Beatrice Bodega

List of Publications by Year
in descending order

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34 papers	5,122 citations	361413 20 h-index	395702 33 g-index
35 all docs	35 docs citations	35 times ranked	11681 citing authors

#	Article	IF	Citations
1	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
2	Genome-wide association between YAP/TAZ/TEAD andÂAP-1 at enhancers drives oncogenic growth. Nature Cell Biology, 2015, 17, 1218-1227.	10.3	865
3	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
4	A Long ncRNA Links Copy Number Variation to a Polycomb/Trithorax Epigenetic Switch in FSHD Muscular Dystrophy. Cell, 2012, 149, 819-831.	28.9	341
5	The long intergenic noncoding RNA landscape of human lymphocytes highlights the regulation of T cell differentiation by linc-MAF-4. Nature Immunology, 2015, 16, 318-325.	14.5	300
6	Identification of New Variants of HumanBMP15Gene in a Large Cohort of Women with Premature Ovarian Failure. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 1976-1979.	3.6	196
7	FANTOM5 CAGE profiles of human and mouse samples. Scientific Data, 2017, 4, 170112.	5.3	195
8	Influence of intermediate and uninterrupted FMR1 CGG expansions in premature ovarian failure manifestation. Human Reproduction, 2006, 21, 952-957.	0.9	162
9	Chromatin regulated interchange between polycomb repressive complex 2 (PRC2)-Ezh2 and PRC2-Ezh1 complexes controls myogenin activation in skeletal muscle cells. Epigenetics and Chromatin, 2011, 4, 16.	3.9	113
10	Lamin A/C sustains PcG protein architecture, maintaining transcriptional repression at target genes. Journal of Cell Biology, 2015, 211, 533-551.	5.2	96
11	Remodeling of the chromatin structure of the facioscapulohumeral muscular dystrophy (FSHD) locus and upregulation of FSHD-related gene 1 (FRG1) expression during human myogenic differentiation. BMC Biology, 2009, 7, 41.	3.8	81
12	Expression Profiling of FSHD-1 and FSHD-2 Cells during Myogenic Differentiation Evidences Common and Distinctive Gene Dysregulation Patterns. PLoS ONE, 2011, 6, e20966.	2.5	39
13	LINE1 are spliced in non-canonical transcript variants to regulate T cell quiescence and exhaustion. Nature Genetics, 2022, 54, 180-193.	21.4	39
14	Mutations in the coding region of the FOXL2 gene are not a major cause of idiopathic premature ovarian failure. Molecular Human Reproduction, 2004, 10, 555-557.	2.8	37
15	Repetitive elements dynamics in cell identity programming, maintenance and disease. Current Opinion in Cell Biology, 2014, 31, 67-73.	5.4	37
16	A cytosolic Ezh1 isoform modulates a PRC2â€“Ezh1 epigenetic adaptive response in postmitotic cells. Nature Structural and Molecular Biology, 2017, 24, 444-452.	8.2	35
17	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. PLoS Biology, 2015, 13, e1002315.	5.6	32
18	Dysfunctional polycomb transcriptional repression contributes to lamin A/Câ€“dependent muscular dystrophy. Journal of Clinical Investigation, 2020, 130, 2408-2421.	8.2	32

#	Article	IF	Citations
19	How Polycombâ€Mediated Cell Memory Deals With a Changing Environment. BioEssays, 2018, 40, e1700137.	2.5	27
20	NIPBL: a new player in myeloid cell differentiation. Haematologica, 2019, 104, 1332-1341.	3.5	22
21	Forced expression of RDH10 gene retards growth of HepG2 cells. Cancer Biology and Therapy, 2007, 6, 238-245.	3.4	21
22	4q-D4Z4 chromatin architecture regulates the transcription of muscle atrophic genes in facioscapulohumeral muscular dystrophy. Genome Research, 2019, 29, 883-895.	5.5	18
23	Early maternal care restores LINE-1 methylation and enhances neurodevelopment in preterm infants. BMC Medicine, 2021, 19, 42.	5.5	17
24	Evolutionary genomic remodelling of the human 4q subtelomere (4q35.2). BMC Evolutionary Biology, 2007, 7, 39.	3.2	11
25	Profound alterations of the chromatin architecture at chromosome 11p15.5 in cells from Beckwith-Wiedemann and Silver-Russell syndromes patients. Scientific Reports, 2020, 10, 8275.	3.3	11
26	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
27	The Sophisticated Transcriptional Response Governed by Transposable Elements in Human Health and Disease. International Journal of Molecular Sciences, 2020, 21, 3201.	4.1	8
28	The boundary of macaque rDNA is constituted by low-copy sequences conserved during evolution. Genomics, 2006, 88, 564-571.	2.9	6
29	Evolutionary history of linked D4Z4 and Beta satellite clusters at the FSHD locus (4q35). Genomics, 2012, 100, 289-296.	2.9	5
30	Chromosome Conformation Capture in Primary Human Cells. Methods in Molecular Biology, 2016, 1480, 213-221.	0.9	5
31	An Algorithm for the Analysis of the 3D Spatial Organization of the Genome. Methods in Molecular Biology, 2021, 2157, 299-320.	0.9	3
32	3D Multicolor DNA FISH Tool to Study Nuclear Architecture in Human Primary Cells. Journal of Visualized Experiments, 2020, , .	0.3	1
33	3D COMBO chrRNAâ€“DNAâ€“ImmunoFISH. Methods in Molecular Biology, 2021, 2157, 281-297.	0.9	1
34	Mutational signatures of early-onset colorectal cancer.. Journal of Clinical Oncology, 2019, 37, e15113-e15113.	1.6	0