Pieter-Jan Volders

List of Publications by Year
in descending order

40 papers	**2,774** citations	304701 **22** h-index	315719 **38** g-index
48 all docs	**48** docs citations	**48** times ranked	**5196** citing authors

#	Article	IF	Citations
1	LNCipedia: a database for annotated human lncRNA transcript sequences and structures. Nucleic Acids Research, 2013, 41, D246-D251.	14.5	488
2	LNCipedia 5: towards a reference set of human long non-coding RNAs. Nucleic Acids Research, 2019, 47, D135-D139.	14.5	403
3	An update on LNCipedia: a database for annotated human lncRNA sequences. Nucleic Acids Research, 2015, 43, D174-D180.	14.5	298
4	RNAcentral: a comprehensive database of non-coding RNA sequences. Nucleic Acids Research, 2017, 45, D128-D134.	14.5	174
5	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. Nucleic Acids Research, 2021, 49, D212-D220.	14.5	160
6	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	14.5	153
7	Long noncoding RNA expression profiling in cancer: Challenges and opportunities. Genes Chromosomes and Cancer, 2019, 58, 191-199.	2.8	117
8	High-throughput functional analysis of lncRNA core promoters elucidates rules governing tissue specificity. Genome Research, 2019, 29, 344-355.	5.5	100
9	The RNA landscape of the human placenta in health and disease. Nature Communications, 2021, 12, 2639.	12.8	75
10	The RNA Atlas expands the catalog of human non-coding RNAs. Nature Biotechnology, 2021, 39, 1453-1465.	17.5	75
11	Closing the circle: current state and perspectives of circular RNA databases. Briefings in Bioinformatics, 2021, 22, 288-297.	6.5	74
12	miRBase Tracker: keeping track of microRNA annotation changes. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	3.0	73
13	The Notch driven long non-coding RNA repertoire in T-cell acute lymphoblastic leukemia. Haematologica, 2014, 99, 1808-1816.	3.5	50
14	Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-4060.	3.7	47
15	ViVar: A Comprehensive Platform for the Analysis and Visualization of Structural Genomic Variation. PLoS ONE, 2014, 9, e113800.	2.5	45
16	Noncoding after All: Biases in Proteomics Data Do Not Explain Observed Absence of lncRNA Translation Products. Journal of Proteome Research, 2017, 16, 2508-2515.	3.7	44
17	Identification of long non-coding RNAs involved in neuronal development and intellectual disability. Scientific Reports, 2016, 6, 28396.	3.3	41
18	Long non-coding RNAs in cutaneous melanoma: clinical perspectives. Oncotarget, 2017, 8, 43470-43480.	1.8	35

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19	Long noncoding RNA signatures define oncogenic subtypes in T-cell acute lymphoblastic leukemia. Leukemia, 2016, 30, 1927-1930.	7.2	32
20	Distinct Notch1 and <i>BCL11B</i> requirements mediate human γδ/αβ T cell development. EMBO Reports, 2020, 21, e49006.	4.5	31
21	Genome wide expression profiling of p53 regulated miRNAs in neuroblastoma. Scientific Reports, 2015, 5, 9027.	3.3	29
22	A comprehensive inventory of TLX1 controlled long non-coding RNAs in T-cell acute lymphoblastic leukemia through polyA+ and total RNA sequencing. Haematologica, 2018, 103, e585-e589.	3.5	20
23	miSTAR: miRNA target prediction through modeling quantitative and qualitative miRNA binding site information in a stacked model structure. Nucleic Acids Research, 2016, 45, gkw1260.	14.5	18
24	COSS: A Fast and User-Friendly Tool for Spectral Library Searching. Journal of Proteome Research, 2020, 19, 2786-2793.	3.7	18
25	decodeRNAâ€" predicting non-coding RNA functions using guilt-by-association. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	16
26	Validation of Circular RNAs Using RTâ€¢qPCR After Effective Removal of Linear RNAs by Ribonuclease R. Current Protocols, 2021, 1, e181.	2.9	15
27	A novel TLX1-driven T-ALL zebrafish model: comparative genomic analysis with other leukemia models. Leukemia, 2020, 34, 3398-3403.	7.2	12
28	MEIS2 Is an Adrenergic Core Regulatory Transcription Factor Involved in Early Initiation of TH-MYCN-Driven Neuroblastoma Formation. Cancers, 2021, 13, 4783.	3.7	12
29	Personalized Proteome: Comparing Proteogenomics and Open Variant Search Approaches for Single Amino Acid Variant Detection. Journal of Proteome Research, 2021, 20, 3353-3364.	3.7	10
30	SPECS: a non-parametric method to identify tissue-specific molecular features for unbalanced sample groups. BMC Bioinformatics, 2020, 21, 58.	2.6	9
31	Sensitive and Specific Spectral Library Searching with CompOmics Spectral Library Searching Tool and Percolator. Journal of Proteome Research, 2022, 21, 1365-1370.	3.7	6
32	CRISPR/Cas9-mediated genome editing in naïve human embryonic stem cells. Scientific Reports, 2017, 7, 16650.	3.3	5
33	Zipper plot: visualizing transcriptional activity of genomic regions. BMC Bioinformatics, 2017, 18, 231.	2.6	5
34	Targeted Genomic Screen Reveals Focal Long Non-Coding RNA Copy Number Alterations in Cancer Cell Lines. Non-coding RNA, 2018, 4, 21.	2.6	5
35	Long non-coding RNA expression profiling in the NCI60 cancer cell line panel using high-throughput RT-qPCR. Scientific Data, 2016, 3, 160052.	5.3	5
36	Orthogonal proteomics methods to unravel the HOTAIR interactome. Scientific Reports, 2022, 12, 1513.	3.3	3

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37	Expanding The TLX1-Regulome In T Cell Acute Lymphoblastic Leukemia Towards Long Non-Coding RNAs. Blood, 2013, 122, 813-813.	1.4	0
38	The NOTCH1 Driven Long Non-Coding RNA Repertoire in T-Cell Acute Lymphoblastic Leukemia. Blood, 2014, 124, 900-900.	1.4	0
39	Abstract A28: Expanding the TLX1 regulome in T-cell acute lymphoblastic leukemia towards long noncoding RNAs. , 2016, , .		0
40	Performance Evaluation of Three DNA Sample Tracking Tools in a Whole Exome Sequencing Workflow. Molecular Diagnosis and Therapy, 2022, 26, 411-419.	3.8	0