Harold E Smith

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A Global Profile of Germline Gene Expression in C. elegans. Molecular Cell, 2000, 6, 605-616.	4.5	567
2	Scalable and Versatile Genome Editing Using Linear DNAs with Microhomology to Cas9 Sites in <i>Caenorhabditis elegans</i> . Genetics, 2014, 198, 1347-1356.	1.2	292
3	E1 Ubiquitin-Activating Enzyme UBA-1 Plays Multiple Roles throughout C. elegans Development. PLoS Genetics, 2008, 4, e1000131.	1.5	55
4	Dynamic sex chromosome expression in Drosophila male germ cells. Nature Communications, 2021, 12, 892.	5.8	53
5	Cytosine base editor 4 but not adenine base editor generates off-target mutations in mouse embryos. Communications Biology, 2020, 3, 19.	2.0	41
6	Mutation frequency is not increased in CRISPR–Cas9-edited mice. Nature Methods, 2018, 15, 756-758.	9.0	38
7	SPE-44 Implements Sperm Cell Fate. PLoS Genetics, 2012, 8, e1002678.	1.5	36
8	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. Genetics, 2016, 204, 1407-1422.	1.2	35
9	The transcriptional response of Escherichia coli to recombinant protein insolubility. Journal of Structural and Functional Genomics, 2007, 8, 27-35.	1.2	29
10	Nematode sperm motility. WormBook, 2014, , 1-15.	5.3	27
11	Rapid and Efficient Identification of Caenorhabditis elegans Legacy Mutations Using Hawaiian SNP-Based Mapping and Whole-Genome Sequencing. G3: Genes, Genomes, Genetics, 2015, 5, 1007-1019.	0.8	23
12	Regulation of sperm gene expression by the GATA factor ELT-1. Developmental Biology, 2009, 333, 397-408.	0.9	22
13	Evaluating alignment and variant-calling software for mutation identification in C. elegans by whole-genome sequencing. PLoS ONE, 2017, 12, e0174446.	1.1	21
14	Sperm motility and MSP. WormBook, 2006, , 1-8.	5.3	21
15	Mapping Challenging Mutations by Whole-Genome Sequencing. G3: Genes, Genomes, Genetics, 2016, 6, 1297-1304.	0.8	19
16	Identification of Suppressors of <i>mbk-2/DYRK</i> by Whole-Genome Sequencing. G3: Genes, Genomes, Genetics, 2014, 4, 231-241.	0.8	15
17	Mutation of NEKL-4/NEK10 and TTLL genes suppress neuronal ciliary degeneration caused by loss of CCPP-1 deglutamylase function. PLoS Genetics, 2020, 16, e1009052.	1.5	15
18	Identifying insertion mutations by whole-genome sequencing. BioTechniques, 2011, 50, 96-97.	0.8	14

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19	The E2F-DP1 Transcription Factor Complex Regulates Centriole Duplication in <i>Caenorhabditis elegans</i> . G3: Genes, Genomes, Genetics, 2016, 6, 709-720.	0.8	14
20	Simultaneous targeting of linked loci in mouse embryos using base editing. Scientific Reports, 2019, 9, 1662.	1.6	12
21	The Paired-box protein PAX-3 regulates the choice between lateral and ventral epidermal cell fates in C. elegans. Developmental Biology, 2016, 412, 191-207.	0.9	11
22	ldentification of Suppressors of <i>top-2</i> Embryonic Lethality in <i>Caenorhabditis elegans</i> . G3: Genes, Genomes, Genetics, 2020, 10, 1183-1191.	0.8	6
23	Mutation Mapping and Identification by Whole-Genome Sequencing. Methods in Molecular Biology, 2022, 2468, 257-269.	0.4	3
24	A complement factor H homolog, heparan sulfation, and syndecan maintain inversin compartment boundaries in C. elegans cilia. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2016698118.	3.3	1
25	Library Construction for Mutation Identification by Whole-Genome Sequencing. Methods in Molecular Biology, 2015, 1327, 1-9.	0.4	0
26	The MLK-1/SCD-4 Mixed Lineage Kinase/MAP3K functions to promote dauer formation upstream of DAF-2/InsR. MicroPublication Biology, 2021, 2021, .	0.1	0