Valentina Boeva

List of Publications by Year
in descending order

41 papers	3,685 citations	218677 26 h-index	276875 41 g-index
45 all docs	45 docs citations	45 times ranked	8955 citing authors

#	Article	IF	Citations
1	Control-FREEC: a tool for assessing copy number and allelic content using next-generation sequencing data. Bioinformatics, 2012, 28, 423-425.	4.1	847
2	Heterogeneity of neuroblastoma cell identity defined by transcriptional circuitries. Nature Genetics, 2017, 49, 1408-1413.	21.4	331
3	Control-free calling of copy number alterations in deep-sequencing data using GC-content normalization. Bioinformatics, 2011, 27, 268-269.	4.1	249
4	Jarid2 Is Implicated in the Initial Xist-Induced Targeting of PRC2 to the Inactive X Chromosome. Molecular Cell, 2014, 53, 301-316.	9.7	221
5	SVDetect: a tool to identify genomic structural variations from paired-end and mate-pair sequencing data. Bioinformatics, 2010, 26, 1895-1896.	4.1	178
6	The Oncogenic EWS-FLI1 Protein Binds In Vivo GGAA Microsatellite Sequences with Potential Transcriptional Activation Function. PLoS ONE, 2009, 4, e4932.	2.5	160
7	Chimeric EWSR1-FLI1 regulates the Ewing sarcoma susceptibility gene EGR2 via a GGAA microsatellite. Nature Genetics, 2015, 47, 1073-1078.	21.4	157
8	Analysis of Genomic Sequence Motifs for Deciphering Transcription Factor Binding and Transcriptional Regulation in Eukaryotic Cells. Frontiers in Genetics, 2016, 7, 24.	2.3	125
9	Changes in correlation between promoter methylation and gene expression in cancer. BMC Genomics, 2015, 16, 873.	2.8	113
10	Multi-factor data normalization enables the detection of copy number aberrations in amplicon sequencing data. Bioinformatics, 2014, 30, 3443-3450.	4.1	109
11	Transcriptional Programs Define Intratumoral Heterogeneity of Ewing Sarcoma at Single-Cell Resolution. Cell Reports, 2020, 30, 1767-1779.e6.	6.4	96
12	Ovarian Cancers Harboring Inactivating Mutations in <i>CDK12</i> Display a Distinct Genomic Instability Pattern Characterized by Large Tandem Duplications. Cancer Research, 2016, 76, 1882-1891.	0.9	95
13	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXM1 reactivation of DREAM targets. Nature Communications, 2018, 9, 4866.	12.8	91
14	Short fuzzy tandem repeats in genomic sequences, identification, and possible role in regulation of gene expression. Bioinformatics, 2006, 22, 676-684.	4.1	88
15	FUN-LDA: A Latent Dirichlet Allocation Model for Predicting Tissue-Specific Functional Effects of Noncoding Variation: Methods and Applications. American Journal of Human Genetics, 2018, 102, 920-942.	6.2	75
16	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	12.8	73
17	Genomic Amplifications and Distal 6q Loss: Novel Markers for Poor Survival in High-risk Neuroblastoma Patients. Journal of the National Cancer Institute, 2018, 110, 1084-1093.	6.3	73
18	De novo motif identification improves the accuracy of predicting transcription factor binding sites in ChIP-Seq data analysis. Nucleic Acids Research, 2010, 38, e126-e126.	14.5	62

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19	Characterization of Rearrangements Involving the *ALK* Gene Reveals a Novel Truncated Form Associated with Tumor Aggressiveness in Neuroblastoma. Cancer Research, 2013, 73, 195-204.	0.9	54
20	Activated ALK signals through the ERK–ETV5–RET pathway to drive neuroblastoma oncogenesis. Oncogene, 2018, 37, 1417-1429.	5.9	45
21	Nebula—a web-server for advanced ChIP-seq data analysis. Bioinformatics, 2012, 28, 2517-2519.	4.1	42
22	Breakpoint Features of Genomic Rearrangements in Neuroblastoma with Unbalanced Translocations and Chromothripsis. PLoS ONE, 2013, 8, e72182.	2.5	42
23	HMCan: a method for detecting chromatin modifications in cancer samples using ChIP-seq data. Bioinformatics, 2013, 29, 2979-2986.	4.1	39
24	Comparative analyses of super-enhancers reveal conserved elements in vertebrate genomes. Genome Research, 2017, 27, 259-268.	5.5	39
25	SV-Bay: structural variant detection in cancer genomes using a Bayesian approach with correction for GC-content and read mappability. Bioinformatics, 2016, 32, 984-992.	4.1	36
26	Learning smoothing models of copy number profiles using breakpoint annotations. BMC Bioinformatics, 2013, 14, 164.	2.6	33
27	Exact p-value calculation for heterotypic clusters of regulatory motifs and its application in computational annotation of cis-regulatory modules. Algorithms for Molecular Biology, 2007, 2, 13.	1.2	29
28	Meta-mining of copy number profiles of high-risk neuroblastoma tumors. Scientific Data, 2018, 5, 180240.	5.3	27
29	CHROMATIX: computing the functional landscape of many-body chromatin interactions in transcriptionally active loci from deconvolved single cells. Genome Biology, 2020, 21, 13.	8.8	22
30	Spi-1/PU.1 activates transcription through clustered DNA occupancy in erythroleukemia. Nucleic Acids Research, 2012, 40, 8927-8941.	14.5	20
31	QuantumClone: clonal assessment of functional mutations in cancer based on a genotype-aware method for clonal reconstruction. Bioinformatics, 2018, 34, 1808-1816.	4.1	20
32	Targeted Therapy of *TERT*-Rearranged Neuroblastoma with BET Bromodomain Inhibitor and Proteasome Inhibitor Combination Therapy. Clinical Cancer Research, 2021, 27, 1438-1451.	7.0	20
33	SegAnnDB: interactive Web-based genomic segmentation. Bioinformatics, 2014, 30, 1539-1546.	4.1	10
34	Deciphering the etiology and role in oncogenic transformation of the CpG island methylator phenotype: a pan-cancer analysis. Briefings in Bioinformatics, 2022, 23, .	6.5	9
35	HMCan-diff: a method to detect changes in histone modifications in cells with different genetic characteristics. Nucleic Acids Research, 2017, 45, gkw1319.	14.5	8
36	CHIPIN: ChIP-seq inter-sample normalization based on signal invariance across transcriptionally constant genes. BMC Bioinformatics, 2021, 22, 407.	2.6	8

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37	RNF: a general framework to evaluate NGS read mappers. Bioinformatics, 2016, 32, 136-139.	4.1	7
38	Calling Chromosome Alterations, DNA Methylation Statuses, and Mutations in Tumors by Simple Targeted Next-Generation Sequencing. Journal of Molecular Diagnostics, 2017, 19, 776-787.	2.8	7
39	Calculating Biological Module Enrichment or Depletion and Visualizing Data on Large-scale Molecular Maps with ACSNMineR and RNaviCell Packages. R Journal, 2016, 8, 293.	1.8	4
40	Chromatin Immunoprecipitation Followed by Next-Generation Sequencing (ChIP-Seq) Analysis in Ewing Sarcoma. Methods in Molecular Biology, 2021, 2226, 265-284.	0.9	2
41	Exploring Pathway-Based Group Lasso for Cancer Survival Analysis: A Special Case of Multi-Task Learning. Frontiers in Genetics, 2021, 12, 771301.	2.3	1