Mehdi Pirooznia

List of Publications by Year
in descending order

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154 papers	5,547 citations	94381 37 h-index	102432 66 g-index
176 all docs	176 docs citations	176 times ranked	11610 citing authors

#	Article	IF	Citations
1	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	9.4	883
2	Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. Cancer Discovery, 2016, 6, 166-175.	7.7	282
3	Genomeâ€wide association study of schizophrenia in Ashkenazi Jews. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 649-659.	1.1	203
4	A comparative study of different machine learning methods on microarray gene expression data. BMC Genomics, 2008, 9, S13.	1.2	199
5	GeneVenn - A web application for comparing gene lists using Venn diagrams. Bioinformation, 2007, 1, 420-422.	0.2	155
6	Whole-genome CNV analysis: advances in computational approaches. Frontiers in Genetics, 2015, 06, 138.	1.1	148
7	A genome-wide association study of attempted suicide. Molecular Psychiatry, 2012, 17, 433-444.	4.1	141
8	Cell-Free DNA to Detect Heart Allograft Acute Rejection. Circulation, 2021, 143, 1184-1197.	1.6	129
9	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	9.4	126
10	Validation and assessment of variant calling pipelines for next-generation sequencing. Human Genomics, 2014, 8, 14.	1.4	121
11	SynaptomeDB: an ontology-based knowledgebase for synaptic genes. Bioinformatics, 2012, 28, 897-899.	1.8	120
12	Polygenic risk, stressful life events and depressive symptoms in older adults: a polygenic score analysis. Psychological Medicine, 2015, 45, 1709-1720.	2.7	98
13	Exome Sequencing of Familial Bipolar Disorder. JAMA Psychiatry, 2016, 73, 590.	6.0	97
14	Human retinoic acidâ€“regulated CD161+ regulatory T cells support wound repair in intestinal mucosa. Nature Immunology, 2018, 19, 1403-1414.	7.0	86
15	Cell-free DNA maps COVID-19 tissue injury and risk of death and can cause tissue injury. JCI Insight, 2021, 6, .	2.3	86
16	Complement receptor CD46 co-stimulates optimal human CD8+ T cell effector function via fatty acid metabolism. Nature Communications, 2018, 9, 4186.	5.8	75
17	Systematic review of genome-wide gene expression studies of bipolar disorder. BMC Psychiatry, 2013, 13, 213.	1.1	70
18	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.	0.3	69

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19	In vivo functional analysis of non-conserved human lncRNAs associated with cardiometabolic traits. Nature Communications, 2020, 11, 45.	5.8	69
20	The transcription factors TFE3 and TFEB amplify p53 dependent transcriptional programs in response to DNA damage. ELife, 2018, 7, .	2.8	69
21	Evaluation of Plasma miR-21 and miR-152 as Diagnostic Biomarkers for Common Types of Human Cancers. Journal of Cancer, 2016, 7, 490-499.	1.2	68
22	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. Nature Biotechnology, 2021, 39, 1141-1150.	9.4	66
23	Genome-wide DNA hydroxymethylation identifies potassium channels in the nucleus accumbens as discriminators of methamphetamine addiction and abstinence. Molecular Psychiatry, 2017, 22, 1196-1204.	4.1	65
24	Mutations in the pancreatic secretory enzymes CPA1 and CPB1 are associated with pancreatic cancer. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4767-4772.	3.3	65
25	Metaâ€analysis of genetic association studies on bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 508-518.	1.1	64
26	Network Analysis and Transcriptome Profiling Identify Autophagic and Mitochondrial Dysfunctions in SARS-CoV-2 Infection. Frontiers in Genetics, 2021, 12, 599261.	1.1	64
27	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, 8195-8202.	4.6	58
28	Genome-wide association of mood-incongruent psychotic bipolar disorder. Translational Psychiatry, 2012, 2, e180-e180.	2.4	58
29	Neutrophil Subsets, Platelets, andÂVascular Disease in Psoriasis. JACC Basic To Translational Science, 2019, 4, 1-14.	1.9	56
30	Cloning, analysis and functional annotation of expressed sequence tags from the Earthworm Eisenia fetida. BMC Bioinformatics, 2007, 8, S7.	1.2	52
31	Circulating mitochondrial DNA is a proinflammatory DAMP in sickle cell disease. Blood, 2021, 137, 3116-3126.	0.6	51
32	Polygenic Risk of Schizophrenia and Cognition in a Population-Based Survey of Older Adults. Schizophrenia Bulletin, 2016, 42, 984-991.	2.3	44
33	DIXDC1 contributes to psychiatric susceptibility by regulating dendritic spine and glutamatergic synapse density via GSK3 and Wnt/Î²-catenin signaling. Molecular Psychiatry, 2018, 23, 467-475.	4.1	44
34	Transcriptomic analysis of RDX and TNT interactive sublethal effects in the earthworm Eisenia fetida. BMC Genomics, 2008, 9, S15.	1.2	42
35	Genomeâ€wide association analysis of age at onset and psychotic symptoms in bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 370-378.	1.1	42
36	Localizing Ashkenazic Jews to Primeval Villages in the Ancient Iranian Lands of Ashkenaz. Genome Biology and Evolution, 2016, 8, 1132-1149.	1.1	41

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37	SVM Classifier â€“ a comprehensive java interface for support vector machine classification of microarray data. BMC Bioinformatics, 2006, 7, S25.	1.2	40
38	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. Scientific Data, 2020, 7, 326.	2.4	40
39	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	1.1	39
40	Genome-wide Methyl-Seq analysis of blood-brain targets of glucocorticoid exposure. Epigenetics, 2017, 12, 637-652.	1.3	39
41	High density lipoprotein proteome is associated with cardiovascular risk factors and atherosclerosis burden as evaluated by coronary CT angiography. Atherosclerosis, 2018, 278, 278-285.	0.4	39
42	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. Nature Biotechnology, 2021, 39, 1151-1160.	9.4	39
43	Pathogenic TERT promoter variants in telomere diseases. Genetics in Medicine, 2019, 21, 1594-1602.	1.1	37
44	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, 168-180.	1.4	34
45	Conserved toxic responses across divergent phylogenetic lineages: a meta-analysis of the neurotoxic effects of RDX among multiple species using toxicogenomics. Ecotoxicology, 2011, 20, 580-594.	1.1	34
46	Distinguishing bipolar from unipolar depression: the importance of clinical symptoms and illness features. Psychological Medicine, 2015, 45, 2437-2446.	2.7	34
47	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-e600.	2.4	33
48	Targeted RNA-sequencing for the quantification of measurable residual disease in acute myeloid leukemia. Haematologica, 2019, 104, 297-304.	1.7	33
49	Electron transport chain biogenesis activated by a JNK-insulin-Myc relay primes mitochondrial inheritance in Drosophila. ELife, 2019, 8, .	2.8	33
50	Batch Blast Extractor: an automated blastx parser application. BMC Genomics, 2008, 9, S10.	1.2	32
51	Data mining approaches for genome-wide association of mood disorders. Psychiatric Genetics, 2012, 22, 55-61.	0.6	32
52	Converging evidence for epistasis between ANK3 and potassium channel gene KCNQ2 in bipolar disorder. Frontiers in Genetics, 2013, 4, 87.	1.1	31
53	High-throughput sequencing of the synaptome in major depressive disorder. Molecular Psychiatry, 2016, 21, 650-655.	4.1	31
54	Fasting-induced FOXO4 blunts human CD4+ T helper cell responsiveness. Nature Metabolism, 2021, 3, 318-326.	5.1	29

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55	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. Genome Biology, 2021, 22, 111.	3.8	29
56	Boosting NAD+ blunts TLR4-induced type I IFN in control and systemic lupus erythematosus monocytes. Journal of Clinical Investigation, 2022, 132, .	3.9	27
57	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways. Nature Neuroscience, 2022, 25, 381-389.	7.1	27
58	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, .	3.3	26
59	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.	0.3	25
60	Mitochondria regulate intestinal stem cell proliferation and epithelial homeostasis through FOXO. Molecular Biology of the Cell, 2020, 31, 1538-1549.	0.9	25
61	RiboaptDB: A Comprehensive Database of Ribozymes and Aptamers. BMC Bioinformatics, 2006, 7, S6.	1.2	23
62	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.	5.1	23
63	Whole-exome sequencing of 81 individuals from 27 multiply affected bipolar disorder families. Translational Psychiatry, 2020, 10, 57.	2.4	23
64	Identification of human long noncoding RNAs associated with nonalcoholic fatty liver disease and metabolic homeostasis. Journal of Clinical Investigation, 2021, 131, .	3.9	23
65	Design, Validation and Annotation of Transcriptome-Wide Oligonucleotide Probes for the Oligochaete Annelid Eisenia fetida. PLoS ONE, 2010, 5, e14266.	1.1	22
66	Gene Expression Analysis of CL-20-Induced Reversible Neurotoxicity Reveals GABA_AReceptors as Potential Targets in the EarthwormEisenia fetida. Environmental Science & Technology, 2012, 46, 1223-1232.	4.6	21
67	GATA-2â€“deficient mast cells limit IgE-mediated immediate hypersensitivity reactions in human subjects. Journal of Allergy and Clinical Immunology, 2019, 144, 613-617.e14.	1.5	21
68	Investigations of transcript expression in fathead minnow (Pimephales promelas) brain tissue reveal toxicological impacts of RDX exposure. Aquatic Toxicology, 2011, 101, 135-145.	1.9	20
69	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	3.8	20
70	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses. PLoS Biology, 2020, 18, e3000981.	2.6	20
71	A Hybrid Likelihood Model for Sequence-Based Disease Association Studies. PLoS Genetics, 2013, 9, e1003224.	1.5	19
72	Reconstructing Druze population history. Scientific Reports, 2016, 6, 35837.	1.6	18

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73	De novo variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 4127-4136.	4.1	18
74	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. Genome Biology, 2022, 23, 2.	3.8	18
75	Metamoodics: meta-analysis and bioinformatics resource for mood disorders. Molecular Psychiatry, 2014, 19, 748-749.	4.1	16
76	Ancient Ancestry Informative Markers for Identifying Fine-Scale Ancient Population Structure in Eurasians. Genes, 2018, 9, 625.	1.0	16
77	IKAPâ€"Identifying K mAjor cell Population groups in single-cell RNA-sequencing analysis. GigaScience, 2019, 8, .	3.3	16
78	Identification and Validation of Nutrient State-Dependent Serum Protein Mediators of Human CD4+ T Cell Responsiveness. Nutrients, 2021, 13, 1492.	1.7	16
79	GCN5L1 interacts with Î±TAT1 and RanBP2 to regulate hepatic Î±-tubulin acetylation and lysosome trafficking. Journal of Cell Science, 2018, 131, .	1.2	15
80	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	4.1	15
81	The immune microenvironment shapes transcriptional and genetic heterogeneity in chronic lymphocytic leukemia. Blood Advances, 2023, 7, 145-158.	2.5	15
82	Genome-Wide Analysis of Off-Target CRISPR/Cas9 Activity in Single-Cell-Derived Human Hematopoietic Stem and Progenitor Cell Clones. Genes, 2020, 11, 1501.	1.0	14
83	Assessment of Whole-Exome Sequence Data in Attempted Suicide within a Bipolar Disorder Cohort. Molecular Neuropsychiatry, 2017, 3, 1-11.	3.0	13
84	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.	1.4	12
85	Discriminating bipolar depression from major depressive disorder with polygenic risk scores. Psychological Medicine, 2020, 51, 1-8.	2.7	12
86	Genomic signatures and gene networking: challenges and promises. BMC Genomics, 2011, 12, I1.	1.2	11
87	The Origins of Ashkenaz, Ashkenazic Jews, and Yiddish. Frontiers in Genetics, 2017, 8, 87.	1.1	11
88	Identification of Genes Contributing to a Long Circadian Period in Drosophila Melanogaster. Journal of Biological Rhythms, 2021, 36, 239-253.	1.4	11
89	ILOOP â€“ a web application for two-channel microarray interwoven loop design. BMC Genomics, 2008, 9, S11.	1.2	10
90	NOTCH-mediated exÂvivo expansion of human hematopoietic stem and progenitor cells by culture under hypoxia. Stem Cell Reports, 2021, 16, 2336-2350.	2.3	10

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91	GOfetcher: a database with complex searching facility for gene ontology. Bioinformatics, 2008, 24, 2561-2563.	1.8	9
92	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.	1.1	9
93	Circulating Lymphangioleiomyomatosis Tumor Cells With Loss of Heterozygosity in the TSC2 Gene Show Increased Aldehyde Dehydrogenase Activity. Chest, 2019, 156, 298-307.	0.4	8
94	Olfactomedin 4 mediation of prostate stem/progenitor-like cell proliferation and differentiation via MYC. Scientific Reports, 2020, 10, 21924.	1.6	7
95	Ultra-Small Lung Cysts Impair Diffusion Without Obstructing Air Flow in Lymphangioleiomyomatosis. Chest, 2021, 160, 199-208.	0.4	7
96	SVAw - a web-based application tool for automated surrogate variable analysis of gene expression studies. Source Code for Biology and Medicine, 2013, 8, 8.	1.7	6
97	Metabolic design in a mammalian model of extreme metabolism, the North American least shrew (Cryptotis parva). Journal of Physiology, 2022, 600, 547-567.	1.3	6
98	Genetic variants of PKLR are associated with acute pain in sickle cell disease. Blood Advances, 2022, 6, 3535-3540.	2.5	6
99	Misregulation of ELK1, AP1, and E12 Transcription Factor Networks Is Associated with Melanoma Progression. Cancers, 2020, 12, 458.	1.7	5
100	Whole genome sequence-based haplotypes reveal a single origin of the 1393 bp HBB deletion. Journal of Medical Genetics, 2020, 57, 567-570.	1.5	5
101	The Genetics of Sudden Infant Death Syndromeâ€"Towards a Gene Reference Resource. Genes, 2021, 12, 216.	1.0	5
102	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.	2.2	5
103	Generation, analysis and functional annotation of expressed sequence tags from the sheepshead minnow (Cyprinodon variegatus). BMC Genomics, 2010, 11, S4.	1.2	3
104	Reducing Fatty Acid Oxidation Improves Cancer-free Survival in a Mouse Model of Li-Fraumeni Syndrome. Cancer Prevention Research, 2021, 14, 31-40.	0.7	3
105	Ogfod1 deletion increases cardiac beta-alanine levels and protects mice against ischaemiaâ€“ reperfusion injury. Cardiovascular Research, 2022, 118, 2847-2858.	1.8	3
106	The PPR domain of mitochondrial RNA polymerase is an exoribonuclease required for mtDNA replication in Drosophila melanogaster. Nature Cell Biology, 2022, 24, 757-765.	4.6	3
107	Affected Sib-Pair Analyses Identify Signaling Networks Associated With Social Behavioral Deficits in Autism. Frontiers in Genetics, 2019, 10, 1186.	1.1	2
108	Effect of non-uniform cyst distribution in lymphangioleiomyomatosis on pulmonary function: a cross-sectional study. European Respiratory Journal, 2021, 57, 2003769.	3.1	2

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109	Circulating microRNA profiling for early detection of non-small cell lung cancer.. Journal of Clinical Oncology, 2014, 32, e22051-e22051.	0.8	2
110	Cell-Free Mitochondrial DNA Is Elevated in Sickle Cell Disease Patients, and Serve As a Potential Proinflammatory DAMP. Blood, 2018, 132, 1068-1068.	0.6	2
111	Mitochondrial DNA Variation in Individuals with Sickle Cell Disease. Blood, 2020, 136, 11-11.	0.6	2
112	Functional Genomics, Genetics, and Bioinformatics 2016. BioMed Research International, 2016, 2016, 1-3.	0.9	1
113	706. Wnt/Î²-Catenin Pathway Contributions to Dendritic Spine and Glutamatergic Synapse Formation Responsive to Lithium-Mediated GSK3 Inhibition. Biological Psychiatry, 2017, 81, S286.	0.7	1
114	Pulmonary Antibody-Mediated Rejection (AMR) Accelerates Aging-Evidence from Whole Genome DNA Methylation Sequencing. Journal of Heart and Lung Transplantation, 2019, 38, S138.	0.3	1
115	Editorial: Machine Learning and Network-Driven Integrative Genomics. Frontiers in Genetics, 2021, 12, 660201.	1.1	1
116	Cardiac Allograft Injury in Patients of African Ancestry: Trends of Donor-Derived Cell-Free DNA Based on Genetic Ancestry. Journal of Heart and Lung Transplantation, 2021, 40, S254.	0.3	1
117	Platelet Phenotype Prediction from Whole Genome Sequencing in 621 Sickle Cell Disease Patients. Blood, 2019, 134, 2295-2295.	0.6	1
118	Bioinformatics Approaches for Functional Prediction of Long Noncoding RNAs. Methods in Molecular Biology, 2021, 2254, 1-13.	0.4	1
119	Diverging Clonal Evolution during Sequential Therapy with Chemoimmunotherapy Followed By BTK Inhibitors. Blood, 2019, 134, 850-850.	0.6	1
120	An Effective Interwoven Loop Design Application for Two-Channel Microarray Experiments. , 2007, , .		0
121	Efficiency of Hybrid Normalization of Microarray Gene Expression: A Simulation Study. , 2007, , .		0
122	Functional Genomics and Molecular Analysis of a Subtropical Harmful Algal Bloom Species, Karenia brevis. , 2011, , 816-828.		0
123	Circulating Xenograft-Derived Cell-Free DNA as a Reliable Marker for Injury After Xenotransplantation. Journal of Heart and Lung Transplantation, 2017, 36, S47.	0.3	0
124	Antibody-mediated Rejection: Should We Wait for Clinical Diagnosis?. Journal of Heart and Lung Transplantation, 2018, 37, S16.	0.3	0
125	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.	2.0	0
126	Variable Cell-free DNA Characteristics With Different Acute Rejection Phenotypes. Journal of Heart and Lung Transplantation, 2018, 37, S95.	0.3	0

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127	Clinically-unrecognized Allograft Injury is Common After Lung Transplantion. Journal of Heart and Lung Transplantation, 2018, 37, S32-S33.	0.3	0
128	Apolipoprotein E Induces CXCL5 Secretion by Asthmatic Airway Epithelial Cells via TLR4-Dependent Activation of TAK1/NF-kB/MAP3K8/JNK Signaling Pathways. , 2019, , .		0
129	Characteristics of Urine Cell-Free DNA in Heart and Lung Transplant. Journal of Heart and Lung Transplantation, 2019, 38, S245-S246.	0.3	0
130	USING WHOLE GENOME SEQUENCING TO IDENTIFY DE NOVO VARIATION IN BIPOLAR DISORDER. European Neuropsychopharmacology, 2019, 29, S827-S828.	0.3	0
131	Ultrahigh-Resolution, Short-Length CT Detects Small Cysts That Are Associated with a Decrease in DLCO but Not FEV1 in Patients with Lymphangioleiomyomatosis. , 2020, , .		0
132	Non-Uniform of Cyst Distribution Influence Pulmonary Function in Lymphangioleiomyomatosis. , 2020, , .		0
133	Early and Late Pulmonary AMR Show Distinct Profiles; Clinical and Epigenetic Analyses. Journal of Heart and Lung Transplantation, 2020, 39, S79.	0.3	0
134	Cell-Free DNA Tissue Damage Mapping in Transplant Patients Infected with COVID-19. Journal of Heart and Lung Transplantation, 2021, 40, S142.	0.3	0
135	Response by Shah et al to Letter Regarding Article, â€œCell-Free DNA to Detect Heart Allograft Acute Rejectionâ€• Circulation, 2021, 144, e198-e199.	1.6	0
136	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.	0.6	0
137	Functional â€˜Omics and Molecular Analysis of a Subtropical Harmful Algal Bloom Species, Karenia brevis. , 2019, , 132-148.		0
138	Abstract 3521: Critical Assessment of CNV Calling Using Next Generation Sequencing. , 2019, , .		0
139	Whole Exome Sequencing Reveals Multiple Driver Events in Chronic Lymphocytic Leukemia Patients with Acquired Ibrutinib Resistance. Blood, 2019, 134, 1287-1287.	0.6	0
140	Spatial Genomic Heterogeneity in Chronic Lymphocytic Leukemia. Blood, 2019, 134, 3017-3017.	0.6	0
141	Pklr Is a Genetic Modifier of Sickle Cell Disease. Blood, 2021, 138, 953-953.	0.6	0
142	Individuals with Sickle Cell Disease Have a Higher Burden of Mitochondrial DNA Heteroplasmy. Blood, 2021, 138, 954-954.	0.6	0
143	Notch-Mediated Expansion of Human Hematopoietic Stem and Progenitor Cells By Culture Under Hypoxia. Blood, 2020, 136, 28-29.	0.6	0
144	RNA Seq Profiles and Bioinformatics Validation in a Large Sample of Sickle Cell Disease Patients. Blood, 2020, 136, 13-14.	0.6	0

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145	Cfcloud: A Cloud-Based Workflow for Cell-Free DNA Data Analysis. Blood, 2020, 136, 31-32.	0.6	0
146	Genome-Wide Cell-Free DNA Methylation Analysis Reveals Significant Recipient Tissue Injury in Allograft Rejection. Journal of Heart and Lung Transplantation, 2022, 41, S301.	0.3	0
147	Abstract 10765: Plasma Cell-Free DNA Predicts Survival and Maps Tissue-Specific Sources of Injury in Pulmonary Arterial Hypertension. Circulation, 2021, 144, .	1.6	0
148	Abstract 3521: Critical Assessment of CNV Calling Using Next Generation Sequencing. , 2019, , .		0
149	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses. , 2020, 18, e3000981.		0
150	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses. , 2020, 18, e3000981.		0
151	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses. , 2020, 18, e3000981.		0
152	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses. , 2020, 18, e3000981.		0
153	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses. , 2020, 18, e3000981.		0
154	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses. , 2020, 18, e3000981.		0