

Harold E Smith

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

1,373
citations

567144

15
h-index

610775

24
g-index

29
all docs

29
docs citations

29
times ranked

1827
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutation Mapping and Identification by Whole-Genome Sequencing. <i>Methods in Molecular Biology</i> , 2022, 2468, 257-269.	0.4	3
2	Dynamic sex chromosome expression in <i>Drosophila</i> male germ cells. <i>Nature Communications</i> , 2021, 12, 892.	5.8	53
3	A complement factor H homolog, heparan sulfation, and syndecan maintain inversin compartment boundaries in <i>C. elegans</i> cilia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2016698118.	3.3	1
4	The MLK-1/SCD-4 Mixed Lineage Kinase/MAP3K functions to promote dauer formation upstream of DAF-2/InsR. <i>MicroPublication Biology</i> , 2021, 2021, .	0.1	0
5	Mutation of NEKL-4/NEK10 and TLL genes suppress neuronal ciliary degeneration caused by loss of CCPP-1 deglutamylase function. <i>PLoS Genetics</i> , 2020, 16, e1009052.	1.5	15
6	Identification of Suppressors of <i>top-2</i> Embryonic Lethality in <i>Caenorhabditis elegans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1183-1191.	0.8	6
7	Cytosine base editor 4 but not adenine base editor generates off-target mutations in mouse embryos. <i>Communications Biology</i> , 2020, 3, 19.	2.0	41
8	Simultaneous targeting of linked loci in mouse embryos using base editing. <i>Scientific Reports</i> , 2019, 9, 1662.	1.6	12
9	Mutation frequency is not increased in CRISPR-Cas9-edited mice. <i>Nature Methods</i> , 2018, 15, 756-758.	9.0	38
10	Evaluating alignment and variant-calling software for mutation identification in <i>C. elegans</i> by whole-genome sequencing. <i>PLoS ONE</i> , 2017, 12, e0174446.	1.1	21
11	Mapping Challenging Mutations by Whole-Genome Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1297-1304.	0.8	19
12	The E2F-DP1 Transcription Factor Complex Regulates Centriole Duplication in <i>Caenorhabditis elegans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 709-720.	0.8	14
13	The Identification of a Novel Mutant Allele of <i>topoisomerase II</i> in <i>Caenorhabditis elegans</i> Reveals a Unique Role in Chromosome Segregation During Spermatogenesis. <i>Genetics</i> , 2016, 204, 1407-1422.	1.2	35
14	The Paired-box protein PAX-3 regulates the choice between lateral and ventral epidermal cell fates in <i>C. elegans</i> . <i>Developmental Biology</i> , 2016, 412, 191-207.	0.9	11
15	Rapid and Efficient Identification of <i>Caenorhabditis elegans</i> Legacy Mutations Using Hawaiian SNP-Based Mapping and Whole-Genome Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1007-1019.	0.8	23
16	Library Construction for Mutation Identification by Whole-Genome Sequencing. <i>Methods in Molecular Biology</i> , 2015, 1327, 1-9.	0.4	0
17	Identification of Suppressors of <i>mbk-2/DYRK</i> by Whole-Genome Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 231-241.	0.8	15
18	Scalable and Versatile Genome Editing Using Linear DNAs with Microhomology to Cas9 Sites in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2014, 198, 1347-1356.	1.2	292

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19	Nematode sperm motility. WormBook, 2014, , 1-15.	5.3	27
20	SPE-44 Implements Sperm Cell Fate. PLoS Genetics, 2012, 8, e1002678.	1.5	36
21	Identifying insertion mutations by whole-genome sequencing. BioTechniques, 2011, 50, 96-97.	0.8	14
22	Regulation of sperm gene expression by the GATA factor ELT-1. Developmental Biology, 2009, 333, 397-408.	0.9	22
23	E1 Ubiquitin-Activating Enzyme UBA-1 Plays Multiple Roles throughout C. elegans Development. PLoS Genetics, 2008, 4, e1000131.	1.5	55
24	The transcriptional response of Escherichia coli to recombinant protein insolubility. Journal of Structural and Functional Genomics, 2007, 8, 27-35.	1.2	29
25	Sperm motility and MSP. WormBook, 2006, , 1-8.	5.3	21
26	A Global Profile of Germline Gene Expression in C. elegans. Molecular Cell, 2000, 6, 605-616.	4.5	567