

Geoffrey G Hicks

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

3,731
citations

257450

24
h-index

330143

37
g-index

40
all docs

40
docs citations

40
times ranked

5649
citing authors

#	ARTICLE	IF	CITATIONS
1	Budget Impact Analysis of an Epigenetic Test Used for Diagnosing Fetal Alcohol Spectrum Disorder from the Perspective of a Laboratory Budget Holder in Manitoba, Canada. <i>Pharmacoeconomics - Open</i> , 2022, 6, 253-263.	1.8	1
2	A novel, ataxic mouse model of ataxia telangiectasia caused by a clinically relevant nonsense mutation. <i>ELife</i> , 2021, 10, .	6.0	11
3	Genomic Analysis of Localized High-Risk Prostate Cancer Circulating Tumor Cells at the Single-Cell Level. <i>Cells</i> , 2020, 9, 1863.	4.1	18
4	The Canadian Rare Diseases Models and Mechanisms (RDMM) Network: Connecting Understudied Genes to Model Organisms. <i>American Journal of Human Genetics</i> , 2020, 106, 143-152.	6.2	30
5	Genome-Wide Transcriptome Landscape of Embryonic Brain-Derived Neural Stem Cells Exposed to Alcohol with Strain-Specific Cross-Examination in BL6 and CD1 Mice. <i>Scientific Reports</i> , 2019, 9, 206.	3.3	25
6	Insights into retinoic acid deficiency and the induction of craniofacial malformations and microcephaly in fetal alcohol spectrum disorder. <i>Genesis</i> , 2019, 57, e23278.	1.6	37
7	Effects of prenatal alcohol exposure (PAE): insights into FASD using mouse models of PAE. <i>Biochemistry and Cell Biology</i> , 2018, 96, 131-147.	2.0	68
8	Copy number variation in fetal alcohol spectrum disorder. <i>Biochemistry and Cell Biology</i> , 2018, 96, 161-166.	2.0	15
9	Translating to the Community (T2C): a protocol paper describing the development of Canada's first social epigenetic FASD biobank. <i>Biochemistry and Cell Biology</i> , 2018, 96, 275-287.	2.0	3
10	ALS/FTD-Linked Mutation in FUS Suppresses Intra-axonal Protein Synthesis and Drives Disease Without Nuclear Loss-of-Function of FUS. <i>Neuron</i> , 2018, 100, 816-830.e7.	8.1	185
11	MicroRNA-200b regulates distal airway development by maintaining epithelial integrity. <i>Scientific Reports</i> , 2017, 7, 6382.	3.3	34
12	FUS/TLS acts as an aggregation-dependent modifier of polyglutamine disease model mice. <i>Scientific Reports</i> , 2016, 6, 35236.	3.3	17
13	FUS/TLS deficiency causes behavioral and pathological abnormalities distinct from amyotrophic lateral sclerosis. <i>Acta Neuropathologica Communications</i> , 2015, 3, 24.	5.2	82
14	FUS-regulated RNA metabolism and DNA damage repair. <i>Rare Diseases (Austin, Tex)</i> , 2014, 2, e29515.	1.8	26
15	ALS-Associated FUS Mutations Result in Compromised FUS Alternative Splicing and Autoregulation. <i>PLoS Genetics</i> , 2013, 9, e1003895.	3.5	166
16	Divergent roles of ALS-linked proteins FUS/TLS and TDP-43 intersect in processing long pre-mRNAs. <i>Nature Neuroscience</i> , 2012, 15, 1488-1497.	14.8	628
17	The mammalian gene function resource: the international knockout mouse consortium. <i>Mammalian Genome</i> , 2012, 23, 580-586.	2.2	292
18	A generalizable pre-clinical research approach for orphan disease therapy. <i>Orphanet Journal of Rare Diseases</i> , 2012, 7, 39.	2.7	32

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19	The emerging functions of the p53-miRNA network in stem cell biology. <i>Cell Cycle</i> , 2012, 11, 2063-2072.	2.6	39
20	miR-34 miRNAs provide a barrier for somatic cell reprogramming. <i>Nature Cell Biology</i> , 2011, 13, 1353-1360.	10.3	347
21	Identification and characterization of Dlc1 isoforms in the mouse and study of the biological function of a single gene trapped isoform. <i>BMC Biology</i> , 2010, 8, 17.	3.8	26
22	Cells deficient in oxidative DNA damage repair genes Myh and Ogg1 are sensitive to oxidants with increased G2/M arrest and multinucleation. <i>Carcinogenesis</i> , 2008, 29, 722-728.	2.8	47
23	Cells deficient in oxidative DNA damage repair genes Myh and Ogg1 are sensitive to oxidants with increased G2/M arrest and multinucleation. <i>Carcinogenesis</i> , 2008, 29, 2432-2432.	2.8	0
24	Regulation of the cellular DNA double-strand break response. <i>Biochemistry and Cell Biology</i> , 2007, 85, 663-674.	2.0	82
25	The International Gene Trap Consortium Website: a portal to all publicly available gene trap cell lines in mouse. <i>Nucleic Acids Research</i> , 2006, 34, D642-D648.	14.5	131
26	Absence of an Immediate G1/S Checkpoint in Primary MEFs Following γ -irradiation Identifies a Novel Checkpoint Switch. <i>Cell Cycle</i> , 2006, 5, 1823-1830.	2.6	13
27	TLS, EWS and TAF15: a model for transcriptional integration of gene expression. <i>Briefings in Functional Genomics & Proteomics</i> , 2006, 5, 8-14.	3.8	172
28	The RNA Binding Protein TLS Is Translocated to Dendritic Spines by mGluR5 Activation and Regulates Spine Morphology. <i>Current Biology</i> , 2005, 15, 587-593.	3.9	327
29	Activation of cryptic 3' splice sites within introns of cellular genes following gene entrapment. <i>Nucleic Acids Research</i> , 2004, 32, 2912-2924.	14.5	15
30	The High-Mobility-Group Box Protein SSRP1/T160 Is Essential for Cell Viability in Day 3.5 Mouse Embryos. <i>Molecular and Cellular Biology</i> , 2003, 23, 5301-5307.	2.3	65
31	Fus deficiency in mice results in defective B-lymphocyte development and activation, high levels of chromosomal instability and perinatal death. <i>Nature Genetics</i> , 2000, 24, 175-179.	21.4	265
32	Apoptosis in megaloblastic anemia occurs during DNA synthesis by a p53-independent, nucleoside-reversible mechanism. <i>Blood</i> , 2000, 96, 3249-3255.	1.4	62
33	Apoptosis in megaloblastic anemia occurs during DNA synthesis by a p53-independent, nucleoside-reversible mechanism. <i>Blood</i> , 2000, 96, 3249-3255.	1.4	1
34	Endogenous p53 regulation and function in early stage Friend virus-induced tumor progression differs from that following DNA damage. <i>Oncogene</i> , 1998, 17, 1119-1130.	5.9	15
35	Functional genomics in mice by tagged sequence mutagenesis. <i>Nature Genetics</i> , 1997, 16, 338-344.	21.4	119
36	H2-M Mutant Mice Are Defective in the Peptide Loading of Class II Molecules, Antigen Presentation, and T Cell Repertoire Selection. <i>Cell</i> , 1996, 84, 543-550.	28.9	316

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37	[17] Retrovirus gene traps. <i>Methods in Enzymology</i> , 1995, 254, 263-275.	1.0	9