whole Genomes from Scaffolds Using Single Cell Strand-Seq Data. International Journal of Molecular Sciences, 2021, 22, 3617.	4.1	5
10	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
11	Single-nucleotide polymorphism rs2070600 regulates AGER splicing and the sputum levels of the COPD biomarker soluble receptor for advanced glycation end-products. ERJ Open Research, 2021, 7, 00947-2020.	2.6	6
12	Estimates of gene ensemble noise highlight critical pathways and predict disease severity in H1N1, COVID-19 and mortality in sepsis patients. Scientific Reports, 2021, 11, 10793.	3.3	8
13	The sputum transcriptome better predicts COPD exacerbations after the withdrawal of inhaled corticosteroids than sputum eosinophils. ERJ Open Research, 2021, 7, 00097-2021.	2.6	7
14	Whole genome sequencing of nearly isogenic WMI and WLI inbred rats identifies genes potentially involved in depression and stress reactivity. Scientific Reports, 2021, 11, 14774.	3.3	8
15	InvertypeR: Bayesian inversion genotyping with Strand-seq data. BMC Genomics, 2021, 22, 582.	2.8	3
16	Deposition Bias of Chromatin Proteins Inverts under DNA Replication Stress Conditions. ACS Chemical Biology, 2021, 16, 2193-2201.	3.4	6
17	The â€˜un-shrunkâ€™ partial correlation in Gaussian graphical models. BMC Bioinformatics, 2021, 22, 424.	2.6	0
18	Telomerase subunit Est2 marks internal sites that are prone to accumulate DNA damage. BMC Biology, 2021, 19, 247.	3.8	4

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19	breakpointR: an R/Bioconductor package to localize strand state changes in Strand-seq data. Bioinformatics, 2020, 36, 1260-1261.	4.1	32
20	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
21	A Novel Role for Bronchial MicroRNAs and Long Noncoding RNAs in Asthma Remission. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 614-618.	5.6	13
22	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
23	Integrated proteogenomic approach identifying a protein signature of COPD and a new splice variant of SORBS1. Thorax, 2020, 75, 180-183.	5.6	16
24	Sperm DNA damage causes genomic instability in early embryonic development. Science Advances, 2020, 6, eaaz7602.	10.3	37
25	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
26	Proteogenomics: From next-generation sequencing (NGS) and mass spectrometry-based proteomics to precision medicine. Clinica Chimica Acta, 2019, 498, 38-46.	1.1	38
27	Exact hypothesis testing for shrinkage-based Gaussian graphical models. Bioinformatics, 2019, 35, 5011-5017.	4.1	8
28	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
29	Gene expression variability: the other dimension in transcriptome analysis. Physiological Genomics, 2019, 51, 145-158.	2.3	61
30	Age-related gene and miRNA expression changes in airways of healthy individuals. Scientific Reports, 2019, 9, 3765.	3.3	34
31	TGF-Î² activation impairs fibroblast ability to support adult lung epithelial progenitor cell organoid formation. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2019, 317, L14-L28.	2.9	53
32	AGER expression and alternative splicing in bronchial biopsies of smokers and never smokers. Respiratory Research, 2019, 20, 70.	3.6	21
33	Gene network approach reveals co-expression patterns in nasal and bronchial epithelium. Scientific Reports, 2019, 9, 15835.	3.3	14
34	Quantification of Aneuploidy in Mammalian Systems. Methods in Molecular Biology, 2019, 1896, 159-190.	0.9	33
35	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
36	Resilience to aging in the regenerationâ€capable flatworm Macrostomum lignano. Aging Cell, 2018, 17, e12739.	6.7	22

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37	BLM helicase suppresses recombination at G-quadruplex motifs in transcribed genes. Nature Communications, 2018, 9, 271.	12.8	83
38	A p300 and SIRT1 Regulated Acetylation Switch of C/EBPÎ± Controls Mitochondrial Function. Cell Reports, 2018, 22, 497-511.	6.4	45
39	Nasal epithelium as a proxy for bronchial epithelium for smoking-induced gene expression and expression Quantitative Trait Loci. Journal of Allergy and Clinical Immunology, 2018, 142, 314-317.e15.	2.9	32
40	Identification of Two Protein-Signaling States Delineating Transcriptionally Heterogeneous Human Medulloblastoma. Cell Reports, 2018, 22, 3206-3216.	6.4	19
41	Parental DNA Methylation States Are Associated with Heterosis in Epigenetic Hybrids. Plant Physiology, 2018, 176, 1627-1645.	4.8	93
42	Lung tissue gene-expression signature for the ageing lung in COPD. Thorax, 2018, 73, 609-617.	5.6	36
43	VEGFC Antibody Therapy Drives Differentiation of AML. Cancer Research, 2018, 78, 5940-5948.	0.9	12
44	MBRS-36. IDENTIFICATION OF TWO PROTEIN-SIGNALING STATES DELINEATING TRANSCRIPTIONALLY HETEROGENEOUS HUMAN MEDULLOBLASTOMA. Neuro-Oncology, 2018, 20, i136-i136.	1.2	0
45	Cigarette smoke exposure decreases CFLAR expression in the bronchial epithelium, augmenting susceptibility for lung epithelial cell death and DAMP release. Scientific Reports, 2018, 8, 12426.	3.3	31
46	Proteomic alterations in early stage cervical cancer. Oncotarget, 2018, 9, 18128-18147.	1.8	20
47	Reduced expression of C/EBPÎ²-LIP extends health and lifespan in mice. ELife, 2018, 7, .	6.0	23
48	Negative selection in humans and fruit flies involves synergistic epistasis. Science, 2017, 356, 539-542.	12.6	103
49	Assessment of variant pathogenicity in a highly admixed population. Human Mutation, 2017, 38, 749-749.	2.5	1
50	Identification of an RNA Polymerase III Regulator Linked to Disease-Associated Protein Aggregation. Molecular Cell, 2017, 65, 1096-1108.e6.	9.7	14
51	Unmasking Transcriptional Heterogeneity in Senescent Cells. Current Biology, 2017, 27, 2652-2660.e4.	3.9	559
52	Efficient transgenesis and annotated genome sequence of the regenerative flatworm model Macrostomum lignano. Nature Communications, 2017, 8, 2120.	12.8	60
53	Dense and accurate whole-chromosome haplotyping of individual genomes. Nature Communications, 2017, 8, 1293.	12.8	83
54	Nasal gene expression differentiates COPD from controls and overlaps bronchial gene expression. Respiratory Research, 2017, 18, 213.	3.6	33

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55	Peptide microarray profiling identifies phospholipase C gamma 1 (PLC-Î³1) as a potential target for t(8;21) AML. Oncotarget, 2017, 8, 67344-67354.	1.8	12
56	Genome-wide mapping of sister chromatid exchange events in single yeast cells using Strand-seq. ELife, 2017, 6, .	6.0	30
57	Single-cell whole genome sequencing reveals no evidence for common aneuploidy in normal and Alzheimerâ€™s disease neurons. Genome Biology, 2016, 17, 116.	8.8	118
58	Proteogenomics: Key Driver for Clinical Discovery and Personalized Medicine. Advances in Experimental Medicine and Biology, 2016, 926, 21-47.	1.6	17
59	Characterizing polymorphic inversions in human genomes by single-cell sequencing. Genome Research, 2016, 26, 1575-1587.	5.5	67
60	Direct chromosome-length haplotyping by single-cell sequencing. Genome Research, 2016, 26, 1565-1574.	5.5	52
61	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
62	Single-cell sequencing reveals karyotype heterogeneity in murine and human malignancies. Genome Biology, 2016, 17, 115.	8.8	178
63	Genomic variability and protein species â€" Improving sequence coverage for proteogenomics. Journal of Proteomics, 2016, 134, 25-36.	2.4	10
64	Genome-wide profiling of nucleosome sensitivity and chromatin accessibility inDrosophila melanogaster. Nucleic Acids Research, 2016, 44, 1036-1051.	14.5	111
65	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
66	Genetic Etiology of Renal Agenesis: Fine Mapping of Renag1 and Identification of Kit as the Candidate Functional Gene. PLoS ONE, 2015, 10, e0118147.	2.5	10
67	Genomic landscape of rat strain and substrain variation. BMC Genomics, 2015, 16, 357.	2.8	84
68	Kinase activity profiling reveals active signal transduction pathways in pediatric acute lymphoblastic leukemia: A new approach for target discovery. Proteomics, 2015, 15, 1245-1254.	2.2	12
69	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
70	Genome-wide patterns and properties of de novo mutations in humans. Nature Genetics, 2015, 47, 822-826.	21.4	384
71	Essential role for cyclic-AMP responsive element binding protein 1 (CREB) in the survival of acute lymphoblastic leukemia. Oncotarget, 2015, 6, 14970-14981.	1.8	25
72	Protein biogenesis machinery is a driver of replicative aging in yeast. ELife, 2015, 4, e08527.	6.0	151

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73	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
74	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
75	Genome-wide RNA Tomography in the Zebrafish Embryo. Cell, 2014, 159, 662-675.	28.9	248
76	Insights in dynamic kinome reprogramming as a consequence of MEK inhibition in MLL-rearranged AML. Leukemia, 2014, 28, 589-599.	7.2	42
77	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	21.4	641
78	Genomes and phenomes of a population of outbred rats and its progenitors. Scientific Data, 2014, 1, 140011.	5.3	25
79	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
80	Kinomic Profiling of Pediatric Acute Myeloid Leukemia for Detailed Cellular Insights. Blood, 2014, 124, 1046-1046.	1.4	0
81	Systematic biases in DNA copy number originate from isolation procedures. Genome Biology, 2013, 14, R33.	9.6	39
82	Improving mammalian genome scaffolding using large insert mate-pair next-generation sequencing. BMC Genomics, 2013, 14, 257.	2.8	35
83	Aging as Accelerated Accumulation of Somatic Variants: Whole-Genome Sequencing of Centenarian and Middle-Aged Monozygotic Twin Pairs. Twin Research and Human Genetics, 2013, 16, 1026-1032.	0.6	40
84	Genome Sequencing Reveals Loci under Artificial Selection that Underlie Disease Phenotypes in the Laboratory Rat. Cell, 2013, 154, 691-703.	28.9	154
85	Quantitative and Qualitative Proteome Characteristics Extracted from In-Depth Integrated Genomics and Proteomics Analysis. Cell Reports, 2013, 5, 1469-1478.	6.4	113
86	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. Nature Genetics, 2013, 45, 767-775.	21.4	176
87	Using a priori knowledge to align sequencing reads to their exact genomic position. Nucleic Acids Research, 2012, 40, e125-e125.	14.5	4
88	Genetic basis of transcriptome differences between the founder strains of the rat HXB/BXH recombinant inbred panel. Genome Biology, 2012, 13, r31.	9.6	32
89	Constitutional Chromothripsis Rearrangements Involve Clustered Double-Stranded DNA Breaks and Nonhomologous Repair Mechanisms. Cell Reports, 2012, 1, 648-655.	6.4	193
90	Chromothripsis is a common mechanism driving genomic rearrangements in primary and metastatic colorectal cancer. Genome Biology, 2011, 12, R103.	9.6	177

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91	Systematic generation of in vivo G protein-coupled receptor mutants in the rat. Pharmacogenomics Journal, 2011, 11, 326-336.	2.0	17
92	Single Nucleotide Polymorphism (SNP) Panels for Rapid Positional Cloning in Zebrafish. Methods in Cell Biology, 2011, 104, 219-235.	1.1	6
93	ALK2 mutation in a patient with Down's syndrome and a congenital heart defect. European Journal of Human Genetics, 2011, 19, 389-393.	2.8	33
94	Chromothripsis as a mechanism driving complex de novo structural rearrangements in the germlineâ€. Human Molecular Genetics, 2011, 20, 1916-1924.	2.9	268
95	An ENU-Mutagenesis Screen in the Mouse: Identification of Novel Developmental Gene Functions. PLoS ONE, 2011, 6, e19357.	2.5	35
96	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. Genome Research, 2010, 20, 791-803.	5.5	84
97	Accurate SNP and mutation detection by targeted custom microarray-based genomic enrichment of short-fragment sequencing libraries. Nucleic Acids Research, 2010, 38, e116-e116.	14.5	79
98	Comparing genome-wide chromatin profiles using ChIP-chip or ChIP-seq. Bioinformatics, 2010, 26, 1000-1006.	4.1	28
99	Efficient Double Fragmentation ChIP-seq Provides Nucleotide Resolution Protein-DNA Binding Profiles. PLoS ONE, 2010, 5, e15092.	2.5	39
100	A novel mutant allele of Ncx1: a single amino acid substitution leads to cardiac dysfunction. International Journal of Developmental Biology, 2010, 54, 1465-1470.	0.6	7
101	Microalterations of Inherently Unstable Genomic Regions in Rat Mammary Carcinomas as Revealed by Long Oligonucleotide Array-Based Comparative Genomic Hybridization. Cancer Research, 2009, 69, 5159-5167.	0.9	15
102	Dominant-Negative ALK2 Allele Associates With Congenital Heart Defects. Circulation, 2009, 119, 3062-3069.	1.6	97
103	Nextâ€generation sequencing approaches in genetic rodent model systems to study functional effects of human genetic variation. FEBS Letters, 2009, 583, 1668-1673.	2.8	16
104	Isolation of deletion alleles by G4 DNA-induced mutagenesis. Nature Methods, 2009, 6, 655-657.	19.0	16
105	Transcription Factor Achaete Scute-Like 2 Controls Intestinal Stem Cell Fate. Cell, 2009, 136, 903-912.	28.9	615
106	SNP and haplotype mapping for genetic analysis in the rat. Nature Genetics, 2008, 40, 560-566.	21.4	172
107	Distribution and functional impact of DNA copy number variation in the rat. Nature Genetics, 2008, 40, 538-545.	21.4	186
108	Improved generation of rat gene knockouts by target-selected mutagenesis in mismatch repair-deficient animals. BMC Genomics, 2008, 9, 460.	2.8	27

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109	A genome-wide SNP panel for mapping and association studies in the rat. BMC Genomics, 2008, 9, 95.	2.8	46
110	Mutagenic Capacity of Endogenous G4 DNA Underlies Genome Instability in FANCJ-Defective C. elegans. Current Biology, 2008, 18, 900-905.	3.9	186
111	Genome-Wide Pattern of TCF7L2/TCF4 Chromatin Occupancy in Colorectal Cancer Cells. Molecular and Cellular Biology, 2008, 28, 2732-2744.	2.3	208
112	Efficient target-selected mutagenesis in Caenorhabditis elegans: Toward a knockout for every gene. Genome Research, 2007, 17, 649-658.	5.5	24
113	Exploring Conservation of Transcription Factor Binding Sites with CONREAL. Methods in Molecular Biology, 2007, 395, 437-448.	0.9	9
114	Haplotype Block Structure Is Conserved across Mammals. PLoS Genetics, 2006, 2, e121.	3.5	66
115	Genetic variation in the zebrafish. Genome Research, 2006, 16, 491-497.	5.5	173
116	Many novel mammalian microRNA candidates identified by extensive cloning and RAKE analysis. Genome Research, 2006, 16, 1289-1298.	5.5	242
117	Generation of gene knockouts and mutant models in the laboratory rat by ENU-driven target-selected mutagenesis. Pharmacogenetics and Genomics, 2006, 16, 159-169.	1.5	161
118	CASCAD: a database of annotated candidate single nucleotide polymorphisms associated with expressed sequences. BMC Genomics, 2005, 6, 10.	2.8	21
119	Efficient single nucleotide polymorphism discovery in laboratory rat strains using wild rat-derived SNP candidates. BMC Genomics, 2005, 6, 170.	2.8	17
120	Identification of a Rat Model for Usher Syndrome Type 1B by N-Ethyl-N-nitrosourea Mutagenesis-Driven Forward Genetics. Genetics, 2005, 170, 1887-1896.	2.9	24
121	CONREAL web server: identification and visualization of conserved transcription factor binding sites. Nucleic Acids Research, 2005, 33, W447-W450.	14.5	78
122	Phylogenetic Shadowing and Computational Identification of Human microRNA Genes. Cell, 2005, 120, 21-24.	28.9	1,194
123	Single Nucleotide Polymorphisms Associated With Rat Expressed Sequences. Genome Research, 2004, 14, 1438-1443.	5.5	50
124	Insertional polymorphism of a non-LTR mobile element (NLRCth1) in European populations of Chironomus riparius (Diptera, Chironomidae) as detected by transposon insertion display. Genome, 2004, 47, 1154-1163.	2.0	22
125	CONREAL: Conserved Regulatory Elements Anchored Alignment Algorithm for Identification of Transcription Factor Binding Sites by Phylogenetic Footprinting. Genome Research, 2003, 14, 170-178.	5.5	78
126	Title is missing!. Invertebrate Systematics, 2002, 16, 599.	1.3	16

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127	Population variability in Chironomus (Camptochironomus) species (Diptera, Nematocera) with a Holarctic distribution: evidence of mitochondrial gene flow. Insect Molecular Biology, 2002, 11, 387-397.	2.0	25
128	Phylogeny of the Genus Chironomus (Diptera) Inferred from DNA Sequences of Mitochondrial Cytochrome b and Cytochrome oxidase I. Molecular Phylogenetics and Evolution, 2001, 19, 9-21.	2.7	67
129	Exploring Conservation of Transcription Factor Binding Sites with CONREAL. , 0, , 437-448.		0