Daoud Sie

List of Publications by Year
in descending order

49	3,066	218677	206112
papers	citations	26 h-index	48 g-index

53	53	53	7463
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Molecular pathways in post-colonoscopy versus detected colorectal cancers: results from a nested caseâ€“control study. British Journal of Cancer, 2022, 126, 865-873.	6.4	6
2	Circular RNA Sequencing of Maternal Platelets: A Novel Tool for the Identification of Pregnancy-Specific Biomarkers. Clinical Chemistry, 2021, 67, 508-517.	3.2	6
3	PCR-Free Shallow Whole Genome Sequencing for Chromosomal Copy Number Detection from Plasma of Cancer Patients Is an Efficient Alternative to the Conventional PCR-Based Approach. Journal of Molecular Diagnostics, 2021, 23, 1553-1563.	2.8	7
4	Fusion transcripts and their genomic breakpoints in polyadenylated and ribosomal RNAâ€“minus RNA sequencing data. GigaScience, 2021, 10, .	6.4	10
5	IBD-Associated Dysplastic Lesions Show More Chromosomal Instability Than Sporadic Adenomas. Inflammatory Bowel Diseases, 2020, 26, 167-180.	1.9	29
6	Expression of let-7i and miR-192 is associated with resistance to cisplatin-based chemoradiotherapy in patients with larynx and hypopharynx cancer. Oral Oncology, 2020, 109, 104851.	1.5	3
7	The bivariate NRIP1/ZEB2 RNA marker permits non-invasive presymptomatic screening of pre-eclampsia. Scientific Reports, 2020, 10, 21857.	3.3	3
8	Clonality analysis of pulmonary tumors by genome-wide copy number profiling. PLoS ONE, 2019, 14, e0223827.	2.5	9
9	Colorectal metastasis to the gallbladder mimicking a primary gallbladder malignancy: histopathological and molecular characteristics. Histopathology, 2019, 75, 394-404.	2.9	8
10	Genomeâ€wide microRNA analysis of HPVâ€positive selfâ€samples yields novel triage markers for early detection of cervical cancer. International Journal of Cancer, 2019, 144, 372-379.	5.1	29
11	ACE: absolute copy number estimation from low-coverage whole-genome sequencing data. Bioinformatics, 2019, 35, 2847-2849.	4.1	50
12	Fetal fraction evaluation in non-invasive prenatal screening (NIPS). European Journal of Human Genetics, 2019, 27, 198-202.	2.8	34
13	Combination of a six microRNA expression profile with four clinicopathological factors for response prediction of systemic treatment in patients with advanced colorectal cancer. PLoS ONE, 2018, 13, e0201809.	2.5	20
14	Molecular heterogeneity in human papillomavirusâ€dependent and â€independent vulvar carcinogenesis. Cancer Medicine, 2018, 7, 4542-4553.	2.8	21
15	Copy number signatures and mutational processes in ovarian carcinoma. Nature Genetics, 2018, 50, 1262-1270.	21.4	320
16	Functional Screening Identifies Human miRNAs that Modulate Adenovirus Propagation in Prostate Cancer Cells. Human Gene Therapy, 2017, 28, 766-780.	2.7	22
17	Cytogenomics of Solid Tumors by Next-Generation Sequencing. , 2017, , 273-279.		0
18	Condensin II mutation causes T-cell lymphoma through tissue-specific genome instability. Genes and Development, 2016, 30, 2173-2186.	5.9	41

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19	Non-classic EGFR mutations in a cohort of Dutch EGFR-mutated NSCLC patients and outcomes following EGFR-TKI treatment. British Journal of Cancer, 2016, 115, 1504-1512.	6.4	55
20	Genomic profiling of stage II and III colon cancers reveals APC mutations to be associated with survival in stage III colon cancer patients. Oncotarget, 2016, 7, 73876-73887.	1.8	9
21	Collembolan Transcriptomes Highlight Molecular Evolution of Hexapods and Provide Clues on the Adaptation to Terrestrial Life. PLoS ONE, 2015, 10, e0130600.	2.5	25
22	Somatic mutation in PIK3CA is a late event in cervical carcinogenesis. Journal of Pathology: Clinical Research, 2015, 1, 207-211.	3.0	24
23	Proper genomic profiling of (BRCA1â€mutated) basalâ€like breast carcinomas requires prior removal of tumor infiltrating lymphocytes. Molecular Oncology, 2015, 9, 877-888.	4.6	16
24	Landscape of chromosomal copy number aberrations in gangliogliomas and dysembryoplastic neuroepithelial tumours. Neuropathology and Applied Neurobiology, 2015, 41, 743-755.	3.2	37
25	MiR expression profiles of paired primary colorectal cancer and metastases by next-generation sequencing. Oncogenesis, 2015, 4, e170-e170.	4.9	53
26	High Prevalence and Clinical Relevance of Genes Affected by Chromosomal Breaks in Colorectal Cancer. PLoS ONE, 2015, 10, e0138141.	2.5	24
27	Spatial and temporal evolution of distal 10q deletion, a prognostically unfavorable event in diffuse low-grade gliomas. Genome Biology, 2014, 15, 471.	8.8	29
28	DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. Genome Research, 2014, 24, 2022-2032.	5.5	362
29	Somatic mutations found in the healthy blood compartment of a 115-yr-old woman demonstrate oligoclonal hematopoiesis. Genome Research, 2014, 24, 733-742.	5.5	136
30	No evidence for active human papillomavirus (<scp>HPV</scp>) in fields surrounding <scp>HPV</scp>â€positive oropharyngeal tumors. Journal of Oral Pathology and Medicine, 2014, 43, 137-142.	2.7	38
31	Performance of amplicon-based next generation DNA sequencing for diagnostic gene mutation profiling in oncopathology. Cellular Oncology (Dordrecht), 2014, 37, 353-361.	4.4	43
32	Targeted sequencing by proximity ligation for comprehensive variant detection and local haplotyping. Nature Biotechnology, 2014, 32, 1019-1025.	17.5	231
33	ShrinkBayes: a versatile R-package for analysis of count-based sequencing data in complex study designs. BMC Bioinformatics, 2014, 15, 116.	2.6	37
34	EGFR mutation analysis in sputum of lung cancer patients: A multitechnique study. Lung Cancer, 2013, 82, 38-43.	2.0	32
35	Novel cases of D-2-hydroxyglutaric aciduria withIDH1orIDH2mosaic mutations identified by amplicon deep sequencing. Journal of Medical Genetics, 2013, 50, 754-759.	3.2	19
36	Search for a Gene Expression Signature of Breast Cancer Local Recurrence in Young Women. Clinical Cancer Research, 2012, 18, 1704-1715.	7.0	67

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37	Diagnosis of Fanconi Anemia: Mutation Analysis by Next-Generation Sequencing. Anemia, 2012, 2012, 1-7.	1.7	44
38	HELLP babies link a novel lincRNA to the trophoblast cell cycle. Journal of Clinical Investigation, 2012, 122, 4003-4011.	8.2	66
39	High-throughput semiquantitative analysis of insertional mutations in heterogeneous tumors. Genome Research, 2011, 21, 2181-2189.	5.5	39
40	To DNA or not to DNA? That Is the Question, When It Comes to Molecular Subtyping for the Clinic!. Clinical Cancer Research, 2011, 17, 4959-4964.	7.0	21
41	MicroRNA Sequence and Expression Analysis in Breast Tumors by Deep Sequencing. Cancer Research, 2011, 71, 4443-4453.	0.9	331
42	A Barcode Screen for Epigenetic Regulators Reveals a Role for the NuB4/HAT-B Histone Acetyltransferase Complex in Histone Turnover. PLoS Genetics, 2011, 7, e1002284.	3.5	25
43	Volatile Anesthetics Modulate Gene Expression in Breast and Brain Tumor Cells. Anesthesia and Analgesia, 2010, 111, 1411-1415.	2.2	49
44	One naive T cell, multiple fates in CD8+ T cell differentiation. Journal of Experimental Medicine, 2010, 207, 1235-1246.	8.5	162
45	Insertional Mutagenesis in Mice Deficient for p15Ink4b, p16Ink4a, p21Cip1, and p27Kip1 Reveals Cancer Gene Interactions and Correlations with Tumor Phenotypes. Cancer Research, 2010, 70, 520-531.	0.9	31
46	Recruitment of Antigen-Specific CD8 ⁺ T Cells in Response to Infection Is Markedly Efficient. Science, 2009, 325, 1265-1269.	12.6	133
47	Large-Scale Mutagenesis in p19ARF- and p53-Deficient Mice Identifies Cancer Genes and Their Collaborative Networks. Cell, 2008, 133, 727-741.	28.9	167
48	Dissecting T cell lineage relationships by cellular barcoding. Journal of Experimental Medicine, 2008, 205, 2309-2318.	8.5	107
49	The T7-Primer Is a Source of Experimental Bias and Introduces Variability between Microarray Platforms. PLoS ONE, 2008, 3, e1980.	2.5	19