Eric LetouzÃ©

List of Publications by Year
in descending order

81 papers	9,551 citations	76196 40 h-index	71532 76 g-index
85 all docs	85 docs citations	85 times ranked	14755 citing authors

#	Article	IF	Citations
1	Hepatitis B virus integrations promote local and distant oncogenic driver alterations in hepatocellular carcinoma. Gut, 2022, 71, 616-626.	6.1	106
2	Comprehensive characterization of viral integrations and genomic aberrations in HBVâ€infected intrahepatic cholangiocarcinomas. Hepatology, 2022, 75, 997-1011.	3.6	16
3	KDM1A inactivation causes hereditary food-dependent Cushing syndrome. Genetics in Medicine, 2022, 24, 374-383.	1.1	27
4	Common genetic variation in alcohol-related hepatocellular carcinoma: a case-control genome-wide association study. Lancet Oncology, The, 2022, 23, 161-171.	5.1	36
5	Detection of acquired TERT amplification in addition to predisposing p53 and Rb pathways alterations in EGFR-mutant lung adenocarcinomas transformed into small-cell lung cancers. Lung Cancer, 2022, 167, 98-106.	0.9	6
6	Structure, Dynamics, and Impact of Replication Stressâ€“Induced Structural Variants in Hepatocellular Carcinoma. Cancer Research, 2022, 82, 1470-1481.	0.4	0
7	H3K27me3 conditions chemotolerance in triple-negative breast cancer. Nature Genetics, 2022, 54, 459-468.	9.4	44
8	Bi-allelic hydroxymethylbilane synthase inactivation defines a homogenous clinico-molecular subtype of hepatocellular carcinoma. Journal of Hepatology, 2022, 77, 1038-1046.	1.8	17
9	HLA-D and PLA2R1 risk alleles associate with recurrent primary membranous nephropathy in kidney transplant recipients. Kidney International, 2021, 99, 671-685.	2.6	24
10	Integrated Genomic Analysis Identifies Driver Genes and Cisplatin-Resistant Progenitor Phenotype in Pediatric Liver Cancer. Cancer Discovery, 2021, 11, 2524-2543.	7.7	41
11	Loss of SDHB Promotes Dysregulated Iron Homeostasis, Oxidative Stress, and Sensitivity to Ascorbate. Cancer Research, 2021, 81, 3480-3494.	0.4	26
12	Multi-site tumor sampling highlights molecular intra-tumor heterogeneity in malignant pleural mesothelioma. Genome Medicine, 2021, 13, 113.	3.6	31
13	DNA Methylation Signatures Reveal the Diversity of Processes Remodeling Hepatocellular Carcinoma Methylomes. Hepatology, 2021, 74, 816-834.	3.6	20
14	A high-risk retinoblastoma subtype with stemness features, dedifferentiated cone states and neuronal/ganglion cell gene expression. Nature Communications, 2021, 12, 5578.	5.8	45
15	Clinical Impact of Genomic Diversity From Early to Advanced Hepatocellular Carcinoma. Hepatology, 2020, 71, 164-182.	3.6	129
16	Adeno-associated virus in the liver: natural history and consequences in tumour development. Gut, 2020, 69, 737-747.	6.1	78
17	Recurrent chromosomal rearrangements of ROS1, FRK and IL6 activating JAK/STAT pathway in inflammatory hepatocellular adenomas. Gut, 2020, 69, 1667-1676.	6.1	17
18	Genomic and Transcriptomic Tumor Heterogeneity in Bilateral Retinoblastoma. JAMA Ophthalmology, 2020, 138, 569.	1.4	17

#	Article	IF	Citations
19	XAF1 as a modifier of p53 function and cancer susceptibility. Science Advances, 2020, 6, eaba3231.	4.7	37
20	TET-Mediated Hypermethylation Primes SDH-Deficient Cells for HIF2Î±-Driven Mesenchymal Transition. Cell Reports, 2020, 30, 4551-4566.e7.	2.9	49
21	PS-047-HSD17B13 loss of function variant protects from hepatocellular carcinoma developed on alcohol related liver disease. Journal of Hepatology, 2019, 70, e29-e30.	1.8	1
22	Analysis of Liver Cancer Cell Lines Identifies Agents With Likely Efficacy Against Hepatocellular Carcinoma and Markers of Response. Gastroenterology, 2019, 157, 760-776.	0.6	141
23	Mutational Processes in Hepatocellular Carcinoma: The Story of Aristolochic Acid. Seminars in Liver Disease, 2019, 39, 334-340.	1.8	24
24	A 17â€Betaâ€Hydroxysteroid Dehydrogenase 13 Variant Protects From Hepatocellular Carcinoma Development in Alcoholic Liver Disease. Hepatology, 2019, 70, 231-240.	3.6	75
25	Hypermethylator Phenotype and Ectopic GIP Receptor in GNAS Mutation-Negative Somatotropinomas. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 1777-1787.	1.8	25
26	APC germline hepatoblastomas demonstrate cisplatin-induced intratumor tertiary lymphoid structures. OncoImmunology, 2019, 8, e1583547.	2.1	31
27	Nonâ€virological factors are drivers of hepatocellular carcinoma in virosuppressed hepatitis B cirrhosis: Results of <scp>ANRS CO</scp>12 CirVir cohort. Journal of Viral Hepatitis, 2019, 26, 384-396.	1.0	16
28	PNPLA3 and TM6SF2 variants as risk factors of hepatocellular carcinoma across various etiologies and severity of underlying liver diseases. International Journal of Cancer, 2019, 144, 533-544.	2.3	72
29	Extrahepatic cancers are the leading cause of death in patients achieving hepatitis B virus control or hepatitis C virus eradication. Hepatology, 2018, 68, 1245-1259.	3.6	33
30	Germline Mutations in the Mitochondrial 2-Oxoglutarate/Malate Carrier SLC25A11 Gene Confer a Predisposition to Metastatic Paragangliomas. Cancer Research, 2018, 78, 1914-1922.	0.4	96
31	Prognostic value of viral eradication for major adverse cardiovascular events in hepatitis C cirrhotic patients. American Heart Journal, 2018, 198, 4-17.	1.2	49
32	Argininosuccinate synthase 1 and periportal gene expression in sonic hedgehog hepatocellular adenomas. Hepatology, 2018, 68, 964-976.	3.6	43
33	Cyclin A2/E1 activation defines a hepatocellular carcinoma subclass with a rearrangement signature of replication stress. Nature Communications, 2018, 9, 5235.	5.8	118
34	Systemic AA Amyloidosis Caused by Inflammatory Hepatocellular Adenoma. New England Journal of Medicine, 2018, 379, 1178-1180.	13.9	15
35	Dual origin of relapses in retinoic-acid resistant acute promyelocytic leukemia. Nature Communications, 2018, 9, 2047.	5.8	35
36	Palimpsest: an R package for studying mutational and structural variant signatures along clonal evolution in cancer. Bioinformatics, 2018, 34, 3380-3381.	1.8	53

#	Article	IF	Citations
37	Compliance With Hepatocellular Carcinoma Surveillance Guidelines Associated With Increased Lead-Time Adjusted Survival of Patients With Compensated Viral Cirrhosis: A Multi-Center Cohort Study. Gastroenterology, 2018, 155, 431-442.e10.	0.6	81
38	Transethnic, Genome-Wide Analysis Reveals Immune-Related Risk Alleles and Phenotypic Correlates in Pediatric Steroid-Sensitive Nephrotic Syndrome. Journal of the American Society of Nephrology: JASN, 2018, 29, 2000-2013.	3.0	72
39	Mutational signature analysis identifies <scp>MUTYH</scp> deficiency in colorectal cancers and adrenocortical carcinomas. Journal of Pathology, 2017, 242, 10-15.	2.1	130
40	Histological subtypes of hepatocellular carcinoma are related to gene mutations and molecular tumour classification. Journal of Hepatology, 2017, 67, 727-738.	1.8	525
41	Germline and somatic DICER1 mutations in familial and sporadic liver tumors. Journal of Hepatology, 2017, 66, 734-742.	1.8	31
42	Molecular Classification of Hepatocellular Adenoma AssociatesÂWith Risk Factors, Bleeding, and Malignant Transformation. Gastroenterology, 2017, 152, 880-894.e6.	0.6	290
43	Combined tumor genomic profiling and exome sequencing in a breast cancer family implicates ATM in tumorigenesis: A proof of principle study. Genes Chromosomes and Cancer, 2017, 56, 788-799.	1.5	5
44	Mutational signatures reveal the dynamic interplay of risk factors and cellular processes during liver tumorigenesis. Nature Communications, 2017, 8, 1315.	5.8	228
45	aCNViewer: Comprehensive genome-wide visualization of absolute copy number and copy neutral variations. PLoS ONE, 2017, 12, e0189334.	1.1	5
46	Characterization of the transcriptional and metabolic responses of pediatric high grade gliomas to mTOR-HIF-1Î± axis inhibition. Oncotarget, 2017, 8, 71597-71617.	0.8	8
47	Genotypeâ€phenotype correlation of CTNNB1 mutations reveals different ÃŸâ€catenin activity associated with liver tumor progression. Hepatology, 2016, 64, 2047-2061.	3.6	222
48	Wild-type AAV Insertions in Hepatocellular Carcinoma Do Not Inform Debate Over Genotoxicity Risk of Vectorized AAV. Molecular Therapy, 2016, 24, 660-661.	3.7	33
49	Integrated multi-omics analysis of oligodendroglial tumours identifies three subgroups of 1p/19q co-deleted gliomas. Nature Communications, 2016, 7, 11263.	5.8	73
50	AAV2 and Hepatocellular Carcinoma. Human Gene Therapy, 2016, 27, 211-213.	1.4	8
51	Whole Exome Analysis of Relapsing Patients with Acute Promyelocytic Leukemia. Blood, 2016, 128, 2892-2892.	0.6	1
52	DNA methylationâ€based prognosis and epidrivers in hepatocellular carcinoma. Hepatology, 2015, 61, 1945-1956.	3.6	367
53	DNA Methylation Profiling in Pheochromocytoma and Paraganglioma Reveals Diagnostic and Prognostic Markers. Clinical Cancer Research, 2015, 21, 3020-3030.	3.2	53
54	Exome sequencing of hepatocellular carcinomas identifies new mutational signatures and potential therapeutic targets. Nature Genetics, 2015, 47, 505-511.	9.4	1,372

#	Article	IF	Citations
55	Multi-omics analysis defines core genomic alterations in pheochromocytomas and paragangliomas. Nature Communications, 2015, 6, 6044.	5.8	153
56	Recurrent AAV2-related insertional mutagenesis in human hepatocellular carcinomas. Nature Genetics, 2015, 47, 1187-1193.	9.4	387
57	TCF12 is mutated in anaplastic oligodendroglioma. Nature Communications, 2015, 6, 7207.	5.8	42
58	Deciphering the molecular basis of invasiveness in Sdhb-deficient cells. Oncotarget, 2015, 6, 32955-32965.	0.8	52
59	Abstract 2973: Exome sequencing of 243 liver tumors identifies new mutational signatures and potential therapeutic targets. , 2015, , .		0
60	Abstract 919: Adeno-associated virus 2 (AAV2) induces recurrent insertional mutagenesis in human hepatocellular carcinomas. , 2015, , .		0
61	SDHB mutations are associated with response to temozolomide in patients with metastatic pheochromocytoma or paraganglioma. International Journal of Cancer, 2014, 135, 2711-2720.	2.3	155
62	EGFR as a potential therapeutic target for a subset of muscle-invasive bladder cancers presenting a basal-like phenotype. Science Translational Medicine, 2014, 6, 244ra91.	5.8	304
63	Contrast enhancement in 1p/19q-codeleted anaplastic oligodendrogliomas is associated with 9p loss, genomic instability, and angiogenic gene expression. Neuro-Oncology, 2014, 16, 662-670.	0.6	59
64	Unsuspected task for an old team: Succinate, fumarate and other Krebs cycle acids in metabolic remodeling. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 1330-1337.	0.5	66
65	Genomic Profiling of Hepatocellular Adenomas Reveals Recurrent FRK-Activating Mutations and the Mechanisms of Malignant Transformation. Cancer Cell, 2014, 25, 428-441.	7.7	240
66	Integrated genomic characterization of adrenocortical carcinoma. Nature Genetics, 2014, 46, 607-612.	9.4	560
67	Oncometabolitesâ€driven tumorigenesis: From genetics to targeted therapy. International Journal of Cancer, 2014, 135, 2237-2248.	2.3	119
68	High-resolution analysis of DNA copy number alterations in rectal cancer. Strahlentherapie Und Onkologie, 2014, 190, 1028-1036.	1.0	4
69	SDH Mutations Establish a Hypermethylator Phenotype in Paraganglioma. Cancer Cell, 2013, 23, 739-752.	7.7	606
70	Recurrent inactivating mutations of ARID2 in nonâ€small cell lung carcinoma. International Journal of Cancer, 2013, 132, 2217-2221.	2.3	70
71	Somatic NF1 inactivation is a frequent event in sporadic pheochromocytoma. Human Molecular Genetics, 2012, 21, 5397-5405.	1.4	126
72	SNP Array Profiling of Childhood Adrenocortical Tumors Reveals Distinct Pathways of Tumorigenesis and Highlights Candidate Driver Genes. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E1284-E1293.	1.8	41

#	Article	IF	Citations
73	Integrated analysis of somatic mutations and focal copy-number changes identifies key genes and pathways in hepatocellular carcinoma. Nature Genetics, 2012, 44, 694-698.	9.4	1,229
74	Identity by Descent Mapping of Founder Mutations in Cancer Using High-Resolution Tumor SNP Data. PLoS ONE, 2012, 7, e35897.	1.1	8
75	Deletion of Chromosomes 13q and 14q Is a Common Feature of Tumors with BRCA2 Mutations. PLoS ONE, 2012, 7, e52079.	1.1	20
76	CDKN2A homozygous deletion is associated with muscle invasion in FGFR3â€mutated urothelial bladder carcinoma. Journal of Pathology, 2012, 227, 315-324.	2.1	90
77	Prognostic value of chromosomal imbalancies and the colon gene expression signatures in rectal cancer.. Journal of Clinical Oncology, 2012, 30, 465-465.	0.8	0
78	Abstract 5121: Acquired inactivating ARID2 mutations in lung non small cell carcinoma. , 2012, , .		0
79	Analysis of the copy number profiles of several tumor samples from the same patient reveals the successive steps in tumorigenesis. Genome Biology, 2010, 11, R76.	13.9	44
80	Analysis of the copy number profiles of several tumor samples from the same patient reveals the successive steps in tumorigenesis. Genome Biology, 2010, 11, P25.	13.9	4
81	Modular Î±-Helical Mimetics with Antiviral Activity against Respiratory Syncitial Virus. Journal of the American Chemical Society, 2006, 128, 13284-13289.	6.6	70