Philippe arnaud

List of Publications by Year in Descending Order

47 papers	2,144 citations	25 h-index	46 g-index
53 ext. papers	2,404 ext. citations	7.7 avg, IF	4.46 L-index

#	Paper	IF	Citations
47	Widespread overexpression from the four DNA hypermethylated HOX clusters in aggressive (IDHwt) glioma is associated with H3K27me3 depletion and alternative promoter usage. *Molecular Oncology*, **2021**, 15, 1995-2010	7.9	1
46	TET3 controls the expression of the H3K27me3 demethylase Kdm6b during neural commitment. *Cellular and Molecular Life Sciences*, **2021**, 78, 757-768	10.3	3
45	HOX gene cluster (de)regulation in brain: from neurodevelopment to malignant glial tumours. *Cellular and Molecular Life Sciences*, **2020**, 77, 3797-3821	10.3	10
44	Transcriptional alterations in glioma result primarily from DNA methylation-independent mechanisms. *Genome Research*, **2019**, 29, 1605-1621	9.7	17
43	DNA methylation profiling reveals a pathological signature that contributes to transcriptional defects of CD34 CD15 cells in early chronic-phase chronic myeloid leukemia. *Molecular Oncology*, **2018**, 12, 814-829	7.9	17
42	CLIFinder: identification of LINE-1 chimeric transcripts in RNA-seq data. *Bioinformatics*, **2018**, 34, 688-690	7.2	6
41	The long non-coding RNA is transcriptionally activated by HOXA9 and is an independent prognostic marker in patients with malignant glioma. *Oncotarget*, **2018**, 9, 15740-15756	3.3	17
40	Detection of the alternative lengthening of telomeres pathway in malignant gliomas for improved molecular diagnosis. *Journal of Neuro-Oncology*, **2017**, 135, 381-390	4.8	14
39	An annotated list of bivalent chromatin regions in human ES cells: a new tool for cancer epigenetic research. *Oncotarget*, **2017**, 8, 4110-4124	3.3	24
38	In Vitro Corticogenesis from Embryonic Stem Cells Recapitulates the In Vivo Epigenetic Control of Imprinted Gene Expression. *Cerebral Cortex*, **2017**, 27, 2418-2433	5.1	11
37	Imprinting control regions (ICRs) are marked by mono-allelic bivalent chromatin when transcriptionally inactive. *Nucleic Acids Research*, **2016**, 44, 621-35	20.1	29
36	The tumoral A genotype of the MGMT rs34180180 single-nucleotide polymorphism in aggressive gliomas is associated with shorter patientsTsurvival. *Carcinogenesis*, **2016**, 37, 169-176	4.6	10
35	Deep sequencing and de novo assembly of the mouse oocyte transcriptome define the contribution of transcription to the DNA methylation landscape. *Genome Biology*, **2015**, 16, 209	18.3	117
34	ICR noncoding RNA expression controls imprinting and DNA replication at the Dlk1-Dio3 domain. *Developmental Cell*, **2014**, 31, 19-33	10.2	53
33	Liver x receptors protect from development of prostatic intra-epithelial neoplasia in mice. *PLoS Genetics*, **2013**, 9, e1003483	6	33
32	Epigenetic Reprogramming in the Mammalian Germline **2013**, 3-34		
31	Characterization of novel paternal ncRNAs at the Plagl1 locus, including Hymai, predicted to interact with regulators of active chromatin. *PLoS ONE*, **2012**, 7, e38907	3.7	21

30	Transcription and histone methylation changes correlate with imprint acquisition in male germ cells. *EMBO Journal*, **2012**, 31, 606-15	13	62
29	Synergic reprogramming of mammalian cells by combined exposure to mitotic Xenopus egg extracts and transcription factors. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 17331-6	11.5	36
28	Human imprinted retrogenes exhibit non-canonical imprint chromatin signatures and reside in non-imprinted host genes. *Nucleic Acids Research*, **2011**, 39, 4577-86	20.1	18
27	Ring1B and Suv39h1 delineate distinct chromatin states at bivalent genes during early mouse lineage commitment. *Development (Cambridge)*, **2010**, 137, 2483-92	6.6	90
26	Genome-wide identification of new imprinted genes. *Briefings in Functional Genomics*, **2010**, 9, 304-14	4.9	40
25	Genomic imprinting in germ cells: imprints are under control. *Reproduction*, **2010**, 140, 411-23	3.8	71
24	Reciprocal imprinting of human GRB10 in placental trophoblast and brain: evolutionary conservation of reversed allelic expression. *Human Molecular Genetics*, **2009**, 18, 3066-74	5.6	70
23	Histone methylation is mechanistically linked to DNA methylation at imprinting control regions in mammals. *Human Molecular Genetics*, **2009**, 18, 3375-83	5.6	105
22	A mono-allelic bivalent chromatin domain controls tissue-specific imprinting at Grb10. *EMBO Journal*, **2008**, 27, 2523-32	13	63
21	Comparative analysis of human chromosome 7q21 and mouse proximal chromosome 6 reveals a placental-specific imprinted gene, TFPI2/Tfpi2, which requires EHMT2 and EED for allelic-silencing. *Genome Research*, **2008**, 18, 1270-81	9.7	69
20	Early mouse embryo development: could epigenetics influence cell fate determination?. *BioEssays*, **2007**, 29, 520-4	4.1	3
19	Identification of the imprinted KLF14 transcription factor undergoing human-specific accelerated evolution. *PLoS Genetics*, **2007**, 3, e65	6	70
18	Chromatin Immunoprecipitation (ChIP) on Unfixed Chromatin from Cells and Tissues to Analyze Histone Modifications. *Cold Spring Harbor Protocols*, **2007**, 2007, pdb.prot4767	1.2	22
17	PCR-Based Analysis of Immunoprecipitated Chromatin. *Cold Spring Harbor Protocols*, **2007**, 2007, pdb.prot4768	1.2	3
16	Stochastic imprinting in the progeny of Dnmt3L-/- females. *Human Molecular Genetics*, **2006**, 15, 589-98	5.6	55
15	Limited evolutionary conservation of imprinting in the human placenta. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 6623-8	11.5	208
14	Imprinting of IGF2 P0 transcript and novel alternatively spliced INS-IGF2 isoforms show differences between mouse and human. *Human Molecular Genetics*, **2006**, 15, 1259-69	5.6	123
13	MEDEA takes control of its own imprinting. *Cell*, **2006**, 124, 468-70	56.2	13

12	Epigenetic deregulation of genomic imprinting in human disorders and following assisted reproduction. *Birth Defects Research Part C: Embryo Today Reviews*, **2005**, 75, 81-97		79
11	Identification and properties of imprinted genes and their control elements. *Cytogenetic and Genome Research*, **2004**, 105, 335-45	1.9	15
10	Imprinted methylation profiles for proximal mouse chromosomes 11 and 7 as revealed by methylation-sensitive representational difference analysis. *Mammalian Genome*, **2003**, 14, 805-16	3.2	13
9	Epigenetic properties and identification of an imprint mark in the Nesp-Gnasxl domain of the mouse Gnas imprinted locus. *Molecular and Cellular Biology*, **2003**, 23, 5475-88	4.8	102
8	Conserved methylation imprints in the human and mouse GRB10 genes with divergent allelic expression suggests differential reading of the same mark. *Human Molecular Genetics*, **2003**, 12, 1005-19	5.6	121
7	The mouse Zac1 locus: basis for imprinting and comparison with human ZAC. *Gene*, **2002**, 292, 101-12	3.8	46
6	Analysis of the SINE S1 Pol III promoter from Brassica; impact of methylation and influence of external sequences. *Plant Journal*, **2001**, 26, 295-305	6.9	27
5	SINE retroposons can be used in vivo as nucleation centers for de novo methylation. *Molecular and Cellular Biology*, **2000**, 20, 3434-41	4.8	79
4	S1 SINE retroposons are methylated at symmetrical and non-symmetrical positions in Brassica napus: identification of a preferred target site for asymmetrical methylation. *Plant Molecular Biology*, **1999**, 39, 243-55	4.6	27
3	Plant S1 SINEs as a model to study retroposition. *Genetica*, **1997**, 100, 155-160	1.5	7
2	Improved thermostability of the North American firefly luciferase: saturation mutagenesis at position 354. *Biochemical Journal*, **1996**, 319 (Pt 2), 343-50	3.8	98
1	A transcriptional analysis of the S1Bn (Brassica napus) family of SINE retroposons. *Plant Molecular Biology*, **1996**, 32, 869-78	4.6	25