Matteo Benelli

List of Publications by Year
in descending order

92 papers	6,027 citations	147801 31 h-index	79698 73 g-index
96 all docs	96 docs citations	96 times ranked	10612 citing authors

#	Article	IF	Citations
1	Allele-specific genomic data elucidate the role of somatic gain and copy-number neutral loss of heterozygosity in cancer. Cell Systems, 2022, 13, 183-193.e7.	6.2	13
2	Serum thymidine kinase activity in patients with hormone receptor-positive and HER2-negative metastatic breast cancer treated with palbociclib and fulvestrant. European Journal of Cancer, 2022, 164, 39-51.	2.8	8
3	Abstract P5-13-13: <i>PIK3CA</i> mutations co-occurring with copy number gain identify patients with adverse outcome and potentially different treatment sensitivity among hormone receptor positive and HER2 negative metastatic breast cancer. Cancer Research, 2022, 82, P5-13-13-P5-13-13.	0.9	0
4	PIK3CA co-occurring mutations and copy-number gain in hormone receptor positive and HER2 negative breast cancer. Npj Breast Cancer, 2022, 8, 24.	5.2	9
5	CDK4/6 inhibitors: A focus on biomarkers of response and post-treatment therapeutic strategies in hormone receptor-positive HER2-negative breast cancer. Cancer Treatment Reviews, 2021, 93, 102136.	7.7	25
6	Activation of the IFN Signaling Pathway is Associated with Resistance to CDK4/6 Inhibitors and Immune Checkpoint Activation in ER-Positive Breast Cancer. Clinical Cancer Research, 2021, 27, 4870-4882.	7.0	49
7	Circulating tumor cells and palbociclib treatment in patients with ER-positive, HER2-negative advanced breast cancer: results from a translational sub-study of the TREnd trial. Breast Cancer Research, 2021, 23, 38.	5.0	14
8	Circulating Biomarkers of CDK4/6 Inhibitors Response in Hormone Receptor Positive and HER2 Negative Breast Cancer. Cancers, 2021, 13, 2640.	3.7	8
9	On the dependence of quantitative diffusion-weighted imaging on scanner system characteristics and acquisition parameters: A large multicenter and multiparametric phantom study with unsupervised clustering analysis. Physica Medica, 2021, 85, 98-106.	0.7	14
10	Genomic and Transcriptomic Analyses of Breast Cancer Primaries and Matched Metastases in AURORA, the Breast International Group (BIG) Molecular Screening Initiative. Cancer Discovery, 2021, 11, 2796-2811.	9.4	79
11	The incremental value of computed tomography of COVID-19 pneumonia in predicting ICU admission. Scientific Reports, 2021, 11, 15619.	3.3	7
12	Charting differentially methylated regions in cancer with Rocker-meth. Communications Biology, 2021, 4, 1249.	4.4	7
13	Exploring Serum NMR-Based Metabolomic Fingerprint of Colorectal Cancer Patients: Effects of Surgery and Possible Associations with Cancer Relapse. Applied Sciences (Switzerland), 2021, 11, 11120.	2.5	3
14	Biomarker-guided implementation of the old drug temozolomide as a novel treatment option for patients with metastatic colorectal cancer. Cancer Treatment Reviews, 2020, 82, 101935.	7.7	17
15	Metabolomics to Assess Response to Immune Checkpoint Inhibitors in Patients with Non-Small-Cell Lung Cancer. Cancers, 2020, 12, 3574.	3.7	42
16	Tumor Necrosis Factor Î± Influences Phenotypic Plasticity and Promotes Epigenetic Changes in Human Basal Forebrain Cholinergic Neuroblasts. International Journal of Molecular Sciences, 2020, 21, 6128.	4.1	17
17	Cell-Free DNA-Methylation-Based Methods and Applications in Oncology. Biomolecules, 2020, 10, 1677.	4.0	31
18	Role of specialized composition of SWI/SNF complexes in prostate cancer lineage plasticity. Nature Communications, 2020, 11, 5549.	12.8	76

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19	Comprehensive Analysis of Radiomic Datasets by RadAR. Cancer Research, 2020, 80, 3170-3174.	0.9	7
20	Glucose Metabolic Reprogramming of ER Breast Cancer in Acquired Resistance to the CDK4/6 Inhibitor Palbociclib+. Cells, 2020, 9, 668.	4.1	23
21	Plasma Thymidine Kinase Activity as a Biomarker in Patients with Luminal Metastatic Breast Cancer Treated with Palbociclib within the TREnd Trial. Clinical Cancer Research, 2020, 26, 2131-2139.	7.0	40
22	Abstract GS2-01: High levels of interferon-response gene signatures are associated withde novoand acquired resistance to CDK4/6 inhibitors in ER+ breast cancer. , 2020, , .		2
23	Genome-wide plasma DNA methylation features of metastatic prostate cancer. Journal of Clinical Investigation, 2020, 130, 1991-2000.	8.2	68
24	Circulating tumor DNA profile recognizes transformation to castration-resistant neuroendocrine prostate cancer. Journal of Clinical Investigation, 2020, 130, 1653-1668.	8.2	122
25	Abstract P4-04-07: A DNA-methylation signature to predict resistance to the CDK4/6 inhibitor palbociclib. , 2020, , .		0
26	Abstract 2488: Characterization of gene fusions in paired primary and metastatic samples of breast cancer in the AURORA molecular screening program. , 2020, , .		0
27	Abstract P5-06-11: Serum thymidine kinase-1 activity (TKa) as a prognostic marker in premenopausal women with hormone receptor positive (HR+) operable breast cancer (BC). , 2020, , .		0
28	Mechanisms of Resistance to CDK4/6 Inhibitors: Potential Implications and Biomarkers for Clinical Practice. Frontiers in Oncology, 2019, 9, 666.	2.8	113
29	LEADeR role of miR-205 host gene as long noncoding RNA in prostate basal cell differentiation. Nature Communications, 2019, 10, 307.	12.8	44
30	Sequencing of a 'mouse azoospermia' gene panel in azoospermic men: identification of RNF212 and STAG3 mutations as novel genetic causes of meiotic arrest. Human Reproduction, 2019, 34, 978-988.	0.9	58
31	Clinical outcomes after palbociclib with or without endocrine therapy in postmenopausal women with hormone receptor positive and HER2-negative metastatic breast cancer enrolled in the TREnd trial. Breast Cancer Research, 2019, 21, 71.	5.0	19
32	Genomic correlates of clinical outcome in advanced prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11428-11436.	7.1	839
33	Prognostic role of serum thymidine kinase 1 activity in patients with hormone receptor–positive metastatic breast cancer: Analysis of the randomised phase III Evaluation of Faslodex versus Exemestane Clinical Trial (EFECT). European Journal of Cancer, 2019, 114, 55-66.	2.8	30
34	Benefit from anti-EGFRs in RAS and BRAF wild-type metastatic transverse colon cancer: a clinical and molecular proof of concept study. ESMO Open, 2019, 4, e000489.	4.5	14
35	Core Biopsies from Prostate Cancer Patients in Active Surveillance Protocols Harbor PTEN and MYC Alterations. European Urology Oncology, 2019, 2, 277-285.	5.4	7
36	An RB-1 loss of function gene signature as a tool to predict response to neoadjuvant chemotherapy plus anti-HER2 agents: a substudy of the NeoALTTO trial (BIG 1-06). Therapeutic Advances in Medical Oncology, 2019, 11, 175883591989160.	3.2	3

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37	Estimating the magnitude of clinical benefit from (neo)adjuvant chemotherapy in patients with ER-positive/HER2-negative breast cancer. Breast, 2019, 48, S81-S84.	2.2	1
38	Abstract 2471: Pan-cancer catalog of Differentially Methylated Regions by Rocker-meth, a new computational method. , 2019, , .		0
39	Abstract 4416: Plasma thymidine kinase activity in patients with luminal metastatic breast cancer treated with Palbociclib within the phase II TREnd trial. , 2019, , .		0
40	Abstract 3012: Single-cell transcriptomic characterization of luminal breast cancer cell lines with acquired resistance to the CDK4/6 inhibitor palbociclib. , 2019, , .		0
41	Tumor purity quantification by clonal DNA methylation signatures. Bioinformatics, 2018, 34, 1642-1649.	4.1	36
42	A gene expression signature of Retinoblastoma loss-of-function predicts resistance to neoadjuvant chemotherapy in ER-positive/HER2-positive breast cancer patients. Breast Cancer Research and Treatment, 2018, 170, 329-341.	2.5	17
43	Contemporary genetic testing in inherited cardiac disease. Journal of Cardiovascular Medicine, 2018, 19, 1-11.	1.5	48
44	ddSeeker: a tool for processing Bio-Rad ddSEQ single cell RNA-seq data. BMC Genomics, 2018, 19, 960.	2.8	22
45	Cyclin E1 and Rb modulation as common events at time of resistance to palbociclib in hormone receptor-positive breast cancer. Npj Breast Cancer, 2018, 4, 38.	5.2	78
46	Dependence of apparent diffusion coefficient measurement on diffusion gradient direction and spatial position â€" A quality assurance intercomparison study of forty-four scanners for quantitative diffusion-weighted imaging. Physica Medica, 2018, 55, 135-141.	0.7	30
47	Patient derived organoids to model rare prostate cancer phenotypes. Nature Communications, 2018, 9, 2404.	12.8	246
48	Role of serum thymidine kinase-1 (TK1) activity in patients (pts) with hormone receptor positive (HR+) advanced breast cancer (ABC) treated with endocrine therapy (ET) in the EFECT trial.. Journal of Clinical Oncology, 2018, 36, 12031-12031.	1.6	1
49	A RB-1 loss of function gene-signature (RBsig) as a tool to predict response to neoadjuvant chemotherapy (CT) plus anti-HER2 agents (H): A substudy of the NeoALTTO trial (BIG 1-06).. Journal of Clinical Oncology, 2018, 36, 570-570.	1.6	0
50	Abstract IA19: Phenotype plasticityâ€"a novel mechanism of targeted therapy resistance. , 2018, , .		0
51	Abstract B040: Differential impact of RB status on E2F1 reprogramming in human cancer. , 2018, , .		0
52	Abstract IA03: Differential impact of RB pathway status on E2F1 reprogramming and disease progression in human prostate cancer. , 2018, , .		0
53	Abstract A078: Towards understanding noncanonical phosphatidylinositol kinases in the maintenance of prostate metabolism. , 2018, , .		0
54	Abstract A042: Modulation of translation regulation by N6-methyladenosine in prostate cancer. , 2018, , .		0

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55	A novel brain tumour model in zebrafish reveals the role of YAP activation in MAPK/PI3K induced malignant growth. DMM Disease Models and Mechanisms, 2017, 10, 15-28.	2.4	58
56	Validation of a method for noninvasive prenatal testing for fetal aneuploidies risk and considerations for its introduction in the Public Health System. Journal of Maternal-Fetal and Neonatal Medicine, 2017, 30, 710-716.	1.5	6
57	*SOX2* promotes lineage plasticity and antiandrogen resistance in *TP53* - and *RB1* -deficient prostate cancer. Science, 2017, 355, 84-88.	12.6	759
58	*CEBPA* â€"double-mutated acute myeloid leukemia displays a unique phenotypic profile: a reliable screening method and insight into biological features. Haematologica, 2017, 102, 529-540.	3.5	61
59	Mechanisms of Resistance to CDK4/6 Inhibitors in Breast Cancer and Potential Biomarkers of Response. Breast Care, 2017, 12, 304-308.	1.4	53
60	A novel founder MYO15A frameshift duplication is the major cause of genetic hearing loss in Oman. Journal of Human Genetics, 2017, 62, 259-264.	2.3	21
61	Differential impact of RB status on E2F1 reprogramming in human cancer. Journal of Clinical Investigation, 2017, 128, 341-358.	8.2	83
62	Whole exome sequencing (WES) of circulating tumor DNA (ctDNA) in patients with neuroendocrine prostate cancer (NEPC) informs tumor heterogeneity.. Journal of Clinical Oncology, 2017, 35, 5011-5011.	1.6	12
63	Abstract LB-122: Tumor heterogeneity in castration resistant neuroendocrine prostate cancer from whole exome sequencing of circulating tumor DNA. , 2017, , .		0
64	Abstract LB-085: RB loss-induced genome wide E2F1 reprogramming drive advanced prostate cancer. , 2017, , .		0
65	Abstract 4165:SOX2promotes lineage plasticity and antiandrogen resistance inTP53andRB1deficient prostate cancer. , 2017, , .		0
66	N-Myc Induces an EZH2-Mediated Transcriptional Program Driving Neuroendocrine Prostate Cancer. Cancer Cell, 2016, 30, 563-577.	16.8	394
67	Divergent clonal evolution of castration-resistant neuroendocrine prostate cancer. Nature Medicine, 2016, 22, 298-305.	30.7	1,193
68	Thin and thick primary cutaneous melanomas reveal distinct patterns of somatic copy number alterations. Oncotarget, 2016, 7, 30365-30378.	1.8	10
69	Multilineage dysplasia as assessed by immunophenotype has no impact on clinical-biological features and outcome of NPM1-mutated acute myeloid leukemia. Experimental Hematology, 2015, 43, 869-879.e22.	0.4	4
70	Exome sequencing in primary melanoma identifies novel drivers of melanoma progression. Journal of Translational Medicine, 2015, 13, P2.	4.4	0
71	Expanding the mutational spectrum of LZTR1 in schwannomatosis. European Journal of Human Genetics, 2015, 23, 963-968.	2.8	58
72	A Systematic Assessment of Accuracy in Detecting Somatic Mosaic Variants by Deep Amplicon Sequencing: Application to NF2 Gene. PLoS ONE, 2015, 10, e0129099.	2.5	16

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73	Abstract B39: Exome sequencing in primary melanoma identifies novel drivers of melanoma progression. , 2015, , .		0
74	16p11.2 de novo microdeletion encompassing SRCAP gene in a patient with speech impairment, global developmental delay and behavioural problems. European Journal of Medical Genetics, 2014, 57, 649-653.	1.3	10
75	<i>H</i> Â3 Â<i>M</i> Â2 : detection of runs of homozygosity from whole-exome sequencing data. Bioinformatics, 2014, 30, 2852-2859.	4.1	88
76	Novel Î±-Actinin 2 Variant Associated With Familial Hypertrophic Cardiomyopathy and Juvenile Atrial Arrhythmias. Circulation: Cardiovascular Genetics, 2014, 7, 741-750.	5.1	74
77	Hypovitaminosis D and osteopenia/osteoporosis in a haemophilia population: a study in <scp>HCV</scp>/<scp>HIV</scp> or <scp>HCV</scp> infected patients. Haemophilia, 2013, 19, 126-133.	2.1	23
78	A systematic analysis of bone marrow cells by flow cytometry defines a specific phenotypic profile beyond GPI deficiency in paroxysmal nocturnal hemoglobinuria. Cytometry Part B - Clinical Cytometry, 2013, 84B, 71-81.	1.5	7
79	Moment estimation in discrete shifting level model applied to fast arrayâ€CGH segmentation. Statistica Neerlandica, 2013, 67, 227-262.	1.6	0
80	EXCAVATOR: detecting copy number variants from whole-exome sequencing data. Genome Biology, 2013, 14, R120.	9.6	213
81	Discovering chimeric transcripts in paired-end RNA-seq data by using EricScript. Bioinformatics, 2012, 28, 3232-3239.	4.1	154
82	Persistence of odd-even staggering in charged-fragment yields from<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"><mml:msup><mml:mrow /><mml:mn>112</mml:mn></mml:msup></mml:math>Sn<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"><mml:mrow><mml:mo>+</mml:mo></mml:mrow></mml:math><mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"><mml:msup><mml:mrow /><mml:	2.9	29
83	Clinical Significance of Rare Copy Number Variations in Epilepsy. Archives of Neurology, 2012, 69, 322.	4.5	61
84	372Âkb microdeletion in 18q12.3 causing SETBP1 haploinsufficiency associated with mild mental retardation and expressive speech impairment. European Journal of Medical Genetics, 2012, 55, 216-221.	1.3	55
85	WNP: A Novel Algorithm for Gene Products Annotation from Weighted Functional Networks. PLoS ONE, 2012, 7, e38767.	2.5	5
86	Read count approach for DNA copy number variants detection. Bioinformatics, 2012, 28, 470-478.	4.1	67
87	EX-HOM (EXome HOMozygosity): A Proof of Principle. Human Heredity, 2011, 72, 45-53.	0.8	27
88	Sphingosine 1-Phosphate Induces Differentiation of Mesoangioblasts towards Smooth Muscle. A Role for GATA6. PLoS ONE, 2011, 6, e20389.	2.5	23
89	Detecting common copy number variants in high-throughput sequencing data by using JointSLM algorithm. Nucleic Acids Research, 2011, 39, e65-e65.	14.5	63
90	A very fast and accurate method for calling aberrations in array-CGH data. Biostatistics, 2010, 11, 515-518.	1.5	16

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91	A shifting level model algorithm that identifies aberrations in array-CGH data. Biostatistics, 2010, 11, 265-280.	1.5	26
92	Bioinformatics for Next Generation Sequencing Data. Genes, 2010, 1, 294-307.	2.4	65