Wim Van Criekinge

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8603829/publications.pdf

Version: 2024-02-01

45 papers

2,673 citations

236925 25 h-index 254184 43 g-index

48 all docs

48 docs citations

48 times ranked

5073 citing authors

#	Article	IF	CITATIONS
1	Technical considerations in PCR-based assay design for diagnostic DNA methylation cancer biomarkers. Clinical Epigenetics, 2022, 14, 56.	4.1	5
2	Spectral Prediction Features as a Solution for the Search Space Size Problem in Proteogenomics. Molecular and Cellular Proteomics, 2021, 20, 100076.	3.8	31
3	Cost-effectiveness of SelectMDx for prostate cancer in four European countries: a comparative modeling study. Prostate Cancer and Prostatic Diseases, 2019, 22, 101-109.	3.9	51
4	PROTEOFORMER 2.0: Further Developments in the Ribosome Profiling-assisted Proteogenomic Hunt for New Proteoforms. Molecular and Cellular Proteomics, 2019, 18, S126-S140.	3.8	43
5	Clinically significant Prostate Cancer diagnosed using a urinary molecular biomarker-based risk score: two case reports. BMC Urology, 2019, 19, 124.	1.4	1
6	<i>MGMT</i> Promoter Methylation Cutoff with Safety Margin for Selecting Glioblastoma Patients into Trials Omitting Temozolomide: A Pooled Analysis of Four Clinical Trials. Clinical Cancer Research, 2019, 25, 1809-1816.	7.0	94
7	Evaluation of an Epigenetic Assay for Predicting Repeat Prostate Biopsy Outcome in African American Men. Urology, 2019, 128, 62-65.	1.0	24
8	Cost-effectiveness of a two-gene urine biomarker assay in MRI strategies for the initial detection of prostate cancer Journal of Clinical Oncology, 2019, 37, 91-91.	1.6	1
9	Clinical utility study of confirms mdx for prostate cancer in a community urology practice Journal of Clinical Oncology, 2019, 37, 94-94.	1.6	3
10	Validation of a two-gene mRNA urine test for detection of high-grade prostate cancer in German men Journal of Clinical Oncology, 2019, 37, 96-96.	1.6	0
11	Epigenetic markers in circulating cellâ€free DNA as prognostic markers for survival of castrationâ€resistant prostate cancer patients. Prostate, 2018, 78, 336-342.	2.3	41
12	Analysis of DNA methylation in cancer: location revisited. Nature Reviews Clinical Oncology, 2018, 15, 459-466.	27.6	486
13	An update on sORFs.org: a repository of small ORFs identified by ribosome profiling. Nucleic Acids Research, 2018, 46, D497-D502.	14.5	135
14	Integrated transcriptomic and epigenomic analysis of ovarian cancer reveals epigenetically silenced GULP1. Cancer Letters, 2018, 433, 242-251.	7.2	16
15	Epigenetic sampling effects: nephrectomy modifies the clear cell renal cell cancer methylome. Cellular Oncology (Dordrecht), 2017, 40, 293-297.	4.4	2
16	Genome-wide DNA Methylation Profiling Reveals Methylation Markers Associated with 3q Gain for Detection of Cervical Precancer and Cancer. Clinical Cancer Research, 2017, 23, 3813-3822.	7.0	68
17	Costâ€effectiveness of a new urinary biomarkerâ€based risk score compared to standard of care in prostate cancer diagnostics – a decision analytical model. BJU International, 2017, 120, 659-665.	2.5	45
18	Differential analysis of genome-wide methylation and gene expression in mesenchymal stem cells of patients with fractures and osteoarthritis. Epigenetics, 2017, 12, 113-122.	2.7	60

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19	A urinary biomarkerâ€based risk score correlates with multiparametric MRI for prostate cancer detection. Prostate, 2017, 77, 1401-1407.	2.3	61
20	Methylome analysis of extreme chemoresponsive patients identifies novel markers of platinum sensitivity in high-grade serous ovarian cancer. BMC Medicine, 2017, 15, 116.	5.5	44
21	A Four-Gene Promoter Methylation Marker Panel Consisting of <i>GREM1, NEURL, LAD1,</i> and <i>NEFH</i> Predicts Survival of Clear Cell Renal Cell Cancer Patients. Clinical Cancer Research, 2017, 23, 2006-2018.	7.0	51
22	Immune cell profiling of melanoma metastases from patients treated with TriMixDC-MEL dendritic cell therapy in combination with ipilimumab Journal of Clinical Oncology, 2017, 35, e21030-e21030.	1.6	0
23	A genome-wide search for epigenetically regulated genes in zebra finch using MethylCap-seq and RNA-seq. Scientific Reports, 2016, 6, 20957.	3.3	9
24	Molecular and epigenetic features of melanomas and tumor immune microenvironment linked to durable remission to ipilimumab-based immunotherapy in metastatic patients. Journal of Translational Medicine, 2016, 14, 232.	4.4	27
25	Detection of High-grade Prostate Cancer Using a Urinary Molecular Biomarker–Based Risk Score. European Urology, 2016, 70, 740-748.	1.9	292
26	<i>WRN</i> Promoter CpG Island Hypermethylation Does Not Predict More Favorable Outcomes for Patients with Metastatic Colorectal Cancer Treated with Irinotecan-Based Therapy. Clinical Cancer Research, 2016, 22, 4612-4622.	7.0	9
27	Identification and validation of <scp><i>WISP</i></scp> <i>111<i>1<i>1<i>2<i>1Identification and validation of <scp><i>WISP</i></scp><i>1 1 2 3 4<</i></i></i></i></i></i>	2.8	28
28	Risk score predicts highâ€grade prostate cancer in DNAâ€methylation positive, histopathologically negative biopsies. Prostate, 2016, 76, 1078-1087.	2.3	74
29	DNA methylation profiling of primary neuroblastoma tumors using methyl-CpG-binding domain sequencing. Scientific Data, 2016, 3, 160004.	5.3	11
30	BMP-SMAD Signaling Regulates Lineage Priming, but Is Dispensable for Self-Renewal in Mouse Embryonic Stem Cells. Stem Cell Reports, 2016, 6, 85-94.	4.8	27
31	Genome-wide methylome analysis using MethylCap-seq uncovers 4 hypermethylated markers with high sensitivity for both adeno- and squamous-cell cervical carcinoma. Oncotarget, 2016, 7, 80735-80750.	1.8	15
32	Dynamic epigenetic changes to <i>VHL</i> occur with sunitinib in metastatic clear cell renal cancer. Oncotarget, 2016, 7, 25241-25250.	1.8	14
33	Genome-wide DNA methylation detection by MethylCap-seq and Infinium HumanMethylation450 BeadChips: an independent large-scale comparison. Scientific Reports, 2015, 5, 15375.	3.3	17
34	MEXPRESS: visualizing expression, DNA methylation and clinical TCGA data. BMC Genomics, 2015, 16, 636.	2.8	257
35	Mining for viral fragments in methylation enriched sequencing data. Frontiers in Genetics, 2015, 6, 16.	2.3	5
36	PROTEOFORMER: deep proteome coverage through ribosome profiling and MS integration. Nucleic Acids Research, 2015, 43, e29-e29.	14.5	132

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37	Systemic Suppression of the Shoot Metabolism upon Rice Root Nematode Infection. PLoS ONE, 2014, 9, e106858.	2.5	13
38	Methylation-mediated repression of PRDM14 contributes to apoptosis evasion in HPV-positive cancers. Carcinogenesis, 2014, 35, 2611-2618.	2.8	35
39	SNP-guided identification of monoallelic DNA-methylation events from enrichment-based sequencing data. Nucleic Acids Research, 2014, 42, e157-e157.	14.5	6
40	Bacterial Diversity Assessment in Antarctic Terrestrial and Aquatic Microbial Mats: A Comparison between Bidirectional Pyrosequencing and Cultivation. PLoS ONE, 2014, 9, e97564.	2.5	60
41	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
42	Food-derived opioid peptides inhibit cysteine uptake with redox and epigenetic consequences. Journal of Nutritional Biochemistry, 2014, 25, 1011-1018.	4.2	85
43	On Cross-Sectional Associations of Leukocyte Telomere Length with Cardiac Systolic, Diastolic and Vascular Function: The Asklepios Study. PLoS ONE, 2014, 9, e115071.	2.5	19
44	Staphylococcal enterotoxin B influences the DNA methylation pattern in nasal polyp tissue: a preliminary study. Allergy, Asthma and Clinical Immunology, 2013, 9, 48.	2.0	13
45	Transcriptional reprogramming by root knot and migratory nematode infection in rice. New Phytologist, 2012, 196, 887-900.	7.3	157