

# Per Stenberg

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9449834/publications.pdf>

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	Alternative Epigenetic Chromatin States of Polycomb Target Genes. <i>PLoS Genetics</i> , 2010, 6, e1000805.	3.5	180
2	Interdependence of PRC1 and PRC2 for recruitment to Polycomb Response Elements. <i>Nucleic Acids Research</i> , 2016, 44, gkw701.	14.5	93
3	Buffering of Segmental and Chromosomal Aneuploidies in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2009, 5, e1000465.	3.5	83
4	Painting of fourth and chromosome-wide regulation of the 4th chromosome in <i>Drosophila melanogaster</i> . <i>EMBO Journal</i> , 2007, 26, 2307-2316.	7.8	65
5	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
6	CBP Regulates Recruitment and Release of Promoter-Proximal RNA Polymerase II. <i>Molecular Cell</i> , 2017, 68, 491-503.e5.	9.7	59
7	POF and HP1 Bind Expressed Exons, Suggesting a Balancing Mechanism for Gene Regulation. <i>PLoS Genetics</i> , 2007, 3, e209.	3.5	54
8	Painting of fourth in genus <i>Drosophila</i> suggests autosome-specific gene regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9728-9733.	7.1	51
9	HP1a Recruitment to Promoters Is Independent of H3K9 Methylation in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012, 8, e1003061.	3.5	50
10	Buffering and the evolution of chromosome-wide gene regulation. <i>Chromosoma</i> , 2011, 120, 213-225.	2.2	49
11	Preferential Genome Targeting of the CBP Co-Activator by Rel and Smad Proteins in Early <i>Drosophila melanogaster</i> Embryos. <i>PLoS Genetics</i> , 2012, 8, e1002769.	3.5	41
12	HP1a, Su(var)3-9, SETDB1 and POF stimulate or repress gene expression depending on genomic position, gene length and expression pattern in <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2013, 41, 4481-4494.	14.5	40
13	Buffering and proteolysis are induced by segmental monosomy in <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2012, 40, 5926-5937.	14.5	32
14	POF Regulates the Expression of Genes on the Fourth Chromosome in <i>Drosophila melanogaster</i> by Binding to Nascent RNA. <i>Molecular and Cellular Biology</i> , 2012, 32, 2121-2134.	2.3	32
15	Non-coding roX RNAs Prevent the Binding of the MSL-complex to Heterochromatic Regions. <i>PLoS Genetics</i> , 2014, 10, e1004865.	3.5	27
16	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
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	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

#	ARTICLE	IF	CITATIONS
19	Airborne microbial biodiversity and seasonality in Northern and Southern Sweden. PeerJ, 2020, 8, e8424.	2.0	22
20	msl2 mRNA is bound by free nuclear MSL complex in Drosophila melanogaster. Nucleic Acids Research, 2011, 39, 6428-6439.	14.5	18
21	Accounting for Bacterial Overlap Between Raw Water Communities and Contaminating Sources Improves the Accuracy of Signature-Based Microbial Source Tracking. Frontiers in Microbiology, 2018, 9, 2364.	3.5	16
22	Highly interacting regions of the human genome are enriched with enhancers and bound by DNA repair proteins. Scientific Reports, 2019, 9, 4577.	3.3	15
23	Atrophia controls developmental signaling pathways via interactions with Trithorax-like. ELife, 2017, 6, .	6.0	15
24	Normalization of High Dimensional Genomics Data Where the Distribution of the Altered Variables Is Skewed. PLoS ONE, 2011, 6, e27942.	2.5	12
25	Organization and regulation of sex-specific thioredoxin encoding genes in the genus Drosophila. Development Genes and Evolution, 2007, 217, 639-650.	0.9	9
26	Genomic 3D compartments emerge from unfolding mitotic chromosomes. Chromosoma, 2019, 128, 15-20.	2.2	8
27	Mapping the spectrum of 3D communities in human chromosome conformation capture data. Scientific Reports, 2019, 9, 6859.	3.3	7
28	Biological amplification of low frequency mutations unravels laboratory culture history of the bio-threat agent Francisella tularensis. Forensic Science International: Genetics, 2020, 45, 102230.	3.1	6
29	PTE, a novel module to target Polycomb Repressive Complex 1 to the human cyclin D2 (CCND2) oncogene. Journal of Biological Chemistry, 2018, 293, 14342-14358.	3.4	5
30	Modeling protein target search in human chromosomes. Physical Review Research, 2021, 3, .	3.6	5
31	Transposon activity, local duplications and propagation of structural variants across haplotypes drive the evolution of the Drosophila S2 cell line. BMC Genomics, 2022, 23, 276.	2.8	4
32	Ploidy Determination in Insects. BioTechniques, 2001, 31, 1268-1269.	1.8	3
33	A likelihood ratio-based approach for improved source attribution in microbiological forensic investigations. Forensic Science International, 2019, 302, 109869.	2.2	3
34	Exploring a Drosophila Transcription Factor Interaction Network to Identify Cis-Regulatory Modules. Journal of Computational Biology, 2020, 27, 1313-1328.	1.6	0