

# Christophe Van Neste

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5247687/publications.pdf>

Version: 2024-02-01

33  
papers

946  
citations

687220

13  
h-index

477173

29  
g-index

39  
all docs

39  
docs citations

39  
times ranked

1480  
citing authors

#	ARTICLE	IF	CITATIONS
1	RRM2 enhances MYCN-driven neuroblastoma formation and acts as a synergistic target with CHK1 inhibition. <i>Science Advances</i> , 2022, 8, .	4.7	15
2	Recurrent chromosomal imbalances provide selective advantage to human embryonic stem cells under enhanced replicative stress conditions. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 272-281.	1.5	3
3	Genes and comorbidities of thyroid cancer. <i>Informatics in Medicine Unlocked</i> , 2021, 25, 100680.	1.9	2
4	MYCN-induced nucleolar stress drives an early senescence-like transcriptional program in hTERT-immortalized RPE cells. <i>Scientific Reports</i> , 2021, 11, 14454.	1.6	6
5	DES-Tcell is a knowledgebase for exploring immunology-related literature. <i>Scientific Reports</i> , 2021, 11, 14344.	1.6	1
6	Machine learning and deep learning methods that use omics data for metastasis prediction. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5008-5018.	1.9	69
7	Cell-to-cell and type-to-type heterogeneity of signaling networks: insights from the crowd. <i>Molecular Systems Biology</i> , 2021, 17, e10402.	3.2	9
8	From DNA Copy Number Gains and Tumor Dependencies to Novel Therapeutic Targets for High-Risk Neuroblastoma. <i>Journal of Personalized Medicine</i> , 2021, 11, 1286.	1.1	2
9	Redox control of vascular biology. <i>BioFactors</i> , 2020, 46, 246-262.	2.6	15
10	Comorbidity network analysis and genetics of colorectal cancer. <i>Informatics in Medicine Unlocked</i> , 2020, 21, 100492.	1.9	9
11	The ETS transcription factor ETV5 is a target of activated ALK in neuroblastoma contributing to increased tumour aggressiveness. <i>Scientific Reports</i> , 2020, 10, 218.	1.6	20
12	DES-ROD: Exploring Literature to Develop New Links between RNA Oxidation and Human Diseases. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-13.	1.9	3
13	Glutathione Redox Homeostasis and Its Relation to Cardiovascular Disease. <i>Oxidative Medicine and Cellular Longevity</i> , 2019, 2019, 1-14.	1.9	89
14	Literature-Based Enrichment Insights into Redox Control of Vascular Biology. <i>Oxidative Medicine and Cellular Longevity</i> , 2019, 2019, 1-16.	1.9	8
15	Hybrid model for efficient prediction of poly(A) signals in human genomic DNA. <i>Methods</i> , 2019, 166, 31-39.	1.9	18
16	ALK positively regulates MYCN activity through repression of HBP1 expression. <i>Oncogene</i> , 2019, 38, 2690-2705.	2.6	17
17	Metastatic State of Colorectal Cancer can be Accurately Predicted with Methylome. , 2019, , .		6
18	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXM1 reactivation of DREAM targets. <i>Nature Communications</i> , 2018, 9, 4866.	5.8	91

#	ARTICLE	IF	CITATIONS
19	In silico discovery of a FOXM1 driven embryonal signaling pathway in therapy resistant neuroblastoma tumors. Scientific Reports, 2018, 8, 17468.	1.6	11
20	DES-Mutation: System for Exploring Links of Mutations and Diseases. Scientific Reports, 2018, 8, 13359.	1.6	13
21	Epigenetic sampling effects: nephrectomy modifies the clear cell renal cell cancer methylome. Cellular Oncology (Dordrecht), 2017, 40, 293-297.	2.1	2
22	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.	1.6	1
23	Flagging False Positives Following Untargeted LC-MS Characterization of Histone Post-Translational Modification Combinations. Journal of Proteome Research, 2017, 16, 655-664.	1.8	11
24	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.	1.6	190
25	Forensic Loci Allele Database (FLAD): Automatically generated, permanent identifiers for sequenced forensic alleles. Forensic Science International: Genetics, 2016, 20, e1-e3.	1.6	7
26	Dynamic epigenetic changes to <i>VHL</i> occur with sunitinib in metastatic clear cell renal cancer. Oncotarget, 2016, 7, 25241-25250.	0.8	14
27	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.	1.6	27
28	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.	0.8	15
29	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.	1.6	75
30	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.	1.3	12
31	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.	3.2	62
32	The Prevalence of Nine Genetic Disorders in a Dog Population from Belgium, the Netherlands and Germany. PLoS ONE, 2013, 8, e74811.	1.1	13
33	Forensic STR analysis using massive parallel sequencing. Forensic Science International: Genetics, 2012, 6, 810-818.	1.6	94