Sandrine Caburet

List of Publications by Year
in descending order

36 papers	2,064 citations	279798 23 h-index	330143 37 g-index
42 all docs	42 docs citations	42 times ranked	3427 citing authors

#	Article	IF	Citations
1	Forkhead transcription factors: key players in health and disease. Trends in Genetics, 2011, 27, 224-232.	6.7	267
2	Mutant Cohesin in Premature Ovarian Failure. New England Journal of Medicine, 2014, 370, 943-949.	27.0	244
3	Eucaryotic genome evolution through the spontaneous duplication of large chromosomal segments. EMBO Journal, 2004, 23, 234-243.	7.8	192
4	Human ribosomal RNA gene arrays display a broad range of palindromic structures. Genome Research, 2005, 15, 1079-1085.	5.5	126
5	A recurrent polyalanine expansion in the transcription factor FOXL2 induces extensive nuclear and cytoplasmic protein aggregation. Journal of Medical Genetics, 2004, 41, 932-936.	3.2	88
6	Transcription factor FOXL2 protects granulosa cells from stress and delays cell cycle: role of its regulation by the SIRT1 deacetylase. Human Molecular Genetics, 2011, 20, 1673-1686.	2.9	81
7	Generic binding sites, generic DNA‐binding domains: where does specific promoter recognition come from?. FASEB Journal, 2010, 24, 346-356.	0.5	74
8	Mechanisms of Mendelian dominance. Clinical Genetics, 2018, 93, 419-428.	2.0	70
9	STAG3 is a strong candidate gene for male infertility. Human Molecular Genetics, 2014, 23, 3421-3431.	2.9	69
10	The transcription factor FOXL2: At the crossroads of ovarian physiology and pathology. Molecular and Cellular Endocrinology, 2012, 356, 55-64.	3.2	67
11	Functional Exploration of the Adult Ovarian Granulosa Cell Tumor-Associated Somatic FOXL2 Mutation p.Cys134Trp (c.402C>G). PLoS ONE, 2010, 5, e8789.	2.5	67
12	A non‐sense <i><scp>MCM9</scp></i> mutation in a familial case of primary ovarian insufficiency. Clinical Genetics, 2016, 89, 603-607.	2.0	60
13	The identification and characterization of a FOXL2 response element provides insights into the pathogenesis of mutant alleles. Human Molecular Genetics, 2008, 17, 3118-3127.	2.9	58
14	A homozygous FANCM mutation underlies a familial case of non-syndromic primary ovarian insufficiency. ELife, 2017, 6, .	6.0	56
15	Molecular analyses of juvenile granulosa cell tumors bearing<i>AKT1</i>mutations provide insights into tumor biology and therapeutic leads. Human Molecular Genetics, 2015, 24, 6687-6698.	2.9	51
16	A truncating MEIOB mutation responsible for familial primary ovarian insufficiency abolishes its interaction with its partner SPATA22 and their recruitment to DNA double-strand breaks. EBioMedicine, 2019, 42, 524-531.	6.1	50
17	The genetic make‐up of ovarian development and function: the focus on the transcription factor <scp>FOXL2</scp>. Clinical Genetics, 2017, 91, 173-182.	2.0	45
18	Coding repeats and evolutionary â€œagilityâ€. BioEssays, 2005, 27, 581-587.	2.5	35

#	Article	IF	Citations
19	Combined comparative genomic hybridization and transcriptomic analyses of ovarian granulosa cell tumors point to novel candidate driver genes. BMC Cancer, 2015, 15, 251.	2.6	33
20	Combing the genome for genomic instability. Trends in Biotechnology, 2002, 20, 344-350.	9.3	30
21	A missense in HSF2BP causing primary ovarian insufficiency affects meiotic recombination by its novel interactor C19ORF57/BRME1. ELife, 2020, 9, .	6.0	29
22	Genome-Wide Linkage in a Highly Consanguineous Pedigree Reveals Two Novel Loci on Chromosome 7 for Non-Syndromic Familial Premature Ovarian Failure. PLoS ONE, 2012, 7, e33412.	2.5	28
23	A Genomic Basis for the Evolution of Vertebrate Transcription Factors Containing Amino Acid Runs. Genetics, 2004, 167, 1813-1820.	2.9	26
24	Homozygous hypomorphic *BRCA2* variant in primary ovarian insufficiency without cancer or Fanconi anaemia trait. Journal of Medical Genetics, 2021, 58, 125-134.	3.2	24
25	The post‚Äêtranslational modification profile of the forkhead transcription factor FOXL2 suggests the existence of parallel processive/concerted modification pathways. Proteomics, 2008, 8, 3118-3123.	2.2	21
26	Compositional Biases and Polyalanine Runs in Humans. Genetics, 2003, 165, 1613-1617.	2.9	21
27	Allelic reduction of Dlx5 and Dlx6 results in early follicular depletion: a new mouse model of primary ovarian insufficiency. Human Molecular Genetics, 2011, 20, 2642-2650.	2.9	20
28	A homozygous mutation of GNRHR in a familial case diagnosed with polycystic ovary syndrome. European Journal of Endocrinology, 2017, 176, K9-K14.	3.7	20
29	A novel variant of *DHH* in a familial case of 46,XY disorder of sex development: Insights from molecular dynamics simulations. Clinical Endocrinology, 2017, 87, 539-544.	2.4	19
30	Premature ovarian failure and forkhead transcription factor FOXL2: blepharophimosis-ptosis-epicanthus inversus syndrome and ovarian dysfunction. Pediatric Endocrinology Reviews, 2005, 2, 653-60.	1.2	19
31	Molecular Combing. Current Protocols in Cytometry, 2001, 16, Unit 8.10.	3.7	14
32	Natural and molecular history of prolactinoma: insights from a *Prlr*-/‚Äì mouse model. Oncotarget, 2018, 9, 6144-6155.	1.8	14
33	Conventional and unconventional interactions of the transcription factor FOXL2 uncovered by a proteome‚Äêwide analysis. FASEB Journal, 2020, 34, 571-587.	0.5	11
34	An exome‚Äêwide exploration of cases of primary ovarian insufficiency uncovers novel sequence variants and candidate genes. Clinical Genetics, 2020, 98, 293-298.	2.0	11
35	Extensive sequence turnover of the signal peptides of members of the GDF/BMP family: exploring their evolutionary landscape. Biology Direct, 2009, 4, 22.	4.6	8
36	Targeting the molecular mechanism of DNA replication. Drug Discovery Today, 2001, 6, 786-792.	6.4	4