Filip Pattyn

List of Publications by Year
in descending order

38 papers	18,650 citations	218592 26 h-index	330025 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. Genome Biology, 2002, 3, research0034.1.	13.9	16,304
2	RTPrimerDB: the Real-Time PCR primer and probe database. Nucleic Acids Research, 2003, 31, 122-123.	6.5	240
3	Distinct transcriptional MYCN/c-MYC activities are associated with spontaneous regression or malignant progression in neuroblastomas. Genome Biology, 2008, 9, R150.	13.9	215
4	Single-Nucleotide Polymorphisms and Other Mismatches Reduce Performance of Quantitative PCR Assays. Clinical Chemistry, 2013, 59, 1470-1480.	1.5	153
5	Targeted Expression of Mutated ALK Induces Neuroblastoma in Transgenic Mice. Science Translational Medicine, 2012, 4, 141ra91.	5.8	147
6	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. Oncogene, 2010, 29, 3583-3592.	2.6	141
7	RTPrimerDB: the portal for real-time PCR primers and probes. Nucleic Acids Research, 2009, 37, D942-D945.	6.5	132
8	RDML: structured language and reporting guidelines for real-time quantitative PCR data. Nucleic Acids Research, 2009, 37, 2065-2069.	6.5	123
9	MYCN/c-MYC-induced microRNAs repress coding gene networks associated with poor outcome in MYCN/c-MYC-activated tumors. Oncogene, 2010, 29, 1394-1404.	2.6	112
10	RTPrimerDB: the real-time PCR primer and probe database, major update 2006. Nucleic Acids Research, 2006, 34, D684-D688.	6.5	107
11	MYCN and HDAC2 cooperate to repress miR-183 signaling in neuroblastoma. Nucleic Acids Research, 2013, 41, 6018-6033.	6.5	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. PLoS Genetics, 2009, 5, e1000522.	1.5	83
13	arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. BMC Bioinformatics, 2005, 6, 124.	1.2	79
14	The microRNA body map: dissecting microRNA function through integrative genomics. Nucleic Acids Research, 2011, 39, e136-e136.	6.5	72
15	Aberrant methylation of candidate tumor suppressor genes in neuroblastoma. Cancer Letters, 2009, 273, 336-346.	3.2	54
16	Neuroblastoma cells with overexpressed MYCN retain their capacity to undergo neuronal differentiation. Laboratory Investigation, 2004, 84, 406-417.	1.7	49
17	Molecular diagnostics for congenital hearing loss including 15 deafness genes using a next generation sequencing platform. BMC Medical Genomics, 2012, 5, 17.	0.7	49
18	<i>Dickkopf‐3</i> is regulated by the MYCN‐induced miR‐17‐92 cluster in neuroblastoma. International Journal of Cancer, 2012, 130, 2591-2598.	2.3	43

#	Article	IF	Citations
19	Meta-mining of Neuroblastoma and Neuroblast Gene Expression Profiles Reveals Candidate Therapeutic Compounds. Clinical Cancer Research, 2009, 15, 3690-3696.	3.2	41
20	Practical Tools to Implement Massive Parallel Pyrosequencing of PCR Products in Next Generation Molecular Diagnostics. PLoS ONE, 2011, 6, e25531.	1.1	40
21	Massively parallel sequencing for early molecular diagnosis in Leber congenital amaurosis. Genetics in Medicine, 2012, 14, 576-585.	1.1	39
22	RNA pre-amplification enables large-scale RT-qPCR gene-expression studies on limiting sample amounts. BMC Research Notes, 2009, 2, 235.	0.6	38
23	Identification of a novel recurrent 1q42.2–1qter deletion in high risk <i>MYCN</i> single copy 11q deleted neuroblastomas. International Journal of Cancer, 2012, 130, 2599-2606.	2.3	37
24	Focal DNA Copy Number Changes in Neuroblastoma Target MYCN Regulated Genes. PLoS ONE, 2013, 8, e52321.	1.1	37
25	methBLAST and methPrimerDB: web-tools for PCR based methylation analysis. BMC Bioinformatics, 2006, 7, 496.	1.2	35
26	The emerging molecular pathogenesis of neuroblastoma: implications for improved risk assessment and targeted therapy. Genome Medicine, 2009, 1, 74.	3.6	34
27	Cost-effective and robust genotyping using double-mismatch allele-specific quantitative PCR. Scientific Reports, 2019, 9, 2150.	1.6	27
28	External oligonucleotide standards enable cross laboratory comparison and exchange of real-time quantitative PCR data. Nucleic Acids Research, 2009, 37, e138-e138.	6.5	25
29	Combined subtractive cDNA cloning and array CGH: an efficient approach for identification of overexpressed genes in DNA amplicons. BMC Genomics, 2004, 5, 11.	1.2	22
30	An Ontology to Standardize Research Output of Nutritional Epidemiology: From Paper-Based Standards to Linked Content. Nutrients, 2019, 11, 1300.	1.7	20
31	Analysing 454 amplicon resequencing experiments using the modular and database oriented Variant Identification Pipeline. BMC Bioinformatics, 2010, 11, 269.	1.2	15
32	Effective Alu Repeat Based RT-Qpcr Normalization in Cancer Cell Perturbation Experiments. PLoS ONE, 2013, 8, e71776.	1.1	13
33	High-throughput PCR assay design for targeted resequencing using primerXL. BMC Bioinformatics, 2017, 18, 400.	1.2	13
34	Unraveling and resolving inefficient glucolipid biosurfactants production through quantitative multiomics analyses of <i>Starmerella bombicola</i> strains. Biotechnology and Bioengineering, 2020, 117, 453-465.	1.7	12
35	Mapping of 5q35 chromosomal rearrangements within a genomically unstable region. Journal of Medical Genetics, 2008, 45, 672-678.	1.5	7
36	methGraph: A genome visualization tool for PCR-based methylation assays. Epigenetics, 2010, 5, 159-163.	1.3	3

#	ARTICLE	IF	CITATIONS
37	Dynamic repair of categorical data with edit rules. Expert Systems With Applications, 2022, 201, 117132.	4.4	2
38	Big linked data ETL benchmark on cloud commodity hardware. , 2016, , .		0