Pierre Martinez

List of Publications by Year
in descending order

21	8,754	567281	752698
papers	citations	15	20
		h-index	g-index

25	25	25	16272
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Intratumor Heterogeneity and Branched Evolution Revealed by Multiregion Sequencing. New England Journal of Medicine, 2012, 366, 883-892.	27.0	6,769
2	Genomic architecture and evolution of clear cell renal cell carcinomas defined by multiregion sequencing. Nature Genetics, 2014, 46, 225-233.	21.4	1,103
3	Systematic Evaluation of the Prognostic Impact and Intratumour Heterogeneity of Clear Cell Renal Cell Carcinoma Biomarkers. European Urology, 2014, 66, 936-948.	1.9	141
4	The evolutionary landscape of colorectal tumorigenesis. Nature Ecology and Evolution, 2018, 2, 1661-1672.	7.8	99
5	Evolutionary history of human colitis-associated colorectal cancer. Gut, 2019, 68, 985-995.	12.1	97
6	Genome‐wide RNA interference analysis of renal carcinoma survival regulators identifies MCT4 as a Warburg effect metabolic target. Journal of Pathology, 2012, 227, 146-156.	4.5	92
7	Parallel evolution of tumour subclones mimics diversity between tumours. Journal of Pathology, 2013, 230, 356-364.	4.5	79
8	Dynamic clonal equilibrium and predetermined cancer risk in Barrett's oesophagus. Nature Communications, 2016, 7, 12158.	12.8	75
9	Comprehensive characterization of claudin-low breast tumors reflects the impact of the cell-of-origin on cancer evolution. Nature Communications, 2020, 11, 3431.	12.8	57
10	Evolution of Barrett's esophagus through space and time at single-crypt and whole-biopsy levels. Nature Communications, 2018, 9, 794.	12.8	47
11	Evolution of oesophageal adenocarcinoma from metaplastic columnar epithelium without goblet cells in Barrett's oesophagus. Gut, 2016, 65, 907-913.	12.1	39
12	Derivation of genetic biomarkers for cancer risk stratification in Barrett's oesophagus: a prospective cohort study. Gut, 2016, 65, 1602-1610.	12.1	39
13	Protein‐Water Interactions in MD Simulations: POPS/POPSCOMP Solvent Accessibility Analysis, Solvation Forces and Hydration Sites. Methods in Molecular Biology, 2012, 819, 375-392.	0.9	22
14	Computational optimisation of targeted DNA sequencing for cancer detection. Scientific Reports, 2013, 3, 3309.	3.3	20
15	Structure and Stability Insights into Tumour Suppressor p53 Evolutionary Related Proteins. PLoS ONE, 2013, 8, e76014.	2.5	20
16	Immunosuppressive niche engineering at the onset of human colorectal cancer. Nature Communications, 2022, 13, 1798.	12.8	19
17	Increased expression of the thyroid hormone nuclear receptor TRα1 characterizes intestinal tumors with high Wnt activity. Oncotarget, 2018, 9, 30979-30996.	1.8	12
18	Quantification of within-sample genetic heterogeneity from SNP-array data. Scientific Reports, 2017, 7, 3248.	3.3	6

#	Article	IF	Citations
19	Quantifying local malignant adaptation in tissue‐specific evolutionary trajectories by harnessing cancer's repeatability at the genetic level. Evolutionary Applications, 2019, 12, 1062-1075.	3.1	2
20	Assessing Cell Activities rather than Identities to Interpret Intra-Tumor Phenotypic Diversity and Its Dynamics. IScience, 2020, 23, 101061.	4.1	1
21	Separating the Local and Malignant Dimensions of Cancer Adaptation. Cancer Informatics, 2019, 18, 117693511987295.	1.9	0