

Tanya Vavouri

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

3,628
citations

304602

22
h-index

434063

31
g-index

33
all docs

33
docs citations

33
times ranked

5984
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly Conserved Non-Coding Sequences Are Associated with Vertebrate Development. <i>PLoS Biology</i> , 2004, 3, e7.	2.6	833
2	Transgenerational transmission of environmental information in <i>C. elegans</i> . <i>Science</i> , 2017, 356, 320-323.	6.0	360
3	Paternal Diet Defines Offspring Chromatin State and Intergenerational Obesity. <i>Cell</i> , 2014, 159, 1352-1364.	13.5	345
4	Intrinsic Protein Disorder and Interaction Promiscuity Are Widely Associated with Dosage Sensitivity. <i>Cell</i> , 2009, 138, 198-208.	13.5	319
5	Tuning in to the signals: noncoding sequence conservation in vertebrate genomes. <i>Trends in Genetics</i> , 2008, 24, 344-352.	2.9	168
6	Trim28 Haploinsufficiency Triggers Bi-stable Epigenetic Obesity. <i>Cell</i> , 2016, 164, 353-364.	13.5	161
7	Human sperm displays rapid responses to diet. <i>PLoS Biology</i> , 2019, 17, e3000559.	2.6	122
8	Parallel evolution of conserved non-coding elements that target a common set of developmental regulatory genes from worms to humans. <i>Genome Biology</i> , 2007, 8, R15.	13.9	117
9	A simple principle concerning the robustness of protein complex activity to changes in gene expression. <i>BMC Systems Biology</i> , 2008, 2, 1.	3.0	112
10	The Polycomb-Dependent Epigenome Controls \hat{I}^2 Cell Dysfunction, Dedifferentiation, and Diabetes. <i>Cell Metabolism</i> , 2018, 27, 1294-1308.e7.	7.2	109
11	Widespread conservation of genetic redundancy during a billion years of eukaryotic evolution. <i>Trends in Genetics</i> , 2008, 24, 485-488.	2.9	108
12	Human genes with CpG island promoters have a distinct transcription-associated chromatin organization. <i>Genome Biology</i> , 2012, 13, R110.	13.9	98
13	Chromatin Organization in Sperm May Be the Major Functional Consequence of Base Composition Variation in the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002036.	1.5	90
14	Ancient duplicated conserved noncoding elements in vertebrates: A genomic and functional analysis. <i>Genome Research</i> , 2006, 16, 451-465.	2.4	88
15	Predicting genetic modifier loci using functional gene networks. <i>Genome Research</i> , 2010, 20, 1143-1153.	2.4	83
16	The small RNA content of human sperm reveals pseudogene-derived piRNAs complementary to protein-coding genes. <i>Rna</i> , 2015, 21, 1085-1095.	1.6	83
17	Defining a genomic radius for long-range enhancer action: duplicated conserved non-coding elements hold the key. <i>Trends in Genetics</i> , 2006, 22, 5-10.	2.9	69
18	Sperm epigenomics: challenges and opportunities. <i>Frontiers in Genetics</i> , 2014, 5, 330.	1.1	67

#	ARTICLE	IF	CITATIONS
19	Prediction of cis-regulatory elements using binding site matrices – the successes, the failures and the reasons for both. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 395-402.	1.5	57
20	The epigenetic landscape of <i>Alu</i> repeats delineates the structural and functional genomic architecture of colon cancer cells. <i>Genome Research</i> , 2017, 27, 118-132.	2.4	51
21	Genomic and proteomic dissection and characterization of the human sperm chromatin. <i>Molecular Human Reproduction</i> , 2014, 20, 1041-1053.	1.3	49
22	Conserved noncoding elements and the evolution of animal body plans. <i>BioEssays</i> , 2009, 31, 727-735.	1.2	30
23	Mechanisms of epigenetic inheritance of variable traits through the germline. <i>Reproduction</i> , 2020, 159, R251-R263.	1.1	18
24	Parallel Evolution of Chordate Cis-Regulatory Code for Development. <i>PLoS Genetics</i> , 2013, 9, e1003904.	1.5	16
25	The Exonuclease Trex2 Shapes Psoriatic Phenotype. <i>Journal of Investigative Dermatology</i> , 2016, 136, 2345-2355.	0.3	15
26	Double deficiency of Trex2 and DNase1L2 nucleases leads to accumulation of DNA in lingual cornifying keratinocytes without activating inflammatory responses. <i>Scientific Reports</i> , 2017, 7, 11902.	1.6	14
27	Assessment of kinship detection using RNA-seq data. <i>Nucleic Acids Research</i> , 2019, 47, e136-e136.	6.5	13
28	Impaired DNA replication derepresses chromatin and generates a transgenerationally inherited epigenetic memory. <i>Science Advances</i> , 2017, 3, e1701143.	4.7	12
29	Molecular characterisation of the SAND protein family: a study based on comparative genomics, structural bioinformatics and phylogeny. <i>Cellular and Molecular Biology Letters</i> , 2004, 9, 739-53.	2.7	11
30	Characterisation of conserved non-coding sequences in vertebrate genomes using bioinformatics, statistics and functional studies. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2006, 1, 46-58.	0.4	5
31	Theatre: a software tool for detailed comparative analysis and visualization of genomic sequence. <i>Nucleic Acids Research</i> , 2003, 31, 3510-3517.	6.5	1