Luca Beltrame

List of Publications by Year
in descending order

61 papers	3,057 citations	218381 26 h-index	161609 54 g-index
63 all docs	63 docs citations	63 times ranked	6577 citing authors

#	Article	IF	Citations
1	Copy number alterations in stage I epithelial ovarian cancer highlight three genomic patterns associated with prognosis. European Journal of Cancer, 2022, 171, 85-95.	1.3	8
2	The miRâ€"181aâ€"SFRP4 Axis Regulates Wnt Activation to Drive Stemness and Platinum Resistance in Ovarian Cancer. Cancer Research, 2021, 81, 2044-2055.	0.4	21
3	Genome-wide Copy-number Alterations in Circulating Tumor DNA as a Novel Biomarker for Patients with High-grade Serous Ovarian Cancer. Clinical Cancer Research, 2021, 27, 2549-2559.	3.2	34
4	Detection of <i>TP53</i> Clonal Variants in Papanicolaou Test Samples Collected up to 6 Years Prior to High-Grade Serous Epithelial Ovarian Cancer Diagnosis. JAMA Network Open, 2020, 3, e207566.	2.8	10
5	Expression profiles of PRKG1, SDF2L1 and PPP1R12A are predictive and prognostic factors for therapy response and survival in highâ€grade serous ovarian cancer. International Journal of Cancer, 2020, 147, 565-574.	2.3	15
6	Abstract LB-268: Detection ofTP53clonal mutations in PAP test collected up to six years prior to high-grade serous epithelial ovarian cancer diagnosis. , 2020, , .		0
7	Musclin, A Myokine Induced by Aerobic Exercise, Retards Muscle Atrophy During Cancer Cachexia in Mice. Cancers, 2019, 11, 1541.	1.7	45
8	Multisite analysis of highâ€grade serous epithelial ovarian cancers identifies genomic regions of focal and recurrent copy number alteration in 3q26.2 and 8q24.3. International Journal of Cancer, 2019, 145, 2670-2681.	2.3	15
9	Transcriptional Characterization of Stage I Epithelial Ovarian Cancer: A Multicentric Study. Cells, 2019, 8, 1554.	1.8	9
10	Bone marrow fibroblasts overexpress miRâ€27b and miRâ€214 in step with multiple myeloma progression, dependent on tumour cellâ€derived exosomes. Journal of Pathology, 2019, 247, 241-253.	2.1	74
11	A systems biology approach to investigate the mechanism of action of trabectedin in a model of myelomonocytic leukemia. Pharmacogenomics Journal, 2018, 18, 56-63.	0.9	8
12	Exome sequencing in an Italian family with Alzheimerâ€™s disease points to a role for seizure-related gene 6 (SEZ6) rare variant R615H. Alzheimer's Research and Therapy, 2018, 10, 106.	3.0	15
13	PL-013 Musclin: a myokine induced by aerobic exercise useful to contrast muscle wasting during cancer. Exercise Biochemistry Review, 2018, 1, .	0.0	0
14	Breast and renal cancerâ€"Derived endothelial colony forming cells share a common gene signature. European Journal of Cancer, 2017, 77, 155-164.	1.3	19
15	FOXM1 expression is significantly associated with chemotherapy resistance and adverse prognosis in non-serous epithelial ovarian cancer patients. Journal of Experimental and Clinical Cancer Research, 2017, 36, 63.	3.5	53
16	Circulating miRNA landscape identifies miR-1246 as promising diagnostic biomarker in high-grade serous ovarian carcinoma: A validation across two independent cohorts. Cancer Letters, 2017, 388, 320-327.	3.2	73
17	Blockade of the IL-1R1/TLR4 pathway mediates disease-modification therapeutic effects in a model of acquired epilepsy. Neurobiology of Disease, 2017, 99, 12-23.	2.1	149
18	Lurbinectedin reduces tumour-associated macrophages and the inflammatory tumour microenvironment in preclinical models. British Journal of Cancer, 2017, 117, 628-638.	2.9	119

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19	Mechanism of action of trabectedin in desmoplastic small round cell tumor cells. BMC Cancer, 2017, 17, 107.	1.1	11
20	MAL gene overexpression as a marker of high-grade serous ovarian carcinoma stem-like cells that predicts chemoresistance and poor prognosis. BMC Cancer, 2017, 17, 366.	1.1	16
21	The orphan nuclear receptor COUP-TFII coordinates hypoxia-independent proangiogenic responses in hepatic stellate cells. Journal of Hepatology, 2017, 66, 754-764.	1.8	19
22	lncRNAs as Novel Indicators of Patients' Prognosis in Stage I Epithelial Ovarian Cancer: A Retrospective and Multicentric Study. Clinical Cancer Research, 2017, 23, 2356-2366.	3.2	57
23	The bromodomain inhibitor OTX015 (MK-8628) exerts anti-tumor activity in triple-negative breast cancer models as single agent and in combination with everolimus. Oncotarget, 2017, 8, 7598-7613.	0.8	79
24	Survival of metastatic melanoma patients after dendritic cell vaccination correlates with expression of leukocyte phosphatidylethanolamine-binding protein 1/Raf kinase inhibitory protein. Oncotarget, 2017, 8, 67439-67456.	0.8	15
25	A prognostic regulatory pathway in stage I epithelial ovarian cancer: new hints for the poor prognosis assessment. Annals of Oncology, 2016, 27, 1511-1519.	0.6	20
26	Identification of high-grade serous ovarian cancer miRNA species associated with survival and drug response in patients receiving neoadjuvant chemotherapy: a retrospective longitudinal analysis using matched tumor biopsies. Annals of Oncology, 2016, 27, 625-634.	0.6	50
27	Regional and temporal heterogeneity of epithelial ovarian cancer tumor biopsies: implications for therapeutic strategies. Oncotarget, 2016, 12, 2404-2417.	0.8	17
28	Electroporated Antigen-Encoding mRNA Is Not a Danger Signal to Human Mature Monocyte-Derived Dendritic Cells. Journal of Immunology Research, 2015, 2015, 1-9.	0.9	9
29	Profiling cancer gene mutations in longitudinal epithelial ovarian cancer biopsies by targeted next-generation sequencing: a retrospective study. Annals of Oncology, 2015, 26, 1363-1371.	0.6	37
30	Abstract 3526: OTX015 effects in triple-negative breast cancer (TNBC) models are independent of hypoxia conditions and synergistic with other anticancer agents. , 2015, , .		2
31	Analysis of Differential miRNA Expression in Primary Tumor and Stroma of Colorectal Cancer Patients. BioMed Research International, 2014, 2014, 1-8.	0.9	49
32	<scp>IL</scp>â€4â€induced gene 1 maintains high <scp>T</scp>ob1 expression that contributes to <scp>TCR</scp> unresponsiveness in human <scp>T</scp> helper 17 cells. European Journal of Immunology, 2014, 44, 654-661.	1.6	36
33	48 Trabectedin and lurbinectedin are effective against leukemic cells derived from patients affected by chronic and juvenile myelomonocytic leukemia. European Journal of Cancer, 2014, 50, 21.	1.3	0
34	580 Evaluation of the pan-BET-bromodomain inhibitor OTX015 as a single agent and in combination with everolimus (RAD001) in triple-negative breast cancer models. European Journal of Cancer, 2014, 50, 187.	1.3	2
35	Wiring miRNAs to pathways: a topological approach to integrate miRNA and mRNA expression profiles. Nucleic Acids Research, 2014, 42, e96-e96.	6.5	41
36	Mode of action of trabectedin in myxoid liposarcomas. Oncogene, 2014, 33, 5201-5210.	2.6	111

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37	Pharmacological blockade of IL-1β/IL-1 receptor type 1 axis during epileptogenesis provides neuroprotection in two rat models of temporal lobe epilepsy. Neurobiology of Disease, 2013, 59, 183-193.	2.1	154
38	Denileukin diftitox (ONTAK) induces a tolerogenic phenotype in dendritic cells and stimulates survival of resting Treg. Blood, 2013, 122, 2185-2194.	0.6	54
39	Resistance to platinum-based chemotherapy is associated with epithelial to mesenchymal transition in epithelial ovarian cancer. European Journal of Cancer, 2013, 49, 520-530.	1.3	141
40	Systems biology of host–mycobiota interactions: Dissecting Dectin-1 and Dectin-2 signalling in immune cells with DC-ATLAS. Immunobiology, 2013, 218, 1428-1437.	0.8	13
41	Role of Macrophage Targeting in the Antitumor Activity of Trabectedin. Cancer Cell, 2013, 23, 249-262.	7.7	721
42	Pathway‐Based Analysis of Microarray and RNAseq Data Using Pathway Processor 2.0. Current Protocols in Bioinformatics, 2013, 41, Unit 7.6.	25.8	0
43	miRNA Landscape in Stage I Epithelial Ovarian Cancer Defines the Histotype Specificities. Clinical Cancer Research, 2013, 19, 4114-4123.	3.2	53
44	Pathway Processor 2.0: a web resource for pathway-based analysis of high-throughput data. Bioinformatics, 2013, 29, 1825-1826.	1.8	6
45	Abstract B18: miRNA landscape analysis of stage I EOC, identifies miR-199a-5p associated to poor prognosis in grade 3 subgroup. , 2013, , .		0
46	666 The Biological Connection Markup Language – a Data Format to Visualize, Annotate and Analyze Biological Pathways. European Journal of Cancer, 2012, 48, S158.	1.3	1
47	Rarity of Human T Helper 17 Cells Is due to Retinoic Acid Orphan Receptor-Dependent Mechanisms that Limit Their Expansion. Immunity, 2012, 36, 201-214.	6.6	103
48	A Systems Biology Approach to Characterize the Regulatory Networks Leading to Trabectedin Resistance in an In Vitro Model of Myxoid Liposarcoma. PLoS ONE, 2012, 7, e35423.	1.1	19
49	Constraints for monocyte‐derived dendritic cell functions under inflammatory conditions. European Journal of Immunology, 2012, 42, 458-469.	1.6	14
50	The Modular Nature of Dendritic Cell Responses to Commensal and Pathogenic Fungi. PLoS ONE, 2012, 7, e42430.	1.1	12
51	Association between miR-200c and the survival of patients with stage I epithelial ovarian cancer: a retrospective study of two independent tumour tissue collections. Lancet Oncology, The, 2011, 12, 273-285.	5.1	173
52	The Biological Connection Markup Language: a SBGN-compliant format for visualization, filtering and analysis of biological pathways. Bioinformatics, 2011, 27, 2127-2133.	1.8	21
53	Inhibition of Immune Synapse by Altered Dendritic Cell Actin Distribution: A New Pathway of Mesenchymal Stem Cell Immune Regulation. Journal of Immunology, 2010, 185, 5102-5110.	0.4	78
54	Differential IL-17 Production and Mannan Recognition Contribute to Fungal Pathogenicity and Commensalism. Journal of Immunology, 2010, 184, 4258-4268.	0.4	59

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55	DC-ATLAS: a systems biology resource to dissect receptor specific signal transduction in dendritic cells. Immunome Research, 2010, 6, 10.	0.1	23
56	Dominant Processes during Human Dendritic Cell Maturation Revealed by Integration of Proteome and Transcriptome at the Pathway Level. Journal of Proteome Research, 2010, 9, 1727-1737.	1.8	45
57	Using Pathway Signatures as Means of Identifying Similarities among Microarray Experiments. PLoS ONE, 2009, 4, e4128.	1.1	25
58	A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets â€. Nucleic Acids Research, 2009, 37, 5057-5070.	6.5	27
59	Genome-wide screening of copy number alterations and LOH events in renal cell carcinomas and integration with gene expression profile. Molecular Cancer, 2008, 7, 6.	7.9	67
60	Assessment of Common Regions and Specific Footprints of DNA Copy Number Aberrations Across Multiple Affymetrix SNP Mapping Arrays. Lecture Notes in Computer Science, 2007, , 674-681.	1.0	0
61	Algorithm for automatic genotype calling of single nucleotide polymorphisms using the full course of TaqMan real-time data. Nucleic Acids Research, 2006, 34, e56-e56.	6.5	10