Pierre-Antoine Defossez

List of Publications by Year
in descending order

47 papers	5,828 citations	159358 30 h-index	197535 49 g-index
55 all docs	55 docs citations	55 times ranked	6942 citing authors

#	Article	IF	Citations
1	Requirement of NAD and SIR2 for Life-Span Extension by Calorie Restriction in Saccharomyces cerevisiae. Science, 2000, 289, 2126-2128.	6.0	1,696
2	Calorie restriction extends Saccharomyces cerevisiae lifespan by increasing respiration. Nature, 2002, 418, 344-348.	13.7	950
3	Elimination of Replication Block Protein Fob1 Extends the Life Span of Yeast Mother Cells. Molecular Cell, 1999, 3, 447-455.	4.5	380
4	A Family of Human Zinc Finger Proteins That Bind Methylated DNA and Repress Transcription. Molecular and Cellular Biology, 2006, 26, 169-181.	1.1	278
5	Born to bind: the BTB proteinâ€“protein interaction domain. BioEssays, 2006, 28, 1194-1202.	1.2	223
6	Methylation of DNA Ligase 1 by G9a/GLP Recruits UHRF1 to Replicating DNA and Regulates DNA Methylation. Molecular Cell, 2017, 67, 550-565.e5.	4.5	151
7	Androgen Receptor-Ets Protein Interaction Is a Novel Mechanism for Steroid Hormone-mediated Down-modulation of Matrix Metalloproteinase Expression. Journal of Biological Chemistry, 1996, 271, 23907-23913.	1.6	147
8	Effects of Mutations in DNA Repair Genes on Formation of Ribosomal DNA Circles and Life Span in Saccharomyces cerevisiae. Molecular and Cellular Biology, 1999, 19, 3848-3856.	1.1	145
9	Differential expression patterns of the PEA3 group transcription factors through murine embryonic development. Oncogene, 1997, 15, 937-952.	2.6	138
10	The Human Proteins MBD5 and MBD6 Associate with Heterochromatin but They Do Not Bind Methylated DNA. PLoS ONE, 2010, 5, e11982.	1.1	97
11	Sequence-specific recognition of methylated DNA by human zinc-finger proteins. Nucleic Acids Research, 2010, 38, 5015-5022.	6.5	92
12	The role of methyl-binding proteins in chromatin organization and epigenome maintenance. Briefings in Functional Genomics, 2012, 11, 251-264.	1.3	92
13	Zbtb4 represses transcription of P21CIP1 and controls the cellular response to p53 activation. EMBO Journal, 2008, 27, 1563-1574.	3.5	91
14	MBD5 and MBD6 interact with the human PRâ€DUB complex through their methylâ€CpGâ€binding domain. Proteomics, 2014, 14, 2179-2189.	1.3	90
15	On how mammalian transcription factors recognize methylated DNA. Epigenetics, 2013, 8, 131-137.	1.3	85
16	Structureâ€“Function Relationships of the PEA3 Group of Ets-Related Transcription Factors. Biochemical and Molecular Medicine, 1997, 61, 127-135.	1.5	84
17	The cell biology of DNA methylation in mammals. Biochimica Et Biophysica Acta - Molecular Cell Research, 2008, 1783, 2167-2173.	1.9	81
18	Biological Functions of Methyl-CpG-Binding Proteins. Progress in Molecular Biology and Translational Science, 2011, 101, 377-398.	0.9	80

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19	The Human Enhancer Blocker CTC-binding Factor Interacts with the Transcription Factor Kaiso. Journal of Biological Chemistry, 2005, 280, 43017-43023.	1.6	76
20	Many paths to one goal? The proteins that recognize methylated DNA in eukaryotes. International Journal of Developmental Biology, 2009, 53, 323-334.	0.3	76
21	Lysine Methylation Regulators Moonlighting outside the Epigenome. Molecular Cell, 2019, 75, 1092-1101.	4.5	73
22	The RBBP6/ZBTB38/MCM10 Axis Regulates DNA Replication and Common Fragile Site Stability. Cell Reports, 2014, 7, 575-587.	2.9	66
23	Staying true to yourself: mechanisms of DNA methylation maintenance in mammals. Nucleic Acids Research, 2021, 49, 3020-3032.	6.5	62
24	Loss of the Methyl-CpGâ€“Binding Protein ZBTB4 Alters Mitotic Checkpoint, Increases Aneuploidy, and Promotes Tumorigenesis. Cancer Research, 2017, 77, 62-73.	0.4	55
25	General Regulatory Factors (GRFs) as Genome Partitioners. Journal of Biological Chemistry, 2002, 277, 41736-41743.	1.6	51
26	The nuclear receptor RXRA controls cellular senescence by regulating calcium signaling. Aging Cell, 2018, 17, e12831.	3.0	45
27	MBD4 cooperates with DNMT1 to mediate methyl-DNA repression and protects mammalian cells from oxidative stress. Epigenetics, 2014, 9, 546-556.	1.3	44
28	Structure of the UHRF1 Tandem Tudor Domain Bound to a Methylated Non-histone Protein, LIG1, Reveals Rules for Binding and Regulation. Structure, 2019, 27, 485-496.e7.	1.6	41
29	Mechanisms of DNA Methyltransferase Recruitment in Mammals. Genes, 2018, 9, 617.	1.0	37
30	Screening of a kinase library reveals novel pro-senescence kinases and their common NF-ÎºB-dependent transcriptional program. Aging, 2015, 7, 986-999.	1.4	36
31	MyoD reprogramming requires Six1 and Six4 homeoproteins: genome-widecis-regulatory module analysis. Nucleic Acids Research, 2016, 44, 8621-8640.	6.5	27
32	Genomic Organization of the Human ERM (ETV5) Gene, a PEA3 Group Member of ETS Transcription Factors. Genomics, 1996, 35, 236-240.	1.3	26
33	Vicious circles: a mechanism for yeast aging. Current Opinion in Microbiology, 1998, 1, 707-711.	2.3	25
34	The vertebrate protein CTCF functions as an insulator in Saccharomyces cerevisiae. Nucleic Acids Research, 2002, 30, 5136-5141.	6.5	25
35	Stabilization of the methyl-CpG binding protein ZBTB38 by the deubiquitinase USP9X limits the occurrence and toxicity of oxidative stress in human cells. Nucleic Acids Research, 2018, 46, 4392-4404.	6.5	22
36	Sound silencing: the Sir2 protein and cellular senescence. BioEssays, 2001, 23, 327-332.	1.2	21

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37	Histone H1 of Saccharomyces cerevisiae Inhibits Transcriptional Silencing. Genetics, 2006, 173, 579-587.	1.2	20
38	Mammalian methylâ€binding proteins: What might they do?. BioEssays, 2010, 32, 1025-1032.	1.2	19
39	Depletion of ZBTB38 potentiates the effects of DNA demethylating agents in cancer cells via CDKN1C mRNA up-regulation. Oncogenesis, 2018, 7, 82.	2.1	14
40	Genetic screens reveal mechanisms for the transcriptional regulation of tissue-specific genes in normal cells and tumors. Nucleic Acids Research, 2019, 47, 3407-3421.	6.5	10
41	Reading DNA Modifications. Journal of Molecular Biology, 2020, 432, 1599-1601.	2.0	9
42	Structure-based screening combined with computational and biochemical analyses identified the inhibitor targeting the binding of DNA Ligase 1 to UHRF1. Bioorganic and Medicinal Chemistry, 2021, 52, 116500.	1.4	8
43	Using reverse electrophoretic mobility shift assay to measure and compare proteinâ€“DNA binding affinities. Analytical Biochemistry, 2006, 357, 156-158.	1.1	7
44	Assessment of sera for chromatin-immunoprecipitation. BioTechniques, 2008, 44, 66-68.	0.8	5
45	Ceci n'est pas une <scp>DNMT</scp>: Recently discovered functions of <scp>DNMT</scp>2 and their relation to methyltransferase activity (<scp>C</scp>omment on) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 417 Td (<scp>DOI</scp>	1.1	
46	Large-Scale Chromatin Rearrangements in Cancer. Cancers, 2022, 14, 2384.	1.7	3
47	Restriction calorique et longÃ©vitÃ© : rÃ©sultats inattendus chez la levure. Medecine/Sciences, 2002, 18, 1191-1193.	0.0	0