Gianmarco Contino

List of Publications by Year
in descending order

26 papers	4,042 citations	430874 18 h-index	526287 27 g-index
54 all docs	54 docs citations	54 times ranked	8457 citing authors

#	Article	IF	Citations
1	Pancreatic cancers require autophagy for tumor growth. Genes and Development, 2011, 25, 717-729.	5.9	1,224
2	Aberrant Overexpression of Satellite Repeats in Pancreatic and Other Epithelial Cancers. Science, 2011, 331, 593-596.	12.6	452
3	RNA sequencing of pancreatic circulating tumour cells implicates WNT signalling in metastasis. Nature, 2012, 487, 510-513.	27.8	439
4	*STAT3* Plays a Critical Role in *KRAS*-Induced Pancreatic Tumorigenesis. Cancer Research, 2011, 71, 5020-5029.	0.9	358
5	Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. Nature Genetics, 2016, 48, 1131-1141.	21.4	332
6	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
7	The landscape of selection in 551 esophageal adenocarcinomas defines genomic biomarkers for the clinic. Nature Genetics, 2019, 51, 506-516.	21.4	166
8	KDM2B promotes pancreatic cancer via Polycomb-dependent and -independent transcriptional programs. Journal of Clinical Investigation, 2013, 123, 727-39.	8.2	144
9	Combined MEK and PI3K Inhibition in a Mouse Model of Pancreatic Cancer. Clinical Cancer Research, 2015, 21, 396-404.	7.0	121
10	Lysine-specific Demethylase 2B (KDM2B)-let-7-Enhancer of Zester Homolog 2 (EZH2) Pathway Regulates Cell Cycle Progression and Senescence in Primary Cells. Journal of Biological Chemistry, 2011, 286, 33061-33069.	3.4	106
11	TGF-β and $\alpha v\beta$6 Integrin Act in a Common Pathway to Suppress Pancreatic Cancer Progression. Cancer Research, 2012, 72, 4840-4845.	0.9	82
12	The Evolving Genomic Landscape of Barrett's Esophagus and Esophageal Adenocarcinoma. Gastroenterology, 2017, 153, 657-673.e1.	1.3	69
13	Identification of Subtypes of Barrett's Esophagus and Esophageal Adenocarcinoma Based on DNA Methylation Profiles and Integration of Transcriptome and Genome Data. Gastroenterology, 2020, 158, 1682-1697.e1.	1.3	58
14	Recurrence and prognostic factors in patients with aggressive fibromatosis. The role of radical surgery and its limitations. World Journal of Surgical Oncology, 2012, 10, 184.	1.9	32
15	Molecular imaging agents: impact on diagnosis and therapeutics in oncology. Expert Reviews in Molecular Medicine, 2010, 12, e20.	3.9	28
16	Whole-genome sequencing of nine esophageal adenocarcinoma cell lines. F1000Research, 2016, 5, 1336.	1.6	23
17	Expression analysis of the gene encoding for the U-box-type ubiquitin ligase UBE4A in human tissues. Gene, 2004, 328, 69-74.	2.2	22
18	Metachronous Colon Metastases from Gastric Adenocarcinoma: A Case Report. Case Reports in Oncology, 2009, 2, 92-96.	0.7	19

#	ARTICLE	IF	CITATIONS
19	Role of genetics in prevention of coronary atherosclerosis. Current Opinion in Cardiology, 2003, 18, 368-371.	1.8	18
20	Transcriptomic profiling reveals three molecular phenotypes of adenocarcinoma at the gastroesophageal junction. International Journal of Cancer, 2019, 145, 3389-3401.	5.1	17
21	Comparison of outcomes between neoadjuvant chemoradiotherapy and neoadjuvant chemotherapy in patients with locally advanced esophageal cancer: A network meta-analysis. EClinicalMedicine, 2021, 42, 101183.	7.1	17
22	Hereditary spastic paraplegia: clinical genomics and pharmacogenetic perspectives. Expert Opinion on Pharmacotherapy, 2006, 7, 1849-1856.	1.8	10
23	Aggressive Treatment Approach for Cloacogenic Carcinoma of the Anorectum: Report from a Single Cancer Center. Digestive Surgery, 2010, 27, 297-301.	1.2	8
24	Rearrangement processes and structural variations show evidence of selection in oesophageal adenocarcinomas. Communications Biology, 2022, 5, 335.	4.4	8
25	Two-year follow-up of wound complications associated with laparoendoscopic single-site adjustable gastric banding. Surgery for Obesity and Related Diseases, 2013, 9, 696-700.	1.2	5
26	Identifying Cancer Drivers Using DRIVE: A Feature-Based Machine Learning Model for a Pan-Cancer Assessment of Somatic Missense Mutations. Cancers, 2021, 13, 2779.	3.7	4