

Frédéric Chalmel

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

3,758
citations

136885

32
h-index

138417

58
g-index

86
all docs

86
docs citations

86
times ranked

5736
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptomic analysis in zebrafish larvae identifies iron-dependent mitochondrial dysfunction as a possible key event of NAFLD progression induced by benzo[a]pyrene/ethanol co-exposure. <i>Cell Biology and Toxicology</i> , 2023, 39, 371-390.	2.4	7
2	FlexDotPlot: a universal and modular dot plot visualization tool for complex multifaceted data. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	1
3	PFOS-induced thyroid hormone system disrupted rats display organ-specific changes in their transcriptomes. <i>Environmental Pollution</i> , 2022, 305, 119340.	3.7	22
4	Multiple metastatic clones assessed by an integrative multiomics strategy in clear cell renal carcinoma: a case study. <i>Journal of Clinical Pathology</i> , 2022, 75, 426-430.	1.0	2
5	Understanding the Underlying Molecular Mechanisms of Meiotic Arrest during In Vitro Spermatogenesis in Rat Prepubertal Testicular Tissue. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5893.	1.8	3
6	Transcriptome analysis of fetal rat testis following intrauterine exposure to the azole fungicides triticonazole and flusilazole reveals subtle changes despite adverse endocrine effects. <i>Chemosphere</i> , 2021, 264, 128468.	4.2	19
7	Cooperative Blockade of CK2 and ATM Kinases Drives Apoptosis in VHL-Deficient Renal Carcinoma Cells through ROS Overproduction. <i>Cancers</i> , 2021, 13, 576.	1.7	19
8	Sperm proteins and cancer testis antigens are released by the seminiferous tubules in mice and men. <i>FASEB Journal</i> , 2021, 35, e21397.	0.2	14
9	Adult female rats perinatally exposed to perfluorohexane sulfonate (PFHxS) and a mixture of endocrine disruptors display increased body/fat weights without a transcriptional footprint in fat cells. <i>Toxicology Letters</i> , 2021, 339, 78-87.	0.4	3
10	Combined RNA/tissue profiling identifies novel Cancer/testis genes. <i>Molecular Oncology</i> , 2021, 15, 3003-3023.	2.1	3
11	The Male Fertility Gene Atlas: a web tool for collecting and integrating OMICS data in the context of male infertility. <i>Human Reproduction</i> , 2020, 35, 1983-1990.	0.4	13
12	Dynamics of the transcriptional landscape during human fetal testis and ovary development. <i>Human Reproduction</i> , 2020, 35, 1099-1119.	0.4	22
13	Characterization of Glyceollins as Novel Aryl Hydrocarbon Receptor Ligands and Their Role in Cell Migration. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1368.	1.8	11
14	RNA profiling of human testicular cells identifies syntenic lncRNAs associated with spermatogenesis. <i>Human Reproduction</i> , 2019, 34, 1278-1290.	0.4	35
15	RUNX1 maintains the identity of the fetal ovary through an interplay with FOXL2. <i>Nature Communications</i> , 2019, 10, 5116.	5.8	59
16	Characterisation and localisation of the endocannabinoid system components in the adult human testis. <i>Scientific Reports</i> , 2019, 9, 12866.	1.6	48
17	Deciphering the Molecular Mechanisms Sustaining the Estrogenic Activity of the Two Major Dietary Compounds Zearalenone and Apigenin in ER-Positive Breast Cancer Cell Lines. <i>Nutrients</i> , 2019, 11, 237.	1.7	22
18	The ReproGenomics Viewer: a multi-omics and cross-species resource compatible with single-cell studies for the reproductive science community. <i>Bioinformatics</i> , 2019, 35, 3133-3139.	1.8	49

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19	Distinct Transcriptional Profiles of the Female, Male, and Finasteride-Induced Feminized Male Anogenital Region in Rat Fetuses. <i>Toxicological Sciences</i> , 2019, 169, 303-311.	1.4	10
20	New transcriptomic tools to understand testis development and functions. <i>Molecular and Cellular Endocrinology</i> , 2018, 468, 47-59.	1.6	14
21	TOXsgN: a cross-species repository for toxicogenomic signatures. <i>Bioinformatics</i> , 2018, 34, 2116-2122.	1.8	22
22	Metabolomics as a powerful tool to decipher the biological effects of environmental contaminants in humans. <i>Current Opinion in Toxicology</i> , 2018, 8, 48-56.	2.6	34
23	Exploiting advances in transcriptomics to improve on human-relevant toxicology. <i>Current Opinion in Toxicology</i> , 2018, 11-12, 43-50.	2.6	3
24	Genome-Wide Transcriptional and Functional Analysis of Human T Lymphocytes Treated with Benzo[\pm]pyrene. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3626.	1.8	13
25	Interplay between transcription regulators RUNX1 and FUBP1 activates an enhancer of the oncogene KIT and amplifies cell proliferation. <i>Nucleic Acids Research</i> , 2018, 46, 11214-11228.	6.5	28
26	Defining the human sperm microtubulome: an integrated genomics approach. <i>Biology of Reproduction</i> , 2017, 96, 93-106.	1.2	15
27	Cytosine modifications modulate the chromatin architecture of transcriptional enhancers. <i>Genome Research</i> , 2017, 27, 947-958.	2.4	34
28	Meiotic Genes Are Enriched in Regions of Reduced Archaic Ancestry. <i>Molecular Biology and Evolution</i> , 2017, 34, 1974-1980.	3.5	35
29	Two hematopoietic transcription factors, RUNX1 and FUBP1, control the expression of KIT oncogene in pre-B lymphoblasts. <i>Experimental Hematology</i> , 2017, 53, S112.	0.2	0
30	Evaluation of apoptotic- and autophagic-related protein expressions before and after IVM of fresh, slow-frozen and vitrified pre-pubertal mouse testicular tissue. <i>Molecular Human Reproduction</i> , 2017, 23, 738-754.	1.3	14
31	Glyceollins trigger anti-proliferative effects through estradiol-dependent and independent pathways in breast cancer cells. <i>Cell Communication and Signaling</i> , 2017, 15, 26.	2.7	21
32	Endogenous IL-33 Deficiency Exacerbates Liver Injury and Increases Hepatic Influx of Neutrophils in Acute Murine Viral Hepatitis. <i>Mediators of Inflammation</i> , 2017, 2017, 1-15.	1.4	9
33	PepPSy: a web server to prioritize gene products in experimental and biocuration workflows. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw070.	1.4	2
34	Cold/menthol TRPM8 receptors initiate the cold shock response and protect germ cells from cold-induced oxidation. <i>FASEB Journal</i> , 2016, 30, 3155-3170.	0.2	17
35	The epigenetic processes of meiosis in male mice are broadly affected by the widely used herbicide atrazine. <i>BMC Genomics</i> , 2015, 16, 885.	1.2	52
36	The ReproGenomics Viewer: an integrative cross-species toolbox for the reproductive science community. <i>Nucleic Acids Research</i> , 2015, 43, W109-W116.	6.5	46

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37	DICER Regulates the Formation and Maintenance of Cell-Cell Junctions in the Mouse Seminiferous Epithelium1. <i>Biology of Reproduction</i> , 2015, 93, 139.	1.2	27
38	Research Resource: The Dynamic Transcriptional Profile of Sertoli Cells During the Progression of Spermatogenesis. <i>Molecular Endocrinology</i> , 2015, 29, 627-642.	3.7	74
39	Combining RNA and Protein Profiling Data with Network Interactions Identifies Genes Associated with Spermatogenesis in Mouse and Human1. <i>Biology of Reproduction</i> , 2015, 92, 71.	1.2	24
40	Linking transcriptomics and proteomics in spermatogenesis. <i>Reproduction</i> , 2015, 150, R149-R157.	1.1	64
41	Androgen-regulated microRNA-135a decreases prostate cancer cell migration and invasion through downregulating ROCK1 and ROCK2. <i>Oncogene</i> , 2015, 34, 2846-2855.	2.6	106
42	C2orf62 and TTC17 Are Involved in Actin Organization and Ciliogenesis in Zebrafish and Human. <i>PLoS ONE</i> , 2014, 9, e86476.	1.1	19
43	An Integrative Omics Strategy to Assess the Germ Cell Secretome and to Decipher Sertoli-Germ Cell Crosstalk in the Mammalian Testis. <i>PLoS ONE</i> , 2014, 9, e104418.	1.1	18
44	Forty-Four Novel Protein-Coding Loci Discovered Using a Proteomics Informed by Transcriptomics (PIT) Approach in Rat Male Germ Cells1. <i>Biology of Reproduction</i> , 2014, 91, 123.	1.2	20
45	High-Resolution Profiling of Novel Transcribed Regions During Rat Spermatogenesis1. <i>Biology of Reproduction</i> , 2014, 91, 5.	1.2	50
46	An atlas of chromatoid body components. <i>Rna</i> , 2014, 20, 483-495.	1.6	92
47	Proteomics and integrative genomics for unraveling the mysteries of spermatogenesis: The strategies of a team. <i>Journal of Proteomics</i> , 2014, 107, 128-143.	1.2	15
48	Expression of HLA-G by mast cells is associated with hepatitis C virus-induced liver fibrosis. <i>Journal of Hepatology</i> , 2014, 60, 245-252.	1.8	58
49	Genome-wide identification of <i>Sox8</i> , and <i>Sox9</i> -dependent genes during early postnatal testis development in the mouse. <i>Andrology</i> , 2013, 1, 281-292.	1.9	14
50	Expression screening of cancer/testis genes in prostate cancer identifies nr6a1 as a novel marker of disease progression and aggressiveness. <i>Prostate</i> , 2013, 73, 1103-1114.	1.2	18
51	Profiling of Androgen Response in Rainbow Trout Pubertal Testis: Relevance to Male Gonad Development and Spermatogenesis. <i>PLoS ONE</i> , 2013, 8, e53302.	1.1	36
52	Systemic Compensatory Response to Neonatal Estradiol Exposure Does Not Prevent Depletion of the Oocyte Pool in the Rat. <i>PLoS ONE</i> , 2013, 8, e82175.	1.1	3
53	GPSy: a cross-species gene prioritization system for conserved biological processes" application in male gamete development. <i>Nucleic Acids Research</i> , 2012, 40, W458-W465.	6.5	20
54	Global human tissue profiling and protein network analysis reveals distinct levels of transcriptional germline-specificity and identifies target genes for male infertility. <i>Human Reproduction</i> , 2012, 27, 3233-3248.	0.4	82

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55	Execution of the meiotic noncoding RNA expression program and the onset of gametogenesis in yeast require the conserved exosome subunit Rrp6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1058-1063.	3.3	124
56	Role of miR-34c microRNA in the late steps of spermatogenesis. <i>Rna</i> , 2010, 16, 720-731.	1.6	239
57	GermOnline 4.0 is a genomics gateway for germline development, meiosis and the mitotic cell cycle. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq030-baq030.	1.4	40
58	Profiling spermatogenic failure in adult testes bearing Sox9-deficient Sertoli cells identifies genes involved in feminization, inflammation and stress. <i>Reproductive Biology and Endocrinology</i> , 2010, 8, 154.	1.4	11
59	Expression profiling of rainbow trout testis development identifies evolutionary conserved genes involved in spermatogenesis. <i>BMC Genomics</i> , 2009, 10, 546.	1.2	76
60	CLPH, a Novel Casein Kinase 2-Phosphorylated Disordered Protein, Is Specifically Associated with Postmeiotic Germ Cells in Rat Spermatogenesis. <i>Journal of Proteome Research</i> , 2009, 8, 2953-2965.	1.8	15
61	Fhl5/Act, a CREM-binding transcriptional activator required for normal sperm maturation and morphology, is not essential for testicular gene expression. <i>Reproductive Biology and Endocrinology</i> , 2009, 7, 133.	1.4	14
62	Temporally Regulated Traffic of HuR and Its Associated ARE-Containing mRNAs from the Chromatoid Body to Polysomes during Mouse Spermatogenesis. <i>PLoS ONE</i> , 2009, 4, e4900.	1.1	40
63	The Annotation, Mapping, Expression and Network (AMEN) suite of tools for molecular systems biology. <i>BMC Bioinformatics</i> , 2008, 9, 86.	1.2	73
64	Chromosomal Gene Movements Reflect the Recent Origin and Biology of Therian Sex Chromosomes. <i>PLoS Biology</i> , 2008, 6, e80.	2.6	182
65	Cross-platform gene expression signature of human spermatogenic failure reveals inflammatory-like response. <i>Human Reproduction</i> , 2007, 22, 2936-2946.	0.4	77
66	The conserved transcriptome in human and rodent male gametogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8346-8351.	3.3	234
67	Rod-derived Cone Viability Factor-2 is a novel bifunctional-thioredoxin-like protein with therapeutic potential. <i>BMC Molecular Biology</i> , 2007, 8, 74.	3.0	58
68	Design and evaluation of Actichip, a thematic microarray for the study of the actin cytoskeleton. <i>BMC Genomics</i> , 2007, 8, 294.	1.2	5
69	Toward Understanding the Core Meiotic Transcriptome in Mammals and Its Implications for Somatic Cancer. <i>Annals of the New York Academy of Sciences</i> , 2007, 1120, 1-15.	1.8	17
70	PromAn: an integrated knowledge-based web server dedicated to promoter analysis. <i>Nucleic Acids Research</i> , 2006, 34, W578-W583.	6.5	13
71	Polyglutamine expansion causes neurodegeneration by altering the neuronal differentiation program. <i>Human Molecular Genetics</i> , 2006, 15, 691-703.	1.4	67
72	Enhancer sequence conservation between vertebrates is favoured in developmental regulator genes. <i>Trends in Genetics</i> , 2005, 21, 207-210.	2.9	59

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73	GOAnno: GO annotation based on multiple alignment. <i>Bioinformatics</i> , 2005, 21, 2095-2096.	1.8	36
74	goCluster integrates statistical analysis and functional interpretation of microarray expression data. <i>Bioinformatics</i> , 2005, 21, 3575-3577.	1.8	24
75	Expression Profiling and Comparative Genomics Identify a Conserved Regulatory Region Controlling Midline Expression in the Zebrafish Embryo. <i>Genome Research</i> , 2004, 14, 228-238.	2.4	34
76	Identification and characterization of rod-derived cone viability factor. <i>Nature Genetics</i> , 2004, 36, 755-759.	9.4	463
77	Identification of genes associated with tumorigenesis and metastatic potential of hypopharyngeal cancer by microarray analysis. <i>Oncogene</i> , 2004, 23, 2484-2498.	2.6	242
78	PipeAlign: a new toolkit for protein family analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3829-3832.	6.5	108
79	Differential Proteomic Analysis of the Mouse Retina. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 494-505.	2.5	42
80	Atrazine exposure of adult mice affect spermatogenesis. <i>Reproduction Abstracts</i> , 0, , .	0.0	0