

# Stephan Beck

## List of Publications by Year in descending order

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Version: 2024-02-01

145  
papers

48,691  
citations

17405

63  
h-index

9073

144  
g-index

159  
all docs

159  
docs citations

159  
times ranked

53456  
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
2	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
3	A beta-mixture quantile normalization method for correcting probe design bias in Illumina Infinium 450 k DNA methylation data. <i>Bioinformatics</i> , 2013, 29, 189-196.	1.8	1,295
4	DNA methylation profiling of human chromosomes 6, 20 and 22. <i>Nature Genetics</i> , 2006, 38, 1378-1385.	9.4	1,212
5	Epigenome-wide association studies for common human diseases. <i>Nature Reviews Genetics</i> , 2011, 12, 529-541.	7.7	1,110
6	Gene map of the extended human MHC. <i>Nature Reviews Genetics</i> , 2004, 5, 889-899.	7.7	949
7	ChAMP: 450k Chip Analysis Methylation Pipeline. <i>Bioinformatics</i> , 2014, 30, 428-430.	1.8	757
8	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. <i>Genome Research</i> , 2010, 20, 440-446.	2.4	740
9	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. <i>Nature Genetics</i> , 2006, 38, 1166-1172.	9.4	686
10	Neoantigen-directed immune escape in lung cancer evolution. <i>Nature</i> , 2019, 567, 479-485.	13.7	639
11	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008, 26, 779-785.	9.4	619
12	ChAMP: updated methylation analysis pipeline for Illumina BeadChips. <i>Bioinformatics</i> , 2017, 33, 3982-3984.	1.8	572
13	The chicken B locus is a minimal essential major histocompatibility complex. <i>Nature</i> , 1999, 401, 923-925.	13.7	568
14	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	3.8	552
15	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
16	An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). <i>Genome Research</i> , 2008, 18, 1518-1529.	2.4	350
17	Downregulation of Death-Associated Protein Kinase 1 (DAPK1) in Chronic Lymphocytic Leukemia. <i>Cell</i> , 2007, 129, 879-890.	13.5	338
18	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	9.4	323

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19	DNA Methylation Profiling of the Human Major Histocompatibility Complex: A Pilot Study for the Human Epigenome Project. <i>PLoS Biology</i> , 2004, 2, e405.	2.6	305
20	Genetic and environmental influences interact with age and sex in shaping the human methylome. <i>Nature Communications</i> , 2016, 7, 11115.	5.8	299
21	A comparison of reference-based algorithms for correcting cell-type heterogeneity in Epigenome-Wide Association Studies. <i>BMC Bioinformatics</i> , 2017, 18, 105.	1.2	297
22	Identification of Type 1 Diabetes-Associated DNA Methylation Variable Positions That Precede Disease Diagnosis. <i>PLoS Genetics</i> , 2011, 7, e1002300.	1.5	295
23	An Epigenetic Signature in Peripheral Blood Predicts Active Ovarian Cancer. <i>PLoS ONE</i> , 2009, 4, e8274.	1.1	291
24	The DNA Methylome of Human Peripheral Blood Mononuclear Cells. <i>PLoS Biology</i> , 2010, 8, e1000533.	2.6	290
25	Variation analysis and gene annotation of eight MHC haplotypes: The MHC Haplotype Project. <i>Immunogenetics</i> , 2008, 60, 1-18.	1.2	286
26	Methylome analysis using MeDIP-seq with low DNA concentrations. <i>Nature Protocols</i> , 2012, 7, 617-636.	5.5	270
27	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	9.4	270
28	Genome-wide DNA methylation analysis for diabetic nephropathy in type 1 diabetes mellitus. <i>BMC Medical Genomics</i> , 2010, 3, 33.	0.7	261
29	Age-associated epigenetic drift: implications, and a case of epigenetic thrift?. <i>Human Molecular Genetics</i> , 2013, 22, R7-R15.	1.4	261
30	Complete MHC Haplotype Sequencing for Common Disease Gene Mapping. <i>Genome Research</i> , 2004, 14, 1176-1187.	2.4	260
31	Molecular dissection of colorectal cancer in pre-clinical models identifies biomarkers predicting sensitivity to EGFR inhibitors. <i>Nature Communications</i> , 2017, 8, 14262.	5.8	260
32	The methylome: approaches for global DNA methylation profiling. <i>Trends in Genetics</i> , 2008, 24, 231-237.	2.9	258
33	A High-Resolution Linkage-Disequilibrium Map of the Human Major Histocompatibility Complex and First Generation of Tag Single-Nucleotide Polymorphisms. <i>American Journal of Human Genetics</i> , 2005, 76, 634-646.	2.6	237
34	From profiles to function in epigenomics. <i>Nature Reviews Genetics</i> , 2017, 18, 51-66.	7.7	233
35	Correlation of an epigenetic mitotic clock with cancer risk. <i>Genome Biology</i> , 2016, 17, 205.	3.8	197
36	Deciphering the genomic, epigenomic, and transcriptomic landscapes of pre-invasive lung cancer lesions. <i>Nature Medicine</i> , 2019, 25, 517-525.	15.2	178

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37	Identification of differentially methylated cell types in epigenome-wide association studies. <i>Nature Methods</i> , 2018, 15, 1059-1066.	9.0	166
38	Glioblastomas acquire myeloid-affiliated transcriptional programs via epigenetic immunoediting to elicit immune evasion. <i>Cell</i> , 2021, 184, 2454-2470.e26.	13.5	165
39	Genetic Analysis of Completely Sequenced Disease-Associated MHC Haplotypes Identifies Shuffling of Segments in Recent Human History. <i>PLoS Genetics</i> , 2006, 2, e9.	1.5	156
40	A second major histocompatibility complex susceptibility locus for multiple sclerosis. <i>Annals of Neurology</i> , 2007, 61, 228-236.	2.8	156
41	From genome to epigenome. <i>Human Molecular Genetics</i> , 2005, 14, R3-R10.	1.4	154
42	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016, 7, 13555.	5.8	142
43	A histone acetylome-wide association study of Alzheimer's disease identifies disease-associated H3K27ac differences in the entorhinal cortex. <i>Nature Neuroscience</i> , 2018, 21, 1618-1627.	7.1	138
44	An Integrative Multi-scale Analysis of the Dynamic DNA Methylation Landscape in Aging. <i>PLoS Genetics</i> , 2015, 11, e1004996.	1.5	132
45	Widespread resetting of DNA methylation in glioblastoma-initiating cells suppresses malignant cellular behavior in a lineage-dependent manner. <i>Genes and Development</i> , 2013, 27, 654-669.	2.7	121
46	A novel cell-type deconvolution algorithm reveals substantial contamination by immune cells in saliva, buccal and cervix. <i>Epigenomics</i> , 2018, 10, 925-940.	1.0	116
47	Using high-density DNA methylation arrays to profile copy number alterations. <i>Genome Biology</i> , 2014, 15, R30.	13.9	113
48	Probe Lasso: A novel method to rope in differentially methylated regions with 450K DNA methylation data. <i>Methods</i> , 2015, 72, 21-28.	1.9	109
49	Analysis pipelines and packages for Infinium HumanMethylation450 BeadChip (450k) data. <i>Methods</i> , 2015, 72, 3-8.	1.9	108
50	Making multi-omics data accessible to researchers. <i>Scientific Data</i> , 2019, 6, 251.	2.4	107
51	Integration of human pancreatic islet genomic data refines regulatory mechanisms at Type 2 Diabetes susceptibility loci. <i>ELife</i> , 2018, 7, .	2.8	103
52	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016, 17, 2137-2150.	2.9	102
53	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , 2017, 18, 18.	3.8	97
54	Comparative methylome analysis of benign and malignant peripheral nerve sheath tumors. <i>Genome Research</i> , 2011, 21, 515-524.	2.4	94

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55	Glioblastoma Stem Cells Respond to Differentiation Cues but Fail to Undergo Commitment and Terminal Cell-Cycle Arrest. <i>Stem Cell Reports</i> , 2015, 5, 829-842.	2.3	93
56	Genome-wide DNA methylation analysis of archival formalin-fixed paraffin-embedded tissue using the Illumina Infinium HumanMethylation27 BeadChip. <i>Methods</i> , 2010, 52, 248-254.	1.9	92
57	Taking the measure of the methylome. <i>Nature Biotechnology</i> , 2010, 28, 1026-1028.	9.4	88
58	eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. <i>Bioinformatics</i> , 2019, 35, 4767-4769.	1.8	84
59	oxBS-450K: A method for analysing hydroxymethylation using 450K BeadChips. <i>Methods</i> , 2015, 72, 9-15.	1.9	83
60	UroMark™ a urinary biomarker assay for the detection of bladder cancer. <i>Clinical Epigenetics</i> , 2017, 9, 8.	1.8	81
61	Tracking the Epigenetic Clock Across the Human Life Course: A Meta-analysis of Longitudinal Cohort Data. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019, 74, 57-61.	1.7	81
62	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. <i>Diabetes</i> , 2019, 68, 2315-2326.	0.3	77
63	Characterization of the Chicken C-Type Lectin-Like Receptors B-NK and B-lec Suggests That the NK Complex and the MHC Share a Common Ancestral Region. <i>Journal of Immunology</i> , 2005, 174, 3475-3483.	0.4	76
64	Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. <i>BioEssays</i> , 2018, 40, 1700148.	1.2	71
65	Increased DNA methylation variability in rheumatoid arthritis-discordant monozygotic twins. <i>Genome Medicine</i> , 2018, 10, 64.	3.6	71
66	A Novel System of Polymorphic and Diverse NK Cell Receptors in Primates. <i>PLoS Genetics</i> , 2009, 5, e1000688.	1.5	64
67	Genome-wide methylation profiling identifies novel methylated genes in neuroblastoma tumors. <i>Epigenetics</i> , 2016, 11, 74-84.	1.3	63
68	Analysis of the Polycomb-related lncRNAs HOTAIR and ANRIL in bladder cancer. <i>Clinical Epigenetics</i> , 2015, 7, 109.	1.8	60
69	Large-scale sequence comparisons reveal unusually high levels of variation in the HLA-DQB1 locus in the class II region of the human MHC. <i>Journal of Molecular Biology</i> , 1998, 282, 71-97.	2.0	59
70	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. <i>Nature Methods</i> , 2017, 14, 216-217.	9.0	59
71	Advances in epigenome-wide association studies for common diseases. <i>Trends in Molecular Medicine</i> , 2014, 20, 541-543.	3.5	58
72	EPISCOPE: cell type deconvolution of bulk tissue DNA methylomes from single-cell RNA-Seq data. <i>Genome Biology</i> , 2020, 21, 221.	3.8	58

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73	Validation of the MethylationEPIC BeadChip for fresh-frozen and formalin-fixed paraffin-embedded tumours. <i>Clinical Epigenetics</i> , 2017, 9, 33.	1.8	57
74	Epigenetic reprogramming of fallopian tube fimbriae in BRCA mutation carriers defines early ovarian cancer evolution. <i>Nature Communications</i> , 2016, 7, 11620.	5.8	56
75	Selfish mutations dysregulating RAS-MAPK signaling are pervasive in aged human testes. <i>Genome Research</i> , 2018, 28, 1779-1790.	2.4	56
76	Accurate Measurement of 5-Methylcytosine and 5-Hydroxymethylcytosine in Human Cerebellum DNA by Oxidative Bisulfite on an Array (OxBS-Array). <i>PLoS ONE</i> , 2015, 10, e0118202.	1.1	54
77	The Dynamics of DNA Methylation Covariation Patterns in Carcinogenesis. <i>PLoS Computational Biology</i> , 2014, 10, e1003709.	1.5	52
78	Epigenetic dysregulation and poorer prognosis in DAXX-deficient pancreatic neuroendocrine tumours. <i>Endocrine-Related Cancer</i> , 2015, 22, L13-L18.	1.6	50
79	G protein-coupled receptor GPR55 promotes colorectal cancer and has opposing effects to cannabinoid receptor 1. <i>International Journal of Cancer</i> , 2018, 142, 121-132.	2.3	49
80	Functional interpretation of non-coding sequence variation: Concepts and challenges. <i>BioEssays</i> , 2014, 36, 191-199.	1.2	47
81	The good, the bad and the ugly: Epigenetic mechanisms in glioblastoma. <i>Molecular Aspects of Medicine</i> , 2013, 34, 849-862.	2.7	46
82	A pan-tissue DNA methylation atlas enables in silico decomposition of human tissue methylomes at cell-type resolution. <i>Nature Methods</i> , 2022, 19, 296-306.	9.0	46
83	DNA methylation analysis of murine hematopoietic side population cells during aging. <i>Epigenetics</i> , 2013, 8, 1114-1122.	1.3	41
84	Tissue-independent and tissue-specific patterns of DNA methylation alteration in cancer. <i>Epigenetics and Chromatin</i> , 2016, 9, 10.	1.8	40
85	EpiDISH web server: Epigenetic Dissection of Intra-Sample-Heterogeneity with online GUI. <i>Bioinformatics</i> , 2020, 36, 1950-1951.	1.8	40
86	A Polycomb-mir200 loop regulates clinical outcome in bladder cancer. <i>Oncotarget</i> , 2015, 6, 42258-42275.	0.8	40
87	Resources for methylome analysis suitable for gene knockout studies of potential epigenome modifiers. <i>GigaScience</i> , 2012, 1, 3.	3.3	39
88	Comparative methylome analysis identifies new tumour subtypes and biomarkers for transformation of nephrogenic rests into Wilms tumour. <i>Genome Medicine</i> , 2015, 7, 11.	3.6	39
89	Non-CG DNA methylation is a biomarker for assessing endodermal differentiation capacity in pluripotent stem cells. <i>Nature Communications</i> , 2016, 7, 10458.	5.8	38
90	Cancer Epigenome. <i>Advances in Genetics</i> , 2010, 70, 247-276.	0.8	37

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91	AutoMeDIP-seq: A high-throughput, whole genome, DNA methylation assay. <i>Methods</i> , 2010, 52, 223-231.	1.9	37
92	Molecular Signatures of Regression of the Canine Transmissible Venereal Tumor. <i>Cancer Cell</i> , 2018, 33, 620-633.e6.	7.7	37
93	A comparison of tagging methods and their tagging space. <i>Human Molecular Genetics</i> , 2005, 14, 2757-2767.	1.4	36
94	Epigenome data release: a participant-centered approach to privacy protection. <i>Genome Biology</i> , 2015, 16, 142.	3.8	34
95	Information recovery from low coverage whole-genome bisulfite sequencing. <i>Nature Communications</i> , 2016, 7, 11306.	5.8	33
96	DNA methylome analysis reveals distinct epigenetic patterns of ascending aortic dissection and bicuspid aortic valve. <i>Cardiovascular Research</i> , 2017, 113, 692-704.	1.8	33
97	The role of epigenetics in psychological resilience. <i>Lancet Psychiatry</i> , 2021, 8, 620-629.	3.7	33
98	Identification of a single killer immunoglobulin-like receptor (KIR) gene in the porcine leukocyte receptor complex on chromosome 6q. <i>Immunogenetics</i> , 2006, 58, 481-486.	1.2	32
99	Assessment of RainDrop BS-seq as a method for large-scale, targeted bisulfite sequencing. <i>Epigenetics</i> , 2014, 9, 678-684.	1.3	28
100	Epigenome-wide association studies for cancer biomarker discovery in circulating cell-free DNA: technical advances and challenges. <i>Current Opinion in Genetics and Development</i> , 2017, 42, 48-55.	1.5	28
101	Points-to-consider on the return of results in epigenetic research. <i>Genome Medicine</i> , 2019, 11, 31.	3.6	27
102	The multi-omic landscape of transcription factor inactivation in cancer. <i>Genome Medicine</i> , 2016, 8, 89.	3.6	26
103	Saturation analysis for whole-genome bisulfite sequencing data. <i>Nature Biotechnology</i> , 2016, 34, 691-693.	9.4	26
104	Genome-Wide Screen for Differential DNA Methylation Associated with Neural Cell Differentiation in Mouse. <i>PLoS ONE</i> , 2011, 6, e26002.	1.1	26
105	DNA methylation-based profiling of bone and soft tissue tumours: a validation study of the DKFZ Sarcoma Classifier™. <i>Journal of Pathology: Clinical Research</i> , 2021, 7, 350-360.	1.3	25
106	Chemotherapy induces canalization of cell state in childhood B-cell precursor acute lymphoblastic leukemia. <i>Nature Cancer</i> , 2021, 2, 835-852.	5.7	25
107	Neuronal methylome reveals CREB-associated neuro-axonal impairment in multiple sclerosis. <i>Clinical Epigenetics</i> , 2019, 11, 86.	1.8	24
108	Overexpression of the Heterochromatinization Factor BAHD1 in HEK293 Cells Differentially Reshapes the DNA Methylome on Autosomes and X Chromosome. <i>Frontiers in Genetics</i> , 2015, 6, 339.	1.1	23

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109	A Blueprint for an International Cancer Epigenome Consortium. A Report from the AACR Cancer Epigenome Task Force. <i>Cancer Research</i> , 2012, 72, 6319-6324.	0.4	22
110	Assessment of patient-derived tumour xenografts (PDXs) as a discovery tool for cancer epigenomics. <i>Genome Medicine</i> , 2014, 6, 116.	3.6	22
111	Human-specific epigenetic variation in the immunological Leukotriene B4 Receptor (LTB4R/BLT1) implicated in common inflammatory diseases. <i>Genome Medicine</i> , 2014, 6, 19.	3.6	21
112	Global hypomethylation in myeloma is associated with poor prognosis. <i>British Journal of Haematology</i> , 2016, 172, 473-475.	1.2	21
113	Brave new epigenomes: the dawn of epigenetic engineering. <i>Genome Medicine</i> , 2015, 7, 59.	3.6	20
114	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. <i>Genome Medicine</i> , 2021, 13, 74.	3.6	20
115	Evolutionary vignettes of natural killer cell receptors. <i>Current Opinion in Immunology</i> , 2007, 19, 553-560.	2.4	19
116	The Personal Genome Project-UK, an open access resource of human multi-omics data. <i>Scientific Data</i> , 2019, 6, 257.	2.4	19
117	Alopecia areata susceptibility variant in MHC region impacts expressions of genes contributing to hair keratinization and is involved in hair loss. <i>EBioMedicine</i> , 2020, 57, 102810.	2.7	19
118	The epigenetic clock: a molecular crystal ball for human aging?. <i>Aging</i> , 2019, 11, 833-835.	1.4	19
119	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. <i>Genome Biology</i> , 2022, 23, 13.	3.8	19
120	Benefits and barriers in the design of harmonized access agreements for international data sharing. <i>Scientific Data</i> , 2019, 6, 297.	2.4	18
121	DNA Methylome Alterations Are Associated with Airway Macrophage Differentiation and Phenotype during Lung Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 204, 954-966.	2.5	17
122	CORALINA: a universal method for the generation of gRNA libraries for CRISPR-based screening. <i>BMC Genomics</i> , 2016, 17, 917.	1.2	16
123	C2c: turning cancer into chronic disease. <i>Genome Medicine</i> , 2014, 6, 38.	3.6	15
124	Differentiation therapy for glioblastoma – too many obstacles?. <i>Molecular and Cellular Oncology</i> , 2016, 3, e1124174.	0.3	15
125	Quantification of tumour evolution and heterogeneity via Bayesian epiallele detection. <i>BMC Bioinformatics</i> , 2017, 18, 354.	1.2	15
126	Molecular signature of response to preoperative radiotherapy in locally advanced breast cancer. <i>Radiation Oncology</i> , 2018, 13, 193.	1.2	15



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127	The missing diversity in human epigenomic studies. <i>Nature Genetics</i> , 2022, 54, 737-739.	9.4	14
128	Sequencing and comparative analysis of the gorilla MHC genomic sequence. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat011.	1.4	13
129	3-methylcytosine in cancer: an underappreciated methyl lesion?. <i>Epigenomics</i> , 2016, 8, 451-454.	1.0	13
130	Diversity in EWAS: current state, challenges, and solutions. <i>Genome Medicine</i> , 2022, 14, .	3.6	13
131	Epigenetic Noise Fuels Cancer Evolution. <i>Cancer Cell</i> , 2014, 26, 775-776.	7.7	12
132	Novel epigenetic network biomarkers for early detection of esophageal cancer. <i>Clinical Epigenetics</i> , 2022, 14, 23.	1.8	11
133	“Epigenome-wide methylation profile of chronic kidney disease-derived arterial DNA uncovers novel pathways in disease-associated cardiovascular pathology.” <i>Epigenetics</i> , 2021, 16, 718-728.	1.3	10
134	Osteosarcoma: Novel prognostic biomarkers using circulating and cell-free tumour DNA. <i>European Journal of Cancer</i> , 2022, 168, 1-11.	1.3	8
135	A donor-specific epigenetic classifier for acute graft-versus-host disease severity in hematopoietic stem cell transplantation. <i>Genome Medicine</i> , 2015, 7, 128.	3.6	7
136	The Relationship between Epigenetic Age and Myocardial Infarction/Acute Coronary Syndrome in a Population-Based Nested Case-Control Study. <i>Journal of Personalized Medicine</i> , 2022, 12, 110.	1.1	6
137	Comparison and imputation-aided integration of five commercial platforms for targeted DNA methylome analysis. <i>Nature Biotechnology</i> , 2022, 40, 1478-1487.	9.4	5
138	GenomeChronicler: The Personal Genome Project UK Genomic Report Generator Pipeline. <i>Frontiers in Genetics</i> , 2020, 11, 518644.	1.1	4
139	RXRB Is an MHC-Encoded Susceptibility Gene Associated with Anti-Topoisomerase I Antibody-Positive Systemic Sclerosis. <i>Journal of Investigative Dermatology</i> , 2017, 137, 1878-1886.	0.3	3
140	Treasure trove for cancer medicine. <i>Nature Materials</i> , 2017, 16, 1056-1057.	13.3	3
141	Getting up close and personal with UK genomics and beyond. <i>Genome Medicine</i> , 2018, 10, 38.	3.6	3
142	A-Z of methylome analysis. <i>Methods</i> , 2010, 52, 201-202.	1.9	2
143	Nano-MeDIP-seq Methylome Analysis Using Low DNA Concentrations. <i>Methods in Molecular Biology</i> , 2015, 1589, 115-138.	0.4	1
144	Editorial: Personal Genomes: Accessing, Sharing, and Interpretation. <i>Frontiers in Genetics</i> , 2021, 12, 687584.	1.1	1

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145	Epigenetics of Inflammatory Bowel Disease. , 2013, , 171-187.		0