## Giorgio Corti

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A Subset of Colorectal Cancers with Cross-Sensitivity to Olaparib and Oxaliplatin. Clinical Cancer Research, 2020, 26, 1372-1384.	7.0	66
2	Patient-Derived Xenografts and Matched Cell Lines Identify Pharmacogenomic Vulnerabilities in Colorectal Cancer. Clinical Cancer Research, 2019, 25, 6243-6259.	7.0	42
3	Evolving neoantigen profiles in colorectal cancers with DNA repair defects. Genome Medicine, 2019, 11, 42.	8.2	42
4	A Genomic Analysis Workflow for Colorectal Cancer Precision Oncology. Clinical Colorectal Cancer, 2019, 18, 91-101.e3.	2.3	29
5	Radiologic and Genomic Evolution of Individual Metastases during HER2 Blockade in Colorectal Cancer. Cancer Cell, 2018, 34, 148-162.e7.	16.8	129
6	Reliance upon ancestral mutations is maintained in colorectal cancers that heterogeneously evolve during targeted therapies. Nature Communications, 2018, 9, 2287.	12.8	18
7	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
8	Tracking colorectal cancer evolution in time and space. Annals of Oncology, 2017, 28, 1163-1165.	1.2	5
9	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
10	Acquired RAS or EGFR mutations and duration of response to EGFR blockade in colorectal cancer. Nature Communications, 2016, 7, 13665.	12.8	170
11	BCAM and LAMA5 Mediate the Recognition between Tumor Cells and the Endothelium in the Metastatic Spreading of KRAS-Mutant Colorectal Cancer. Clinical Cancer Research, 2016, 22, 4923-4933.	7.0	50
12	Molecular Landscape of Acquired Resistance to Targeted Therapy Combinations in <i>BRAF</i> -Mutant Colorectal Cancer. Cancer Research, 2016, 76, 4504-4515.	0.9	91
13	Tumor Heterogeneity and Lesion-Specific Response to Targeted Therapy in Colorectal Cancer. Cancer Discovery, 2016, 6, 147-153.	9.4	338
14	Acquired Resistance to the TRK Inhibitor Entrectinib in Colorectal Cancer. Cancer Discovery, 2016, 6, 36-44.	9.4	258
15	Clonal evolution and resistance to EGFR blockade in the blood of colorectal cancer patients. Nature Medicine, 2015, 21, 795-801.	30.7	809
16	Emergence of Multiple <i>EGFR</i> Extracellular Mutations during Cetuximab Treatment in Colorectal Cancer. Clinical Cancer Research, 2015, 21, 2157-2166.	7.0	227
17	The molecular landscape of colorectal cancer cell lines unveils clinically actionable kinase targets. Nature Communications, 2015, 6, 7002.	12.8	251
18	A Genomic, Transcriptomic and Proteomic Look at the GE2270 Producer Planobispora rosea, an Uncommon Actinomycete. PLoS ONE, 2015, 10, e0133705.	2.5	14

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19	Enly: Improving Draft Genomes through Reads Recycling. Journal of Genomics, 2014, 2, 89-93.	0.9	3
20	Small Noncoding RNAs in Cells Transformed by Human T-Cell Leukemia Virus Type 1: a Role for a tRNA Fragment as a Primer for Reverse Transcriptase. Journal of Virology, 2014, 88, 3612-3622.	3.4	116
21	A Glycosylated, Labionin-Containing Lanthipeptide with Marked Antinociceptive Activity. ACS Chemical Biology, 2014, 9, 398-404.	3.4	89
22	Comparative genomics revealed key molecular targets to rapidly convert a reference rifamycin-producing bacterial strain into an overproducer by genetic engineering. Metabolic Engineering, 2014, 26, 1-16.	7.0	29
23	The genome sequence of the hydrocarbon-degrading Acinetobacter venetianus VE-C3. Research in Microbiology, 2013, 164, 439-449.	2.1	30
24	Amplification of the <i>MET</i> Receptor Drives Resistance to Anti-EGFR Therapies in Colorectal Cancer. Cancer Discovery, 2013, 3, 658-673.	9.4	585
25	Origins and Evolution of the Etruscans' mtDNA. PLoS ONE, 2013, 8, e55519.	2.5	40
26	Specific inactivation of two immunomodulatory <i>SIGLEC</i> genes during human evolution. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9935-9940.	7.1	64
27	Comparative genomics and transcriptional profiles of Saccharopolyspora erythraea NRRL 2338 and a classically improved erythromycin over-producing strain. Microbial Cell Factories, 2012, 11, 32.	4.0	36
28	Phylogenetic Position of a Copper Age Sheep (Ovis aries) Mitochondrial DNA. PLoS ONE, 2012, 7, e33792.	2.5	20
29	The Complete Mitochondrial Genome of an 11,450-year-old Aurochsen (Bos primigenius) from Central Italy. BMC Evolutionary Biology, 2011, 11, 32.	3.2	39
30	Complete genome sequence of a serotype 11A, ST62 Streptococcus pneumoniaeinvasive isolate. BMC Microbiology, 2011, 11, 25.	3.3	36
31	High-definition mapping of retroviral integration sites identifies active regulatory elements in human multipotent hematopoietic progenitors. Blood, 2010, 116, 5507-5517.	1.4	150
32	The Microcephalin Ancestral Allele in a Neanderthal Individual. PLoS ONE, 2010, 5, e10648.	2.5	31
33	Characterization of Nucleotide Misincorporation Patterns in the Iceman's Mitochondrial DNA. PLoS ONE, 2010, 5, e8629.	2.5	18
34	An Ariadne's thread to the identification and annotation of noncoding RNAs in eukaryotes. Briefings in Bioinformatics, 2009, 10, 475-489.	6.5	25
35	Phenotypes and gene expression profiles of Saccharopolyspora erythraea rifampicin-resistant (rif) mutants affected in erythromycin production. Microbial Cell Factories, 2009, 8, 18.	4.0	45
36	Complete Mitochondrial Genome Sequence of the Tyrolean Iceman. Current Biology, 2008, 18, 1687-1693.	3.9	101

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37	Complete gene expression profiling of Saccharopolyspora erythraea using GeneChip DNA microarrays. Microbial Cell Factories, 2007, 6, 37.	4.0	25