Sandrine Caburet

List of Publications by Year
in descending order

36	2,064	279798 23	330143 37
papers	citations	h-index	g-index

42	42	42	3427
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Conventional and unconventional interactions of the transcription factor FOXL2 uncovered by a proteomeâ€wide analysis. FASEB Journal, 2020, 34, 571-587.	0.5	11
3	An exomeâ€wide exploration of cases of primary ovarian insufficiency uncovers novel sequence variants and candidate genes. Clinical Genetics, 2020, 98, 293-298.	2.0	11
4	A missense in HSF2BP causing primary ovarian insufficiency affects meiotic recombination by its novel interactor C19ORF57/BRME1. ELife, 2020, 9, .	6.0	29
5	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
6	Mechanisms of Mendelian dominance. Clinical Genetics, 2018, 93, 419-428.	2.0	70
7	Natural and molecular history of prolactinoma: insights from aPrlr-/â€“ mouse model. Oncotarget, 2018, 9, 6144-6155.	1.8	14
8	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
9	A novel variant of <scp>DHH</scp> in a familial case of 46,<scp>XY</scp> disorder of sex development: Insights from molecular dynamics simulations. Clinical Endocrinology, 2017, 87, 539-544.	2.4	19
10	The genetic makeâ€up of ovarian development and function: the focus on the transcription factor <scp>FOXL2</scp>. Clinical Genetics, 2017, 91, 173-182.	2.0	45
11	A homozygous FANCM mutation underlies a familial case of non-syndromic primary ovarian insufficiency. ELife, 2017, 6, .	6.0	56
12	A nonâ€sense <scp>MCM9</scp> mutation in a familial case of primary ovarian insufficiency. Clinical Genetics, 2016, 89, 603-607.	2.0	60
13	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
14	Molecular analyses of juvenile granulosa cell tumors bearingAKT1mutations provide insights into tumor biology and therapeutic leads. Human Molecular Genetics, 2015, 24, 6687-6698.	2.9	51
15	STAG3 is a strong candidate gene for male infertility. Human Molecular Genetics, 2014, 23, 3421-3431.	2.9	69
16	Mutant Cohesin in Premature Ovarian Failure. New England Journal of Medicine, 2014, 370, 943-949.	27.0	244
17	The transcription factor FOXL2: At the crossroads of ovarian physiology and pathology. Molecular and Cellular Endocrinology, 2012, 356, 55-64.	3.2	67
18	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

#	Article	IF	Citations
19	Forkhead transcription factors: key players in health and disease. Trends in Genetics, 2011, 27, 224-232.	6.7	267
20	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
21	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
22	Generic binding sites, generic DNAâ€binding domains: where does specific promoter recognition come from?. FASEB Journal, 2010, 24, 346-356.	0.5	74
23	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
24	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
25	The postâ€translational 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	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
27	Coding repeats and evolutionary â€œagilityâ€. BioEssays, 2005, 27, 581-587.	2.5	35
28	Human ribosomal RNA gene arrays display a broad range of palindromic structures. Genome Research, 2005, 15, 1079-1085.	5.5	126
29	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
30	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
31	A Genomic Basis for the Evolution of Vertebrate Transcription Factors Containing Amino Acid Runs. Genetics, 2004, 167, 1813-1820.	2.9	26
32	Eucaryotic genome evolution through the spontaneous duplication of large chromosomal segments. EMBO Journal, 2004, 23, 234-243.	7.8	192
33	Compositional Biases and Polyalanine Runs in Humans. Genetics, 2003, 165, 1613-1617.	2.9	21
34	Combing the genome for genomic instability. Trends in Biotechnology, 2002, 20, 344-350.	9.3	30
35	Targeting the molecular mechanism of DNA replication. Drug Discovery Today, 2001, 6, 786-792.	6.4	4
36	Molecular Combing. Current Protocols in Cytometry, 2001, 16, Unit 8.10.	3.7	14