Giovanni Crisafulli

List of Publications by Year
in descending order

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39	3,482	361413	526287
papers	citations	20 h-index	27 g-index

41	41	41	6336
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Liquid biopsies to monitor and direct cancer treatment in colorectal cancer. British Journal of Cancer, 2022, 127, 394-407.	6.4	41
2	Temozolomide Treatment Alters Mismatch Repair and Boosts Mutational Burden in Tumor and Blood of Colorectal Cancer Patients. Cancer Discovery, 2022, 12, 1656-1675.	9.4	48
3	A modified fluctuation-test framework characterizes the population dynamics and mutation rate of colorectal cancer persister cells. Nature Genetics, 2022, 54, 976-984.	21.4	23
4	Werner Helicase Is a Synthetic-Lethal Vulnerability in Mismatch Repairâ€“Deficient Colorectal Cancer Refractory to Targeted Therapies, Chemotherapy, and Immunotherapy. Cancer Discovery, 2021, 11, 1923-1937.	9.4	48
5	Assessment of HER2 (ERBB2) amplification (HER2amp) using blood-based circulating tumor DNA (ctDNA) next generation sequencing (NGS) and correlation with tissue-based testing in metastatic colorectal cancer (mCRC).. Journal of Clinical Oncology, 2021, 39, 3589-3589.	1.6	2
6	PARP1 Inhibitor and Trabectedin Combination Does Not Increase Tumor Mutational Burden in Advanced Sarcomasâ€”A Preclinical and Translational Study. Cancers, 2021, 13, 6295.	3.7	0
7	Abstract B11: Whole-exome sequencing analysis of urine transrenal tumor DNA in metastatic colorectal cancer patients. , 2020, , .		0
8	Adaptive mutability of colorectal cancers in response to targeted therapies. Science, 2019, 366, 1473-1480.	12.6	290
9	A Genomic Analysis Workflow for Colorectal Cancer Precision Oncology. Clinical Colorectal Cancer, 2019, 18, 91-101.e3.	2.3	29
10	Whole exome sequencing analysis of urine trans-renal tumour DNA in metastatic colorectal cancer patients. ESMO Open, 2019, 4, e000572.	4.5	27
11	Pembrolizumab in MMR-proficient metastatic colorectal cancer pharmacologically primed to trigger dynamic hypermutation status: The ARETHUSA trial.. Journal of Clinical Oncology, 2019, 37, TPS2659-TPS2659.	1.6	10
12	Abstract B069: Temozolomide drives mismatch repair deficiency and fosters neoantigen generation in tumor cells. , 2019, , .		0
13	Abstract A120: Adaptive mutability of colorectal cancers in response to targeted therapies. , 2019, , .		0
14	Radiologic and Genomic Evolution of Individual Metastases during HER2 Blockade in Colorectal Cancer. Cancer Cell, 2018, 34, 148-162.e7.	16.8	129
15	Abstract 5723: Inactivation of DNA repair triggers neoantigen generation and impairs tumor growth. Cancer Research, 2018, 78, 5723-5723.	0.9	5
16	Abstract 2848: Radiographic and genomic evolution of individual metastases during HER2 blockade in colorectal cancer. , 2018, , .		1
17	Abstract 2743: Accumulation of predicted neoantigens by MMR deficiency triggered by temozolomide treatment of human colorectal cancer. , 2018, , .		0
18	Tracking aCAD-ALK gene rearrangement in urine and blood of a colorectal cancer patient treated with an ALK inhibitor. Annals of Oncology, 2017, 28, 1302-1308.	1.2	32

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19	Loss of AXIN1 drives acquired resistance to <scp>WNT</scp> pathway blockade in colorectal cancer cells carrying <scp>RSPO</scp> 3 fusions. EMBO Molecular Medicine, 2017, 9, 293-303.	6.9	54
20	Tracking colorectal cancer evolution in time and space. Annals of Oncology, 2017, 28, 1163-1165.	1.2	5
21	Genetic Evolution of Glioblastoma Stem-Like Cells From Primary to Recurrent Tumor. Stem Cells, 2017, 35, 2218-2228.	3.2	47
22	Inactivation of DNA repair triggers neoantigen generation and impairs tumour growth. Nature, 2017, 552, 116-120.	27.8	480
23	Genotyping tumour DNA in cerebrospinal fluid and plasma of a HER2-positive breast cancer patient with brain metastases. ESMO Open, 2017, 2, e000253.	4.5	56
24	Emergence of MET hyper-amplification at progression to MET and BRAF inhibition in colorectal cancer. British Journal of Cancer, 2017, 117, 347-352.	6.4	31
25	Abstract 3834: Tracking CAD-ALK gene translocation in urine and plasma of a colorectal cancer patient treated with ALK blockade. , 2017, , .		0
26	Abstract 2913: Emergence ofRASorEGFRmutant clones affects duration of response to EGFR blockade in colorectal cancers. , 2017, , .		0
27	Acquired RAS or EGFR mutations and duration of response to EGFR blockade in colorectal cancer. Nature Communications, 2016, 7, 13665.	12.8	170
28	Molecular Landscape of Acquired Resistance to Targeted Therapy Combinations in BRAF-Mutant Colorectal Cancer. Cancer Research, 2016, 76, 4504-4515.	0.9	91
29	Tumor Heterogeneity and Lesion-Specific Response to Targeted Therapy in Colorectal Cancer. Cancer Discovery, 2016, 6, 147-153.	9.4	338
30	Acquired Resistance to the TRK Inhibitor Entrectinib in Colorectal Cancer. Cancer Discovery, 2016, 6, 36-44.	9.4	258
31	Abstract 878: Tumor heterogeneity and lesion-specific response to targeted therapy in colorectal cancer. , 2016, , .		1
32	Clonal evolution and resistance to EGFR blockade in the blood of colorectal cancer patients. Nature Medicine, 2015, 21, 795-801.	30.7	809
33	Emergence of Multiple EGFR Extracellular Mutations during Cetuximab Treatment in Colorectal Cancer. Clinical Cancer Research, 2015, 21, 2157-2166.	7.0	227
34	Abstract PR01: Acquisition of resistance to anti-EGFR therapy drives genomic heterogeneity and lesion-specific responses in colorectal cancer. , 2015, , .		1
35	Raise and decline of KRAS mutant clones in colorectal cancers (CRCs) treated with multiple rounds of anti-EGFR antibodies.. Journal of Clinical Oncology, 2015, 33, 11073-11073.	1.6	0
36	Abstract 616: Blood-based molecular landscapes of resistance to EGFR blockade in colorectal cancer patients. , 2015, , .		0

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37	Abstract 3588: Emergence of multiple EGFR extracellular mutations during cetuximab treatment in colorectal cancer. , 2015, , .		0
38	An extended multi-locus molecular typing schema for Streptococcus pneumoniae demonstrates that a limited number of capsular switch events is responsible for serotype heterogeneity of closely related strains from different countries. Infection, Genetics and Evolution, 2013, 13, 151-161.	2.3	9
39	Sequence Analysis of 96 Genomic Regions Identifies Distinct Evolutionary Lineages within CC156, the Largest Streptococcus pneumoniae Clonal Complex in the MLST Database. PLoS ONE, 2013, 8, e61003.	2.5	8