

# Ludovic Barault

## List of Publications by Year in descending order

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Version: 2024-02-01

29  
papers

3,037  
citations

331670

21  
h-index

526287

27  
g-index

31  
all docs

31  
docs citations

31  
times ranked

6200  
citing authors

#	ARTICLE	IF	CITATIONS
1	Temozolomide Treatment Alters Mismatch Repair and Boosts Mutational Burden in Tumor and Blood of Colorectal Cancer Patients. <i>Cancer Discovery</i> , 2022, 12, 1656-1675.	9.4	48
2	True conversions from RAS mutant to RAS wild-type in circulating tumor DNA from metastatic colorectal cancer patients as assessed by methylation and mutational signature. <i>Cancer Letters</i> , 2021, 507, 89-96.	7.2	10
3	Circulating Methylated DNA to Monitor the Dynamics of RAS Mutation Clearance in Plasma from Metastatic Colorectal Cancer Patients. <i>Cancers</i> , 2020, 12, 3633.	3.7	7
4	Capecitabine and Temozolomide versus FOLFIRI in RAS-Mutated, MGMT-Methylated Metastatic Colorectal Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 1017-1024.	7.0	22
5	High Circulating Methylated DNA Is a Negative Predictive and Prognostic Marker in Metastatic Colorectal Cancer Patients Treated With Regorafenib. <i>Frontiers in Oncology</i> , 2019, 9, 622.	2.8	22
6	Evolving neoantigen profiles in colorectal cancers with DNA repair defects. <i>Genome Medicine</i> , 2019, 11, 42.	8.2	42
7	A randomized, multicenter, phase 2 trial comparing CAPTEM versus FOLFIRI as second-line treatment for MGMT-methylated, RAS-mutated metastatic colorectal cancer patients. <i>Annals of Oncology</i> , 2019, 30, iv135.	1.2	0
8	A Genomic Analysis Workflow for Colorectal Cancer Precision Oncology. <i>Clinical Colorectal Cancer</i> , 2019, 18, 91-101.e3.	2.3	29
9	Whole exome sequencing analysis of urine trans-renal tumour DNA in metastatic colorectal cancer patients. <i>ESMO Open</i> , 2019, 4, e000572.	4.5	27
10	Refining the selection of patients with metastatic colorectal cancer for treatment with temozolomide using proteomic analysis of O6-methylguanine-DNA-methyltransferase. <i>European Journal of Cancer</i> , 2019, 107, 164-174.	2.8	9
11	Colorectal cancer early methylation alterations affect the crosstalk between cell and surrounding environment, tracing a biomarker signature specific for this tumor. <i>International Journal of Cancer</i> , 2018, 143, 907-920.	5.1	41
12	Temozolomide and irinotecan (TEMIRI regimen) as salvage treatment of irinotecan-sensitive advanced colorectal cancer patients bearing MGMT methylation. <i>Annals of Oncology</i> , 2018, 29, 1800-1806.	1.2	32
13	Discovery of methylated circulating DNA biomarkers for comprehensive non-invasive monitoring of treatment response in metastatic colorectal cancer. <i>Gut</i> , 2018, 67, 1995-2005.	12.1	188
14	Digital PCR assessment of MGMT promoter methylation coupled with reduced protein expression optimises prediction of response to alkylating agents in metastatic colorectal cancer patients. <i>European Journal of Cancer</i> , 2017, 71, 43-50.	2.8	27
15	Inactivation of DNA repair triggers neoantigen generation and impairs tumour growth. <i>Nature</i> , 2017, 552, 116-120.	27.8	480
16	MET-Driven Resistance to Dual EGFR and BRAF Blockade May Be Overcome by Switching from EGFR to MET Inhibition in BRAF-Mutated Colorectal Cancer. <i>Cancer Discovery</i> , 2016, 6, 963-971.	9.4	85
17	Molecular Landscape of Acquired Resistance to Targeted Therapy Combinations in BRAF-Mutant Colorectal Cancer. <i>Cancer Research</i> , 2016, 76, 4504-4515.	0.9	91
18	Tumor MGMT promoter hypermethylation changes over time limit temozolomide efficacy in a phase II trial for metastatic colorectal cancer. <i>Annals of Oncology</i> , 2016, 27, 1062-1067.	1.2	35

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19	Digital PCR quantification of MGMT methylation refines prediction of clinical benefit from alkylating agents in glioblastoma and metastatic colorectal cancer. <i>Annals of Oncology</i> , 2015, 26, 1994-1999.	1.2	105
20	Aberrant methylation of imprinted genes is associated with negative hormone receptor status in invasive breast cancer. <i>International Journal of Cancer</i> , 2015, 137, 537-547.	5.1	39
21	The prevalence of loss of imprinting of <i>H19</i> and <i>IGF2</i> at birth. <i>FASEB Journal</i> , 2013, 27, 3335-3343.	0.5	33
22	<i>BRAF</i> V600E Is a Determinant of Sensitivity to Proteasome Inhibitors. <i>Molecular Cancer Therapeutics</i> , 2013, 12, 2950-2961.	4.1	18
23	Leukocyte DNA as Surrogate for the Evaluation of Imprinted Loci Methylation in Mammary Tissue DNA. <i>PLoS ONE</i> , 2013, 8, e55896.	2.5	18
24	DNA methylation of stress-related genes and LINE-1 repetitive elements across the healthy human placenta. <i>Placenta</i> , 2012, 33, 183-187.	1.5	31
25	Laboratory Methods in <i>Epigenetic Epidemiology.</i> , 2012, , 37-56.		4
26	Birthweight, Maternal Weight Trajectories and Global DNA Methylation of LINE-1 Repetitive Elements. <i>PLoS ONE</i> , 2011, 6, e25254.	2.5	135
27	Immunogenic death of colon cancer cells treated with oxaliplatin. <i>Oncogene</i> , 2010, 29, 482-491.	5.9	937
28	Mutations in the RAS/MAPK, PI(3)K (phosphatidylinositol 3-OH kinase) signaling network correlate with poor survival in a population-based series of colon cancers. <i>International Journal of Cancer</i> , 2008, 122, 2255-2259.	5.1	273
29	Hypermethylator Phenotype in Sporadic Colon Cancer: Study on a Population-Based Series of 582 Cases. <i>Cancer Research</i> , 2008, 68, 8541-8546.	0.9	247