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	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
2	Targeted Therapy of <i>TERT</i>-Rearranged Neuroblastoma with BET Bromodomain Inhibitor and Proteasome Inhibitor Combination Therapy. Clinical Cancer Research, 2021, 27, 1438-1451.	7.0	20
3	CHIPIN: ChIP-seq inter-sample normalization based on signal invariance across transcriptionally constant genes. BMC Bioinformatics, 2021, 22, 407.	2.6	8
4	Chromatin Immunoprecipition Followed by Next-Generation Sequencing (ChIP-Seq) Analysis in Ewing Sarcoma. Methods in Molecular Biology, 2021, 2226, 265-284.	0.9	2
5	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
6	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
7	Transcriptional Programs Define Intratumoral Heterogeneity of Ewing Sarcoma at Single-Cell Resolution. Cell Reports, 2020, 30, 1767-1779.e6.	6.4	96
8	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
9	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
10	Activated ALK signals through the ERK–ETV5–RET pathway to drive neuroblastoma oncogenesis. Oncogene, 2018, 37, 1417-1429.	5.9	45
11	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
12	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXM1 reactivation of DREAM targets. Nature Communications, 2018, 9, 4866.	12.8	91
13	Meta-mining of copy number profiles of high-risk neuroblastoma tumors. Scientific Data, 2018, 5, 180240.	5.3	27
14	Comparative analyses of super-enhancers reveal conserved elements in vertebrate genomes. Genome Research, 2017, 27, 259-268.	5.5	39
15	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
16	Heterogeneity of neuroblastoma cell identity defined by transcriptional circuitries. Nature Genetics, 2017, 49, 1408-1413.	21.4	331
17	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
18	RNF: a general framework to evaluate NGS read mappers. Bioinformatics, 2016, 32, 136-139.	4.1	7

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19	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
20	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	12.8	73
21	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
22	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
23	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
24	Changes in correlation between promoter methylation and gene expression in cancer. BMC Genomics, 2015, 16, 873.	2.8	113
25	Chimeric EWSR1-FLI1 regulates the Ewing sarcoma susceptibility gene EGR2 via a GGAA microsatellite. Nature Genetics, 2015, 47, 1073-1078.	21.4	157
26	SegAnnDB: interactive Web-based genomic segmentation. Bioinformatics, 2014, 30, 1539-1546.	4.1	10
27	Multi-factor data normalization enables the detection of copy number aberrations in amplicon sequencing data. Bioinformatics, 2014, 30, 3443-3450.	4.1	109
28	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
29	Characterization of Rearrangements Involving the <i>ALK</i> Gene Reveals a Novel Truncated Form Associated with Tumor Aggressiveness in Neuroblastoma. Cancer Research, 2013, 73, 195-204.	0.9	54
30	HMCan: a method for detecting chromatin modifications in cancer samples using ChIP-seq data. Bioinformatics, 2013, 29, 2979-2986.	4.1	39
31	Learning smoothing models of copy number profiles using breakpoint annotations. BMC Bioinformatics, 2013, 14, 164.	2.6	33
32	Breakpoint Features of Genomic Rearrangements in Neuroblastoma with Unbalanced Translocations and Chromothripsis. PLoS ONE, 2013, 8, e72182.	2.5	42
33	Spi-1/PU.1 activates transcription through clustered DNA occupancy in erythroleukemia. Nucleic Acids Research, 2012, 40, 8927-8941.	14.5	20
34	Control-FREEC: a tool for assessing copy number and allelic content using next-generation sequencing data. Bioinformatics, 2012, 28, 423-425.	4.1	847
35	Nebulaâ€"a web-server for advanced ChIP-seq data analysis. Bioinformatics, 2012, 28, 2517-2519.	4.1	42
36	Control-free calling of copy number alterations in deep-sequencing data using GC-content normalization. Bioinformatics, 2011, 27, 268-269.	4.1	249

#	Article	IF	Citations
37	SVDetect: a tool to identify genomic structural variations from paired-end and mate-pair sequencing data. Bioinformatics, 2010, 26, 1895-1896.	4.1	178
38	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
39	The Oncogenic EWS-FLI1 Protein Binds In Vivo GGAA Microsatellite Sequences with Potential Transcriptional Activation Function. PLoS ONE, 2009, 4, e4932.	2.5	160
40	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
41	Short fuzzy tandem repeats in genomic sequences, identification, and possible role in regulation of gene expression. Bioinformatics, 2006, 22, 676-684.	4.1	88