

# Steffen Durinck

## List of Publications by Year in descending order

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Version: 2024-02-01

31  
papers

11,902  
citations

218677

26  
h-index

414414

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.	12.8	25
2	Embryonic lethality and defective mammary gland development of activatorâ€œfunction impaired conditional knockâ€œin <i>ErbB3</i> <sup>V943R</sup> mice. Genetics & Genomics Next, 2021, 2, e10036.	1.5	1
3	The Indian cobra reference genome and transcriptome enables comprehensive identification of venom toxins. Nature Genetics, 2020, 52, 106-117.	21.4	139
4	Accurate assembly of the olive baboon ( <i>Papio anubis</i> ) genome using long-read and Hi-C data. GigaScience, 2020, 9, .	6.4	18
5	Integrated genomic analysis reveals mutated ELF3 as a potential gallbladder cancer vaccine candidate. Nature Communications, 2020, 11, 4225.	12.8	47
6	Actionable Activating Oncogenic ERBB2/HER2 Transmembrane and Juxtamembrane Domain Mutations. Cancer Cell, 2018, 34, 792-806.e5.	16.8	102
7	ERK Mutations and Amplification Confer Resistance to ERK-Inhibitor Therapy. Clinical Cancer Research, 2018, 24, 4044-4055.	7.0	36
8	CRISPR off-target analysis in genetically engineered rats and mice. Nature Methods, 2018, 15, 512-514.	19.0	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.	9.4	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.	2.5	4
11	Single-cell RNA sequencing identifies distinct mouse medial ganglionic eminence cell types. Scientific Reports, 2017, 7, 45656.	3.3	67
12	â€œSilencing of retrotransposons by SETDB1 inhibits the interferon response in acute myeloid leukemiaâ€œ. Journal of Cell Biology, 2017, 216, 3535-3549.	5.2	144
13	Comprehensive genomic analysis of malignant pleural mesothelioma identifies recurrent mutations, gene fusions and splicing alterations. Nature Genetics, 2016, 48, 407-416.	21.4	730
14	Targeting PTPRK-RSPO3 colon tumours promotes differentiation and loss of stem-cell function. Nature, 2016, 529, 97-100.	27.8	203
15	The BioMart community portal: an innovative alternative to large, centralized data repositories. Nucleic Acids Research, 2015, 43, W589-W598.	14.5	682
16	A comprehensive transcriptional portrait of human cancer cell lines. Nature Biotechnology, 2015, 33, 306-312.	17.5	556
17	Spectrum of diverse genomic alterations define nonâ€œclear cell renal carcinoma subtypes. Nature Genetics, 2015, 47, 13-21.	21.4	310
18	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. Nature Communications, 2014, 5, 3830.	12.8	77

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19	Oncogenic ERBB3 Mutations in Human Cancers. <i>Cancer Cell</i> , 2013, 23, 603-617.	16.8	318
20	Modeling precision treatment of breast cancer. <i>Genome Biology</i> , 2013, 14, R110.	9.6	264
21	Recurrent R-spondin fusions in colon cancer. <i>Nature</i> , 2012, 488, 660-664.	27.8	862
22	Comprehensive genomic analysis identifies SOX2 as a frequently amplified gene in small-cell lung cancer. <i>Nature Genetics</i> , 2012, 44, 1111-1116.	21.4	906
23	Subtype and pathway specific responses to anticancer compounds in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2724-2729.	7.1	417
24	Temporal Dissection of Tumorigenesis in Primary Cancers. <i>Cancer Discovery</i> , 2011, 1, 137-143.	9.4	240
25	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. <i>Molecular Cancer Research</i> , 2010, 8, 961-974.	3.4	121
26	GenomeGraphs: integrated genomic data visualization with R. <i>BMC Bioinformatics</i> , 2009, 10, 2.	2.6	68
27	Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt. <i>Nature Protocols</i> , 2009, 4, 1184-1191.	12.0	3,084
28	BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. <i>Bioinformatics</i> , 2005, 21, 3439-3440.	4.1	1,781
29	Benchmarking the CATMA Microarray. A Novel Tool for Arabidopsis Transcriptome Analysis. <i>Plant Physiology</i> , 2005, 137, 588-601.	4.8	91
30	Importing MAGE-ML format microarray data into BioConductor. <i>Bioinformatics</i> , 2004, 20, 3641-3642.	4.1	8
31	Versatile Gene-Specific Sequence Tags for Arabidopsis Functional Genomics: Transcript Profiling and Reverse Genetics Applications. <i>Genome Research</i> , 2004, 14, 2176-2189.	5.5	282