## Giovanni Nassa

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	RNA sequencing identifies specific PIWI-interacting small non-coding RNA expression patterns in breast cancer. Oncotarget, 2014, 5, 9901-9910.	1.8	145
2	Global analysis of estrogen receptor beta binding to breast cancer cell genome reveals an extensive interplay with estrogen receptor alpha for target gene regulation. BMC Genomics, 2011, 12, 36.	2.8	140
3	TNF-alpha and metalloproteases as key players in melanoma cells aggressiveness. Journal of Experimental and Clinical Cancer Research, 2018, 37, 326.	8.6	73
4	Inhibition of histone methyltransferase DOT1L silences ERα gene and blocks proliferation of antiestrogen-resistant breast cancer cells. Science Advances, 2019, 5, eaav5590.	10.3	70
5	Splicing of platelet resident pre-mRNAs upon activation by physiological stimuli results in functionally relevant proteome modifications. Scientific Reports, 2018, 8, 498.	3.3	65
6	The nuclear receptor ERÎ <sup>2</sup> engages AGO2 in regulation of gene transcription, RNA splicing and RISC loading. Genome Biology, 2017, 18, 189.	8.8	63
7	Specific patterns of PIWI-interacting small noncoding RNA expression in dysplastic liver nodules and hepatocellular carcinoma. Oncotarget, 2016, 7, 54650-54661.	1.8	63
8	iMir: An integrated pipeline for high-throughput analysis of small non-coding RNA data obtained by smallRNA-Seq. BMC Bioinformatics, 2013, 14, 362.	2.6	62
9	Identification of a Hormone-regulated Dynamic Nuclear Actin Network Associated with Estrogen Receptor α in Human Breast Cancer Cell Nuclei. Molecular and Cellular Proteomics, 2010, 9, 1352-1367.	3.8	59
10	Atrial myxomas arise from multipotent cardiac stem cells. European Heart Journal, 2020, 41, 4332-4345.	2.2	51
11	Small non-coding RNA deregulation in endometrial carcinogenesis. Oncotarget, 2015, 6, 4677-4691.	1.8	49
12	Timed regulation of P-element-induced wimpy testis-interacting RNA expression during rat liver regeneration. Hepatology, 2014, 60, 798-806.	7.3	48
13	Lack of pathogenic mutations in six patients with MMPSI. Epilepsy Research, 2014, 108, 340-344.	1.6	40
14	Activating stimuli induce platelet microRNA modulation and proteome reorganisation. Thrombosis and Haemostasis, 2015, 114, 96-108.	3.4	40
15	Comparative analysis of nuclear estrogen receptor alpha and beta interactomes in breast cancer cells. Molecular BioSystems, 2011, 7, 667-676.	2.9	39
16	A large set of estrogen receptor βâ€interacting proteins identified by tandem affinity purification in hormoneâ€responsive human breast cancer cell nuclei. Proteomics, 2011, 11, 159-165.	2.2	36
17	Identification of proteins associated with ligandâ€activated estrogen receptor α in human breast cancer cell nuclei by tandem affinity purification and nano LCâ€MS/MS. Proteomics, 2011, 11, 172-179.	2.2	35
18	Post-transcriptional Regulation of Human Breast Cancer Cell Proteome by Unliganded Estrogen Receptor β via microRNAs. Molecular and Cellular Proteomics, 2014, 13, 1076-1090.	3.8	33

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19	Insights into the Role of Estrogen Receptor Î <sup>2</sup> in Triple-Negative Breast Cancer. Cancers, 2020, 12, 1477.	3.7	33
20	Molecular Mechanisms of Selective Estrogen Receptor Modulator Activity in Human Breast Cancer Cells: Identification of Novel Nuclear Cofactors of Antiestrogen–ERα Complexes by Interaction Proteomics. Journal of Proteome Research, 2013, 12, 421-431.	3.7	32
21	Large-scale profiling of signalling pathways reveals an asthma specific signature in bronchial smooth muscle cells. Oncotarget, 2016, 7, 25150-25161.	1.8	32
22	Carcinogenic risk and Bisphenol A exposure: A focus on molecular aspects in endoderm derived glands. Molecular and Cellular Endocrinology, 2017, 457, 20-34.	3.2	32
23	Small RNA profiling reveals deregulated phosphatase and tensin homolog (PTEN)/phosphoinositide 3-kinase (PI3K)/Akt pathway in bronchial smooth muscle cells from asthmatic patients. Journal of Allergy and Clinical Immunology, 2016, 137, 58-67.	2.9	30
24	Estrogen receptor beta impacts hormone-induced alternative mRNA splicing in breast cancer cells. BMC Genomics, 2015, 16, 367.	2.8	28
25	The "busy life―of unliganded estrogen receptors. Proteomics, 2016, 16, 288-300.	2.2	26
26	Small Non-Coding RNA Profiling Identifies miR-181a-5p as a Mediator of Estrogen Receptor Beta-Induced Inhibition of Cholesterol Biosynthesis in Triple-Negative Breast Cancer. Cells, 2020, 9, 874.	4.1	25
27	Expression of functional tissue factor in activated T-lymphocytes in vitro and in vivo : A possible contribution of immunity to thrombosis?. International Journal of Cardiology, 2016, 218, 188-195.	1.7	24
28	The Histone Methyltransferase DOT1L Is a Functional Component of Estrogen Receptor Alpha Signaling in Ovarian Cancer Cells. Cancers, 2019, 11, 1720.	3.7	24
29	PDGFR-alpha inhibits melanoma growth via CXCL10/IP-10: a multi-omics approach. Oncotarget, 2016, 7, 77257-77275.	1.8	22
30	Quantitative mapping of RNA-mediated nuclear estrogen receptor Î <sup>2</sup> interactome in human breast cancer cells. Scientific Data, 2018, 5, 180031.	5.3	22
31	WIND (Workflow for pIRNAs aNd beyonD): a strategy for in-depth analysis of small RNA-seq data. F1000Research, 2021, 10, 1.	1.6	22
32	Histone Methyltransferase DOT1L as a Promising Epigenetic Target for Treatment of Solid Tumors. Frontiers in Genetics, 2022, 13, 864612.	2.3	22
33	iSmaRT: a toolkit for a comprehensive analysis of small RNA-Seq data. Bioinformatics, 2017, 33, 938-940.	4.1	21
34	Metabolic Regulation of Epigenetic Modifications and Cell Differentiation in Cancer. Cancers, 2020, 12, 3788.	3.7	21
35	An Overview of Candidate Therapeutic Target Genes in Ovarian Cancer. Cancers, 2020, 12, 1470.	3.7	20
36	The RNA-mediated estrogen receptor α interactome of hormone-dependent human breast cancer cell nuclei. Scientific Data, 2019, 6, 173.	5.3	18

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37	Interaction Proteomics Identifies ERbeta Association with Chromatin Repressive Complexes to Inhibit Cholesterol Biosynthesis and Exert An Oncosuppressive Role in Triple-negative Breast Cancer. Molecular and Cellular Proteomics, 2020, 19, 245-260.	3.8	18
38	ldentification of cytoplasmic proteins interacting with unliganded estrogen receptor α and β in human breast cancer cells. Proteomics, 2015, 15, 1801-1807.	2.2	17
39	KCTD15 is overexpressed in human childhood B-cell acute lymphoid leukemia. Scientific Reports, 2019, 9, 20108.	3.3	17
40	Molecular and Functional Characterization of the Somatic PIWIL1/piRNA Pathway in Colorectal Cancer Cells. Cells, 2019, 8, 1390.	4.1	16
41	Global Transcriptome Profiles of Italian Mediterranean Buffalo Embryos with Normal and Retarded Growth. PLoS ONE, 2014, 9, e90027.	2.5	14
42	Global View of Candidate Therapeutic Target Genes in Hormone-Responsive Breast Cancer. International Journal of Molecular Sciences, 2020, 21, 4068.	4.1	13
43	Regulation of Metabolic Reprogramming by Long Non-Coding RNAs in Cancer. Cancers, 2021, 13, 3485.	3.7	12
44	HOME-BIO (sHOtgun MEtagenomic analysis of BIOlogical entities): a specific and comprehensive pipeline for metagenomic shotgun sequencing data analysis. BMC Bioinformatics, 2021, 22, 106.	2.6	9
45	Phenytoin neurotoxicity in a child carrying new STXBP1 and CYP2C9 gene mutations. Seizure: the Journal of the British Epilepsy Association, 2016, 34, 26-28.	2.0	7
46	ldentification of a novel truncating mutation in PALB2 gene by a multigene sequencing panel for mutational screening of breast cancer riskâ€associated and related genes. Journal of Clinical Laboratory Analysis, 2018, 32, e22418.	2.1	5
47	WIND (Workflow for pIRNAs aNd beyonD): a strategy for in-depth analysis of small RNA-seq data. F1000Research, 2021, 10, 1.	1.6	5
48	Identification of long nonâ€์coding RNA expression patterns useful for molecular‑based classification of type2I endometrial cancers. Oncology Reports, 2018, 41, 1209-1217.	2.6	4
49	Identification of Antiestrogenâ€Bound Estrogen Receptor α Interactomes in Hormoneâ€Responsive Human Breast Cancer Cell Nuclei. Proteomics, 2020, 20, 2000135.	2.2	4
50	Single-Cell States in the Estrogen Response of Breast Cancer Cell Lines. PLoS ONE, 2014, 9, e88485.	2.5	4
51	New Insights on Estrogen Receptor Actions in Hormone-Responsive Breast Cancer Cells by Interaction Proteomics. , 2013, , 149-174.		1