Babak Alipanahi Ramandi

List of Publications by Year
in descending order

36 papers	7,431 citations	304368 22 h-index	344852 36 g-index

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

#	Article	IF	Citations
1	Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning. Nature Biotechnology, 2015, 33, 831-838.	9.4	2,206
2	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
3	The human splicing code reveals new insights into the genetic determinants of disease. Science, 2015, 347, 1254806.	6.0	1,053
4	Widespread intron retention in mammals functionally tunes transcriptomes. Genome Research, 2014, 24, 1774-1786.	2.4	554
5	MBNL proteins repress ES-cell-specific alternative splicing and reprogramming. Nature, 2013, 498, 241-245.	13.7	326
6	Whole-genome sequencing expands diagnostic utility and improves clinical management in paediatric medicine. Npj Genomic Medicine, 2016, 1, .	1.7	295
7	Genome-wide characteristics of de novo mutations in autism. Npj Genomic Medicine, 2016, 1, 160271-1602710.	1.7	200
8	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
9	Machine Learning in Genomic Medicine: A Review of Computational Problems and Data Sets. Proceedings of the IEEE, 2016, 104, 176-197.	16.4	186
10	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
11	Replication and characterization of CADM2 and MSRA genes on human behavior. Heliyon, 2017, 3, e00349.	1.4	80
12	The effect of LRRK2 loss-of-function variants in humans. Nature Medicine, 2020, 26, 869-877.	15.2	79
13	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	3.8	63
14	Correspondence between cerebral glucose metabolism and BOLD reveals relative power and cost in human brain. Nature Communications, 2019, 10, 690.	5.8	62
15	PICKY: a novel SVD-based NMR spectra peak picking method. Bioinformatics, 2009, 25, i268-i275.	1.8	61
16	Disease risk scores for skin cancers. Nature Communications, 2021, 12, 160.	5.8	46
17	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
18	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

#	Article	IF	Citations
19	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
20	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
21	Genome-wide association studies of antidepressant class response and treatment-resistant depression. Translational Psychiatry, 2020, 10, 360.	2.4	33
22	Genomewide Association Studies of <scp>LRRK2</scp> Modifiers of Parkinson's Disease. Annals of Neurology, 2021, 90, 76-88.	2.8	30
23	Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. American Journal of Human Genetics, 2017, 101, 913-924.	2.6	29
24	Network cleanup. Nature Biotechnology, 2013, 31, 714-715.	9.4	26
25	Insights into the genetic basis of retinal detachment. Human Molecular Genetics, 2020, 29, 689-702.	1.4	26
26	Determining Protein Structures from NOESY Distance Constraints by Semidefinite Programming. Journal of Computational Biology, 2013, 20, 296-310.	0.8	25
27	PROTEIN SECONDARY STRUCTURE PREDICTION USING NMR CHEMICAL SHIFT DATA. Journal of Bioinformatics and Computational Biology, 2010, 08, 867-884.	0.3	19
28	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
29	ERROR TOLERANT NMR BACKBONE RESONANCE ASSIGNMENT AND AUTOMATED STRUCTURE GENERATION. Journal of Bioinformatics and Computational Biology, 2011, 09, 15-41.	0.3	18
30	DeepNull models non-linear covariate effects to improve phenotypic prediction and association power. Nature Communications, 2022, 13, 241.	5.8	17
31	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
32	Guided Locally Linear Embedding. Pattern Recognition Letters, 2011, 32, 1029-1035.	2.6	15
33	Does conservation account for splicing patterns?. BMC Genomics, 2016, 17, 787.	1.2	15
34	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
35	Protein Structure by Semidefinite Facial Reduction. Lecture Notes in Computer Science, 2012, , 1-11.	1.0	2
36	How Accurately Can We Model Protein Structures with Dihedral Angles?. Lecture Notes in Computer Science, 2012, , 274-287.	1.0	0