

# Heiko M MÃ¼ller

## List of Publications by Year in descending order

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Version: 2024-02-01

31  
papers

3,606  
citations

394286

19  
h-index

434063

31  
g-index

31  
all docs

31  
docs citations

31  
times ranked

5902  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Large Fraction of Extragenic RNA Pol II Transcription Sites Overlap Enhancers. <i>PLoS Biology</i> , 2010, 8, e1000384.	2.6	762
2	Apaf-1 is a transcriptional target for E2F and p53. <i>Nature Cell Biology</i> , 2001, 3, 552-558.	4.6	552
3	Cyclin D1 protein expression and function in human breast cancer. <i>International Journal of Cancer</i> , 1994, 57, 353-361.	2.3	480
4	Selective transcriptional regulation by Myc in cellular growth control and lymphomagenesis. <i>Nature</i> , 2014, 511, 488-492.	13.7	411
5	Acute myeloid leukemia fusion proteins deregulate genes involved in stem cell maintenance and DNA repair. <i>Journal of Clinical Investigation</i> , 2003, 112, 1751-1761.	3.9	223
6	E2F-6: a novel member of the E2F family is an inhibitor of E2F-dependent transcription. <i>Oncogene</i> , 1998, 17, 611-623.	2.6	183
7	Degradation dynamics of microRNAs revealed by a novel pulse-chase approach. <i>Genome Research</i> , 2016, 26, 554-565.	2.4	155
8	The E2F transcription factors: key regulators of cell proliferation. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2000, 1470, M1-M12.	3.3	150
9	[20] Analysis of altered gene expression by differential display. <i>Methods in Enzymology</i> , 1995, 254, 304-321.	0.4	114
10	Identification of Target Genes of the p16INK4A-pRB-E2F Pathway. <i>Journal of Biological Chemistry</i> , 2003, 278, 46124-46137.	1.6	107
11	GenoMetric Query Language: a novel approach to large-scale genomic data management. <i>Bioinformatics</i> , 2015, 31, 1881-1888.	1.8	79
12	IsomiRage: From Functional Classification to Differential Expression of miRNA Isoforms. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 38.	2.0	61
13	Molecular signature of retinoic acid treatment in acute promyelocytic leukemia. <i>Oncogene</i> , 2005, 24, 3358-3368.	2.6	52
14	VCF.Filter: interactive prioritization of disease-linked genetic variants from sequencing data. <i>Nucleic Acids Research</i> , 2017, 45, W567-W572.	6.5	37
15	Localizing hotspots of antisense transcription. <i>Nucleic Acids Research</i> , 2007, 35, 1488-1500.	6.5	30
16	Lap2&alpha; Expression is Controlled by E2F and Deregulated in Various Human Tumors. <i>Cell Cycle</i> , 2006, 5, 1331-1341.	1.3	29
17	Role of the Mad2 Dimerization Interface in the Spindle Assembly Checkpoint Independent of Kinetochores. <i>Current Biology</i> , 2012, 22, 1900-1908.	1.8	26
18	Mining published lists of cancer related microarray experiments: Identification of a gene expression signature having a critical role in cell-cycle control. <i>BMC Bioinformatics</i> , 2005, 6, S14.	1.2	22

#	ARTICLE	IF	CITATIONS
19	E2F1-mediated transcriptional inhibition of the plasminogen activator inhibitor type 1 gene. FEBS Journal, 2001, 268, 4969-4978.	0.2	20
20	Identification and Analysis of Co-Occurrence Networks with NetCutter. PLoS ONE, 2008, 3, e3178.	1.1	20
21	Graph-based identification of cancer signaling pathways from published gene expression signatures using PubLiME. Nucleic Acids Research, 2007, 35, 2343-2355.	6.5	17
22	SMITH: a LIMS for handling next-generation sequencing workflows. BMC Bioinformatics, 2014, 15, S3.	1.2	16
23	GenePicker: replicate analysis of Affymetrix gene expression microarrays. Bioinformatics, 2004, 20, 3670-3672.	1.8	15
24	Targeted mutation screening of 292 candidate genes in 38 children with inborn haematological cytopenias efficiently identifies novel disease-causing mutations. British Journal of Haematology, 2018, 182, 251-258.	1.2	12
25	The MI bundle: enabling network and structural biology in genome visualization tools: Fig. 1.. Bioinformatics, 2015, 31, 3679-3681.	1.8	9
26	AnnotateGenomicRegions: a web application. BMC Bioinformatics, 2014, 15, S8.	1.2	8
27	TGF $\beta$ -dependent gene expression shows that senescence correlates with abortive differentiation along several lineages in Myc-induced lymphomas. Cell Cycle, 2010, 9, 4622-4626.	1.3	6
28	Genome and network visualization facilitates the analyses of the effects of drugs and mutations on protein-protein and drug-protein networks. BMC Bioinformatics, 2016, 17, 54.	1.2	4
29	Topological Properties of Co-Occurrence Networks in Published Gene Expression Signatures. Bioinformatics and Biology Insights, 2008, 2, BBI.S518.	1.0	3
30	Automated DNA chip annotation tables at IFOM: the importance of synchronisation and cross-referencing of sequence databases. Applied Bioinformatics, 2003, 2, 245-9.	1.7	2
31	Aberrant somatic hypermutation of CCND1 generates non-coding drivers of mantle cell lymphomagenesis. Cancer Gene Therapy, 2022, , .	2.2	1