

Per Stenberg

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

1,137
citations

471509

17
h-index

414414

32
g-index

36
all docs

36
docs citations

36
times ranked

1386
citing authors

#	ARTICLE	IF	CITATIONS
1	Transposon activity, local duplications and propagation of structural variants across haplotypes drive the evolution of the <i>Drosophila</i> S2 cell line. <i>BMC Genomics</i> , 2022, 23, 276.	2.8	4
2	Modeling protein target search in human chromosomes. <i>Physical Review Research</i> , 2021, 3, .	3.6	5
3	Biological amplification of low frequency mutations unravels laboratory culture history of the bio-threat agent <i>Francisella tularensis</i> . <i>Forensic Science International: Genetics</i> , 2020, 45, 102230.	3.1	6
4	Exploring a <i>Drosophila</i> Transcription Factor Interaction Network to Identify Cis-Regulatory Modules. <i>Journal of Computational Biology</i> , 2020, 27, 1313-1328.	1.6	0
5	Airborne microbial biodiversity and seasonality in Northern and Southern Sweden. <i>PeerJ</i> , 2020, 8, e8424.	2.0	22
6	A likelihood ratio-based approach for improved source attribution in microbiological forensic investigations. <i>Forensic Science International</i> , 2019, 302, 109869.	2.2	3
7	Mapping the spectrum of 3D communities in human chromosome conformation capture data. <i>Scientific Reports</i> , 2019, 9, 6859.	3.3	7
8	Highly interacting regions of the human genome are enriched with enhancers and bound by DNA repair proteins. <i>Scientific Reports</i> , 2019, 9, 4577.	3.3	15
9	Genomic 3D compartments emerge from unfolding mitotic chromosomes. <i>Chromosoma</i> , 2019, 128, 15-20.	2.2	8
10	Accounting for Bacterial Overlap Between Raw Water Communities and Contaminating Sources Improves the Accuracy of Signature-Based Microbial Source Tracking. <i>Frontiers in Microbiology</i> , 2018, 9, 2364.	3.5	16
11	The gut microbiome participates in transgenerational inheritance of low-temperature responses in <i>Drosophila melanogaster</i> . <i>FEBS Letters</i> , 2018, 592, 4078-4086.	2.8	23
12	PTE, a novel module to target Polycomb Repressive Complex 1 to the human cyclin D2 (CCND2) oncogene. <i>Journal of Biological Chemistry</i> , 2018, 293, 14342-14358.	3.4	5
13	CBP Regulates Recruitment and Release of Promoter-Proximal RNA Polymerase II. <i>Molecular Cell</i> , 2017, 68, 491-503.e5.	9.7	59
14	Genome contact map explorer: a platform for the comparison, interactive visualization and analysis of genome contact maps. <i>Nucleic Acids Research</i> , 2017, 45, e152-e152.	14.5	26
15	Atrophia controls developmental signaling pathways via interactions with Trithorax-like. <i>ELife</i> , 2017, 6, .	6.0	15
16	Interdependence of PRC1 and PRC2 for recruitment to Polycomb Response Elements. <i>Nucleic Acids Research</i> , 2016, 44, gkw701.	14.5	93
17	CBP binding outside of promoters and enhancers in <i>Drosophila melanogaster</i> . <i>Epigenetics and Chromatin</i> , 2015, 8, 48.	3.9	24
18	Combinatorial Interactions Are Required for the Efficient Recruitment of Pho Repressive Complex (PhoRC) to Polycomb Response Elements. <i>PLoS Genetics</i> , 2014, 10, e1004495.	3.5	59

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19	Non-coding roX RNAs Prevent the Binding of the MSL-complex to Heterochromatic Regions. PLoS Genetics, 2014, 10, e1004865.	3.5	27
20	HP1a, Su(var)3-9, SETDB1 and POF stimulate or repress gene expression depending on genomic position, gene length and expression pattern in Drosophila melanogaster. Nucleic Acids Research, 2013, 41, 4481-4494.	14.5	40
21	HP1a Recruitment to Promoters Is Independent of H3K9 Methylation in Drosophila melanogaster. PLoS Genetics, 2012, 8, e1003061.	3.5	50
22	Buffering and proteolysis are induced by segmental monosomy in Drosophila melanogaster. Nucleic Acids Research, 2012, 40, 5926-5937.	14.5	32
23	Preferential Genome Targeting of the CBP Co-Activator by Rel and Smad Proteins in Early Drosophila melanogaster Embryos. PLoS Genetics, 2012, 8, e1002769.	3.5	41
24	POF Regulates the Expression of Genes on the Fourth Chromosome in <i>Drosophila melanogaster</i> by Binding to Nascent RNA. Molecular and Cellular Biology, 2012, 32, 2121-2134.	2.3	32
25	Buffering and the evolution of chromosome-wide gene regulation. Chromosoma, 2011, 120, 213-225.	2.2	49
26	msl2 mRNA is bound by free nuclear MSL complex in Drosophila melanogaster. Nucleic Acids Research, 2011, 39, 6428-6439.	14.5	18
27	Normalization of High Dimensional Genomics Data Where the Distribution of the Altered Variables Is Skewed. PLoS ONE, 2011, 6, e27942.	2.5	12
28	Alternative Epigenetic Chromatin States of Polycomb Target Genes. PLoS Genetics, 2010, 6, e1000805.	3.5	180
29	Buffering of Segmental and Chromosomal Aneuploidies in Drosophila melanogaster. PLoS Genetics, 2009, 5, e1000465.	3.5	83
30	POF and HP1 Bind Expressed Exons, Suggesting a Balancing Mechanism for Gene Regulation. PLoS Genetics, 2007, 3, e209.	3.5	54
31	Painting of fourth and chromosome-wide regulation of the 4th chromosome in Drosophila melanogaster. EMBO Journal, 2007, 26, 2307-2316.	7.8	65
32	Organization and regulation of sex-specific thioredoxin encoding genes in the genus Drosophila. Development Genes and Evolution, 2007, 217, 639-650.	0.9	9
33	Painting of fourth in genus Drosophila suggests autosome-specific gene regulation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9728-9733.	7.1	51
34	Ploidy Determination in Insects. BioTechniques, 2001, 31, 1268-1269.	1.8	3