

Traver Hart

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

6,510
citations

172457

29
h-index

182427

51
g-index

72
all docs

72
docs citations

72
times ranked

11021
citing authors

#	ARTICLE	IF	CITATIONS
1	HumanNet v3: an improved database of human gene networks for disease research. <i>Nucleic Acids Research</i> , 2022, 50, D632-D639.	14.5	53
2	Genome-wide CRISPR screens using isogenic cells reveal vulnerabilities conferred by loss of tumor suppressors. <i>Science Advances</i> , 2022, 8, eabm6638.	10.3	17
3	Integrated screens uncover a cell surface tumor suppressor gene <i>KIRREL</i> involved in Hippo pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	10
4	Dynamic rewiring of biological activity across genotype and lineage revealed by context-dependent functional interactions. <i>Genome Biology</i> , 2022, 23, .	8.8	9
5	Genetic vulnerabilities upon inhibition of DNA damage response. <i>Nucleic Acids Research</i> , 2021, 49, 8214-8231.	14.5	17
6	AR-negative prostate cancer is vulnerable to loss of JMJD1C demethylase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	6
7	Improved analysis of CRISPR fitness screens and reduced off-target effects with the BAGEL2 gene essentiality classifier. <i>Genome Medicine</i> , 2021, 13, 2.	8.2	60
8	Discovery of putative tumor suppressors from CRISPR screens reveals rewired lipid metabolism in acute myeloid leukemia cells. <i>Nature Communications</i> , 2021, 12, 6506.	12.8	13
9	Common computational tools for analyzing CRISPR screens. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 779-788.	2.6	10
10	Multiplex enCas12a screens detect functional buffering among paralogs otherwise masked in monogenic Cas9 knockout screens. <i>Genome Biology</i> , 2020, 21, 262.	8.8	62
11	Copper bioavailability is a KRAS-specific vulnerability in colorectal cancer. <i>Nature Communications</i> , 2020, 11, 3701.	12.8	128
12	C17orf53 is identified as a novel gene involved in inter-strand crosslink repair. <i>DNA Repair</i> , 2020, 95, 102946.	2.8	14
13	Functional genomic landscape of cancer-intrinsic evasion of killing by T cells. <i>Nature</i> , 2020, 586, 120-126.	27.8	249
14	DNA polymerase $\hat{1}$ compensates for Fanconi anemia pathway deficiency by countering DNA replication stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33436-33445.	7.1	13
15	CRISPR/CAS9-based DNA damage response screens reveal gene-drug interactions. <i>DNA Repair</i> , 2020, 87, 102803.	2.8	23
16	Genome-wide In Vivo CNS Screening Identifies Genes that Modify CNS Neuronal Survival and mHTT Toxicity. <i>Neuron</i> , 2020, 106, 76-89.e8.	8.1	62
17	Genome-wide CRISPR screen uncovers a synergistic effect of combining Haspin and Aurora kinase B inhibition. <i>Oncogene</i> , 2020, 39, 4312-4322.	5.9	16
18	IPO11 mediates $\hat{2}$ catenin nuclear import in a subset of colorectal cancers. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	27

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19	Identifying chemogenetic interactions from CRISPR screens with drugZ. <i>Genome Medicine</i> , 2019, 11, 52.	8.2	127
20	Pooled library screening with multiplexed Cpf1 library. <i>Nature Communications</i> , 2019, 10, 3144.	12.8	37
21	A consensus set of genetic vulnerabilities to ATR inhibition. <i>Open Biology</i> , 2019, 9, 190156.	3.6	81
22	Genome-Wide CRISPR-Cas9 Screens Expose Genetic Vulnerabilities and Mechanisms of Temozolomide Sensitivity in Glioblastoma Stem Cells. <i>Cell Reports</i> , 2019, 27, 971-986.e9.	6.4	139
23	Chemogenetic interactions in human cancer cells. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1318-1325.	4.1	8
24	HumanNet v2: human gene networks for disease research. <i>Nucleic Acids Research</i> , 2019, 47, D573-D580.	14.5	161
25	A network of human functional gene interactions from knockout fitness screens in cancer cells. <i>Life Science Alliance</i> , 2019, 2, e201800278.	2.8	81
26	PICKLES: the database of pooled in-vitro CRISPR knockout library essentiality screens. <i>Nucleic Acids Research</i> , 2018, 46, D776-D780.	14.5	74
27	Microdroplet PCR for Highly Multiplexed Targeted Bisulfite Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1708, 333-348.	0.9	2
28	Expression of the miR-150 tumor suppressor is restored by and synergizes with rapamycin in a human leukemia T-cell line. <i>Leukemia Research</i> , 2018, 74, 1-9.	0.8	9
29	CRISPR screens identify genomic ribonucleotides as a source of PARP-trapping lesions. <i>Nature</i> , 2018, 559, 285-289.	27.8	297
30	The shieldin complex mediates 53BP1-dependent DNA repair. <i>Nature</i> , 2018, 560, 117-121.	27.8	445
31	Identification of FZD5 as Genetic Vulnerability in RNF43 Mutant Cancer. <i>FASEB Journal</i> , 2018, 32, 804.31.	0.5	0
32	All for One, and One for All. <i>Cell Systems</i> , 2017, 5, 314-316.	6.2	2
33	Evaluation and Design of Genome-Wide CRISPR/SpCas9 Knockout Screens. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2719-2727.	1.8	417
34	Genome-wide CRISPR screens reveal a Wnt- β -catenin-FZD5 signaling circuit as a druggable vulnerability of RNF43-mutant pancreatic tumors. <i>Nature Medicine</i> , 2017, 23, 60-68.	30.7	261
35	BAGEL: a computational framework for identifying essential genes from pooled library screens. <i>BMC Bioinformatics</i> , 2016, 17, 164.	2.6	216
36	Extensive mapping of an innate immune network with CRISPR. <i>Molecular Systems Biology</i> , 2015, 11, 821.	7.2	2

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37	Genome-wide CRISPR-Cas9 Screens Reveal Loss of Redundancy between PKMYT1 and WEE1 in Glioblastoma Stem-like Cells. <i>Cell Reports</i> , 2015, 13, 2425-2439.	6.4	146
38	Defining CD4 T Cell Memory by the Epigenetic Landscape of CpG DNA Methylation. <i>Journal of Immunology</i> , 2015, 194, 1565-1579.	0.8	59
39	Natural Variation in Gene Expression Modulates the Severity of Mutant Phenotypes. <i>Cell</i> , 2015, 162, 391-402.	28.9	129
40	High-Resolution CRISPR Screens Reveal Fitness Genes and Genotype-Specific Cancer Liabilities. <i>Cell</i> , 2015, 163, 1515-1526.	28.9	1,339
41	Genome-wide RNAi analysis reveals that simultaneous inhibition of specific mevalonate pathway genes potentiates tumor cell death. <i>Oncotarget</i> , 2015, 6, 26909-26921.	1.8	52
42	Measuring error rates in genomic perturbation screens: gold standards for human functional genomics. <i>Molecular Systems Biology</i> , 2014, 10, 733.	7.2	322
43	Finding the active genes in deep RNA-seq gene expression studies. <i>BMC Genomics</i> , 2013, 14, 778.	2.8	193
44	Scaling up the systematic hunt for mammalian genetic interactions. <i>Nature Methods</i> , 2013, 10, 397-399.	19.0	4
45	A Census of Human Soluble Protein Complexes. <i>Cell</i> , 2012, 150, 1068-1081.	28.9	781
46	Method for improved Illumina sequencing library preparation using NuGEN Ovation RNA-Seq System. <i>BioTechniques</i> , 2011, 50, 177-181.	1.8	27
47	Application of microdroplet PCR for large-scale targeted bisulfite sequencing. <i>Genome Research</i> , 2011, 21, 1738-1745.	5.5	36
48	MicroRNA Regulation of Molecular Networks Mapped by Global MicroRNA, mRNA, and Protein Expression in Activated T Lymphocytes. <i>Journal of Immunology</i> , 2011, 187, 2233-2243.	0.8	86
49	Systematic Definition of Protein Constituents along the Major Polarization Axis Reveals an Adaptive Reuse of the Polarization Machinery in Pheromone-Treated Budding Yeast. <i>Journal of Proteome Research</i> , 2009, 8, 6-19.	3.7	28
50	Human Cell Chips: Adapting DNA Microarray Spotting Technology to Cell-Based Imaging Assays. <i>PLoS ONE</i> , 2009, 4, e7088.	2.5	22
51	A map of human protein interactions derived from co-expression of human mRNAs and their orthologs. <i>Molecular Systems Biology</i> , 2008, 4, 180.	7.2	77
52	Systematic profiling of cellular phenotypes and gene function using spotted cellular microarrays. <i>FASEB Journal</i> , 2006, 20, LB61.	0.5	0
53	The Functional Genomic Circuitry of Human Glioblastoma Stem Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0