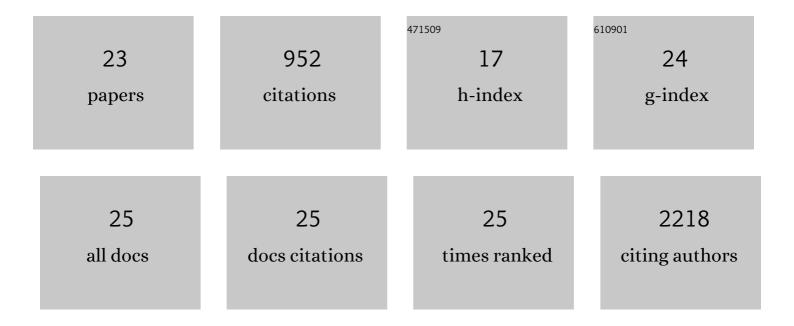
Andrei L Turinsky

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5055523/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	CHARGE and Kabuki Syndromes: Gene-Specific DNA Methylation Signatures Identify Epigenetic Mechanisms Linking These Clinically Overlapping Conditions. American Journal of Human Genetics, 2017, 100, 773-788.	6.2	166
2	Prevalence and Clinical Features of Inflammatory Bowel Diseases Associated With Monogenic Variants, Identified by Whole-Exome Sequencing in 1000 Children at a Single Center. Gastroenterology, 2020, 158, 2208-2220.	1.3	81
3	Multilocus loss of DNA methylation in individuals with mutations in the histone H3 Lysine 4 Demethylase KDM5C. BMC Medical Genomics, 2013, 6, 1.	1.5	80
4	Human-Chromatin-Related Protein Interactions Identify a Demethylase Complex Required for Chromosome Segregation. Cell Reports, 2014, 8, 297-310.	6.4	72
5	Impact of assisted reproduction, infertility, sex and paternal factors on the placental DNA methylome. Human Molecular Genetics, 2019, 28, 372-385.	2.9	61
6	DNA Methylation Signature for EZH2 Functionally Classifies Sequence Variants in Three PRC2 Complex Genes. American Journal of Human Genetics, 2020, 106, 596-610.	6.2	59
7	Intercellular network structure and regulatory motifs in the human hematopoietic system. Molecular Systems Biology, 2014, 10, 741.	7.2	57
8	Literature curation of protein interactions: measuring agreement across major public databases. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq026-baq026.	3.0	54
9	Genome-wide placental DNA methylation analysis of severely growth-discordant monochorionic twins reveals novel epigenetic targets for intrauterine growth restriction. Clinical Epigenetics, 2016, 8, 70.	4.1	51
10	The missing indels: an estimate of indel variation in a human genome and analysis of factors that impede detection. Nucleic Acids Research, 2015, 43, 7217-7228.	14.5	47
11	Anatomy of DNA methylation signatures: Emerging insights and applications. American Journal of Human Genetics, 2021, 108, 1359-1366.	6.2	36
12	Extracting high confidence protein interactions from affinity purification data: At the crossroads. Journal of Proteomics, 2015, 118, 63-80.	2.4	30
13	Obsessive-compulsive disorder and attention-deficit/hyperactivity disorder: distinct associations with DNA methylation and genetic variation. Journal of Neurodevelopmental Disorders, 2020, 12, 23.	3.1	27
14	New insights into DNA methylation signatures: SMARCA2 variants in Nicolaides-Baraitser syndrome. BMC Medical Genomics, 2019, 12, 105.	1.5	25
15	DNA methylation signature is prognostic of choroid plexus tumor aggressiveness. Clinical Epigenetics, 2019, 11, 117.	4.1	21
16	DAnCER: Disease-Annotated Chromatin Epigenetics Resource. Nucleic Acids Research, 2011, 39, D889-D894.	14.5	19
17	Navigating the Clobal Protein–Protein Interaction Landscape Using iRefWeb. Methods in Molecular Biology, 2014, 1091, 315-331.	0.9	19
18	EpigenCentral: Portal for DNA methylation data analysis and classification in rare diseases. Human Mutation, 2020, 41, 1722-1733.	2.5	15

#	Article	IF	CITATIONS
19	Role of STAT5 and epigenetics in lactation-associated upregulation of multidrug transporter ABCG2 in the mammary gland. American Journal of Physiology - Endocrinology and Metabolism, 2014, 307, E596-E610.	3.5	11
20	Don't brush off buccal data heterogeneity. Epigenetics, 2019, 14, 109-117.	2.7	8
21	MetaFusion: a high-confidence metacaller for filtering and prioritizing RNA-seq gene fusion candidates. Bioinformatics, 2021, 37, 3144-3151.	4.1	6
22	Genomics4RD: An integrated platform to share Canadian deep-phenotype and multiomic data for international rare disease gene discovery Human Mutation, 2022, , .	2.5	4
23	Navigating the Global Protein–Protein Interaction Landscape Using iRefWeb. Methods in Molecular Biology, 2021, 2199, 191-207.	0.9	2