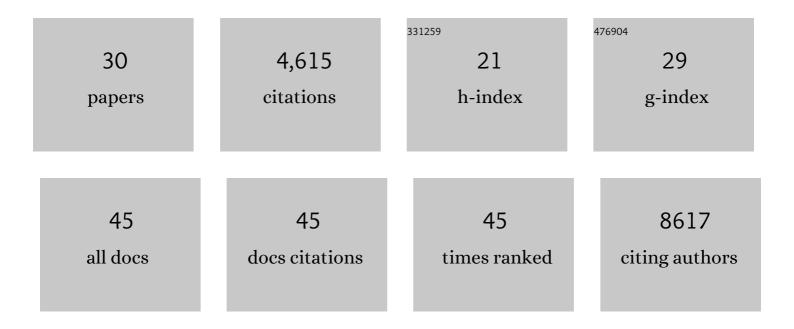
## Jaroslav Bendl

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2389269/publications.pdf Version: 2024-02-01



INDOSLAV RENDL

#	Article	IF	CITATIONS
1	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805
2	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	6.0	618
3	PredictSNP: Robust and Accurate Consensus Classifier for Prediction of Disease-Related Mutations. PLoS Computational Biology, 2014, 10, e1003440.	1.5	593
4	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
5	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data, 2018, 5, 180185.	2.4	320
6	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	6.0	220
7	An atlas of chromatin accessibility in the adult human brain. Genome Research, 2018, 28, 1243-1252.	2.4	170
8	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180.	2.4	149
9	PredictSNP2: A Unified Platform for Accurately Evaluating SNP Effects by Exploiting the Different Characteristics of Variants in Distinct Genomic Regions. PLoS Computational Biology, 2016, 12, e1004962.	1.5	149
10	FireProt: Energy- and Evolution-Based Computational Design of Thermostable Multiple-Point Mutants. PLoS Computational Biology, 2015, 11, e1004556.	1.5	144
11	Integration of Alzheimer's disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. Nature Communications, 2021, 12, 1610.	5.8	118
12	Common genetic variation influencing human white matter microstructure. Science, 2021, 372, .	6.0	106
13	FireProt: web server for automated design of thermostable proteins. Nucleic Acids Research, 2017, 45, W393-W399.	6.5	104
14	HotSpot Wizard 2.0: automated design of site-specific mutations and smart libraries in protein engineering. Nucleic Acids Research, 2016, 44, W479-W487.	6.5	76
15	Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. Nature Communications, 2020, 11, 5581.	5.8	53
16	Multi-ancestry eQTL meta-analysis of human brain identifies candidate causal variants for brain-related traits. Nature Genetics, 2022, 54, 161-169.	9.4	49
17	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	5.8	48
18	Computer-Assisted Engineering of the Synthetic Pathway for Biodegradation of a Toxic Persistent Pollutant. ACS Synthetic Biology, 2014, 3, 172-181.	1.9	39

JAROSLAV BENDL

#	Article	IF	CITATIONS
19	Functional interpretation of genetic variants using deep learning predicts impact on chromatin accessibility and histone modification. Nucleic Acids Research, 2019, 47, 10597-10611.	6.5	39
20	Sex Differences in the Human Brain Transcriptome of Cases With Schizophrenia. Biological Psychiatry, 2022, 91, 92-101.	0.7	38
21	Common variants contribute to intrinsic human brain functional networks. Nature Genetics, 2022, 54, 508-517.	9.4	37
22	Maximizing the Efficiency of Multienzyme Process by Stoichiometry Optimization. ChemBioChem, 2014, 15, 1891-1895.	1.3	31
23	A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. Genome Medicine, 2020, 12, 19.	3.6	31
24	Chromatin domain alterations linked to 3D genome organization in a large cohort of schizophrenia and bipolar disorder brains. Nature Neuroscience, 2022, 25, 474-483.	7.1	25
25	Computational Tools for Designing Smart Libraries. Methods in Molecular Biology, 2014, 1179, 291-314.	0.4	21
26	NewProt – a protein engineering portal. Protein Engineering, Design and Selection, 2017, 30, 441-447.	1.0	11
27	decorate: differential epigenetic correlation test. Bioinformatics, 2020, 36, 2856-2861.	1.8	11
28	Unbiased identification of novel transcription factors in striatal compartmentation and striosome maturation. ELife, 2021, 10, .	2.8	9
29	Impact of schizophrenia GWAS loci converge onto distinct pathways in cortical interneurons vs glutamatergic neurons during development. Molecular Psychiatry, 2022, 27, 4218-4233.	4.1	6

30 ATAC-seq and psychiatric disorders. , 2021, , 143-162.

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