Babak Alipanahi Ramandi

List of Publications by Year
in descending order

36	7,431	304602	345118
papers	citations	22 h-index	36 g-index

43	43	43	14247
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. Human Reproduction, 2022, 37, 366-383.	0.4	19
2	DeepNull models non-linear covariate effects to improve phenotypic prediction and association power. Nature Communications, 2022, 13, 241.	5.8	17
3	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. Human Genetics, 2021, 140, 529-552.	1.8	36
4	Disease risk scores for skin cancers. Nature Communications, 2021, 12, 160.	5.8	46
5	Genomewide Association Studies of <scp>LRRK2</scp> Modifiers of Parkinson's Disease. Annals of Neurology, 2021, 90, 76-88.	2.8	30
6	Large-scale machine-learning-based phenotyping significantly improves genomic discovery for optic nerve head morphology. American Journal of Human Genetics, 2021, 108, 1217-1230.	2.6	35
7	Insights into the genetic basis of retinal detachment. Human Molecular Genetics, 2020, 29, 689-702.	1.4	26
8	Genome-wide association studies of antidepressant class response and treatment-resistant depression. Translational Psychiatry, 2020, 10, 360.	2.4	33
9	The effect of LRRK2 loss-of-function variants in humans. Nature Medicine, 2020, 26, 869-877.	15.2	79
10	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2019, 18, 1091-1102.	4.9	1,414
11	The Parkinsonâ€™s phenomeâ€”traits associated with Parkinsonâ€™s disease in a broadly phenotyped cohort. Npj Parkinson's Disease, 2019, 5, 4.	2.5	34
12	Correspondence between cerebral glucose metabolism and BOLD reveals relative power and cost in human brain. Nature Communications, 2019, 10, 690.	5.8	62
13	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€“Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100.	1.1	16
14	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	3.8	63
15	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. Lancet Neurology, The, 2017, 16, 898-907.	4.9	191
16	Replication and characterization of CADM2 and MSRA genes on human behavior. Heliyon, 2017, 3, e00349.	1.4	80
17	Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. American Journal of Human Genetics, 2017, 101, 913-924.	2.6	29
18	Does conservation account for splicing patterns?. BMC Genomics, 2016, 17, 787.	1.2	15

#	Article	IF	Citations
19	Whole-genome sequencing expands diagnostic utility and improves clinical management in paediatric medicine. Npj Genomic Medicine, 2016, 1, .	1.7	295
20	Genome-wide characteristics of de novo mutations in autism. Npj Genomic Medicine, 2016, 1, 160271-1602710.	1.7	200
21	Machine Learning in Genomic Medicine: A Review of Computational Problems and Data Sets. Proceedings of the IEEE, 2016, 104, 176-197.	16.4	186
22	Whole-Genome Sequencing Suggests Schizophrenia Risk Mechanisms in Humans with 22q11.2 Deletion Syndrome. G3: Genes, Genomes, Genetics, 2015, 5, 2453-2461.	0.8	43
23	Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning. Nature Biotechnology, 2015, 33, 831-838.	9.4	2,206
24	The human splicing code reveals new insights into the genetic determinants of disease. Science, 2015, 347, 1254806.	6.0	1,053
25	Brain-expressed exons under purifying selection are enriched for de novo mutations in autism spectrum disorder. Nature Genetics, 2014, 46, 742-747.	9.4	149
26	Widespread intron retention in mammals functionally tunes transcriptomes. Genome Research, 2014, 24, 1774-1786.	2.4	554
27	Protein Structure Idealization: How accurately is it possible to model protein structures with dihedral angles?. Algorithms for Molecular Biology, 2013, 8, 5.	0.3	2
28	Network cleanup. Nature Biotechnology, 2013, 31, 714-715.	9.4	26
29	Determining Protein Structures from NOESY Distance Constraints by Semidefinite Programming. Journal of Computational Biology, 2013, 20, 296-310.	0.8	25
30	MBNL proteins repress ES-cell-specific alternative splicing and reprogramming. Nature, 2013, 498, 241-245.	13.7	326
31	Protein Structure by Semidefinite Facial Reduction. Lecture Notes in Computer Science, 2012, , 1-11.	1.0	2
32	How Accurately Can We Model Protein Structures with Dihedral Angles?. Lecture Notes in Computer Science, 2012, , 274-287.	1.0	0
33	Guided Locally Linear Embedding. Pattern Recognition Letters, 2011, 32, 1029-1035.	2.6	15
34	ERROR TOLERANT NMR BACKBONE RESONANCE ASSIGNMENT AND AUTOMATED STRUCTURE GENERATION. Journal of Bioinformatics and Computational Biology, 2011, 09, 15-41.	0.3	18
35	PROTEIN SECONDARY STRUCTURE PREDICTION USING NMR CHEMICAL SHIFT DATA. Journal of Bioinformatics and Computational Biology, 2010, 08, 867-884.	0.3	19
36	PICKY: a novel SVD-based NMR spectra peak picking method. Bioinformatics, 2009, 25, i268-i275.	1.8	61