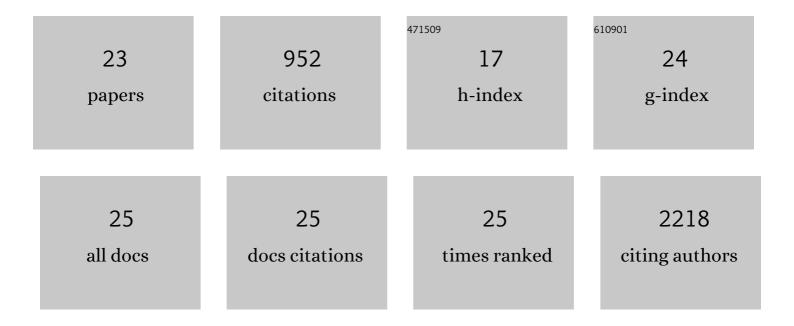
Andrei L Turinsky

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 |