Florian Heigwer

List of Publications by Year
in descending order

24 papers	2,454 citations	623699 14 h-index	888047 17 g-index
35 all docs	35 docs citations	35 times ranked	4385 citing authors

#	Article	IF	Citations
1	SARS-CoV-2 infection induces a pro-inflammatory cytokine response through cGAS-STING and NF-κB. Communications Biology, 2022, 5, 45.	4.4	133
2	Cloud-Based Design of Short Guide RNA (sgRNA) Libraries for CRISPR Experiments. Methods in Molecular Biology, 2021, 2162, 3-22.	0.9	0
3	A large-scale resource for tissue-specific CRISPR mutagenesis in Drosophila. ELife, 2020, 9, .	6.0	115
4	Toward an integrated map of genetic interactions in cancer cells. Molecular Systems Biology, 2018, 14, e7656.	7.2	64
5	RNA Interference (RNAi) Screening in <i>Drosophila</i>. Genetics, 2018, 208, 853-874.	2.9	90
6	Machine learning and image-based profiling in drug discovery. Current Opinion in Systems Biology, 2018, 10, 43-52.	2.6	128
7	Time-resolved mapping of genetic interactions to model rewiring of signaling pathways. ELife, 2018, 7, .	6.0	21
8	HTSvis: a web app for exploratory data analysis and visualization of arrayed high-throughput screens. Bioinformatics, 2017, 33, 2960-2962.	4.1	5
9	Data-analysis strategies for image-based cell profiling. Nature Methods, 2017, 14, 849-863.	19.0	535
10	GenomeCRISPR - a database for high-throughput CRISPR/Cas9 screens. Nucleic Acids Research, 2017, 45, D679-D686.	14.5	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. Genome Biology, 2016, 17, 55.	8.8	68
17	caRpools: an R package for exploratory data analysis and documentation of pooled CRISPR/Cas9 screens. Bioinformatics, 2016, 32, 632-634.	4.1	54
18	Microscopy-Based High-Content Screening. Cell, 2015, 163, 1314-1325.	28.9	312

#	Article	IF	Citations
19	E-CRISP: fast CRISPR target site identification. Nature Methods, 2014, 11, 122-123.	19.0	719
20	E-TALEN: a web tool to design TALENs for genome engineering. Nucleic Acids Research, 2013, 41, e190-e190.	14.5	60
21	Acetic acid treatment in S. cerevisiae creates significant energy deficiency and nutrient starvation that is dependent on the activity of the mitochondrial transcriptional complex Hap2-3-4-5. Frontiers in Oncology, 2012, 2, 118.	2.8	18
22	KOMA: ELISA-microarray calibration and data analysis based on kinetic signal amplification. Journal of Immunological Methods, 2012, 380, 10-15.	1.4	10
23	Microarrayâ€based kinetic colorimetric detection for quantitative multiplex protein phosphorylation analysis. Proteomics, 2011, 11, 2129-2133.	2.2	14
24	Targeting euchromatic histone lysine methyltransferases sensitizes colorectal cancer to histone deacetylase inhibitors. International Journal of Cancer, 0, , .	5.1	2