Mehdi Pirooznia

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/4411745/mehdi-pirooznia-publications-by-year.pdf
Version: 2024-04-26

135 papers	3,513 citations	31 h-index	56 g-index
176 ext. papers	4,761 ext. citations	7.7 avg, IF	5.95 L-index

#	Paper	IF	Citations
135	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing.. *Genome Biology*, **2022**, 23, 2	18.3	3
134	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways.. *Nature Neuroscience*, **2022**, 25, 381-389	25.5	2
133	Discriminating bipolar depression from major depressive disorder with polygenic risk scores. *Psychological Medicine*, **2021**, 51, 1451-1458	6.9	6
132	Pklr Is a Genetic Modifier of Sickle Cell Disease. *Blood*, **2021**, 138, 953-953	2.2	
131	Individuals with Sickle Cell Disease Have a Higher Burden of Mitochondrial DNA Heteroplasmy. *Blood*, **2021**, 138, 954-954	2.2	
130	Early Myeloid Derived Suppressor Cells (eMDSCs) Are Associated With High Donor Myeloid Chimerism Following Haploidentical HSCT for Sickle Cell Disease.. *Frontiers in Immunology*, **2021**, 12, 757279	8.4	0
129	Bioinformatics Approaches for Functional Prediction of Long Noncoding RNAs. *Methods in Molecular Biology*, **2021**, 2254, 1-13	1.4	1
128	Fasting-induced FOXO4 blunts human CD4 T helper cell responsiveness. *Nature Metabolism*, **2021**, 3, 318-326	14.6	3
127	Cell-Free DNA to Detect Heart Allograft Acute Rejection. *Circulation*, **2021**, 143, 1184-1197	16.7	36
126	Network Analysis and Transcriptome Profiling Identify Autophagic and Mitochondrial Dysfunctions in SARS-CoV-2 Infection. *Frontiers in Genetics*, **2021**, 12, 599261	4.5	31
125	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. *Nature Biotechnology*, **2021**, 39, 1115-1128	44.5	31
124	Identification and Validation of Nutrient State-Dependent Serum Protein Mediators of Human CD4 T Cell Responsiveness. *Nutrients*, **2021**, 13,	6.7	2
123	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. *Genome Biology*, **2021**, 22, 109	18.3	6
122	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. *Genome Biology*, **2021**, 22, 111	18.3	8
121	Cell-free DNA maps COVID-19 tissue injury and risk of death and can cause tissue injury. *JCI Insight*, **2021**, 6,	9.9	18
120	Cell-Free DNA Tissue Damage Mapping in Transplant Patients Infected with COVID-19. *Journal of Heart and Lung Transplantation*, **2021**, 40, S142	5.8	78
119	Circulating mitochondrial DNA is a proinflammatory DAMP in sickle cell disease. *Blood*, **2021**, 137, 3116-3126	2.2	12

118	Ultra-Small Lung Cysts Impair Diffusion Without Obstructing Air Flow in Lymphangioleiomyomatosis. *Chest*, **2021**, 160, 199-208	5.3	1
117	De novo variation in bipolar disorder. *Molecular Psychiatry*, **2021**, 26, 4127-4136	15.1	7
116	Identification of Genes Contributing to a Long Circadian Period in. *Journal of Biological Rhythms*, **2021**, 36, 239-253	3.2	1
115	Reducing Fatty Acid Oxidation Improves Cancer-free Survival in a Mouse Model of Li-Fraumeni Syndrome. *Cancer Prevention Research*, **2021**, 14, 31-40	3.2	1
114	The secretome mouse provides a genetic platform to delineate tissue-specific in vivo secretion. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	8
113	Identification of human long noncoding RNAs associated with nonalcoholic fatty liver disease and metabolic homeostasis. *Journal of Clinical Investigation*, **2021**, 131,	15.9	6
112	The Genetics of Sudden Infant Death Syndrome-Towards a Gene Reference Resource. *Genes*, **2021**, 12,	4.2	3
111	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. *Nature Biotechnology*, **2021**, 39, 1141-1150	44.5	11
110	Response by Shah et al to Letter Regarding Article, "Cell-Free DNA to Detect Heart Allograft Acute Rejection". *Circulation*, **2021**, 144, e198-e199	16.7	
109	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. *Nature Biotechnology*, **2021**, 39, 1151-1160	44.5	5
108	NOTCH-mediated ex vivo expansion of human hematopoietic stem and progenitor cells by culture under hypoxia. *Stem Cell Reports*, **2021**, 16, 2336-2350	8	3
107	Effect of non-uniform cyst distribution in lymphangioleiomyomatosis on pulmonary function: a cross-sectional study. *European Respiratory Journal*, **2021**, 57,	13.6	0
106	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. *Molecular Psychiatry*, **2021**, 26, 5239-5250	15.1	3
105	Olfactomedin 4 mediation of prostate stem/progenitor-like cell proliferation and differentiation via MYC. *Scientific Reports*, **2020**, 10, 21924	4.9	1
104	Apolipoprotein E Signals via TLR4 to Induce CXCL5 Secretion by Asthmatic Airway Epithelial Cells. *American Journal of Respiratory Cell and Molecular Biology*, **2020**, 63, 185-197	5.7	6
103	Sequential CRISPR-Based Screens Identify LITAF and CDIP1 as the Bacillus cereus Hemolysin BL Toxin Host Receptors. *Cell Host and Microbe*, **2020**, 28, 402-410.e5	23.4	14
102	Misregulation of ELK1, AP1, and E12 Transcription Factor Networks Is Associated with Melanoma Progression. *Cancers*, **2020**, 12,	6.6	1
101	Mitochondria regulate intestinal stem cell proliferation and epithelial homeostasis through FOXO. *Molecular Biology of the Cell*, **2020**, 31, 1538-1549	3.5	8

100	Whole-exome sequencing of 81 individuals from 27 multiply affected bipolar disorder families. *Translational Psychiatry*, **2020**, 10, 57	8.6	7
99	Whole genome sequence-based haplotypes reveal a single origin of the 1393 bp deletion. *Journal of Medical Genetics*, **2020**, 57, 567-570	5.8	2
98	Notch-Mediated Expansion of Human Hematopoietic Stem and Progenitor Cells By Culture Under Hypoxia. *Blood*, **2020**, 136, 28-29	2.2	
97	Mitochondrial DNA Variation in Individuals with Sickle Cell Disease. *Blood*, **2020**, 136, 11-11	2.2	0
96	RNA Seq Profiles and Bioinformatics Validation in a Large Sample of Sickle Cell Disease Patients. *Blood*, **2020**, 136, 13-14	2.2	
95	Cfcloud: A Cloud-Based Workflow for Cell-Free DNA Data Analysis. *Blood*, **2020**, 136, 31-32	2.2	
94	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses. *PLoS Biology*, **2020**, 18, e3000981	9.7	8
93	Network Analysis and Transcriptome Profiling Identify Autophagic and Mitochondrial Dysfunctions in SARS-CoV-2 Infection **2020**,		11
92	In vivo functional analysis of non-conserved human lncRNAs associated with cardiometabolic traits. *Nature Communications*, **2020**, 11, 45	17.4	29
91	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. *Scientific Data*, **2020**, 7, 326	8.2	16
90	Genome-Wide Analysis of Off-Target CRISPR/Cas9 Activity in Single-Cell-Derived Human Hematopoietic Stem and Progenitor Cell Clones. *Genes*, **2020**, 11,	4.2	1
89	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses **2020**, 18, e3000981		
88	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses **2020**, 18, e3000981		
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85	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses **2020**, 18, e3000981		
84	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses **2020**, 18, e3000981		
83	IKAP-Identifying K mAjor cell Population groups in single-cell RNA-sequencing analysis. *GigaScience*, **2019**, 8,	7.6	7

82	GATA-2-deficient mast cells limit IgE-mediated immediate hypersensitivity reactions in human subjects. *Journal of Allergy and Clinical Immunology*, **2019**, 144, 613-617.e14	11.5	14
81	Circulating Lymphangioleiomyomatosis Tumor Cells With Loss of Heterozygosity in the TSC2 Gene Show Increased Aldehyde Dehydrogenase Activity. *Chest*, **2019**, 156, 298-307	5.3	4
80	Neutrophil Subsets, Platelets, and Vascular Disease in Psoriasis. *JACC Basic To Translational Science*, **2019**, 4, 1-14	8.7	36
79	Platelet Phenotype Prediction from Whole Genome Sequencing in 621 Sickle Cell Disease Patients. *Blood*, **2019**, 134, 2295-2295	2.2	1
78	Electron transport chain biogenesis activated by a JNK-insulin-Myc relay primes mitochondrial inheritance in. *ELife*, **2019**, 8,	8.9	13
77	Author response: Electron transport chain biogenesis activated by a JNK-insulin-Myc relay primes mitochondrial inheritance in Drosophila **2019**,		3
76	Functional Omics and Molecular Analysis of a Subtropical Harmful Algal Bloom Species, Karenia brevis **2019**, 132-148		
75	Diverging Clonal Evolution during Sequential Therapy with Chemoimmunotherapy Followed By BTK Inhibitors. *Blood*, **2019**, 134, 850-850	2.2	1
74	Whole Exome Sequencing Reveals Multiple Driver Events in Chronic Lymphocytic Leukemia Patients with Acquired Ibrutinib Resistance. *Blood*, **2019**, 134, 1287-1287	2.2	
73	Spatial Genomic Heterogeneity in Chronic Lymphocytic Leukemia. *Blood*, **2019**, 134, 3017-3017	2.2	
72	Affected Sib-Pair Analyses Identify Signaling Networks Associated With Social Behavioral Deficits in Autism. *Frontiers in Genetics*, **2019**, 10, 1186	4.5	2
71	Targeted RNA-sequencing for the quantification of measurable residual disease in acute myeloid leukemia. *Haematologica*, **2019**, 104, 297-304	6.6	22
70	Pathogenic TERT promoter variants in telomere diseases. *Genetics in Medicine*, **2019**, 21, 1594-1602	8.1	18
69	Late manifestation of alloantibody-associated injury and clinical pulmonary antibody-mediated rejection: Evidence from cell-free DNA analysis. *Journal of Heart and Lung Transplantation*, **2018**, 37, 925-932	5.8	40
68	Mutations in the pancreatic secretory enzymes and are associated with pancreatic cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 4767-4772	11.5	34
67	Circulating cell-free DNA as a biomarker of tissue injury: Assessment in a cardiac xenotransplantation model. *Journal of Heart and Lung Transplantation*, **2018**, 37, 967-975	5.8	16
66	DIXDC1 contributes to psychiatric susceptibility by regulating dendritic spine and glutamatergic synapse density via GSK3 and Wnt/β-catenin signaling. *Molecular Psychiatry*, **2018**, 23, 467-475	15.1	34
65	The transcription factors TFE3 and TFEB amplify p53 dependent transcriptional programs in response to DNA damage. *ELife*, **2018**, 7,	8.9	44

64	Cell-Free Mitochondrial DNA Is Elevated in Sickle Cell Disease Patients, and Serve As a Potential Proinflammatory DAMP. *Blood*, **2018**, 132, 1068-1068	2.2	1
63	Red Blood Cell and Platelet Phenotype Prediction from Whole Genome Sequencing in 621 Sickle Cell Disease Patients: Correlation with Alloimmunization History, Serology and Other Genotyping Methods. *Blood*, **2018**, 132, 2388-2388	2.2	
62	Evaluation of Early Biomarkers Associated with Graft Rejection in Patients with Sickle Cell Disease Undergoing Haploidentical Hematopoietic Stem Cell Transplantation. *Biology of Blood and Marrow Transplantation*, **2018**, 24, S298	4.7	
61	Human retinoic acid-regulated CD161 regulatory T cells support wound repair in intestinal mucosa. *Nature Immunology*, **2018**, 19, 1403-1414	19.1	58
60	Ancient Ancestry Informative Markers for Identifying Fine-Scale Ancient Population Structure in Eurasians. *Genes*, **2018**, 9,	4.2	10
59	High density lipoprotein proteome is associated with cardiovascular risk factors and atherosclerosis burden as evaluated by coronary CT angiography. *Atherosclerosis*, **2018**, 278, 278-285	3.1	27
58	Complement receptor CD46 co-stimulates optimal human CD8 T cell effector function via fatty acid metabolism. *Nature Communications*, **2018**, 9, 4186	17.4	38
57	GCN5L1 interacts with □TAT1 and RanBP2 to regulate hepatic □tubulin acetylation and lysosome trafficking. *Journal of Cell Science*, **2018**, 131,	5.3	7
56	Assessment of Whole-Exome Sequence Data in Attempted Suicide within a Bipolar Disorder Cohort. *Molecular Neuropsychiatry*, **2017**, 3, 1-11	4.9	11
55	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. *Human Mutation*, **2017**, 38, 1182-1192	4.7	28
54	Genome-wide Methyl-Seq analysis of blood-brain targets of glucocorticoid exposure. *Epigenetics*, **2017**, 12, 637-652	5.7	23
53	Genome-wide DNA hydroxymethylation identifies potassium channels in the nucleus accumbens as discriminators of methamphetamine addiction and abstinence. *Molecular Psychiatry*, **2017**, 22, 1196-1204	15.1	45
52	The Diversity of REcent and Ancient huMan (DREAM): A New Microarray for Genetic Anthropology and Genealogy, Forensics, and Personalized Medicine. *Genome Biology and Evolution*, **2017**, 9, 3225-3237	3.9	7
51	The Origins of Ashkenaz, Ashkenazic Jews, and Yiddish. *Frontiers in Genetics*, **2017**, 8, 87	4.5	8
50	High-throughput sequencing of the synaptome in major depressive disorder. *Molecular Psychiatry*, **2016**, 21, 650-5	15.1	27
49	Reconstructing Druze population history. *Scientific Reports*, **2016**, 6, 35837	4.9	12
48	Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. *Cancer Discovery*, **2016**, 6, 166-75	24.4	206
47	Polygenic Risk of Schizophrenia and Cognition in a Population-Based Survey of Older Adults. *Schizophrenia Bulletin*, **2016**, 42, 984-91	1.3	28

46	Localizing Ashkenazic Jews to Primeval Villages in the Ancient Iranian Lands of Ashkenaz. *Genome Biology and Evolution*, **2016**, 8, 1132-49	3.9	28
45	Evaluation of Plasma miR-21 and miR-152 as Diagnostic Biomarkers for Common Types of Human Cancers. *Journal of Cancer*, **2016**, 7, 490-9	4.5	47
44	Exome Sequencing of Familial Bipolar Disorder. *JAMA Psychiatry*, **2016**, 73, 590-7	14.5	69
43	Search for common targets of lithium and valproic acid identifies novel epigenetic effects of lithium on the rat leptin receptor gene. *Translational Psychiatry*, **2015**, 5, e600	8.6	26
42	Whole-genome CNV analysis: advances in computational approaches. *Frontiers in Genetics*, **2015**, 6, 138	4.5	100
41	Polygenic risk, stressful life events and depressive symptoms in older adults: a polygenic score analysis. *Psychological Medicine*, **2015**, 45, 1709-20	6.9	71
40	Distinguishing bipolar from unipolar depression: the importance of clinical symptoms and illness features. *Psychological Medicine*, **2015**, 45, 2437-46	6.9	30
39	Genome-wide association study of schizophrenia in Ashkenazi Jews. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2015**, 168, 649-59	3.5	128
38	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. *Nature Biotechnology*, **2014**, 32, 903-14	44.5	618
37	Metamoodics: meta-analysis and bioinformatics resource for mood disorders. *Molecular Psychiatry*, **2014**, 19, 748-9	15.1	7
36	Validation and assessment of variant calling pipelines for next-generation sequencing. *Human Genomics*, **2014**, 8, 14	6.8	79
35	Circulating microRNA profiling for early detection of non-small cell lung cancer.. *Journal of Clinical Oncology*, **2014**, 32, e22051-e22051	2.2	2
34	SVAw - a web-based application tool for automated surrogate variable analysis of gene expression studies. *Source Code for Biology and Medicine*, **2013**, 8, 8	1.9	6
33	Systematic review of genome-wide gene expression studies of bipolar disorder. *BMC Psychiatry*, **2013**, 13, 213	4.2	63
32	A hybrid likelihood model for sequence-based disease association studies. *PLoS Genetics*, **2013**, 9, e1003224	6	16
31	Converging Evidence for Epistasis between ANK3 and Potassium Channel Gene KCNQ2 in Bipolar Disorder. *Frontiers in Genetics*, **2013**, 4, 87	4.5	27
30	Gene expression analysis of CL-20-induced reversible neurotoxicity reveals GABA(A) receptors as potential targets in the earthworm Eisenia fetida. *Environmental Science & Technology*, **2012**, 46, 1223-32	10.3	19
29	Meta-analysis of genetic association studies on bipolar disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2012**, 159B, 508-18	3.5	54

28	A genome-wide association study of attempted suicide. *Molecular Psychiatry*, **2012**, 17, 433-44	15.1	117
27	SynaptomeDB: an ontology-based knowledgebase for synaptic genes. *Bioinformatics*, **2012**, 28, 897-9	7.2	77
26	Data mining approaches for genome-wide association of mood disorders. *Psychiatric Genetics*, **2012**, 22, 55-61	2.9	18
25	Genome-wide association of mood-incongruent psychotic bipolar disorder. *Translational Psychiatry*, **2012**, 2, e180	8.6	51
24	Investigations of transcript expression in fathead minnow (Pimephales promelas) brain tissue reveal toxicological impacts of RDX exposure. *Aquatic Toxicology*, **2011**, 101, 135-45	5.1	19
23	Functional Genomics and Molecular Analysis of a Subtropical Harmful Algal Bloom Species, Karenia brevis **2011**, 816-828		
22	Conserved toxic responses across divergent phylogenetic lineages: a meta-analysis of the neurotoxic effects of RDX among multiple species using toxicogenomics. *Ecotoxicology*, **2011**, 20, 580-94	2.9	33
21	Genome-wide association analysis of age at onset and psychotic symptoms in bipolar disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2011**, 156B, 370-8	3.5	39
20	Design, validation and annotation of transcriptome-wide oligonucleotide probes for the oligochaete annelid Eisenia fetida. *PLoS ONE*, **2010**, 5, e14266	3.7	17
19	Generation, analysis and functional annotation of expressed sequence tags from the sheepshead minnow (Cyprinodon variegatus). *BMC Genomics*, **2010**, 11 Suppl 2, S4	4.5	3
18	Neurotoxicogenomic investigations to assess mechanisms of action of the munitions constituents RDX and 2,6-DNT in Northern bobwhite (Colinus virginianus). *Toxicological Sciences*, **2009**, 110, 168-80	4.4	32
17	A comparative study of different machine learning methods on microarray gene expression data. *BMC Genomics*, **2008**, 9 Suppl 1, S13	4.5	140
16	Transcriptomic analysis of RDX and TNT interactive sublethal effects in the earthworm Eisenia fetida. *BMC Genomics*, **2008**, 9 Suppl 1, S15	4.5	37
15	Batch Blast Extractor: an automated blastx parser application. *BMC Genomics*, **2008**, 9 Suppl 2, S10	4.5	16
14	ILOOP--a web application for two-channel microarray interwoven loop design. *BMC Genomics*, **2008**, 9 Suppl 2, S11	4.5	6
13	GOfetcher: a database with complex searching facility for gene ontology. *Bioinformatics*, **2008**, 24, 2561-3	7.2	9
12	Toxicogenomic analysis provides new insights into molecular mechanisms of the sublethal toxicity of 2,4,6-trinitrotoluene in Eisenia fetida. *Environmental Science & Technology*, **2007**, 41, 8195-202	10.3	49
11	Cloning, analysis and functional annotation of expressed sequence tags from the Earthworm Eisenia fetida. *BMC Bioinformatics*, **2007**, 8 Suppl 7, S7	3.6	39

10	GeneVenn - A web application for comparing gene lists using Venn diagrams. *Bioinformation*, **2007**, 1, 420-2	1.1	135
9	RiboaptDB: a comprehensive database of ribozymes and aptamers. *BMC Bioinformatics*, **2006**, 7 Suppl 2, S6	3.6	16
8	SVM Classifier - a comprehensive java interface for support vector machine classification of microarray data. *BMC Bioinformatics*, **2006**, 7 Suppl 4, S25	3.6	25
7	lncRNAKB: A comprehensive knowledgebase of long non-coding RNAs		1
6	Acetylation-mediated phase control of the nucleolus regulates cellular acetyl-CoA responses		1
5	Ancient ancestry informative markers for identifying fine-scale ancient population structure in Eurasians		1
4	Establishing reference samples for detection of somatic mutations and germline variants with NGS technologies		5
3	Achieving reproducibility and accuracy in cancer mutation detection with whole-genome and whole-exome sequencing		5
2	Metabolic design in a model of extreme mammalian metabolism, the North American least shrew (Cryptotis parva)		1
1	Comprehensive Assessment of Somatic Copy Number Variation Calling Using Next-Generation Sequencing Data		2