Veronica J Buckle

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7753140/publications.pdf

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25 papers	1,848 citations	516710 16 h-index	642732 23 g-index
32 all docs	32 docs citations	32 times ranked	3337 citing authors

#	Article	IF	Citations
1	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	21.4	310
2	Association between active genes occurs at nuclear speckles and is modulated by chromatin environment. Journal of Cell Biology, 2008, 182, 1083-1097.	5.2	231
3	Coregulated human globin genes are frequently in spatial proximity when active. Journal of Cell Biology, 2006, 172, 177-187.	5.2	192
4	Single-allele chromatin interactions identify regulatory hubs in dynamic compartmentalized domains. Nature Genetics, 2018, 50, 1744-1751.	21.4	150
5	Stabilization of chromatin topology safeguards genome integrity. Nature, 2019, 574, 571-574.	27.8	136
6	Cohesin Disrupts Polycomb-Dependent Chromosome Interactions in Embryonic Stem Cells. Cell Reports, 2020, 30, 820-835.e10.	6.4	129
7	Predicting the three-dimensional folding of cis-regulatory regions in mammalian genomes using bioinformatic data and polymer models. Genome Biology, 2016, 17, 59.	8.8	97
8	Chromatin arranges in chains of mesoscale domains with nanoscale functional topography independent of cohesin. Science Advances, 2020, 6, .	10.3	97
9	Dynamics of the 4D genome during in vivo lineage specification and differentiation. Nature Communications, 2020, 11, 2722.	12.8	79
10	Homozygous mutations in a predicted endonuclease are a novel cause of congenital dyserythropoietic anemia type I. Haematologica, 2013, 98, 1383-1387.	3.5	71
11	A tissue-specific self-interacting chromatin domain forms independently of enhancer-promoter interactions. Nature Communications, 2018, 9, 3849.	12.8	62
12	Codanin-1 mutations in congenital dyserythropoietic anemia type 1 affect HP1Î± localization in erythroblasts. Blood, 2011, 117, 6928-6938.	1.4	58
13	A Dynamic Folded Hairpin Conformation Is Associated with Î±-Globin Activation in Erythroid Cells. Cell Reports, 2020, 30, 2125-2135.e5.	6.4	38
14	High-resolution targeted 3C interrogation of cis-regulatory element organization at genome-wide scale. Nature Communications, 2021, 12, 531.	12.8	32
15	De novoand rare inherited mutations implicate the transcriptional coregulator TCF20/SPBP in autism spectrum disorder. Journal of Medical Genetics, 2014, 51, 737-747.	3.2	31
16	Expanded GAA repeats impair FXN gene expression and reposition the FXN locus to the nuclear lamina in single cells. Human Molecular Genetics, 2015, 24, 3457-3471.	2.9	25
17	Detection of Nascent RNA Transcripts by Fluorescence In Situ Hybridization. Methods in Molecular Biology, 2010, 659, 33-50.	0.9	17
18	Robust CRISPR/Cas9 Genome Editing of the HUDEP-2 Erythroid Precursor Line Using Plasmids and Single-Stranded Oligonucleotide Donors. Methods and Protocols, 2018, 1, 28.	2.0	17

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19	Majeed syndrome: description of a novel mutation and therapeutic response to bisphosphonates and IL-1 blockade with anakinra. Rheumatology, 2020, 59, 448-451.	1.9	15
20	Recapitulation of erythropoiesis in congenital dyserythropoietic anemia type I (CDA-I) identifies defects in differentiation and nucleolar abnormalities. Haematologica, 2021, 106, 2960-2970.	3.5	10
21	RASER-FISH: non-denaturing fluorescence in situ hybridization for preservation of three-dimensional interphase chromatin structure. Nature Protocols, 2022, 17, 1306-1331.	12.0	10
22	Genetic and functional insights into CDA-I prevalence and pathogenesis. Journal of Medical Genetics, 2021, 58, 185-195.	3.2	9
23	ATR-16 syndrome: mechanisms linking monosomy to phenotype. Journal of Medical Genetics, 2020, 57, 414-421.	3.2	7
24	The Application of SEM-Based EDS Microanalysis to the Study of Congenital Dyserythropoietic Anaemia Type-1 (CDA-I). Microscopy and Microanalysis, 2019, 25, 1104-1105.	0.4	0
25	Functional impairment of erythropoiesis in Congenital Dyserythropoietic Anaemia type I arises at the progenitor level. British Journal of Haematology, 2022, , .	2.5	0