Anastasia A Samsonova

List of Publications by Year
in descending order

35 papers	3,860 citations	393982 19 h-index	377514 34 g-index
36 all docs	36 docs citations	36 times ranked	6860 citing authors

#	Article	IF	Citations
1	A genome-wide association study identifies a gene network associated with paranoid schizophrenia and antipsychotics-induced tardive dyskinesia. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2021, 105, 110134.	2.5	4
2	A Genomic Blueprint of Flax Fungal Parasite Fusarium oxysporum f. sp. lini. International Journal of Molecular Sciences, 2021, 22, 2665.	1.8	6
3	Immune modulation underpins the anti€cancer activity of HDAC inhibitors. Molecular Oncology, 2021, 15, 3280-3298.	2.1	18
4	A comprehensive dataset of flax (Linum uitatissimum L.) phenotypes. Data in Brief, 2021, 37, 107224.	0.5	5
5	Genomic Regions Associated with Fusarium Wilt Resistance in Flax. International Journal of Molecular Sciences, 2021, 22, 12383.	1.8	10
6	Stochastic Effects in Retrotransposon Dynamics Revealed by Modeling under Competition for Cellular Resources. Life, 2021, 11, 1209.	1.1	2
7	Current challenges and possible future developments in personalized psychiatry with an emphasis on psychotic disorders. Heliyon, 2020, 6, e03990.	1.4	15
8	PRMT5 promotes cancer cell migration and invasion through the E2F pathway. Cell Death and Disease, 2020, 11, 572.	2.7	20
9	The Genome Sequence of Five Highly Pathogenic Isolates of Fusarium oxysporum f. sp. lini. Molecular Plant-Microbe Interactions, 2020, 33, 1112-1115.	1.4	14
10	Arginine methylation expands the regulatory mechanisms and extends the genomic landscape under E2F control. Science Advances, 2019, 5, eaaw4640.	4.7	19
11	Clinical whole-genome sequencing from routine formalin-fixed, paraffin-embedded specimens: pilot study for the 100,000 Genomes Project. Genetics in Medicine, 2018, 20, 1196-1205.	1.1	125
12	RASSF1A uncouples Wnt from Hippo signalling and promotes YAP mediated differentiation via p73. Nature Communications, 2018, 9, 424.	5.8	72
13	Human Accelerated Regions and Other Human-Specific Sequence Variations in the Context of Evolution and Their Relevance for Brain Development. Genome Biology and Evolution, 2018, 10, 166-188.	1.1	61
14	Development and validation of response markers to predict survival and pleurodesis success in patients with malignant pleural effusion (PROMISE): a multicohort analysis. Lancet Oncology, The, 2018, 19, 930-939.	5.1	92
15	Late Breaking Abstract - Prognostic and therapeutic markers of malignant pleural effusion â€" The PROMISE study. , 2017, , .		0
16	Multivalent Histone and DNA Engagement by a PHD/BRD/PWWP Triple Reader Cassette Recruits ZMYND8 to K14ac-Rich Chromatin. Cell Reports, 2016, 17, 2724-2737.	2.9	86
17	Promiscuous targeting of bromodomains by bromosporine identifies BET proteins as master regulators of primary transcription response in leukemia. Science Advances, 2016, 2, e1600760.	4.7	90
18	SmD1 Modulates the miRNA Pathway Independently of Its Pre-mRNA Splicing Function. PLoS Genetics, 2015, 11, e1005475.	1.5	26

#	Article	IF	Citations
19	Regulators of Autophagosome Formation in Drosophila Muscles. PLoS Genetics, 2015, 11, e1005006.	1.5	46
20	Diversity and dynamics of the Drosophila transcriptome. Nature, 2014, 512, 393-399.	13.7	647
21	Integrating protein-protein interaction networks with phenotypes reveals signs of interactions. Nature Methods, 2014, 11, 94-99.	9.0	130
22	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	13.7	289
23	Conserved Regulators of Nucleolar Size Revealed by Global Phenotypic Analyses. Science Signaling, 2013, 6, ra70.	1.6	68
24	False negative rates in Drosophila cell-based RNAi screens: a case study. BMC Genomics, 2011, 12, 50.	1.2	43
25	Deep annotation of *Drosophila melanogaster* microRNAs yields insights into their processing, modification, and emergence. Genome Research, 2011, 21, 203-215.	2.4	207
26	The transcriptional diversity of 25 *Drosophila* cell lines. Genome Research, 2011, 21, 301-314.	2.4	235
27	Identification of Functional Elements and Regulatory Circuits by *Drosophila* modENCODE. Science, 2010, 330, 1787-1797.	6.0	1,124
28	GCPReg package for registration of the segmentation gene expression data in Drosophila. Fly, 2009, 3, 151-156.	0.9	11
29	Methods for acquisition of quantitative data from confocal images of gene expression in situ. Cell and Tissue Biology, 2008, 2, 200-215.	0.2	12
30	Characterization of the Drosophila segment determination morphome. Developmental Biology, 2008, 313, 844-862.	0.9	200
31	Pipeline for acquisition of quantitative data on segmentation gene expression from confocal images. Fly, 2008, 2, 58-66.	0.9	44
32	Prediction of Gene Expression in Embryonic Structures of Drosophila melanogaster. PLoS Computational Biology, 2007, 3, e144.	1.5	13
33	Determination of the Developmental Age of a Drosophila Embryo from Confocal Images of its Segmentation Gene Expression Patterns. , 2006, , 467-478.		0
34	Spatial Registration of Data on in situ Gene Expression. Molecular Biology, 2001, 35, 955-960.	0.4	4
35	Registration of the expression patterns of Drosophila segmentation genes by two independent methods. Bioinformatics, 2001, 17, 3-12.	1.8	118