

# Joerg Tost

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

185  
papers

12,194  
citations

53  
h-index

108  
g-index

213  
ext. papers

14,512  
ext. citations

6.9  
avg, IF

6.29  
L-index

#	Paper	IF	Citations
185	International network of cancer genome projects. <i>Nature</i> , <b>2010</b> , 464, 993-8	50.4	1613
184	Plant genetics. Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. <i>Science</i> , <b>2014</b> , 345, 950-3	33.3	1348
183	DNA methylation analysis by pyrosequencing. <i>Nature Protocols</i> , <b>2007</b> , 2, 2265-75	18.8	522
182	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 680-96	11	489
181	Complete pipeline for Infinium(®) Human Methylation 450K BeadChip data processing using subset quantile normalization for accurate DNA methylation estimation. <i>Epigenomics</i> , <b>2012</b> , 4, 325-41	4.4	336
180	DNA methylation profiling of the human major histocompatibility complex: a pilot study for the human epigenome project. <i>PLoS Biology</i> , <b>2004</b> , 2, e405	9.7	265
179	Identification of type 1 diabetes-associated DNA methylation variable positions that precede disease diagnosis. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002300	6	255
178	Analysis and quantification of multiple methylation variable positions in CpG islands by Pyrosequencing. <i>BioTechniques</i> , <b>2003</b> , 35, 152-6	2.5	226
177	De novo quantitative bisulfite sequencing using the pyrosequencing technology. <i>Analytical Biochemistry</i> , <b>2004</b> , 333, 119-27	3.1	225
176	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 726-37	44.5	204
175	The epigenetics of breast cancer. <i>Molecular Oncology</i> , <b>2010</b> , 4, 242-54	7.9	200
174	Quantitative analysis of DNA methylation profiles in lung cancer identifies aberrant DNA methylation of specific genes and its association with gender and cancer risk factors. <i>Cancer Research</i> , <b>2009</b> , 69, 243-52	10.1	193
173	Specific epigenetic alterations of IGF2-H19 locus in spermatozoa from infertile men. <i>European Journal of Human Genetics</i> , <b>2010</b> , 18, 73-80	5.3	183
172	Sex- and diet-specific changes of imprinted gene expression and DNA methylation in mouse placenta under a high-fat diet. <i>PLoS ONE</i> , <b>2010</b> , 5, e14398	3.7	174
171	A DEMETER-like DNA demethylase governs tomato fruit ripening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 10804-9	11.5	173
170	DNA methylation: an introduction to the biology and the disease-associated changes of a promising biomarker. <i>Molecular Biotechnology</i> , <b>2010</b> , 44, 71-81	3	159
169	Increased regulatory T-cell numbers are associated with farm milk exposure and lower atopic sensitization and asthma in childhood. <i>Journal of Allergy and Clinical Immunology</i> , <b>2014</b> , 133, 551-9	11.5	143

168	In utero undernutrition in male mice programs liver lipid metabolism in the second-generation offspring involving altered Lxra DNA methylation. <i>Cell Metabolism</i> , <b>2014</b> , 19, 941-51	24.6	137
167	Epigenetic regulation in murine offspring as a novel mechanism for transmaternal asthma protection induced by microbes. <i>Journal of Allergy and Clinical Immunology</i> , <b>2011</b> , 128, 618-25.e1-7	11.5	136
166	Epigenetics and allergy: from basic mechanisms to clinical applications. <i>Epigenomics</i> , <b>2017</b> , 9, 539-571	4.4	134
165	Genotyping single nucleotide polymorphisms by MALDI mass spectrometry in clinical applications. <i>Clinical Biochemistry</i> , <b>2005</b> , 38, 335-50	3.5	132
164	Aberrant DNA methylation distinguishes hepatocellular carcinoma associated with HBV and HCV infection and alcohol intake. <i>Journal of Hepatology</i> , <b>2011</b> , 54, 705-15	13.4	127
163	Variation in genomic landscape of clear cell renal cell carcinoma across Europe. <i>Nature Communications</i> , <b>2014</b> , 5, 5135	17.4	123
162	Farm exposure and time trends in early childhood may influence DNA methylation in genes related to asthma and allergy. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , <b>2013</b> , 68, 355-64	9.3	123
161	Identification of regions correlating MGMT promoter methylation and gene expression in glioblastomas. <i>Neuro-Oncology</i> , <b>2009</b> , 11, 348-56	1	119
160	DNA methylation based biomarkers: practical considerations and applications. <i>Biochimie</i> , <b>2012</b> , 94, 2314-27	3.7	118
159	Frequent aberrant DNA methylation of ABCB1, FOXC1, PPP2R2B and PTEN in ductal carcinoma in situ and early invasive breast cancer. <i>Breast Cancer Research</i> , <b>2010</b> , 12, R3	8.3	113
158	Perinatal undernutrition affects the methylation and expression of the leptin gene in adults: implication for the understanding of metabolic syndrome. <i>FASEB Journal</i> , <b>2011</b> , 25, 3271-8	0.9	111
157	Genotyping single nucleotide polymorphisms by mass spectrometry. <i>Mass Spectrometry Reviews</i> , <b>2002</b> , 21, 388-418	11	111
156	NRAS mutation is the sole recurrent somatic mutation in large congenital melanocytic nevi. <i>Journal of Investigative Dermatology</i> , <b>2014</b> , 134, 1067-1074	4.3	109
155	DNA methylation profiling in doxorubicin treated primary locally advanced breast tumours identifies novel genes associated with survival and treatment response. <i>Molecular Cancer</i> , <b>2010</b> , 9, 68	42.1	109
154	Genome-wide DNA methylation profiles in progression to in situ and invasive carcinoma of the breast with impact on gene transcription and prognosis. <i>Genome Biology</i> , <b>2014</b> , 15, 435	18.3	108
153	Expressional and epigenetic alterations of placental serine protease inhibitors: SERPINA3 is a potential marker of preeclampsia. <i>Hypertension</i> , <b>2007</b> , 49, 76-83	8.5	104
152	Methylation profiling with a panel of cancer related genes: association with estrogen receptor, TP53 mutation status and expression subtypes in sporadic breast cancer. <i>Molecular Oncology</i> , <b>2011</b> , 5, 61-76	7.9	100
151	Analysis and accurate quantification of CpG methylation by MALDI mass spectrometry. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, e50	20.1	97

150	Placentas from pregnancies conceived by IVF/ICSI have a reduced DNA methylation level at the H19 and MEST differentially methylated regions. <i>Human Reproduction</i> , <b>2013</b> , 28, 1117-26	5.7	94
149	Genome-wide DNA methylation profiles in progression to <b>2014</b> , 15, 435		90
148	Germline and somatic genetic variations of TNFAIP3 in lymphoma complicating primary Sjogren's syndrome. <i>Blood</i> , <b>2013</b> , 122, 4068-76	2.2	84
147	Comprehensive evaluation of methods to isolate, quantify, and characterize circulating cell-free DNA from small volumes of plasma. <i>Analytical and Bioanalytical Chemistry</i> , <b>2015</b> , 407, 6873-8	4.4	77
146	DNA methylation: an introduction to the biology and the disease-associated changes of a promising biomarker. <i>Methods in Molecular Biology</i> , <b>2009</b> , 507, 3-20	1.4	77
145	DNA methylation at enhancers identifies distinct breast cancer lineages. <i>Nature Communications</i> , <b>2017</b> , 8, 1379	17.4	71
144	Individual and combined effects of DNA methylation and copy number alterations on miRNA expression in breast tumors. <i>Genome Biology</i> , <b>2013</b> , 14, R126	18.3	65
143	Epigenetic mechanisms and the relationship to childhood asthma. <i>European Respiratory Journal</i> , <b>2010</b> , 36, 950-61	13.6	64
142	Analysis of gene-specific DNA methylation patterns by pyrosequencing technology. <i>Methods in Molecular Biology</i> , <b>2007</b> , 373, 89-102	1.4	64
141	Deregulation of microRNA expression in purified T and B lymphocytes from patients with primary Sjogren's syndrome. <i>Annals of the Rheumatic Diseases</i> , <b>2018</b> , 77, 133-140	2.4	62
140	Modulation of imprinted gene network in placenta results in normal development of in vitro manipulated mouse embryos. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 1779-90	5.6	62
139	Recurrent NRAS mutations in pulmonary Langerhans cell histiocytosis. <i>European Respiratory Journal</i> , <b>2016</b> , 47, 1785-96	13.6	59
138	C5-DNA methyltransferase inhibitors: from screening to effects on zebrafish embryo development. <i>ChemBioChem</i> , <b>2011</b> , 12, 1337-45	3.8	58
137	Overlap between differentially methylated DNA regions in blood B lymphocytes and genetic at-risk loci in primary Sjogren's syndrome. <i>Annals of the Rheumatic Diseases</i> , <b>2016</b> , 75, 933-40	2.4	57
136	Quantitative DNA methylation analyses reveal stage dependent DNA methylation and association to clinico-pathological factors in breast tumors. <i>BMC Cancer</i> , <b>2013</b> , 13, 456	4.8	57
135	Improving breast cancer survival analysis through competition-based multidimensional modeling. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003047	5	57
134	Serial pyrosequencing for quantitative DNA methylation analysis. <i>BioTechniques</i> , <b>2006</b> , 40, 721-2, 724, 726	2.5	57
133	Hypermethylation of the IGF2 differentially methylated region 2 is a specific event in insulinomas leading to loss-of-imprinting and overexpression. <i>Endocrine-Related Cancer</i> , <b>2009</b> , 16, 939-52	5.7	53

132	Genome-wide DNA methylation analyses in lung adenocarcinomas: Association with EGFR, KRAS and TP53 mutation status, gene expression and prognosis. <i>Molecular Oncology</i> , <b>2016</b> , 10, 330-43	7.9	52
131	Pregnancy exposure to atmospheric pollution and meteorological conditions and placental DNA methylation. <i>Environment International</i> , <b>2018</b> , 118, 334-347	12.9	51
130	Identification and quantification of differentially methylated loci by the pyrosequencing technology. <i>Methods in Molecular Biology</i> , <b>2009</b> , 507, 189-205	1.4	51
129	Altered gene expression in human placentas after IVF/ICSI. <i>Human Reproduction</i> , <b>2014</b> , 29, 2821-31	5.7	47
128	Gata3 hypermethylation and Foxp3 hypomethylation are associated with sustained protection and bystander effect following epicutaneous immunotherapy in peanut-sensitized mice. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , <b>2019</b> , 74, 152-164	9.3	46
127	Gene expression profiling in insulinomas of Men1 beta-cell mutant mice reveals early genetic and epigenetic events involved in pancreatic beta-cell tumorigenesis. <i>Endocrine-Related Cancer</i> , <b>2006</b> , 13, 1223-36	5.7	45
126	DNA analysis by mass spectrometry-past, present and future. <i>Journal of Mass Spectrometry</i> , <b>2006</b> , 41, 981-95	2.2	43
125	Molecular haplotyping at high throughput. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, e96	20.1	43
124	Twin DNA Methylation Profiling Reveals Flare-Dependent Interferon Signature and B Cell Promoter Hypermethylation in Systemic Lupus Erythematosus. <i>Arthritis and Rheumatology</i> , <b>2018</b> , 70, 878-890	9.5	41
123	GSTP1 promoter haplotypes affect DNA methylation levels and promoter activity in breast carcinomas. <i>Cancer Research</i> , <b>2008</b> , 68, 5562-71	10.1	41
122	Hypoxia inducible factor-1 mediates the expression of the immune checkpoint HLA-G in glioma cells through hypoxia response element located in exon 2. <i>Oncotarget</i> , <b>2016</b> , 7, 63690-63707	3.3	40
121	A General Framework for Interrogation of mRNA Stability Programs Identifies RNA-Binding Proteins that Govern Cancer Transcriptomes. <i>Cell Reports</i> , <b>2018</b> , 23, 1639-1650	10.6	39
120	DNA methylation status of key cell-cycle regulators such as CDKN2A/p16 and CCNA1 correlates with treatment response to doxorubicin and 5-fluorouracil in locally advanced breast tumors. <i>Clinical Cancer Research</i> , <b>2014</b> , 20, 6357-66	12.9	38
119	Epigenetic Changes in Chronic Inflammatory Diseases. <i>Advances in Protein Chemistry and Structural Biology</i> , <b>2017</b> , 106, 139-189	5.3	35
118	Epigenome-wide DNA methylation analysis in siblings and monozygotic twins discordant for sporadic Parkinson's disease revealed different epigenetic patterns in peripheral blood mononuclear cells. <i>Neurogenetics</i> , <b>2017</b> , 18, 7-22	3	35
117	Sensitive detection of KRAS mutations using enhanced-ice-COLD-PCR mutation enrichment and direct sequence identification. <i>Human Mutation</i> , <b>2013</b> , 34, 1568-80	4.7	34
116	miRNA profiling identifies deregulated miRNAs associated with osteosarcoma development and time to metastasis in two large cohorts. <i>Molecular Oncology</i> , <b>2018</b> , 12, 114-131	7.9	34
115	Genome-Wide Methylation Analysis Identifies Specific Epigenetic Marks In Severely Obese Children. <i>Scientific Reports</i> , <b>2017</b> , 7, 46311	4.9	33

114	A translational perspective on epigenetics in allergic diseases. <i>Journal of Allergy and Clinical Immunology</i> , <b>2018</b> , 142, 715-726	11.5	33
113	Integrated analysis of high-resolution DNA methylation profiles, gene expression, germline genotypes and clinical end points in breast cancer patients. <i>International Journal of Cancer</i> , <b>2014</b> , 134, 2615-25	7.5	32
112	DNA methylation associated with polycomb repression in retinoic acid receptor $\beta$ silencing. <i>FASEB Journal</i> , <b>2013</b> , 27, 1468-78	0.9	32
111	Recent findings in the genetics and epigenetics of asthma and allergy. <i>Seminars in Immunopathology</i> , <b>2020</b> , 42, 43-60	12	31
110	DNMT3L interacts with transcription factors to target DNMT3L/DNMT3B to specific DNA sequences: role of the DNMT3L/DNMT3B/p65-NFB complex in the (de-)methylation of TRAF1. <i>Biochimie</i> , <b>2014</b> , 104, 36-49	4.6	30
109	Pulmonary endothelial cell DNA methylation signature in pulmonary arterial hypertension. <i>Oncotarget</i> , <b>2017</b> , 8, 52995-53016	3.3	30
108	Parental vitamin D deficiency during pregnancy is associated with increased blood pressure in offspring via Panx1 hypermethylation. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , <b>2016</b> , 311, H1459-H1469	5.2	29
107	A polymorphism in the TH 2 locus control region is associated with changes in DNA methylation and gene expression. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , <b>2014</b> , 69, 1171-80	9.3	26
106	Establishment and characterization of a highly tumourigenic and cancer stem cell enriched pancreatic cancer cell line as a well defined model system. <i>PLoS ONE</i> , <b>2012</b> , 7, e48503	3.7	26
105	Epigenetics in Forest Trees: State of the Art and Potential Implications for Breeding and Management in a Context of Climate Change. <i>Advances in Botanical Research</i> , <b>2018</b> , 88, 387-453	2.2	26
104	Differential DNA methylation analysis of breast cancer reveals the impact of immune signaling in radiation therapy. <i>International Journal of Cancer</i> , <b>2014</b> , 135, 2085-95	7.5	25
103	Synergistic chromatin repression of the tumor suppressor gene RARB in human prostate cancers. <i>Epigenetics</i> , <b>2014</b> , 9, 477-82	5.7	25
102	A novel tumor suppressor function of Kindlin-3 in solid cancer. <i>Oncotarget</i> , <b>2014</b> , 5, 8970-85	3.3	25
101	Loss of chromosome Y leads to down regulation of KDM5D and KDM6C epigenetic modifiers in clear cell renal cell carcinoma. <i>Scientific Reports</i> , <b>2017</b> , 7, 44876	4.9	24
100	Upregulation of membrane-bound CD40L on CD4+ T cells in women with primary Sjögren's syndrome. <i>Scandinavian Journal of Immunology</i> , <b>2014</b> , 79, 37-42	3.4	24
99	MeQA: a pipeline for MeDIP-seq data quality assessment and analysis. <i>Bioinformatics</i> , <b>2012</b> , 28, 587-8	7.2	24
98	Rapid identification of promoter hypermethylation in hepatocellular carcinoma by pyrosequencing of etiologically homogeneous sample pools. <i>Journal of Molecular Diagnostics</i> , <b>2007</b> , 9, 510-20	5.1	24
97	A Summary of the Biological Processes, Disease-Associated Changes, and Clinical Applications of DNA Methylation. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1708, 3-30	1.4	24

96	Ultrasensitive detection and identification of BRAF V600 mutations in fresh frozen, FFPE, and plasma samples of melanoma patients by E-ice-COLD-PCR. <i>Analytical and Bioanalytical Chemistry</i> , <b>2014</b> , 406, 5513-20	4.4	23
95	Inactivation and Mutation Drive a Convergence toward Loss of Function of H3K36 Writers in Clear Cell Renal Cell Carcinomas. <i>Cancer Research</i> , <b>2017</b> , 77, 4835-4845	10.1	23
94	Epigenetic changes in inflammatory and autoimmune diseases. <i>Sub-Cellular Biochemistry</i> , <b>2013</b> , 61, 455-485	7.5	23
93	Comparison of the quantification of KRAS mutations by digital PCR and E-ice-COLD-PCR in circulating-cell-free DNA from metastatic colorectal cancer patients. <i>Clinica Chimica Acta</i> , <b>2017</b> , 465, 1-4	6.2	22
92	DNA methylation profiles distinguish different subtypes of gastroenteropancreatic neuroendocrine tumors. <i>Epigenomics</i> , <b>2015</b> , 7, 1245-58	4.4	22
91	IGF2/H19 hypomethylation in a patient with very low birthweight, precocious pubarche and insulin resistance. <i>BMC Medical Genetics</i> , <b>2012</b> , 13, 42	2.1	22
90	COLD-PCR Technologies in the Area of Personalized Medicine: Methodology and Applications. <i>Molecular Diagnosis and Therapy</i> , <b>2017</b> , 21, 269-283	4.5	21
89	The 5p12 breast cancer susceptibility locus affects MRPS30 expression in estrogen-receptor positive tumors. <i>Molecular Oncology</i> , <b>2014</b> , 8, 273-84	7.9	21
88	Combination of promoter hypomethylation and PDX1 overexpression leads to TBX15 decrease in vascular IUGR placentas. <i>Epigenetics</i> , <b>2011</b> , 6, 247-55	5.7	21
87	Methylation profile of the promoter region of IRF5 in primary Sjögren's syndrome. <i>European Cytokine Network</i> , <b>2012</b> , 23, 166-72	3.3	21
86	Whole-Genome Bisulfite Sequencing for the Analysis of Genome-Wide DNA Methylation and Hydroxymethylation Patterns at Single-Nucleotide Resolution. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1767, 311-349	1.4	19
85	Current and Emerging Technologies for the Analysis of the Genome-Wide and Locus-Specific DNA Methylation Patterns. <i>Advances in Experimental Medicine and Biology</i> , <b>2016</b> , 945, 343-430	3.6	19
84	Dramatic transient improvement of metastatic BRAF(V600E)-mutated Langerhans cell sarcoma under treatment with dabrafenib. <i>Blood</i> , <b>2015</b> , 126, 2649-52	2.2	19
83	Circulating miRNAs as Biomarker in Cancer. <i>Recent Results in Cancer Research</i> , <b>2020</b> , 215, 277-298	1.5	19
82	BRAF(V600) mutation levels predict response to vemurafenib in metastatic melanoma. <i>Melanoma Research</i> , <b>2014</b> , 24, 415-8	3.3	18
81	Identification of susceptibility genes for peritoneal, ovarian, and deep infiltrating endometriosis using a pooled sample-based genome-wide association study. <i>BioMed Research International</i> , <b>2015</b> , 2015, 461024	3	18
80	Lentiviral transduction of CD34(+) cells induces genome-wide epigenetic modifications. <i>PLoS ONE</i> , <b>2012</b> , 7, e48943	3.7	18
79	The impact of microRNAs on alterations of gene regulatory networks in allergic diseases. <i>Advances in Protein Chemistry and Structural Biology</i> , <b>2020</b> , 120, 237-312	5.3	17

78	Copy number variations alter methylation and parallel IGF2 overexpression in adrenal tumors. <i>Endocrine-Related Cancer</i> , <b>2015</b> , 22, 953-67	5.7	16
77	Involvement of Tumor Necrosis Factor Receptor Type II in FoxP3 Stability and as a Marker of Treg Cells Specifically Expanded by Anti-Tumor Necrosis Factor Treatments in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , <b>2020</b> , 72, 576-587	9.5	16
76	Quantitative DNA Methylation Analysis at Single-Nucleotide Resolution by Pyrosequencing. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1708, 427-445	1.4	16
75	Improved reproducibility in genome-wide DNA methylation analysis for PAXgene-fixed samples compared with restored formalin-fixed and paraffin-embedded DNA. <i>Analytical Biochemistry</i> , <b>2015</b> , 468, 50-8	3.1	15
74	Exhaustive methylation analysis revealed uneven profiles of methylation at IGF2/ICR1/H19 11p15 loci in Russell Silver syndrome. <i>Journal of Medical Genetics</i> , <b>2015</b> , 52, 53-60	5.8	15
73	White Blood Cell BRCA1 Promoter Methylation Status and Ovarian Cancer Risk. <i>Annals of Internal Medicine</i> , <b>2018</b> , 168, 326-334	8	15
72	Accurate CpG and non-CpG cytosine methylation analysis by high-throughput locus-specific pyrosequencing in plants. <i>Plant Molecular Biology</i> , <b>2015</b> , 88, 471-85	4.6	14
71	Heterogeneous DNA Methylation Patterns in the GSTP1 Promoter Lead to Discordant Results between Assay Technologies and Impede Its Implementation as Epigenetic Biomarkers in Breast Cancer. <i>Genes</i> , <b>2015</b> , 6, 878-900	4.2	14
70	DNA methylation signature (SAM40) identifies subgroups of the Luminal A breast cancer samples with distinct survival. <i>Oncotarget</i> , <b>2017</b> , 8, 1074-1082	3.3	14
69	Pyrosequencing-Based Identification of Low-Frequency Mutations Enriched Through Enhanced-ice-COLD-PCR. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1315, 83-101	1.4	14
68	Deregulation of microRNA expression in monocytes and CD4 T lymphocytes from patients with axial spondyloarthritis. <i>Arthritis Research and Therapy</i> , <b>2019</b> , 21, 51	5.7	14
67	Epigenome-wide DNA methylation profiling in Progressive Supranuclear Palsy reveals major changes at DLX1. <i>Nature Communications</i> , <b>2018</b> , 9, 2929	17.4	13
66	Dynamic changes of DNA methylation and lung disease in cystic fibrosis: lessons from a monogenic disease. <i>Epigenomics</i> , <b>2018</b> , 10, 1131-1145	4.4	12
65	Consequences of combining siRNA-mediated DNA methyltransferase 1 depletion with 5-aza-2-Deoxycytidine in human leukemic KG1 cells. <i>Oncotarget</i> , <b>2015</b> , 6, 15265-82	3.3	12
64	Multiplexing of E-ice-COLD-PCR Assays for Mutation Detection and Identification. <i>Clinical Chemistry</i> , <b>2016</b> , 62, 1155-8	5.5	12
63	Genome-wide association study in breast cancer survivors reveals SNPs associated with gene expression of genes belonging to MHC class I and II. <i>Genomics</i> , <b>2013</b> , 102, 278-87	4.3	11
62	Immediate and durable effects of maternal tobacco consumption alter placental DNA methylation in enhancer and imprinted gene-containing regions. <i>BMC Medicine</i> , <b>2020</b> , 18, 306	11.4	11
61	Whole-Genome Bisulfite Sequencing Using the Ovation Ultralow Methyl-Seq Protocol. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1708, 83-104	1.4	11



60	Clonogenic cell subpopulations maintain congenital melanocytic nevi. <i>Journal of Investigative Dermatology</i> , <b>2015</b> , 135, 824-833	4.3	10
59	Systemic epigenetic response to recombinant lentiviral vectors independent of proviral integration. <i>Epigenetics and Chromatin</i> , <b>2016</b> , 9, 29	5.8	10
58	GFRA3 promoter methylation may be associated with decreased postoperative survival in gastric cancer. <i>BMC Cancer</i> , <b>2016</b> , 16, 225	4.8	10
57	New technologies for DNA analysis--a review of the READNA Project. <i>New Biotechnology</i> , <b>2016</b> , 33, 311-324	3.4	10
56	Epigenetic modulation of ARL1 and increased HLA expression in brains of multiple system atrophy patients. <i>Acta Neuropathologica Communications</i> , <b>2020</b> , 8, 29	7.3	9
55	Consequences of VHL Loss on Global DNA Methylome. <i>Scientific Reports</i> , <b>2018</b> , 8, 3313	4.9	9
54	Non-random, individual-specific methylation profiles are present at the sixth CTCF binding site in the human H19/IGF2 imprinting control region. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 5438-48	20.1	9
53	Loss of fragile X mental retardation protein precedes Lewy pathology in Parkinson's disease. <i>Acta Neuropathologica</i> , <b>2020</b> , 139, 319-345	14.3	9
52	Epigenetics of the immune system and alterations in inflammation and autoimmunity. <i>Epigenomics</i> , <b>2017</b> , 9, 371-373	4.4	8
51	Clinical value of early detection of circulating tumour DNA- in patients with metastatic melanoma treated with a BRAF inhibitor. <i>ESMO Open</i> , <b>2017</b> , 2, e000173	6	8
50	Specific hypomethylated CpGs at the IGF2 locus act as an epigenetic biomarker for familial adenomatous polyposis colorectal cancer. <i>Epigenomics</i> , <b>2010</b> , 2, 365-75	4.4	8
49	Methylation of specific CpG sites in the P2 promoter of parathyroid hormone-related protein determines the invasive potential of breast cancer cell lines. <i>Epigenetics</i> , <b>2011</b> , 6, 1035-46	5.7	8
48	Demethylation by low-dose 5-aza-2-deoxycytidine impairs 3D melanoma invasion partially through miR-199a-3p expression revealing the role of this miR in melanoma. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 9	7.7	7
47	Data integration from two microarray platforms identifies bi-allelic genetic inactivation of RIC8A in a breast cancer cell line. <i>BMC Medical Genomics</i> , <b>2009</b> , 2, 26	3.7	7
46	Molecular Mechanisms of Trophoblast Dysfunction Mediated by Imbalance between STOX1 Isoforms. <i>iScience</i> , <b>2020</b> , 23, 101086	6.1	7
45	Contrasting DCIS and invasive breast cancer by subtype suggests basal-like DCIS as distinct lesions. <i>Npj Breast Cancer</i> , <b>2020</b> , 6, 26	7.8	6
44	DNA methylation signatures in circulating cell-free DNA for the monitoring of at-risk populations progressing to lung cancer. <i>EBioMedicine</i> , <b>2015</b> , 2, 798-9	8.8	6
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