

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	Dynamic repair of categorical data with edit rules. Expert Systems With Applications, 2022, 201, 117132.	7.6	2
2	Unraveling and resolving inefficient glucolipid biosurfactants production through quantitative multiomics analyses of <i>Starmerella bombicola</i> strains. Biotechnology and Bioengineering, 2020, 117, 453-465.	3.3	12
3	An Ontology to Standardize Research Output of Nutritional Epidemiology: From Paper-Based Standards to Linked Content. Nutrients, 2019, 11, 1300.	4.1	20
4	Cost-effective and robust genotyping using double-mismatch allele-specific quantitative PCR. Scientific Reports, 2019, 9, 2150.	3.3	27
5	High-throughput PCR assay design for targeted resequencing using primerXL. BMC Bioinformatics, 2017, 18, 400.	2.6	13
6	Big linked data ETL benchmark on cloud commodity hardware. , 2016, , .		0
7	Single-Nucleotide Polymorphisms and Other Mismatches Reduce Performance of Quantitative PCR Assays. Clinical Chemistry, 2013, 59, 1470-1480.	3.2	153
8	MYCN and HDAC2 cooperate to repress miR-183 signaling in neuroblastoma. Nucleic Acids Research, 2013, 41, 6018-6033.	14.5	87
9	Effective Alu Repeat Based RT-Qpcr Normalization in Cancer Cell Perturbation Experiments. PLoS ONE, 2013, 8, e71776.	2.5	13
10	Focal DNA Copy Number Changes in Neuroblastoma Target MYCN Regulated Genes. PLoS ONE, 2013, 8, e52321.	2.5	37
11	Targeted Expression of Mutated ALK Induces Neuroblastoma in Transgenic Mice. Science Translational Medicine, 2012, 4, 141ra91.	12.4	147
12	Massively parallel sequencing for early molecular diagnosis in Leber congenital amaurosis. Genetics in Medicine, 2012, 14, 576-585.	2.4	39
13	Molecular diagnostics for congenital hearing loss including 15 deafness genes using a next generation sequencing platform. BMC Medical Genomics, 2012, 5, 17.	1.5	49
14	<i>Dickkopf3</i> is regulated by the MYCN-induced miR-17-92 cluster in neuroblastoma. International Journal of Cancer, 2012, 130, 2591-2598.	5.1	43
15	Identification of a novel recurrent 1q42.2qter deletion in high risk MYCN single copy 11q deleted neuroblastomas. International Journal of Cancer, 2012, 130, 2599-2606.	5.1	37
16	The microRNA body map: dissecting microRNA function through integrative genomics. Nucleic Acids Research, 2011, 39, e136-e136.	14.5	72
17	Practical Tools to Implement Massive Parallel Pyrosequencing of PCR Products in Next Generation Molecular Diagnostics. PLoS ONE, 2011, 6, e25531.	2.5	40
18	Analysing 454 amplicon resequencing experiments using the modular and database oriented Variant Identification Pipeline. BMC Bioinformatics, 2010, 11, 269.	2.6	15

#	ARTICLE	IF	CITATIONS
19	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
20	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. <i>Oncogene</i> , 2010, 29, 3583-3592.	5.9	141
21	methGraph: A genome visualization tool for PCR-based methylation assays. <i>Epigenetics</i> , 2010, 5, 159-163.	2.7	3
22	RDML: structured language and reporting guidelines for real-time quantitative PCR data. <i>Nucleic Acids Research</i> , 2009, 37, 2065-2069.	14.5	123
23	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
24	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
25	RTPrimerDB: the portal for real-time PCR primers and probes. <i>Nucleic Acids Research</i> , 2009, 37, D942-D945.	14.5	132
26	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
27	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
28	Aberrant methylation of candidate tumor suppressor genes in neuroblastoma. <i>Cancer Letters</i> , 2009, 273, 336-346.	7.2	54
29	The emerging molecular pathogenesis of neuroblastoma: implications for improved risk assessment and targeted therapy. <i>Genome Medicine</i> , 2009, 1, 74.	8.2	34
30	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
31	Mapping of 5q35 chromosomal rearrangements within a genomically unstable region. <i>Journal of Medical Genetics</i> , 2008, 45, 672-678.	3.2	7
32	methBLAST and methPrimerDB: web-tools for PCR based methylation analysis. <i>BMC Bioinformatics</i> , 2006, 7, 496.	2.6	35
33	RTPrimerDB: the real-time PCR primer and probe database, major update 2006. <i>Nucleic Acids Research</i> , 2006, 34, D684-D688.	14.5	107
34	arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. <i>BMC Bioinformatics</i> , 2005, 6, 124.	2.6	79
35	Neuroblastoma cells with overexpressed MYCN retain their capacity to undergo neuronal differentiation. <i>Laboratory Investigation</i> , 2004, 84, 406-417.	3.7	49
36	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

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37	RTPrimerDB: the Real-Time PCR primer and probe database. <i>Nucleic Acids Research</i> , 2003, 31, 122-123.	14.5	240
38	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