

# Ondrej Libiger

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10726967/publications.pdf>

Version: 2024-02-01

27  
papers

3,941  
citations

471509

17  
h-index

552781

26  
g-index

27  
all docs

27  
docs citations

27  
times ranked

7110  
citing authors

#	ARTICLE	IF	CITATIONS
1	Impacts of personal DNA ancestry testing. <i>Journal of Community Genetics</i> , 2021, 12, 37-52.	1.2	12
2	Anxiety is related to indices of cortical maturation in typically developing children and adolescents. <i>Brain Structure and Function</i> , 2016, 221, 3013-3025.	2.3	43
3	Dyslexia and language impairment associated genetic markers influence cortical thickness and white matter in typically developing children. <i>Brain Imaging and Behavior</i> , 2016, 10, 272-282.	2.1	27
4	The Pediatric Imaging, Neurocognition, and Genetics (PING) Data Repository. <i>NeuroImage</i> , 2016, 124, 1149-1154.	4.2	251
5	Partial Least Squares Regression Can Aid in Detecting Differential Abundance of Multiple Features in Sets of Metagenomic Samples. <i>Frontiers in Genetics</i> , 2015, 6, 350.	2.3	3
6	Family income, parental education and brain structure in children and adolescents. <i>Nature Neuroscience</i> , 2015, 18, 773-778.	14.8	979
7	Chip-based direct genotyping of coding variants in genome wide association studies: Utility, issues and prospects. <i>Gene</i> , 2014, 540, 104-109.	2.2	10
8	Correlation analysis of genetic admixture and social identification with body mass index in a Native American Community. <i>American Journal of Human Biology</i> , 2014, 26, 347-360.	1.6	13
9	The NIH Toolbox Cognition Battery: Results from a large normative developmental sample (PING).. <i>Neuropsychology</i> , 2014, 28, 1-10.	1.3	163
10	Admixture and Clinical Phenotypic Variation. <i>Human Heredity</i> , 2014, 77, 73-86.	0.8	20
11	Patterns of population epigenomic diversity. <i>Nature</i> , 2013, 495, 193-198.	27.8	543
12	Complex Patterns of Genomic Admixture within Southern Africa. <i>PLoS Genetics</i> , 2013, 9, e1003309.	3.5	94
13	A Method for Inferring an Individual's Genetic Ancestry and Degree of Admixture Associated with Six Major Continental Populations. <i>Frontiers in Genetics</i> , 2013, 3, 322.	2.3	33
14	Genomic Risk Models Improve Prediction of Longitudinal Lipid Levels in Children and Young Adults. <i>Frontiers in Genetics</i> , 2013, 4, 86.	2.3	6
15	Long-term influence of normal variation in neonatal characteristics on human brain development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20089-20094.	7.1	158
16	Multimodal imaging of the self-regulating developing brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19620-19625.	7.1	192
17	Clinical Implications of Human Population Differences in Genome-Wide Rates of Functional Genotypes. <i>Frontiers in Genetics</i> , 2012, 3, 211.	2.3	29
18	Transgenerational Epigenetic Instability Is a Source of Novel Methylation Variants. <i>Science</i> , 2011, 334, 369-373.	12.6	635

#	ARTICLE	IF	CITATIONS
19	AN APPLICATION AND EMPIRICAL COMPARISON OF STATISTICAL ANALYSIS METHODS FOR ASSOCIATING RARE VARIANTS TO A COMPLEX PHENOTYPE. , 2010, , 76-87.		10
20	Statistical analysis strategies for association studies involving rare variants. Nature Reviews Genetics, 2010, 11, 773-785.	16.3	426
21	Comparison of Genetic Distance Measures Using Human SNP Genotype Data. Human Biology, 2009, 81, 389-406.	0.2	29
22	Accommodating Linkage Disequilibrium in Genetic-Association Analyses via Ridge Regression. American Journal of Human Genetics, 2008, 82, 375-385.	6.2	115
23	Generalized Analysis of Molecular Variance. PLoS Genetics, 2007, 3, e51.	3.5	75
24	Detecting genetic variation in microarray expression data. Genome Research, 2007, 17, 1228-1235.	5.5	10
25	DNA variation and brain region-specific expression profiles exhibit different relationships between inbred mouse strains: implications for eQTL mapping studies. Genome Biology, 2007, 8, R25.	9.6	57
26	A simulation-based analysis of chromosome segment sharing among a group of arbitrarily related individuals. European Journal of Human Genetics, 2007, 15, 1260-1268.	2.8	6
27	Simulation-based homozygosity mapping with the GAW14 COGA dataset on alcoholism. BMC Genetics, 2005, 6, S35.	2.7	2