

# Bã©la Molnã;r

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/70423/publications.pdf>

Version: 2024-02-01

56  
papers

2,994  
citations

159585

30  
h-index

161849

54  
g-index

59  
all docs

59  
docs citations

59  
times ranked

3876  
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA Methylation Biomarkers for Blood-Based Colorectal Cancer Screening. <i>Clinical Chemistry</i> , 2008, 54, 414-423.	3.2	436
2	Sensitive Detection of Colorectal Cancer in Peripheral Blood by Septin 9 DNA Methylation Assay. <i>PLoS ONE</i> , 2008, 3, e3759.	2.5	333
3	Performance of Epigenetic Markers SEPT9 and ALX4 in Plasma for Detection of Colorectal Precancerous Lesions. <i>PLoS ONE</i> , 2010, 5, e9061.	2.5	158
4	Detection of Methylated SEPT9 in Plasma Is a Reliable Screening Method for Both Left- and Right-Sided Colon Cancers. <i>PLoS ONE</i> , 2012, 7, e46000.	2.5	155
5	Aberrant septin 9 DNA methylation in colorectal cancer is restricted to a single CpG island. <i>BMC Cancer</i> , 2013, 13, 398.	2.6	111
6	Aristaless-like Homeobox-4 Gene Methylation Is a Potential Marker for Colorectal Adenocarcinomas. <i>Gastroenterology</i> , 2006, 131, 1418-1430.	1.3	106
7	Inflammation, Adenoma and Cancer: Objective Classification of Colon Biopsy Specimens with Gene Expression Signature. <i>Disease Markers</i> , 2008, 25, 1-16.	1.3	92
8	Colorectal adenoma and cancer detection based on altered methylation pattern of <i>SFRP1</i> , <i>SFRP2</i> , <i>SDC2</i> , and <i>PRIMA1</i> in plasma samples. <i>Epigenetics</i> , 2017, 12, 751-763.	2.7	92
9	Detection of Methylated Septin 9 in Tissue and Plasma of Colorectal Patients with Neoplasia and the Relationship to the Amount of Circulating Cell-Free DNA. <i>PLoS ONE</i> , 2014, 9, e115415.	2.5	87
10	Diagnostic and prognostic potential of tissue and circulating long non-coding RNAs in colorectal tumors. <i>World Journal of Gastroenterology</i> , 2019, 25, 5026-5048.	3.3	81
11	Diagnostic mRNA Expression Patterns of Inflamed, Benign, and Malignant Colorectal Biopsy Specimen and their Correlation with Peripheral Blood Results. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 2835-2845.	2.5	68
12	Aberrant DNA methylation of WNT pathway genes in the development and progression of CIMP-negative colorectal cancer. <i>Epigenetics</i> , 2016, 11, 588-602.	2.7	67
13	Serrated pathway: Alternative route to colorectal cancer. <i>World Journal of Gastroenterology</i> , 2013, 19, 607.	3.3	61
14	Identification and Validation of Colorectal Neoplasia-Specific Methylation Markers for Accurate Classification of Disease. <i>Molecular Cancer Research</i> , 2007, 5, 153-163.	3.4	60
15	DNA hypermethylation and decreased mRNA expression of MAL, PRIMA1, PTGDR and SFRP1 in colorectal adenoma and cancer. <i>BMC Cancer</i> , 2015, 15, 736.	2.6	53
16	Dysplasia-Carcinoma Transition Specific Transcripts in Colonic Biopsy Samples. <i>PLoS ONE</i> , 2012, 7, e48547.	2.5	52
17	Ageing related methylation influences the gene expression of key control genes in colorectal cancer and adenoma. <i>World Journal of Gastroenterology</i> , 2016, 22, 10325.	3.3	49
18	Plasma methylated septin 9: a colorectal cancer screening marker. <i>Expert Review of Molecular Diagnostics</i> , 2015, 15, 171-184.	3.1	45

#	ARTICLE	IF	CITATIONS
19	Gene promoter and exon DNA methylation changes in colon cancer development â€“ mRNA expression and tumor mutation alterations. <i>BMC Cancer</i> , 2018, 18, 695.	2.6	45
20	Comprehensive DNA Methylation Analysis Reveals a Common Ten-Gene Methylation Signature in Colorectal Adenomas and Carcinomas. <i>PLoS ONE</i> , 2015, 10, e0133836.	2.5	42
21	Colorectal adenoma and carcinoma specific miRNA profiles in biopsy and their expression in plasma specimens. <i>Clinical Epigenetics</i> , 2017, 9, 22.	4.1	40
22	Blood Collection and Cell-Free DNA Isolation Methods Influence the Sensitivity of Liquid Biopsy Analysis for Colorectal Cancer Detection. <i>Pathology and Oncology Research</i> , 2019, 25, 915-923.	1.9	39
23	Gene expression analysis of normal and colorectal cancer tissue samples from fresh frozen and matched formalin-fixed, paraffin-embedded (FFPE) specimens after manual and automated RNA isolation. <i>Methods</i> , 2013, 59, S16-S19.	3.8	37
24	Genome-Wide Screening of Genes Regulated by DNA Methylation in Colon Cancer Development. <i>PLoS ONE</i> , 2012, 7, e46215.	2.5	37
25	Circulating cell-free nucleic acids as biomarkers in colorectal cancer screening and diagnosis. <i>Expert Review of Molecular Diagnostics</i> , 2016, 16, 239-252.	3.1	36
26	Genome-wide expression profiling in colorectal cancer focusing on lncRNAs in the adenoma-carcinoma transition. <i>BMC Cancer</i> , 2019, 19, 1059.	2.6	36
27	Comparison of Circulating miRNAs Expression Alterations in Matched Tissue and Plasma Samples During Colorectal Cancer Progression. <i>Pathology and Oncology Research</i> , 2019, 25, 97-105.	1.9	36
28	Molecular Pathogenesis of <i>Helicobacter pylori</i> Infection: The Role of Bacterial Virulence Factors. <i>Digestive Diseases</i> , 2010, 28, 604-608.	1.9	34
29	Importance of carcinoma-associated fibroblast-derived proteins in clinical oncology. <i>Journal of Clinical Pathology</i> , 2014, 67, 1026-1031.	2.0	33
30	Exosomes in colorectal carcinoma formation: ALIX under the magnifying glass. <i>Modern Pathology</i> , 2016, 29, 928-938.	5.5	33
31	Cell Free DNA of Tumor Origin Induces a â€“Metastaticâ€™ Expression Profile in HT-29 Cancer Cell Line. <i>PLoS ONE</i> , 2015, 10, e0131699.	2.5	32
32	Myofibroblast-Derived SFRP1 as Potential Inhibitor of Colorectal Carcinoma Field Effect. <i>PLoS ONE</i> , 2014, 9, e106143.	2.5	32
33	Elevation in Peripheral Blood Circulating Tumor Cell Number Correlates with Macroscopic Progression in UICC Stage IV Colorectal Cancer Patients. <i>Disease Markers</i> , 2008, 24, 141-150.	1.3	31
34	MMP3 and CXCL1 are potent stromal protein markers of dysplasiaâ€“carcinoma transition in sporadic colorectal cancer. <i>European Journal of Cancer Prevention</i> , 2014, 23, 336-343.	1.3	29
35	<i>En bloc</i> release of MVBâ€like small extracellular vesicle clusters by colorectal carcinoma cells. <i>Journal of Extracellular Vesicles</i> , 2019, 8, 1596668.	12.2	29
36	Role of DNA Methylation in Colorectal Carcinogenesis. <i>Digestive Diseases</i> , 2012, 30, 310-315.	1.9	27

#	ARTICLE	IF	CITATIONS
37	Peripheral Blood Based Discrimination of Ulcerative Colitis and Crohn's Disease from Non-IBD Colitis by Genome-Wide Gene Expression Profiling. <i>Disease Markers</i> , 2011, 30, 1-17.	1.3	26
38	Circulating cell-free nucleic acids as biomarkers in colorectal cancer screening and diagnosis - an update. <i>Expert Review of Molecular Diagnostics</i> , 2019, 19, 477-498.	3.1	26
39	Perspective: bidirectional exosomal transport between cancer stem cells and their fibroblast-rich microenvironment during metastasis formation. <i>Npj Breast Cancer</i> , 2018, 4, 18.	5.2	23
40	Promoter Hypermethylation-Related Reduced Somatostatin Production Promotes Uncontrolled Cell Proliferation in Colorectal Cancer. <i>PLoS ONE</i> , 2015, 10, e0118332.	2.5	22
41	Comparison of Automated and Manual DNA Isolation Methods for DNA Methylation Analysis of Biopsy, Fresh Frozen, and Formalin-Fixed, Paraffin-Embedded Colorectal Cancer Samples. <i>Journal of the Association for Laboratory Automation</i> , 2015, 20, 642-651.	2.8	19
42	S-Adenosylmethionine Treatment of Colorectal Cancer Cell Lines Alters DNA Methylation, DNA Repair and Tumor Progression-Related Gene Expression. <i>Cells</i> , 2020, 9, 1864.	4.1	16
43	miR-21 expression analysis in budding colon cancer cells by confocal slide scanning microscopy. <i>Clinical and Experimental Metastasis</i> , 2018, 35, 819-830.	3.3	15
44	Comprehensive DNA Methylation and Mutation Analyses Reveal a Methylation Signature in Colorectal Sessile Serrated Adenomas. <i>Pathology and Oncology Research</i> , 2017, 23, 589-594.	1.9	13
45	miRNA Isolation from FFPET Specimen: A Technical Comparison of miRNA and Total RNA Isolation Methods. <i>Pathology and Oncology Research</i> , 2016, 22, 505-513.	1.9	12
46	Promoter Hypomethylation and Increased Expression of the Long Non-coding RNA LINC00152 Support Colorectal Carcinogenesis. <i>Pathology and Oncology Research</i> , 2020, 26, 2209-2223.	1.9	11
47	Association of Self-DNA Mediated TLR9-Related Gene, DNA Methyltransferase, and Cytokeratin Protein Expression Alterations in HT29-Cells to DNA Fragment Length and Methylation Status. <i>Scientific World Journal, The</i> , 2013, 2013, 1-8.	2.1	10
48	Applicability of Antibody and mRNA Expression Microarrays for Identifying Diagnostic and Progression Markers of Early and Late Stage Colorectal Cancer. <i>Disease Markers</i> , 2010, 28, 1-14.	1.3	10
49	Gene-expression analysis of a colorectal cancer-specific discriminatory transcript set on formalin-fixed, paraffin-embedded (FFPE) tissue samples. <i>Diagnostic Pathology</i> , 2015, 10, 126.	2.0	7
50	Construction of a multiplex mutation hot spot PCR panel: the first step towards colorectal cancer genotyping on the GS Junior platform. <i>Journal of Cancer</i> , 2017, 8, 162-173.	2.5	7
51	A Liquid Biopsy-Based Approach for Monitoring Treatment Response in Post-Operative Colorectal Cancer Patients. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3774.	4.1	6
52	Hierarchy and control of ageing-related methylation networks. <i>PLoS Computational Biology</i> , 2021, 17, e1009327.	3.2	5
53	Folic Acid Treatment Directly Influences the Genetic and Epigenetic Regulation along with the Associated Cellular Maintenance Processes of HT-29 and SW480 Colorectal Cancer Cell Lines. <i>Cancers</i> , 2022, 14, 1820.	3.7	5
54	Detecting low intensity nuclei on propidium iodide stained digital slides. , 2014, , .		2

#	ARTICLE	IF	CITATIONS
55	Republished: Importance of carcinoma-associated fibroblast-derived proteins in clinical oncology. Postgraduate Medical Journal, 2015, 91, 291-296.	1.8	2
56	Abstract 2945: Comprehensive analysis of tissue and plasma-related genetic alterations in Hungarian colorectal cancer patients. Cancer Research, 2022, 82, 2945-2945.	0.9	0