Steffen Durinck

List of Publications by Year
in descending order

31 papers	11,902 citations	218381 26 h-index	414034 32 g-index
32 all docs	32 docs citations	32 times ranked	27417 citing authors

#	Article	IF	Citations
1	Determinants of renal cell carcinoma invasion and metastatic competence. Nature Communications, 2021, 12, 5760.	5.8	25
2	Embryonic lethality and defective mammary gland development of activator‐function impaired conditional knock‐in *Erbb3*^{*V943R*} mice. Genetics & Genomics Next, 2021, 2, e10036.	0.8	1
3	The Indian cobra reference genome and transcriptome enables comprehensive identification of venom toxins. Nature Genetics, 2020, 52, 106-117.	9.4	139
4	Accurate assembly of the olive baboon (*Papio anubis*) genome using long-read and Hi-C data. GigaScience, 2020, 9, .	3.3	18
5	Integrated genomic analysis reveals mutated ELF3 as a potential gallbladder cancer vaccine candidate. Nature Communications, 2020, 11, 4225.	5.8	47
6	Actionable Activating Oncogenic ERBB2/HER2 Transmembrane and Juxtamembrane Domain Mutations. Cancer Cell, 2018, 34, 792-806.e5.	7.7	102
7	ERK Mutations and Amplification Confer Resistance to ERK-Inhibitor Therapy. Clinical Cancer Research, 2018, 24, 4044-4055.	3.2	36
8	CRISPR off-target analysis in genetically engineered rats and mice. Nature Methods, 2018, 15, 512-514.	9.0	176
9	An Empirical Approach Leveraging Tumorgrafts to Dissect the Tumor Microenvironment in Renal Cell Carcinoma Identifies Missing Link to Prognostic Inflammatory Factors. Cancer Discovery, 2018, 8, 1142-1155.	7.7	138
10	Homozygous KSR1 deletion attenuates morbidity but does not prevent tumor development in a mouse model of RAS-driven pancreatic cancer. PLoS ONE, 2018, 13, e0194998.	1.1	4
11	Single-cell RNA sequencing identifies distinct mouse medial ganglionic eminence cell types. Scientific Reports, 2017, 7, 45656.	1.6	67
12	ÂÂÂSilencing of retrotransposons by SETDB1 inhibits the interferon response in acute myeloid leukemiaÂÂ. Journal of Cell Biology, 2017, 216, 3535-3549.	2.3	144
13	Comprehensive genomic analysis of malignant pleural mesothelioma identifies recurrent mutations, gene fusions and splicing alterations. Nature Genetics, 2016, 48, 407-416.	9.4	730
14	Targeting PTPRK-RSPO3 colon tumours promotes differentiation and loss of stem-cell function. Nature, 2016, 529, 97-100.	13.7	203
15	The BioMart community portal: an innovative alternative to large, centralized data repositories. Nucleic Acids Research, 2015, 43, W589-W598.	6.5	682
16	A comprehensive transcriptional portrait of human cancer cell lines. Nature Biotechnology, 2015, 33, 306-312.	9.4	556
17	Spectrum of diverse genomic alterations define non‐clear cell renal carcinoma subtypes. Nature Genetics, 2015, 47, 13-21.	9.4	310
18	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. Nature Communications, 2014, 5, 3830.	5.8	77

#	Article	IF	Citations
19	Oncogenic ERBB3 Mutations in Human Cancers. Cancer Cell, 2013, 23, 603-617.	7.7	318
20	Modeling precision treatment of breast cancer. Genome Biology, 2013, 14, R110.	13.9	264
21	Recurrent R-spondin fusions in colon cancer. Nature, 2012, 488, 660-664.	13.7	862
22	Comprehensive genomic analysis identifies SOX2 as a frequently amplified gene in small-cell lung cancer. Nature Genetics, 2012, 44, 1111-1116.	9.4	906
23	Subtype and pathway specific responses to anticancer compounds in breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2724-2729.	3.3	417
24	Temporal Dissection of Tumorigenesis in Primary Cancers. Cancer Discovery, 2011, 1, 137-143.	7.7	240
25	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. Molecular Cancer Research, 2010, 8, 961-974.	1.5	121
26	GenomeGraphs: integrated genomic data visualization with R. BMC Bioinformatics, 2009, 10, 2.	1.2	68
27	Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. Nature Protocols, 2009, 4, 1184-1191.	5.5	3,084
28	BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics, 2005, 21, 3439-3440.	1.8	1,781
29	Benchmarking the CATMA Microarray. A Novel Tool forArabidopsis Transcriptome Analysis. Plant Physiology, 2005, 137, 588-601.	2.3	91
30	Importing MAGE-ML format microarray data into BioConductor. Bioinformatics, 2004, 20, 3641-3642.	1.8	8
31	Versatile Gene-Specific Sequence Tags for Arabidopsis Functional Genomics: Transcript Profiling and Reverse Genetics Applications. Genome Research, 2004, 14, 2176-2189.	2.4	282