

# Iva A Tchasovnikarova

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2622832/publications.pdf>

Version: 2024-02-01

13  
papers

915  
citations

933447

10  
h-index

1125743

13  
g-index

16  
all docs

16  
docs citations

16  
times ranked

1636  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic silencing by the HUSH complex mediates position-effect variegation in human cells. <i>Science</i> , 2015, 348, 1481-1485.	12.6	250
2	The HUSH complex cooperates with TRIM28 to repress young retrotransposons and new genes. <i>Genome Research</i> , 2018, 28, 836-845.	5.5	141
3	Hyperactivation of HUSH complex function by Charcot-Marie-Tooth disease mutation in MORC2. <i>Nature Genetics</i> , 2017, 49, 1035-1044.	21.4	105
4	ATF7IP-Mediated Stabilization of the Histone Methyltransferase SETDB1 Is Essential for Heterochromatin Formation by the HUSH Complex. <i>Cell Reports</i> , 2016, 17, 653-659.	6.4	94
5	Genetic dissection of mammalian ERAD through comparative haploid and CRISPR forward genetic screens. <i>Nature Communications</i> , 2016, 7, 11786.	12.8	64
6	De Novo Variants in the ATPase Module of MORC2 Cause a Neurodevelopmental Disorder with Growth Retardation and Variable Craniofacial Dysmorphism. <i>American Journal of Human Genetics</i> , 2020, 107, 352-363.	6.2	64
7	TASOR is a pseudo-PARP that directs HUSH complex assembly and epigenetic transposon control. <i>Nature Communications</i> , 2020, 11, 4940.	12.8	59
8	Neuropathic MORC2 mutations perturb GHKL ATPase dimerization dynamics and epigenetic silencing by multiple structural mechanisms. <i>Nature Communications</i> , 2018, 9, 651.	12.8	58
9	Position-effect variegation revisited: HUSHing up heterochromatin in human cells. <i>BioEssays</i> , 2016, 38, 333-343.	2.5	36
10	Periphilin self-association underpins epigenetic silencing by the HUSH complex. <i>Nucleic Acids Research</i> , 2020, 48, 10313-10328.	14.5	15
11	Beyond the Histone Code: A Physical Map of Chromatin States. <i>Molecular Cell</i> , 2018, 69, 5-7.	9.7	10
12	Differential viral accessibility (DIVA) identifies alterations in chromatin architecture through large-scale mapping of lentiviral integration sites. <i>Nature Protocols</i> , 2019, 14, 153-170.	12.0	7
13	TRACE generates fluorescent human reporter cell lines to characterize epigenetic pathways. <i>Molecular Cell</i> , 2022, 82, 479-491.e7.	9.7	7