

# Mehdi Pirooznia

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/4411745/mehdi-pirooznia-publications-by-citations.pdf>

**Version:** 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 903-14	44.5	618
134	Whole Genome Sequencing Defines the Genetic Heterogeneity of Familial Pancreatic Cancer. <i>Cancer Discovery</i> , <b>2016</b> , 6, 166-75	24.4	206
133	A comparative study of different machine learning methods on microarray gene expression data. <i>BMC Genomics</i> , <b>2008</b> , 9 Suppl 1, S13	4.5	140
132	GeneVenn - A web application for comparing gene lists using Venn diagrams. <i>Bioinformatics</i> , <b>2007</b> , 1, 420-2	1.1	135
131	Genome-wide association study of schizophrenia in Ashkenazi Jews. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2015</b> , 168, 649-59	3.5	128
130	A genome-wide association study of attempted suicide. <i>Molecular Psychiatry</i> , <b>2012</b> , 17, 433-44	15.1	117
129	Whole-genome CNV analysis: advances in computational approaches. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 138	4.5	100
128	Validation and assessment of variant calling pipelines for next-generation sequencing. <i>Human Genomics</i> , <b>2014</b> , 8, 14	6.8	79
127	Cell-Free DNA Tissue Damage Mapping in Transplant Patients Infected with COVID-19. <i>Journal of Heart and Lung Transplantation</i> , <b>2021</b> , 40, S142	5.8	78
126	SynaptomeDB: an ontology-based knowledgebase for synaptic genes. <i>Bioinformatics</i> , <b>2012</b> , 28, 897-9	7.2	77
125	Polygenic risk, stressful life events and depressive symptoms in older adults: a polygenic score analysis. <i>Psychological Medicine</i> , <b>2015</b> , 45, 1709-20	6.9	71
124	Exome Sequencing of Familial Bipolar Disorder. <i>JAMA Psychiatry</i> , <b>2016</b> , 73, 590-7	14.5	69
123	Systematic review of genome-wide gene expression studies of bipolar disorder. <i>BMC Psychiatry</i> , <b>2013</b> , 13, 213	4.2	63
122	Human retinoic acid-regulated CD161 regulatory T cells support wound repair in intestinal mucosa. <i>Nature Immunology</i> , <b>2018</b> , 19, 1403-1414	19.1	58
121	Meta-analysis of genetic association studies on bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2012</b> , 159B, 508-18	3.5	54
120	Genome-wide association of mood-incongruent psychotic bipolar disorder. <i>Translational Psychiatry</i> , <b>2012</b> , 2, e180	8.6	51
119	Toxicogenomic analysis provides new insights into molecular mechanisms of the sublethal toxicity of 2,4,6-trinitrotoluene in <i>Eisenia fetida</i> . <i>Environmental Science &amp; Technology</i> , <b>2007</b> , 41, 8195-202	10.3	49

118	Evaluation of Plasma miR-21 and miR-152 as Diagnostic Biomarkers for Common Types of Human Cancers. <i>Journal of Cancer</i> , <b>2016</b> , 7, 490-9	4.5	47
117	Genome-wide DNA hydroxymethylation identifies potassium channels in the nucleus accumbens as discriminators of methamphetamine addiction and abstinence. <i>Molecular Psychiatry</i> , <b>2017</b> , 22, 1196-1204	15.1	45
116	The transcription factors TFE3 and TFEB amplify p53 dependent transcriptional programs in response to DNA damage. <i>ELife</i> , <b>2018</b> , 7,	8.9	44
115	Late manifestation of alloantibody-associated injury and clinical pulmonary antibody-mediated rejection: Evidence from cell-free DNA analysis. <i>Journal of Heart and Lung Transplantation</i> , <b>2018</b> , 37, 925-932	5.8	40
114	Genome-wide association analysis of age at onset and psychotic symptoms in bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2011</b> , 156B, 370-8	3.5	39
113	Cloning, analysis and functional annotation of expressed sequence tags from the Earthworm <i>Eisenia fetida</i> . <i>BMC Bioinformatics</i> , <b>2007</b> , 8 Suppl 7, S7	3.6	39
112	Complement receptor CD46 co-stimulates optimal human CD8 T cell effector function via fatty acid metabolism. <i>Nature Communications</i> , <b>2018</b> , 9, 4186	17.4	38
111	Transcriptomic analysis of RDX and TNT interactive sublethal effects in the earthworm <i>Eisenia fetida</i> . <i>BMC Genomics</i> , <b>2008</b> , 9 Suppl 1, S15	4.5	37
110	Neutrophil Subsets, Platelets, and Vascular Disease in Psoriasis. <i>JACC Basic To Translational Science</i> , <b>2019</b> , 4, 1-14	8.7	36
109	Cell-Free DNA to Detect Heart Allograft Acute Rejection. <i>Circulation</i> , <b>2021</b> , 143, 1184-1197	16.7	36
108	Mutations in the pancreatic secretory enzymes and are associated with pancreatic cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 4767-4772	11.5	34
107	DIXDC1 contributes to psychiatric susceptibility by regulating dendritic spine and glutamatergic synapse density via GSK3 and Wnt/ $\beta$ -catenin signaling. <i>Molecular Psychiatry</i> , <b>2018</b> , 23, 467-475	15.1	34
106	Conserved toxic responses across divergent phylogenetic lineages: a meta-analysis of the neurotoxic effects of RDX among multiple species using toxicogenomics. <i>Ecotoxicology</i> , <b>2011</b> , 20, 580-94	2.9	33
105	Neurotoxicogenomic investigations to assess mechanisms of action of the munitions constituents RDX and 2,6-DNT in Northern bobwhite ( <i>Colinus virginianus</i> ). <i>Toxicological Sciences</i> , <b>2009</b> , 110, 168-80	4.4	32
104	Network Analysis and Transcriptome Profiling Identify Autophagic and Mitochondrial Dysfunctions in SARS-CoV-2 Infection. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 599261	4.5	31
103	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 1115-1128	44.5	31
102	Distinguishing bipolar from unipolar depression: the importance of clinical symptoms and illness features. <i>Psychological Medicine</i> , <b>2015</b> , 45, 2437-46	6.9	30
101	In vivo functional analysis of non-conserved human lncRNAs associated with cardiometabolic traits. <i>Nature Communications</i> , <b>2020</b> , 11, 45	17.4	29

100	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , <b>2017</b> , 38, 1182-1192	4.7	28
99	Polygenic Risk of Schizophrenia and Cognition in a Population-Based Survey of Older Adults. <i>Schizophrenia Bulletin</i> , <b>2016</b> , 42, 984-91	1.3	28
98	Localizing Ashkenazic Jews to Primeval Villages in the Ancient Iranian Lands of Ashkenaz. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 1132-49	3.9	28
97	High-throughput sequencing of the synaptome in major depressive disorder. <i>Molecular Psychiatry</i> , <b>2016</b> , 21, 650-5	15.1	27
96	Converging Evidence for Epistasis between ANK3 and Potassium Channel Gene KCNQ2 in Bipolar Disorder. <i>Frontiers in Genetics</i> , <b>2013</b> , 4, 87	4.5	27
95	High density lipoprotein proteome is associated with cardiovascular risk factors and atherosclerosis burden as evaluated by coronary CT angiography. <i>Atherosclerosis</i> , <b>2018</b> , 278, 278-285	3.1	27
94	Search for common targets of lithium and valproic acid identifies novel epigenetic effects of lithium on the rat leptin receptor gene. <i>Translational Psychiatry</i> , <b>2015</b> , 5, e600	8.6	26
93	SVM Classifier - a comprehensive java interface for support vector machine classification of microarray data. <i>BMC Bioinformatics</i> , <b>2006</b> , 7 Suppl 4, S25	3.6	25
92	Genome-wide Methyl-Seq analysis of blood-brain targets of glucocorticoid exposure. <i>Epigenetics</i> , <b>2017</b> , 12, 637-652	5.7	23
91	Targeted RNA-sequencing for the quantification of measurable residual disease in acute myeloid leukemia. <i>Haematologica</i> , <b>2019</b> , 104, 297-304	6.6	22
90	Gene expression analysis of CL-20-induced reversible neurotoxicity reveals GABA(A) receptors as potential targets in the earthworm <i>Eisenia fetida</i> . <i>Environmental Science &amp; Technology</i> , <b>2012</b> , 46, 1223-32	10.3	19
89	Investigations of transcript expression in fathead minnow ( <i>Pimephales promelas</i> ) brain tissue reveal toxicological impacts of RDX exposure. <i>Aquatic Toxicology</i> , <b>2011</b> , 101, 135-45	5.1	19
88	Data mining approaches for genome-wide association of mood disorders. <i>Psychiatric Genetics</i> , <b>2012</b> , 22, 55-61	2.9	18
87	Cell-free DNA maps COVID-19 tissue injury and risk of death and can cause tissue injury. <i>JCI Insight</i> , <b>2021</b> , 6,	9.9	18
86	Pathogenic TERT promoter variants in telomere diseases. <i>Genetics in Medicine</i> , <b>2019</b> , 21, 1594-1602	8.1	18
85	Design, validation and annotation of transcriptome-wide oligonucleotide probes for the oligochaete annelid <i>Eisenia fetida</i> . <i>PLoS ONE</i> , <b>2010</b> , 5, e14266	3.7	17
84	Circulating cell-free DNA as a biomarker of tissue injury: Assessment in a cardiac xenotransplantation model. <i>Journal of Heart and Lung Transplantation</i> , <b>2018</b> , 37, 967-975	5.8	16
83	A hybrid likelihood model for sequence-based disease association studies. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003324	16	16

82	Batch Blast Extractor: an automated blastx parser application. <i>BMC Genomics</i> , <b>2008</b> , 9 Suppl 2, S10	4.5	16
81	RiboaptDB: a comprehensive database of ribozymes and aptamers. <i>BMC Bioinformatics</i> , <b>2006</b> , 7 Suppl 2, S6	3.6	16
80	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. <i>Scientific Data</i> , <b>2020</b> , 7, 326	8.2	16
79	GATA-2-deficient mast cells limit IgE-mediated immediate hypersensitivity reactions in human subjects. <i>Journal of Allergy and Clinical Immunology</i> , <b>2019</b> , 144, 613-617.e14	11.5	14
78	Sequential CRISPR-Based Screens Identify LITAF and CDIP1 as the Bacillus cereus Hemolysin BL Toxin Host Receptors. <i>Cell Host and Microbe</i> , <b>2020</b> , 28, 402-410.e5	23.4	14
77	Electron transport chain biogenesis activated by a JNK-insulin-Myc relay primes mitochondrial inheritance in. <i>ELife</i> , <b>2019</b> , 8,	8.9	13
76	Reconstructing Druze population history. <i>Scientific Reports</i> , <b>2016</b> , 6, 35837	4.9	12
75	Circulating mitochondrial DNA is a proinflammatory DAMP in sickle cell disease. <i>Blood</i> , <b>2021</b> , 137, 3116-3126		12
74	Assessment of Whole-Exome Sequence Data in Attempted Suicide within a Bipolar Disorder Cohort. <i>Molecular Neuropsychiatry</i> , <b>2017</b> , 3, 1-11	4.9	11
73	Network Analysis and Transcriptome Profiling Identify Autophagic and Mitochondrial Dysfunctions in SARS-CoV-2 Infection <b>2020</b> ,		11
72	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 1141-1150	44.5	11
71	Ancient Ancestry Informative Markers for Identifying Fine-Scale Ancient Population Structure in Eurasians. <i>Genes</i> , <b>2018</b> , 9,	4.2	10
70	GOfetcher: a database with complex searching facility for gene ontology. <i>Bioinformatics</i> , <b>2008</b> , 24, 2561-2	3.2	9
69	Mitochondria regulate intestinal stem cell proliferation and epithelial homeostasis through FOXO. <i>Molecular Biology of the Cell</i> , <b>2020</b> , 31, 1538-1549	3.5	8
68	The Origins of Ashkenaz, Ashkenazic Jews, and Yiddish. <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 87	4.5	8
67	Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses. <i>PLoS Biology</i> , <b>2020</b> , 18, e3000981	9.7	8
66	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , <b>2021</b> , 22, 111	18.3	8
65	The secretome mouse provides a genetic platform to delineate tissue-specific in vivo secretion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	8

64	IKAP-Identifying K mAjor cell Population groups in single-cell RNA-sequencing analysis. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	7
63	Whole-exome sequencing of 81 individuals from 27 multiply affected bipolar disorder families. <i>Translational Psychiatry</i> , <b>2020</b> , 10, 57	8.6	7
62	Metamoodics: meta-analysis and bioinformatics resource for mood disorders. <i>Molecular Psychiatry</i> , <b>2014</b> , 19, 748-9	15.1	7
61	The Diversity of REcent and Ancient huMan (DREAM): A New Microarray for Genetic Anthropology and Genealogy, Forensics, and Personalized Medicine. <i>Genome Biology and Evolution</i> , <b>2017</b> , 9, 3225-3237 <sup>3,9</sup>	3.9	7
60	De novo variation in bipolar disorder. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 4127-4136	15.1	7
59	GCN5L1 interacts with $\beta$ TAT1 and RanBP2 to regulate hepatic $\beta$ tubulin acetylation and lysosome trafficking. <i>Journal of Cell Science</i> , <b>2018</b> , 131,	5.3	7
58	Apolipoprotein E Signals via TLR4 to Induce CXCL5 Secretion by Asthmatic Airway Epithelial Cells. <i>American Journal of Respiratory Cell and Molecular Biology</i> , <b>2020</b> , 63, 185-197	5.7	6
57	Discriminating bipolar depression from major depressive disorder with polygenic risk scores. <i>Psychological Medicine</i> , <b>2021</b> , 51, 1451-1458	6.9	6
56	SVaw - a web-based application tool for automated surrogate variable analysis of gene expression studies. <i>Source Code for Biology and Medicine</i> , <b>2013</b> , 8, 8	1.9	6
55	ILOOP--a web application for two-channel microarray interwoven loop design. <i>BMC Genomics</i> , <b>2008</b> , 9 Suppl 2, S11	4.5	6
54	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , <b>2021</b> , 22, 109	18.3	6
53	Identification of human long noncoding RNAs associated with nonalcoholic fatty liver disease and metabolic homeostasis. <i>Journal of Clinical Investigation</i> , <b>2021</b> , 131,	15.9	6
52	Establishing reference samples for detection of somatic mutations and germline variants with NGS technologies		
51	Achieving reproducibility and accuracy in cancer mutation detection with whole-genome and whole-exome sequencing		5
50	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 1151-1160	44.5	5
49	Circulating Lymphangioliomyomatosis Tumor Cells With Loss of Heterozygosity in the TSC2 Gene Show Increased Aldehyde Dehydrogenase Activity. <i>Chest</i> , <b>2019</b> , 156, 298-307	5.3	4
48	Generation, analysis and functional annotation of expressed sequence tags from the sheepshead minnow ( <i>Cyprinodon variegatus</i> ). <i>BMC Genomics</i> , <b>2010</b> , 11 Suppl 2, S4	4.5	3
47	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing.. <i>Genome Biology</i> , <b>2022</b> , 23, 2	18.3	3

46	Author response: Electron transport chain biogenesis activated by a JNK-insulin-Myc relay primes mitochondrial inheritance in <i>Drosophila</i> <b>2019</b> ,		3
45	Fasting-induced FOXO4 blunts human CD4 T helper cell responsiveness. <i>Nature Metabolism</i> , <b>2021</b> , 3, 318-326	14.6	3
44	The Genetics of Sudden Infant Death Syndrome-Towards a Gene Reference Resource. <i>Genes</i> , <b>2021</b> , 12,	4.2	3
43	NOTCH-mediated ex vivo expansion of human hematopoietic stem and progenitor cells by culture under hypoxia. <i>Stem Cell Reports</i> , <b>2021</b> , 16, 2336-2350	8	3
42	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 5239-5250	15.1	3
41	Whole genome sequence-based haplotypes reveal a single origin of the 1393 bp deletion. <i>Journal of Medical Genetics</i> , <b>2020</b> , 57, 567-570	5.8	2
40	Circulating microRNA profiling for early detection of non-small cell lung cancer.. <i>Journal of Clinical Oncology</i> , <b>2014</b> , 32, e22051-e22051	2.2	2
39	Identification and Validation of Nutrient State-Dependent Serum Protein Mediators of Human CD4 T Cell Responsiveness. <i>Nutrients</i> , <b>2021</b> , 13,	6.7	2
38	Affected Sib-Pair Analyses Identify Signaling Networks Associated With Social Behavioral Deficits in Autism. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1186	4.5	2
37	Comprehensive Assessment of Somatic Copy Number Variation Calling Using Next-Generation Sequencing Data		2
36	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways.. <i>Nature Neuroscience</i> , <b>2022</b> , 25, 381-389	25.5	2
35	Olfactomedin 4 mediation of prostate stem/progenitor-like cell proliferation and differentiation via MYC. <i>Scientific Reports</i> , <b>2020</b> , 10, 21924	4.9	1
34	Misregulation of ELK1, AP1, and E12 Transcription Factor Networks Is Associated with Melanoma Progression. <i>Cancers</i> , <b>2020</b> , 12,	6.6	1
33	Platelet Phenotype Prediction from Whole Genome Sequencing in 621 Sickle Cell Disease Patients. <i>Blood</i> , <b>2019</b> , 134, 2295-2295	2.2	1
32	Bioinformatics Approaches for Functional Prediction of Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2254, 1-13	1.4	1
31	Cell-Free Mitochondrial DNA Is Elevated in Sickle Cell Disease Patients, and Serve As a Potential Proinflammatory DAMP. <i>Blood</i> , <b>2018</b> , 132, 1068-1068	2.2	1
30	lncRNAKB: A comprehensive knowledgebase of long non-coding RNAs		1
29	Diverging Clonal Evolution during Sequential Therapy with Chemoimmunotherapy Followed By BTK Inhibitors. <i>Blood</i> , <b>2019</b> , 134, 850-850	2.2	1

28	Acetylation-mediated phase control of the nucleolus regulates cellular acetyl-CoA responses		1
27	Ancient ancestry informative markers for identifying fine-scale ancient population structure in Eurasians		1
26	Genome-Wide Analysis of Off-Target CRISPR/Cas9 Activity in Single-Cell-Derived Human Hematopoietic Stem and Progenitor Cell Clones. <i>Genes</i> , <b>2020</b> , 11,	4.2	1
25	Metabolic design in a model of extreme mammalian metabolism, the North American least shrew ( <i>Cryptotis parva</i> )		1
24	Ultra-Small Lung Cysts Impair Diffusion Without Obstructing Air Flow in Lymphangiomyomatosis. <i>Chest</i> , <b>2021</b> , 160, 199-208	5.3	1
23	Identification of Genes Contributing to a Long Circadian Period in. <i>Journal of Biological Rhythms</i> , <b>2021</b> , 36, 239-253	3.2	1
22	Reducing Fatty Acid Oxidation Improves Cancer-free Survival in a Mouse Model of Li-Fraumeni Syndrome. <i>Cancer Prevention Research</i> , <b>2021</b> , 14, 31-40	3.2	1
21	Mitochondrial DNA Variation in Individuals with Sickle Cell Disease. <i>Blood</i> , <b>2020</b> , 136, 11-11	2.2	0
20	Early Myeloid Derived Suppressor Cells (eMDSCs) Are Associated With High Donor Myeloid Chimerism Following Haploidentical HSCT for Sickle Cell Disease.. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 757279	8.4	0
19	Effect of non-uniform cyst distribution in lymphangiomyomatosis on pulmonary function: a cross-sectional study. <i>European Respiratory Journal</i> , <b>2021</b> , 57,	13.6	0
18	Functional Genomics and Molecular Analysis of a Subtropical Harmful Algal Bloom Species, <i>Karenia brevis</i> <b>2011</b> , 816-828		
17	Notch-Mediated Expansion of Human Hematopoietic Stem and Progenitor Cells By Culture Under Hypoxia. <i>Blood</i> , <b>2020</b> , 136, 28-29	2.2	
16	RNA Seq Profiles and Bioinformatics Validation in a Large Sample of Sickle Cell Disease Patients. <i>Blood</i> , <b>2020</b> , 136, 13-14	2.2	
15	Cfcloud: A Cloud-Based Workflow for Cell-Free DNA Data Analysis. <i>Blood</i> , <b>2020</b> , 136, 31-32	2.2	
14	Pklr Is a Genetic Modifier of Sickle Cell Disease. <i>Blood</i> , <b>2021</b> , 138, 953-953	2.2	
13	Individuals with Sickle Cell Disease Have a Higher Burden of Mitochondrial DNA Heteroplasmy. <i>Blood</i> , <b>2021</b> , 138, 954-954	2.2	
12	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. <i>Blood</i> , <b>2018</b> , 132, 2388-2388	2.2	
11	Functional Genomics and Molecular Analysis of a Subtropical Harmful Algal Bloom Species, <i>Karenia brevis</i> <b>2019</b> , 132-148		



- 10 Whole Exome Sequencing Reveals Multiple Driver Events in Chronic Lymphocytic Leukemia Patients with Acquired Ibrutinib Resistance. *Blood*, **2019**, 134, 1287-1287 2.2
- 9 Spatial Genomic Heterogeneity in Chronic Lymphocytic Leukemia. *Blood*, **2019**, 134, 3017-3017 2.2
- 8 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
- 7 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
- 6 Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses **2020**, 18, e3000981
- 5 Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses **2020**, 18, e3000981
- 4 Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses **2020**, 18, e3000981
- 3 Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses **2020**, 18, e3000981
- 2 Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses **2020**, 18, e3000981
- 1 Acetylation-mediated remodeling of the nucleolus regulates cellular acetyl-CoA responses **2020**, 18, e3000981