Matthias Ziehm

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	MYCN mediates cysteine addiction and sensitizes neuroblastoma to ferroptosis. Nature Cancer, 2022, 3, 471-485.	5.7	73
2	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. Nature Communications, 2021, 12, 1269.	5.8	46
3	Comprehensive micro-scaled proteome and phosphoproteome characterization of archived retrospective cancer repositories. Nature Communications, 2021, 12, 3576.	5.8	39
4	Neuroblastoma signalling models unveil combination therapies targeting feedback-mediated resistance. PLoS Computational Biology, 2021, 17, e1009515.	1.5	5
5	Proteomic Analysis Reveals Upregulation of ACE2 (Angiotensin-Converting Enzyme 2), the Putative SARS-CoV-2 Receptor in Pressure–but Not Volume-Overloaded Human Hearts. Hypertension, 2020, 76, e41-e43.	1.3	6
6	Drug repurposing for aging research using model organisms. Aging Cell, 2017, 16, 1006-1015.	3.0	34
7	Two forms of death in ageing Caenorhabditis elegans. Nature Communications, 2017, 8, 15458.	5.8	73
8	Longevity GWAS Using the <i>Drosophila</i> Genetic Reference Panel. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 1470-1478.	1.7	105
9	SurvCurv database and online survival analysis platform update. Bioinformatics, 2015, 31, 3878-3880.	1.8	13
10	MDL-1, a growth- and tumor-suppressor, slows aging and prevents germline hyperplasia and hypertrophy in C. elegans. Aging, 2014, 6, 98-117.	1.4	27
11	Analysing variation in <i><scp>D</scp>rosophila</i> aging across independent experimental studies: a metaâ€analysis of survival data. Aging Cell, 2013, 12, 917-922.	3.0	27
12	Transcriptional feedback in the insulin signalling pathway modulates ageing in both Caenorhabditis elegans and Drosophila melanogaster. Molecular BioSystems, 2013, 9, 1756.	2.9	4
13	Unlocking the potential of survival data for model organisms through a new database and online analysis platform: <scp>S</scp> urv <scp>C</scp> urv. Aging Cell, 2013, 12, 910-916.	3.0	24
14	Using Answer Set Programming to Integrate RNA Expression with Signalling Pathway Information to Infer How Mutations Affect Ageing. PLoS ONE, 2012, 7, e50881.	1.1	13
15	POPISK: T-cell reactivity prediction using support vector machines and string kernels. BMC Bioinformatics, 2011, 12, 446.	1.2	79
16	T-cell epitope prediction based on self-tolerance. , 2011, , .		5
17	Computational biology for ageing. Philosophical Transactions of the Royal Society B: Biological Sciences, 2011, 366, 51-63.	1.8	35