Carlos S Moreno

List of Publications by Year
in descending order

118 papers	**7,105** citations	47006 **47** h-index	58581 **82** g-index
123 all docs	**123** docs citations	**123** times ranked	**12218** citing authors

#	Article	IF	Citations
1	MTA3, a Mi-2/NuRD Complex Subunit, Regulates an Invasive Growth Pathway in Breast Cancer. Cell, 2003, 113, 207-219.	28.9	483
2	MR Imaging Predictors of Molecular Profile and Survival: Multi-institutional Study of the TCGA Glioblastoma Data Set. Radiology, 2013, 267, 560-569.	7.3	362
3	Expression Profiling of Renal Epithelial Neoplasms. American Journal of Pathology, 2001, 158, 1639-1651.	3.8	300
4	Relative Burden of Large CNVs on a Range of Neurodevelopmental Phenotypes. PLoS Genetics, 2011, 7, e1002334.	3.5	293
5	Sex-Determining Region Y Box 4 Is a Transforming Oncogene in Human Prostate Cancer Cells. Cancer Research, 2006, 66, 4011-4019.	0.9	264
6	The Tumor Microenvironment Strongly Impacts Master Transcriptional Regulators and Gene Expression Class of Glioblastoma. American Journal of Pathology, 2012, 180, 2108-2119.	3.8	220
7	Wnt signaling in triple negative breast cancer is associated with metastasis. BMC Cancer, 2013, 13, 537.	2.6	210
8	Novel Molecular Signaling and Classification of Human Clinically Nonfunctional Pituitary Adenomas Identified by Gene Expression Profiling and Proteomic Analyses. Cancer Research, 2005, 65, 10214-10222.	0.9	189
9	Tumor-Infiltrating Lymphocytes in Glioblastoma Are Associated with Specific Genomic Alterations and Related to Transcriptional Class. Clinical Cancer Research, 2013, 19, 4951-4960.	7.0	182
10	Consolidation of the cancer genome into domains of repressive chromatin by long-range epigenetic silencing (LRES) reduces transcriptional plasticity. Nature Cell Biology, 2010, 12, 235-246.	10.3	178
11	Genome-Wide Promoter Analysis of the <i>SOX4</i> Transcriptional Network in Prostate Cancer Cells. Cancer Research, 2009, 69, 709-717.	0.9	176
12	CREB Regulates MHC Class II Expression in a CIITA-Dependent Manner. Immunity, 1999, 10, 143-151.	14.3	170
13	WD40 Repeat Proteins Striatin and S/G2 Nuclear Autoantigen Are Members of a Novel Family of Calmodulin-binding Proteins That Associate with Protein Phosphatase 2A. Journal of Biological Chemistry, 2000, 275, 5257-5263.	3.4	169
14	The OncoPPi network of cancer-focused protein–protein interactions to inform biological insights and therapeutic strategies. Nature Communications, 2017, 8, 14356.	12.8	151
15	Methylation of the Protein Phosphatase 2A Catalytic Subunit Is Essential for Association of Bα Regulatory Subunit But Not SG2NA, Striatin, or Polyomavirus Middle Tumor Antigen. Molecular Biology of the Cell, 2001, 12, 185-199.	2.1	148
16	Molecular analysis of G1B and G3A IFNγ mutants reveals that defects in CIITA or RFX result in defective class II MHC and Ii gene induction. Immunity, 1994, 1, 687-697.	14.3	136
17	An expanded universe of cancer targets. Cell, 2021, 184, 1142-1155.	28.9	135
18	Wnt signaling blockage inhibits cell proliferation and migration, and induces apoptosis in triple-negative breast cancer cells. Journal of Translational Medicine, 2013, 11, 280.	4.4	131

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19	Molecular Classification of Renal Tumors by Gene Expression Profiling. Journal of Molecular Diagnostics, 2005, 7, 206-218.	2.8	130
20	The Proneural Molecular Signature Is Enriched in Oligodendrogliomas and Predicts Improved Survival among Diffuse Gliomas. PLoS ONE, 2010, 5, e12548.	2.5	125
21	Carboxymethylation of the PP2A Catalytic Subunit in Saccharomyces cerevisiae Is Required for Efficient Interaction with the B-type Subunits Cdc55p and Rts1p. Journal of Biological Chemistry, 2001, 276, 1570-1577.	3.4	116
22	SOX4: The unappreciated oncogene. Seminars in Cancer Biology, 2020, 67, 57-64.	9.6	114
23	Global Transcriptome Analysis of Formalin-Fixed Prostate Cancer Specimens Identifies Biomarkers of Disease Recurrence. Cancer Research, 2014, 74, 3228-3237.	0.9	111
24	Identification of a Novel Small Molecule HIF-1α Translation Inhibitor. Clinical Cancer Research, 2009, 15, 6128-6136.	7.0	102
25	Protein-Coding and MicroRNA Biomarkers of Recurrence of Prostate Cancer Following Radical Prostatectomy. American Journal of Pathology, 2011, 179, 46-54.	3.8	92
26	Machine-Based Morphologic Analysis of Glioblastoma Using Whole-Slide Pathology Images Uncovers Clinically Relevant Molecular Correlates. PLoS ONE, 2013, 8, e81049.	2.5	91
27	Human <i>Brat</i> Ortholog <i>TRIM3</i> Is a Tumor Suppressor That Regulates Asymmetric Cell Division in Glioblastoma. Cancer Research, 2014, 74, 4536-4548.	0.9	90
28	Molecular pathogenesis of human prolactinomas identified by gene expression profiling, RT-qPCR, and proteomic analyses. Pituitary, 2008, 11, 231-245.	2.9	89
29	Loss of HOXC6 expression induces apoptosis in prostate cancer cells. Oncogene, 2005, 24, 188-198.	5.9	87
30	A Mammalian Homolog of Yeast MOB1 Is Both a Member and a Putative Substrate of Striatin Family-Protein Phosphatase 2A Complexes. Journal of Biological Chemistry, 2001, 276, 24253-24260.	3.4	83
31	Protein phosphatase 2a (PP2A) binds within the oligomerization domain of striatin and regulates the phosphorylation and activation of the mammalian Ste20-Like kinase Mst3. BMC Biochemistry, 2011, 12, 54.	4.4	82
32	Integrated morphologic analysis for the identification and characterization of disease subtypes. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 317-323.	4.4	82
33	Sox7 Is an Independent Checkpoint for β-Catenin Function in Prostate and Colon Epithelial Cells. Molecular Cancer Research, 2008, 6, 1421-1430.	3.4	81
34	Optimization of RNA extraction from FFPE tissues for expression profiling in the DASL assay. BioTechniques, 2008, 44, 417-423.	1.8	81
35	<i>Cosmc</i> is an X-linked inflammatory bowel disease risk gene that spatially regulates gut microbiota and contributes to sex-specific risk. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14787-14792.	7.1	77
36	SOX4 Is Essential for Prostate Tumorigenesis Initiated by PTEN Ablation. Cancer Research, 2016, 76, 1112-1121.	0.9	67

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37	The Sex-Determining Region Y-Box 4 and Homeobox C6 Transcriptional Networks in Prostate Cancer Progression. American Journal of Pathology, 2010, 176, 518-527.	3.8	64
38	Aurora kinase inhibitors synergize with paclitaxel to induce apoptosis in ovarian cancer cells. Journal of Translational Medicine, 2008, 6, 79.	4.4	62
39	Genome-Wide Analysis of the Homeobox C6 Transcriptional Network in Prostate Cancer. Cancer Research, 2008, 68, 1988-1996.	0.9	62
40	Prostate cancer genes associated with TMPRSS2â€"ERG gene fusion and prognostic of biochemical recurrence in multiple cohorts. British Journal of Cancer, 2010, 102, 570-576.	6.4	61
41	Effects of genistein supplementation on genome-wide DNA methylation and gene expression in patients with localized prostate cancer. International Journal of Oncology, 2017, 51, 223-234.	3.3	61
42	Integrative, Multimodal Analysis of Glioblastoma Using TCGA Molecular Data, Pathology Images, and Clinical Outcomes. IEEE Transactions on Biomedical Engineering, 2011, 58, 3469-3474.	4.2	57
43	CONFAC: automated application of comparative genomic promoter analysis to DNA microarray datasets. Nucleic Acids Research, 2004, 32, W475-W484.	14.5	56
44	Signaling and Transcriptional Changes Critical for Transformation of Human Cells by Simian Virus 40 Small Tumor Antigen or Protein Phosphatase 2A B56Î³ Knockdown. Cancer Research, 2004, 64, 6978-6988.	0.9	53
45	An Integrative Approach for In Silico Glioma Research. IEEE Transactions on Biomedical Engineering, 2010, 57, 2617-2621.	4.2	53
46	Genistein cooperates with the histone deacetylase inhibitor vorinostat to induce cell death in prostate cancer cells. BMC Cancer, 2012, 12, 145.	2.6	53
47	Evidence that p53-Mediated Cell-Cycle-Arrest Inhibits Chemotherapeutic Treatment of Ovarian Carcinomas. PLoS ONE, 2007, 2, e441.	2.5	51
48	E2F Activators Signal and Maintain Centrosome Amplification in Breast Cancer Cells. Molecular and Cellular Biology, 2014, 34, 2581-2599.	2.3	49
49	SOX4 interacts with plakoglobin in a Wnt3a-dependent manner in prostate cancer cells. BMC Cell Biology, 2011, 12, 50.	3.0	47
50	Evaluating intra- and inter-individual variation in the human placental transcriptome. Genome Biology, 2015, 16, 54.	8.8	45
51	The OncoPPi Portal: an integrative resource to explore and prioritize proteinâ€"protein interactions for cancer target discovery. Bioinformatics, 2018, 34, 1183-1191.	4.1	41
52	Gene expression profiling of clear cell papillary renal cell carcinoma: comparison with clear cell renal cell carcinoma and papillary renal cell carcinoma. Modern Pathology, 2014, 27, 222-230.	5.5	38
53	Phosphoinositide 3-Kinase Signaling Can Modulate MHC Class I and II Expression. Molecular Cancer Research, 2019, 17, 2395-2409.	3.4	36
54	Combined HER3-EGFR score in triple-negative breast cancer provides prognostic and predictive significance superior to individual biomarkers. Scientific Reports, 2020, 10, 3009.	3.3	34

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55	High throughput, label-free isolation of circulating tumor cell clusters in meshed microwells. Nature Communications, 2022, 13, .	12.8	33
56	Detection of prostate cancerâ€specific transcripts in extracellular vesicles isolated from postâ€DRE urine. Prostate, 2017, 77, 990-999.	2.3	29
57	EZH2 has a non-catalytic and PRC2-independent role in stabilizing DDB2 to promote nucleotide excision repair. Oncogene, 2020, 39, 4798-4813.	5.9	29
58	Lycopene in the prevention of renal cell cancer in the TSC2 mutant Eker rat model. Archives of Biochemistry and Biophysics, 2015, 572, 36-39.	3.0	28
59	AKT1, LKB1, and YAP1 Revealed as MYC Interactors with NanoLuc-Based Protein-Fragment Complementation Assay. Molecular Pharmacology, 2017, 91, 339-347.	2.3	27
60	The BCL6-associated transcriptional co-repressor, MTA3, is selectively expressed by germinal centre B cells and lymphomas of putative germinal centre derivation. Journal of Pathology, 2007, 213, 106-115.	4.5	25
61	Heterogeneity of primary glioblastoma cells in the expression of caspase-8 and the response to TRAIL-induced apoptosis. Apoptosis: an International Journal on Programmed Cell Death, 2011, 16, 1150-1164.	4.9	25
62	The biology of castration-resistant prostate cancer. Current Problems in Cancer, 2015, 39, 17-28.	2.0	22
63	Identification of the Transcription Factor Relationships Associated with Androgen Deprivation Therapy Response and Metastatic Progression in Prostate Cancer. Cancers, 2018, 10, 379.	3.7	21
64	Integrated Analysis of Whole-Genome Paired-End and Mate-Pair Sequencing Data for Identifying Genomic Structural Variations in Multiple Myeloma. Cancer Informatics, 2014, 13s2, CIN.S13783.	1.9	20
65	SOX4 regulates invasion of bladder cancer cells via repression of WNT5a. International Journal of Oncology, 2019, 55, 359-370.	3.3	20
66	The E2F activators control multiple mitotic regulators and maintain genomic integrity through Sgo1 and BubR1. Oncotarget, 2017, 8, 77649-77672.	1.8	19
67	Morphological signatures and genomic correlates in glioblastoma. , 2011, , 1624-1627.		18
68	Hierarchical Feature Selection Incorporating Known and Novel Biological Information: Identifying Genomic Features Related to Prostate Cancer Recurrence. Journal of the American Statistical Association, 2016, 111, 1427-1439.	3.1	18
69	Cross-platform expression profiling demonstrates that SV40 small tumor antigen activates Notch, Hedgehog, and Wnt signaling in human cells. BMC Cancer, 2006, 6, 54.	2.6	17
70	Claudin-based barrier differentiation in the colonic epithelial crypt niche involves Hopx/Klf4 and Tcf7l2/Hnf4-Î± cascades. Tissue Barriers, 2016, 4, e1214038.	3.2	17
71	The JNK inhibitor AS602801 Synergizes with Enzalutamide to Kill Prostate Cancer Cells In Vitro and In Vivo and Inhibit Androgen Receptor Expression. Translational Oncology, 2020, 13, 100751.	3.7	17
72	Systematic discovery of mutation-directed neo-protein-protein interactions in cancer. Cell, 2022, 185, 1974-1985.e12.	28.9	17

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73	RNA biomarkers to facilitate the identification of aggressive prostate cancer. Molecular Aspects of Medicine, 2015, 45, 37-46.	6.4	16
74	Molecular characterisation of formalin-fixed paraffin-embedded (FFPE) breast tumour specimens using a custom 512-gene breast cancer bead array-based platform. British Journal of Cancer, 2011, 105, 1574-1581.	6.4	15
75	Identification of Candidate Genes for Histiocytoid Cardiomyopathy (HC) Using Whole Genome Expression Analysis: Analyzing Material from the HC Registry. Pediatric and Developmental Pathology, 2011, 14, 370-377.	1.0	14
76	Assessing needs and assets for building a regional network infrastructure to reduce cancer related health disparities. Evaluation and Program Planning, 2014, 44, 14-25.	1.6	13
77	Risk prediction for prostate cancer recurrence through regularized estimation with simultaneous adjustment for nonlinear clinical effects. Annals of Applied Statistics, 2011, 5, 2003-2023.	1.1	12
78	Gene integrated set profile analysis: a context-based approach for inferring biological endpoints. Nucleic Acids Research, 2016, 44, e69-e69.	14.5	11
79	Computational identification of conserved transcription factor binding sites upstream of genes induced in rat brain by transient focal ischemic stroke. Brain Research, 2013, 1495, 76-85.	2.2	10
80	Pan-cancer analysis of pathway-based gene expression pattern at the individual level reveals biomarkers of clinical prognosis. Cell Reports Methods, 2021, 1, 100050.	2.9	10
81	Enriching gene expression profiles will help personalize prostate cancer management for African-Americans: A perspective. Urologic Oncology: Seminars and Original Investigations, 2017, 35, 315-321.	1.6	8
82	Androgen attenuates the inactivating phospho–Ser-127 modification of yes-associated protein 1 (YAP1) and promotes YAP1 nuclear abundance and activity. Journal of Biological Chemistry, 2020, 295, 8550-8559.	3.4	8
83	Variation of microRNA expression in the human placenta driven by population identity and sex of the newborn. BMC Genomics, 2021, 22, 286.	2.8	8
84	Procedure for developing linear and Bayesian classification models based on immunosensor measurements. Sensors and Actuators B: Chemical, 2014, 190, 165-170.	7.8	6
85	MELK kinase holds promise as a new radiosensitizing target and biomarker in triple-negative breast cancer. Journal of Thoracic Disease, 2016, 8, E1367-E1368.	1.4	6
86	Evaluation of a 24–gene signature for prognosis of metastatic events and prostate cancer–specific mortality. BJU International, 2017, 119, 961-967.	2.5	6
87	Genomic copy number variation correlates with survival outcomes in WHO grade IV glioma. Scientific Reports, 2020, 10, 7355.	3.3	6
88	Characterization of exosome release and extracellular vesicle-associated miRNAs for human bronchial epithelial cells irradiated with high charge and energy ions. Life Sciences in Space Research, 2021, 28, 11-17.	2.3	6
89	High-performance computational analysis of glioblastoma pathology images with database support identifies molecular and survival correlates. , 2013, , 229-236.		4
90	MEDICI: Mining Essentiality Data to Identify Critical Interactions for Cancer Drug Target Discovery and Development. PLoS ONE, 2017, 12, e0170339.	2.5	4

#	ARTICLE	IF	CITATIONS
91	Expression microarray analysis of brain tumors what have we learned so far. Frontiers in Bioscience - Landmark, 2002, 7, c74-82.	3.0	2
92	Use of Everolimus and Trastuzumab in Addition to Endocrine Therapy in Hormone-Refractory Metastatic Breast Cancer. Clinical Breast Cancer, 2019, 19, 188-196.	2.4	2
93	The need for new test verification and regulatory support for innovative diagnostics. Nature Biotechnology, 2021, 39, 1060-1062.	17.5	2
94	Genomic Promoter Analysis Predicts Functional Transcription Factor Binding. Advances in Bioinformatics, 2008, 2008, 1-9.	5.7	1
95	PROTEIN-CODING AND MICRORNA BIOMARKER GENE PANELS PREDICTIVE OF CLINICAL RECURRENCE IN PROSTATE CANCER. Journal of Urology, 2009, 181, 776-776.	0.4	1
96	Transcriptomic landscape of male and female reproductive cancers: Similar pathways and molecular signatures predicting response to endocrine therapy. Molecular and Cellular Endocrinology, 2021, 535, 111393.	3.2	1
97	Abstract 113: The TCGA proneural subtype predicts improved clinical outcome for low-grade oligodendrogliomas. , 2010, , .		1
98	Overexpression of SOX4 induces up-regulation of miR-126 and miR-195 in LNCaP prostate cancer cell line. Cytotechnology, 2020, 72, 527-537.	1.6	1
99	Institutional Profile: The Emory Biomarker Service Center. Biomarkers in Medicine, 2009, 3, 567-571.	1.4	0
100	Reduced Rap1 Signaling Contributes to Prostate Cancer Progression. FASEB Journal, 2007, 21, A78.	0.5	0
101	Genome‐wide Analysis of the HOXC6 Transcriptional Network in Prostate Cancer. FASEB Journal, 2008, 22, 470.4.	0.5	0
102	Protein‐coding and MicroRNA Biomarker Gene Panels Predictive of Clinical Recurrence in Prostate Cancer. FASEB Journal, 2009, 23, 361.2.	0.5	0
103	Abstract 3912: Comprehensive Characterization of SOX4 Protein Complexes in Prostate Cancer Cells. , 2010, , .		0
104	ETV1 Is a Survival Gene That Is Expressed in a Subset of Multiple Myeloma. Blood, 2011, 118, 2884-2884.	1.4	0
105	Abstract LB-101: Quantitative imaging of protein expression using multiplex quantum dot immunohistochemistry. , 2012, , .		0
106	Integrative, Multi-Platform, Whole-Genome Analyses Identify Clinically Relevant Common- and Cell-Specific Signatures in Multiple Myeloma. Blood, 2012, 120, 3974-3974.	1.4	0
107	Abstract B40: Methylation signatures specific to triple negative breast cancer subtypes. , 2013, , .		0
108	Abstract C68: Global transcriptome sequencing of ethnically diverse formalin-fixed patient samples identifies biomarkers of recurrence in prostate cancer. , 2014, , .		0

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109	Abstract PR15: Predicting the essentialities of protein-protein interactions in cancer. , 2015, , .		0
110	Abstract A46: Effects of genistein supplementation on genome-wide DNA methylation and gene expression in patients with localized prostate cancer. , 2016, , .		0
111	Abstract 2023: SOX4 is essential for PTEN-mediated prostate tumorigenesis in vivo. , 2016, , .		0
112	Abstract 2269: Transcription factor relationships associated with androgen-deprivation therapy response and metastatic progression in prostate cancer. , 2018, , .		0
113	Abstract 4373: AR signaling in concert with PP2A/B regulates YAP1 expression in prostate cancer cells. , 2018, , .		0
114	Abstract 284: Combination therapies to prevent resistance to androgen deprivation therapies in prostate cancer. , 2019, , .		0
115	Abstract 2436: Systematic computational analysis of histologic-genomic associations in triple-negative infiltrating ductal carcinomas of the breast. , 2019, , .		0
116	Abstract C028: Hypoxia-associated genes on disparities in the aggressiveness of prostate cancer. , 2020, , .		0
117	Mutation of murine Sox4 untranslated regions results in partially penetrant perinatal lethality. In Vivo, 2014, 28, 709-18.	1.3	0
118	The Movember Global Action Plan 1 (GAP1): Unique Prostate Cancer Tissue Microarray Resource. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 715-727.	2.5	0