

# Angelika Merkel

## 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.

25  
papers

20,902  
citations

17  
h-index

27  
g-index

27  
ext. papers

25,292  
ext. citations

17.4  
avg, IF

8.14  
L-index

#	Paper	IF	Citations
25	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , <b>2012</b> , 489, 57-74	50.4	11449
24	Landscape of transcription in human cells. <i>Nature</i> , <b>2012</b> , 489, 101-8	50.4	3544
23	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , <b>2012</b> , 22, 1775-89	9.7	3408
22	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , <b>2011</b> , 9, e1001046	9.7	1060
21	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , <b>2008</b> , 453, 175-83	50.4	545
20	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , <b>2015</b> , 47, 746-56	36.3	209
19	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , <b>2018</b> , 24, 868-880	50.5	103
18	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , <b>2015</b> , 25, 478-87	9.7	92
17	Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures and over time. <i>Biotechnology and Bioengineering</i> , <b>2016</b> , 113, 2241-53	4.9	88
16	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. <i>Cancer Cell</i> , <b>2016</b> , 30, 806-821	24.3	73
15	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , <b>2017</b> , 18, 18	18.3	70
14	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , <b>2018</b> , 24, 2784-2794	10.6	54
13	Detecting short tandem repeats from genome data: opening the software black box. <i>Briefings in Bioinformatics</i> , <b>2008</b> , 9, 355-66	13.4	50
12	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. <i>Cell Reports</i> , <b>2016</b> , 17, 2101-2111	10.6	42
11	Epigenetic regulation of gene expression in Chinese Hamster Ovary cells in response to the changing environment of a batch culture. <i>Biotechnology and Bioengineering</i> , <b>2019</b> , 116, 677-692	4.9	27
10	Grape RNA-Seq analysis pipeline environment. <i>Bioinformatics</i> , <b>2013</b> , 29, 614-21	7.2	23
9	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. <i>Cell Reports</i> , <b>2019</b> , 26, 1059-1069.e6	10.6	19

8	gemBS: high throughput processing for DNA methylation data from bisulfite sequencing. <i>Bioinformatics</i> , <b>2019</b> , 35, 737-742	7.2	14
7	Whole-genome DNA hyper-methylation in iPSC-derived dopaminergic neurons from Parkinson's disease patients. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 108	7.7	11
6	GEMBS [high through-put processing for DNA methylation data from Whole Genome Bisulfite Sequencing (WGBS)		3
5	Comparative analysis of neutrophil and monocyte epigenomes		2
4	Evolution of Microsatellite DNA <b>2008</b> ,		1
3	Experimental and Bioinformatic Approaches to Studying DNA Methylation in Cancer.. <i>Cancers</i> , <b>2022</b> , 14,	6.6	1
2	Review of [rap-analysis gene expression] <i>BioEssays</i> , <b>2011</b> , 33, 233-234	4.1	
1	DNA Methylation Assays Using Bisulphite Sequencing and Next-Generation Sequencing. <i>Comprehensive Analytical Chemistry</i> , <b>2018</b> , 107-136	1.9	