

Florian Heigwer

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

2,454
citations

706676

14
h-index

993246

17
g-index

35
all docs

35
docs citations

35
times ranked

4892
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 infection induces a pro-inflammatory cytokine response through cGAS-STING and NF- κ B. <i>Communications Biology</i> , 2022, 5, 45.	2.0	133
2	Cloud-Based Design of Short Guide RNA (sgRNA) Libraries for CRISPR Experiments. <i>Methods in Molecular Biology</i> , 2021, 2162, 3-22.	0.4	0
3	A large-scale resource for tissue-specific CRISPR mutagenesis in <i>Drosophila</i> . <i>ELife</i> , 2020, 9, .	2.8	115
4	Toward an integrated map of genetic interactions in cancer cells. <i>Molecular Systems Biology</i> , 2018, 14, e7656.	3.2	64
5	RNA Interference (RNAi) Screening in <i>Drosophila</i> . <i>Genetics</i> , 2018, 208, 853-874.	1.2	90
6	Machine learning and image-based profiling in drug discovery. <i>Current Opinion in Systems Biology</i> , 2018, 10, 43-52.	1.3	128
7	Time-resolved mapping of genetic interactions to model rewiring of signaling pathways. <i>ELife</i> , 2018, 7, .	2.8	21
8	HTSvis: a web app for exploratory data analysis and visualization of arrayed high-throughput screens. <i>Bioinformatics</i> , 2017, 33, 2960-2962.	1.8	5
9	Data-analysis strategies for image-based cell profiling. <i>Nature Methods</i> , 2017, 14, 849-863.	9.0	535
10	GenomeCRISPR - a database for high-throughput CRISPR/Cas9 screens. <i>Nucleic Acids Research</i> , 2017, 45, D679-D686.	6.5	65
11	Abstract 5766: High-content microscopy-based screening of colorectal organoids. , 2017, , .		0
12	Abstract A10: CRISPR-AnalyzeR (caR): Web-based, interactive and exploratory analysis and documentation of pooled CRISPR/Cas9 screens. , 2017, , .		0
13	Abstract B16: Epistatic mapping of signaling and chromatin regulators. , 2017, , .		0
14	Abstract B06: HTSvis: An user-friendly application for analysis of arrayed high-throughput experiments by interactive data representations. , 2017, , .		0
15	Abstract A23: Multi-parametric genetic interactions map dynamic genetic network rewiring upon anti-proliferative treatment. , 2017, , .		0
16	CRISPR library designer (CLD): software for multispecies design of single guide RNA libraries. <i>Genome Biology</i> , 2016, 17, 55.	3.8	68
17	caRpools: an R package for exploratory data analysis and documentation of pooled CRISPR/Cas9 screens. <i>Bioinformatics</i> , 2016, 32, 632-634.	1.8	54
18	Microscopy-Based High-Content Screening. <i>Cell</i> , 2015, 163, 1314-1325.	13.5	312

#	ARTICLE	IF	CITATIONS
19	E-CRISP: fast CRISPR target site identification. <i>Nature Methods</i> , 2014, 11, 122-123.	9.0	719
20	E-TALEN: a web tool to design TALENs for genome engineering. <i>Nucleic Acids Research</i> , 2013, 41, e190-e190.	6.5	60
21	Acetic acid treatment in <i>S. cerevisiae</i> creates significant energy deficiency and nutrient starvation that is dependent on the activity of the mitochondrial transcriptional complex Hap2-3-4-5. <i>Frontiers in Oncology</i> , 2012, 2, 118.	1.3	18
22	KOMA: ELISA-microarray calibration and data analysis based on kinetic signal amplification. <i>Journal of Immunological Methods</i> , 2012, 380, 10-15.	0.6	10
23	Microarray-based kinetic colorimetric detection for quantitative multiplex protein phosphorylation analysis. <i>Proteomics</i> , 2011, 11, 2129-2133.	1.3	14
24	Targeting euchromatic histone lysine methyltransferases sensitizes colorectal cancer to histone deacetylase inhibitors. <i>International Journal of Cancer</i> , 0, , .	2.3	2