

Filip Pattyn

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

18,650
citations

218677

26
h-index

330143

37
g-index

39
all docs

39
docs citations

39
times ranked

32411
citing authors

#	ARTICLE	IF	CITATIONS
1	Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. <i>Genome Biology</i> , 2002, 3, RESEARCH0034.	9.6	16,304
2	RTPrimerDB: the Real-Time PCR primer and probe database. <i>Nucleic Acids Research</i> , 2003, 31, 122-123.	14.5	240
3	Distinct transcriptional MYCN/c-MYC activities are associated with spontaneous regression or malignant progression in neuroblastomas. <i>Genome Biology</i> , 2008, 9, R150.	9.6	215
4	Single-Nucleotide Polymorphisms and Other Mismatches Reduce Performance of Quantitative PCR Assays. <i>Clinical Chemistry</i> , 2013, 59, 1470-1480.	3.2	153
5	Targeted Expression of Mutated ALK Induces Neuroblastoma in Transgenic Mice. <i>Science Translational Medicine</i> , 2012, 4, 141ra91.	12.4	147
6	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. <i>Oncogene</i> , 2010, 29, 3583-3592.	5.9	141
7	RTPrimerDB: the portal for real-time PCR primers and probes. <i>Nucleic Acids Research</i> , 2009, 37, D942-D945.	14.5	132
8	RDML: structured language and reporting guidelines for real-time quantitative PCR data. <i>Nucleic Acids Research</i> , 2009, 37, 2065-2069.	14.5	123
9	MYCN/c-MYC-induced microRNAs repress coding gene networks associated with poor outcome in MYCN/c-MYC-activated tumors. <i>Oncogene</i> , 2010, 29, 1394-1404.	5.9	112
10	RTPrimerDB: the real-time PCR primer and probe database, major update 2006. <i>Nucleic Acids Research</i> , 2006, 34, D684-D688.	14.5	107
11	MYCN and HDAC2 cooperate to repress miR-183 signaling in neuroblastoma. <i>Nucleic Acids Research</i> , 2013, 41, 6018-6033.	14.5	87
12	Disease-Causing 7.4 kb Cis-Regulatory Deletion Disrupting Conserved Non-Coding Sequences and Their Interaction with the FOXL2 Promotor: Implications for Mutation Screening. <i>PLoS Genetics</i> , 2009, 5, e1000522.	3.5	83
13	arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. <i>BMC Bioinformatics</i> , 2005, 6, 124.	2.6	79
14	The microRNA body map: dissecting microRNA function through integrative genomics. <i>Nucleic Acids Research</i> , 2011, 39, e136-e136.	14.5	72
15	Aberrant methylation of candidate tumor suppressor genes in neuroblastoma. <i>Cancer Letters</i> , 2009, 273, 336-346.	7.2	54
16	Neuroblastoma cells with overexpressed MYCN retain their capacity to undergo neuronal differentiation. <i>Laboratory Investigation</i> , 2004, 84, 406-417.	3.7	49
17	Molecular diagnostics for congenital hearing loss including 15 deafness genes using a next generation sequencing platform. <i>BMC Medical Genomics</i> , 2012, 5, 17.	1.5	49
18	miR-17-92 is regulated by the MYCN-induced miR-17-92 cluster in neuroblastoma. <i>International Journal of Cancer</i> , 2012, 130, 2591-2598.	5.1	43

#	ARTICLE	IF	CITATIONS
19	Meta-mining of Neuroblastoma and Neuroblast Gene Expression Profiles Reveals Candidate Therapeutic Compounds. <i>Clinical Cancer Research</i> , 2009, 15, 3690-3696.	7.0	41
20	Practical Tools to Implement Massive Parallel Pyrosequencing of PCR Products in Next Generation Molecular Diagnostics. <i>PLoS ONE</i> , 2011, 6, e25531.	2.5	40
21	Massively parallel sequencing for early molecular diagnosis in Leber congenital amaurosis. <i>Genetics in Medicine</i> , 2012, 14, 576-585.	2.4	39
22	RNA pre-amplification enables large-scale RT-qPCR gene-expression studies on limiting sample amounts. <i>BMC Research Notes</i> , 2009, 2, 235.	1.4	38
23	Identification of a novel recurrent 1q42.2â€”qter deletion in high risk <i>MYCN</i> single copy 11q deleted neuroblastomas. <i>International Journal of Cancer</i> , 2012, 130, 2599-2606.	5.1	37
24	Focal DNA Copy Number Changes in Neuroblastoma Target <i>MYCN</i> Regulated Genes. <i>PLoS ONE</i> , 2013, 8, e52321.	2.5	37
25	methBLAST and methPrimerDB: web-tools for PCR based methylation analysis. <i>BMC Bioinformatics</i> , 2006, 7, 496.	2.6	35
26	The emerging molecular pathogenesis of neuroblastoma: implications for improved risk assessment and targeted therapy. <i>Genome Medicine</i> , 2009, 1, 74.	8.2	34
27	Cost-effective and robust genotyping using double-mismatch allele-specific quantitative PCR. <i>Scientific Reports</i> , 2019, 9, 2150.	3.3	27
28	External oligonucleotide standards enable cross laboratory comparison and exchange of real-time quantitative PCR data. <i>Nucleic Acids Research</i> , 2009, 37, e138-e138.	14.5	25
29	Combined subtractive cDNA cloning and array CGH: an efficient approach for identification of overexpressed genes in DNA amplicons. <i>BMC Genomics</i> , 2004, 5, 11.	2.8	22
30	An Ontology to Standardize Research Output of Nutritional Epidemiology: From Paper-Based Standards to Linked Content. <i>Nutrients</i> , 2019, 11, 1300.	4.1	20
31	Analysing 454 amplicon resequencing experiments using the modular and database oriented Variant Identification Pipeline. <i>BMC Bioinformatics</i> , 2010, 11, 269.	2.6	15
32	Effective Alu Repeat Based RT-Qpcr Normalization in Cancer Cell Perturbation Experiments. <i>PLoS ONE</i> , 2013, 8, e71776.	2.5	13
33	High-throughput PCR assay design for targeted resequencing using primerXL. <i>BMC Bioinformatics</i> , 2017, 18, 400.	2.6	13
34	Unraveling and resolving inefficient glucolipid biosurfactants production through quantitative multiomics analyses of <i>Starmerella bombicola</i> strains. <i>Biotechnology and Bioengineering</i> , 2020, 117, 453-465.	3.3	12
35	Mapping of 5q35 chromosomal rearrangements within a genomically unstable region. <i>Journal of Medical Genetics</i> , 2008, 45, 672-678.	3.2	7
36	methGraph: A genome visualization tool for PCR-based methylation assays. <i>Epigenetics</i> , 2010, 5, 159-163.	2.7	3

#	ARTICLE	IF	CITATIONS
37	Dynamic repair of categorical data with edit rules. Expert Systems With Applications, 2022, 201, 117132.	7.6	2
38	Big linked data ETL benchmark on cloud commodity hardware. , 2016, , .		0