Christophe Van Neste

List of Publications by Year
in descending order

33 papers	946 citations	687363 13 h-index	477307 29 g-index
39 all docs	39 docs citations	39 times ranked	1480 citing authors

#	Article	IF	Citations
1	Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements. Forensic Science International: Genetics, 2016, 22, 54-63.	3.1	190
2	Forensic STR analysis using massive parallel sequencing. Forensic Science International: Genetics, 2012, 6, 810-818.	3.1	94
3	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXM1 reactivation of DREAM targets. Nature Communications, 2018, 9, 4866.	12.8	91
4	Glutathione "Redox Homeostasis" and Its Relation to Cardiovascular Disease. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-14.	4.0	89
5	My-Forensic-Loci-queries (MyFLq) framework for analysis of forensic STR data generated by massive parallel sequencing. Forensic Science International: Genetics, 2014, 9, 1-8.	3.1	75
6	Machine learning and deep learning methods that use omics data for metastasis prediction. Computational and Structural Biotechnology Journal, 2021, 19, 5008-5018.	4.1	69
7	The Effect of VEGF-Targeted Therapy on Biomarker Expression in Sequential Tissue from Patients with Metastatic Clear Cell Renal Cancer. Clinical Cancer Research, 2013, 19, 6924-6934.	7.0	62
8	Forensic massively parallel sequencing data analysis tool: Implementation of MyFLq as a standalone web- and Illumina BaseSpace®-application. Forensic Science International: Genetics, 2015, 15, 2-7.	3.1	27
9	The ETS transcription factor ETV5 is a target of activated ALK in neuroblastoma contributing to increased tumour aggressiveness. Scientific Reports, 2020, 10, 218.	3.3	20
10	Hybrid model for efficient prediction of poly(A) signals in human genomic DNA. Methods, 2019, 166, 31-39.	3.8	18
11	ALK positively regulates MYCN activity through repression of HBP1 expression. Oncogene, 2019, 38, 2690-2705.	5.9	17
12	Differential transcriptome analysis of the common shrimp Crangon crangon: Special focus on the nuclear receptors and RNAi-related genes. General and Comparative Endocrinology, 2015, 212, 163-177.	1.8	15
13	Redox control of vascular biology. BioFactors, 2020, 46, 246-262.	5.4	15
14	RRM2 enhances MYCN-driven neuroblastoma formation and acts as a synergistic target with CHK1 inhibition. Science Advances, 2022, 8, .	10.3	15
15	Dynamic epigenetic changes to *VHL* occur with sunitinib in metastatic clear cell renal cancer. Oncotarget, 2016, 7, 25241-25250.	1.8	14
16	The Prevalence of Nine Genetic Disorders in a Dog Population from Belgium, the Netherlands and Germany. PLoS ONE, 2013, 8, e74811.	2.5	13
17	DES-Mutation: System for Exploring Links of Mutations and Diseases. Scientific Reports, 2018, 8, 13359.	3.3	13
18	Retrospective study of the impact of miniSTRs on forensic DNA profiling of touch DNA samples. Science and Justice - Journal of the Forensic Science Society, 2014, 54, 369-372.	2.1	12

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19	Flagging False Positives Following Untargeted LC–MS Characterization of Histone Post-Translational Modification Combinations. Journal of Proteome Research, 2017, 16, 655-664.	3.7	11
20	In silico discovery of a FOXM1 driven embryonal signaling pathway in therapy resistant neuroblastoma tumors. Scientific Reports, 2018, 8, 17468.	3.3	11
21	Comorbidity network analysis and genetics of colorectal cancer. Informatics in Medicine Unlocked, 2020, 21, 100492.	3.4	9
22	Cell–to–cell and type–to–type heterogeneity of signaling networks: insights from the crowd. Molecular Systems Biology, 2021, 17, e10402.	7.2	9
23	Literature-Based Enrichment Insights into Redox Control of Vascular Biology. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-16.	4.0	8
24	Forensic Loci Allele Database (FLAD): Automatically generated, permanent identifiers for sequenced forensic alleles. Forensic Science International: Genetics, 2016, 20, e1-e3.	3.1	7
25	MYCN-induced nucleolar stress drives an early senescence-like transcriptional program in hTERT-immortalized RPE cells. Scientific Reports, 2021, 11, 14454.	3.3	6
26	Metastatic State of Colorectal Cancer can be Accurately Predicted with Methylome. , 2019, , .		6
27	DES-ROD: Exploring Literature to Develop New Links between RNA Oxidation and Human Diseases. Oxidative Medicine and Cellular Longevity, 2020, 2020, 1-13.	4.0	3
28	Recurrent chromosomal imbalances provide selective advantage to human embryonic stem cells under enhanced replicative stress conditions. Genes Chromosomes and Cancer, 2021, 60, 272-281.	2.8	3
29	Epigenetic sampling effects: nephrectomy modifies the clear cell renal cell cancer methylome. Cellular Oncology (Dordrecht), 2017, 40, 293-297.	4.4	2
30	Genes and comorbidities of thyroid cancer. Informatics in Medicine Unlocked, 2021, 25, 100680.	3.4	2
31	From DNA Copy Number Gains and Tumor Dependencies to Novel Therapeutic Targets for High-Risk Neuroblastoma. Journal of Personalized Medicine, 2021, 11, 1286.	2.5	2
32	RMNE calculation in forensic profiles with a high number of loci and allelic drop-outs using polynomial expansion. Forensic Science International: Genetics, 2017, 26, e14-e16.	3.1	1
33	DES-Tcell is a knowledgebase for exploring immunology-related literature. Scientific Reports, 2021, 11, 14344.	3.3	1