

Jacob J Hughey

List of Publications by Citations

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

154
papers

11,837
citations

46
h-index

108
g-index

186
ext. papers

16,506
ext. citations

11.3
avg, IF

6.83
L-index

#	Paper	IF	Citations
154	xCell: digitally portraying the tissue cellular heterogeneity landscape. <i>Genome Biology</i> , 2017 , 18, 220	18.3	1050
153	Ten years of pathway analysis: current approaches and outstanding challenges. <i>PLoS Computational Biology</i> , 2012 , 8, e1002375	5	974
152	Reference-based analysis of lung single-cell sequencing reveals a transitional profibrotic macrophage. <i>Nature Immunology</i> , 2019 , 20, 163-172	19.1	752
151	Single-cell NF-kappaB dynamics reveal digital activation and analogue information processing. <i>Nature</i> , 2010 , 466, 267-71	50.4	606
150	Variation in the human immune system is largely driven by non-heritable influences. <i>Cell</i> , 2015 , 160, 37-47	46.2	586
149	Systematic pan-cancer analysis of tumour purity. <i>Nature Communications</i> , 2015 , 6, 8971	17.4	555
148	Discovery and preclinical validation of drug indications using compendia of public gene expression data. <i>Science Translational Medicine</i> , 2011 , 3, 96ra77	17.5	542
147	Computational repositioning of the anticonvulsant topiramate for inflammatory bowel disease. <i>Science Translational Medicine</i> , 2011 , 3, 96ra76	17.5	430
146	ImmPort: disseminating data to the public for the future of immunology. <i>Immunologic Research</i> , 2014 , 58, 234-9	4.3	392
145	An Environment-Wide Association Study (EWAS) on type 2 diabetes mellitus. <i>PLoS ONE</i> , 2010 , 5, e107463	3.7	372
144	Clinical interpretation and implications of whole-genome sequencing. <i>JAMA - Journal of the American Medical Association</i> , 2014 , 311, 1035-45	27.4	333
143	High-sensitivity measurements of multiple kinase activities in live single cells. <i>Cell</i> , 2014 , 157, 1724-34	56.2	296
142	SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer. <i>Nature</i> , 2014 , 510, 283-7	50.4	259
141	Network-based elucidation of human disease similarities reveals common functional modules enriched for pluripotent drug targets. <i>PLoS Computational Biology</i> , 2010 , 6, e1000662	5	234
140	ImmPort, toward repurposing of open access immunological assay data for translational and clinical research. <i>Scientific Data</i> , 2018 , 5, 180015	8.2	233
139	Comprehensive analysis of normal adjacent to tumor transcriptomes. <i>Nature Communications</i> , 2017 , 8, 1077	17.4	216
138	A longitudinal big data approach for precision health. <i>Nature Medicine</i> , 2019 , 25, 792-804	50.5	183

137	Creation and implications of a phenome-genome network. <i>Nature Biotechnology</i> , 2006 , 24, 55-62	44.5	176
136	A common rejection module (CRM) for acute rejection across multiple organs identifies novel therapeutics for organ transplantation. <i>Journal of Experimental Medicine</i> , 2013 , 210, 2205-21	16.6	166
135	Autoimmune disease classification by inverse association with SNP alleles. <i>PLoS Genetics</i> , 2009 , 5, e1000792	129	
134	Guidelines for Genome-Scale Analysis of Biological Rhythms. <i>Journal of Biological Rhythms</i> , 2017 , 32, 380-393	3.2	127
133	Microfluidic platform for real-time signaling analysis of multiple single T cells in parallel. <i>Lab on a Chip</i> , 2008 , 8, 1700-12	7.2	113
132	Aging disrupts cell subpopulation dynamics and diminishes the function of mesenchymal stem cells. <i>Scientific Reports</i> , 2014 , 4, 7144	4.9	108
131	A meta-analysis of lung cancer gene expression identifies PTK7 as a survival gene in lung adenocarcinoma. <i>Cancer Research</i> , 2014 , 74, 2892-902	10.1	108
130	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. <i>Science</i> , 2018 , 359, 1233-1239	33.3	101
129	A noisy paracrine signal determines the cellular NF-kappaB response to lipopolysaccharide. <i>Science Signaling</i> , 2009 , 2, ra65	8.8	101
128	Translational bioinformatics: coming of age. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2008 , 15, 709-14	8.6	101
127	Cross-tissue Analysis of Gene and Protein Expression in Normal and Cancer Tissues. <i>Scientific Reports</i> , 2016 , 6, 24799	4.9	96
126	Type 2 diabetes risk alleles demonstrate extreme directional differentiation among human populations, compared to other diseases. <i>PLoS Genetics</i> , 2012 , 8, e1002621	6	95
125	Minimum information about clinical artificial intelligence modeling: the MI-CLAIM checklist. <i>Nature Medicine</i> , 2020 , 26, 1320-1324	50.5	87
124	Systematic identification of interaction effects between genome- and environment-wide associations in type 2 diabetes mellitus. <i>Human Genetics</i> , 2013 , 132, 495-508	6.3	86
123	Reversal of cancer gene expression correlates with drug efficacy and reveals therapeutic targets. <i>Nature Communications</i> , 2017 , 8, 16022	17.4	85
122	Robust meta-analysis of gene expression using the elastic net. <i>Nucleic Acids Research</i> , 2015 , 43, e79	20.1	76
121	Defective Signaling in the JAK-STAT Pathway Tracks with Chronic Inflammation and Cardiovascular Risk in Aging Humans. <i>Cell Systems</i> , 2016 , 3, 374-384.e4	10.6	73
120	Assessment of a Deep Learning Model Based on Electronic Health Record Data to Forecast Clinical Outcomes in Patients With Rheumatoid Arthritis. <i>JAMA Network Open</i> , 2019 , 2, e190606	10.4	67

119	PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. <i>Cancer Research</i> , 2017 , 77, e62-e66	10.1	65
118	Prototype of running clinical trials in an untrustworthy environment using blockchain. <i>Nature Communications</i> , 2019 , 10, 917	17.4	65
117	Releasing a preprint is associated with more attention and citations for the peer-reviewed article. <i>ELife</i> , 2019 , 8,	8.9	59
116	Analysis of the genetic basis of disease in the context of worldwide human relationships and migration. <i>PLoS Genetics</i> , 2013 , 9, e1003447	6	58
115	Diabetes irreversibly depletes bone marrow-derived mesenchymal progenitor cell subpopulations. <i>Diabetes</i> , 2014 , 63, 3047-56	0.9	55
114	Population-level rhythms in human skin with implications for circadian medicine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 12313-12318	11.5	54
113	Sex differences in disease risk from reported genome-wide association study findings. <i>Human Genetics</i> , 2012 , 131, 353-64	6.3	50
112	Live-cell measurements of kinase activity in single cells using translocation reporters. <i>Nature Protocols</i> , 2018 , 13, 155-169	18.8	49
111	Anti-CD44 antibody treatment lowers hyperglycemia and improves insulin resistance, adipose inflammation, and hepatic steatosis in diet-induced obese mice. <i>Diabetes</i> , 2015 , 64, 867-75	0.9	47
110	ZeitZeiger: supervised learning for high-dimensional data from an oscillatory system. <i>Nucleic Acids Research</i> , 2016 , 44, e80	20.1	47
109	Extreme evolutionary disparities seen in positive selection across seven complex diseases. <i>PLoS ONE</i> , 2010 , 5, e12236	3.7	46
108	Computational modeling of mammalian signaling networks. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010 , 2, 194-209	6.6	46
107	Widespread parainflammation in human cancer. <i>Genome Biology</i> , 2016 , 17, 145	18.3	45
106	Medicine. The ultimate model organism. <i>Science</i> , 2008 , 320, 325-7	33.3	43
105	Computational Discovery of Niclosamide Ethanolamine, a Repurposed Drug Candidate That Reduces Growth of Hepatocellular Carcinoma Cells In Vitro and in Mice by Inhibiting Cell Division Cycle 37 Signaling. <i>Gastroenterology</i> , 2017 , 152, 2022-2036	13.3	42
104	Achieving high-sensitivity for clinical applications using augmented exome sequencing. <i>Genome Medicine</i> , 2015 , 7, 71	14.4	41
103	Whole genome sequencing in support of wellness and health maintenance. <i>Genome Medicine</i> , 2013 , 5, 58	14.4	40
102	Investigation of maternal environmental exposures in association with self-reported preterm birth. <i>Reproductive Toxicology</i> , 2014 , 45, 1-7	3.4	37

101	The Case for Algorithmic Stewardship for Artificial Intelligence and Machine Learning Technologies. <i>JAMA - Journal of the American Medical Association</i> , 2020 , 324, 1397-1398	27.4	37
100	Microfluidic single-cell transcriptional analysis rationally identifies novel surface marker profiles to enhance cell-based therapies. <i>Nature Communications</i> , 2016 , 7, 11945	17.4	36
99	Machine learning identifies a compact gene set for monitoring the circadian clock in human blood. <i>Genome Medicine</i> , 2017 , 9, 19	14.4	34
98	Single-cell variation leads to population invariance in NF- κ B signaling dynamics. <i>Molecular Biology of the Cell</i> , 2015 , 26, 583-90	3.5	33
97	Disease risk factors identified through shared genetic architecture and electronic medical records. <i>Science Translational Medicine</i> , 2014 , 6, 234ra57	17.5	33
96	Evidence for widespread dysregulation of circadian clock progression in human cancer. <i>PeerJ</i> , 2018 , 6, e4327	3.1	33
95	Repurpose terbutaline sulfate for amyotrophic lateral sclerosis using electronic medical records. <i>Scientific Reports</i> , 2015 , 5, 8580	4.9	32
94	Finding disease-related genomic experiments within an international repository: first steps in translational bioinformatics 2006 , 106-10	0.7	32
93	Solving Immunology?. <i>Trends in Immunology</i> , 2017 , 38, 116-127	14.4	28
92	Peptidomic Identification of Serum Peptides Diagnosing Preeclampsia. <i>PLoS ONE</i> , 2013 , 8, e65571	3.7	28
91	MetaCyto: A Tool for Automated Meta-analysis of Mass and Flow Cytometry Data. <i>Cell Reports</i> , 2018 , 24, 1377-1388	10.6	27
90	Are minor alleles more likely to be risk alleles?. <i>BMC Medical Genomics</i> , 2018 , 11, 3	3.7	27
89	In silico and in vitro drug screening identifies new therapeutic approaches for Ewing sarcoma. <i>Oncotarget</i> , 2017 , 8, 4079-4095	3.3	26
88	Differential Phasing between Circadian Clocks in the Brain and Peripheral Organs in Humans. <i>Journal of Biological Rhythms</i> , 2016 , 31, 588-597	3.2	26
87	LimoRhyde: A Flexible Approach for Differential Analysis of Rhythmic Transcriptome Data. <i>Journal of Biological Rhythms</i> , 2019 , 34, 5-18	3.2	25
86	Organ size control is dominant over Rb family inactivation to restrict proliferation in vivo. <i>Cell Reports</i> , 2014 , 8, 371-81	10.6	24
85	Protein microarrays discover angiotensinogen and PRKRIP1 as novel targets for autoantibodies in chronic renal disease. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.000497	7.6	24
84	The 10,000 Immunomes Project: Building a Resource for Human Immunology. <i>Cell Reports</i> , 2018 , 25, 513-522.e3	10.6	22

83	A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth. <i>Scientific Reports</i> , 2018 , 8, 226	4.9	21
82	Expression-Based Genome-Wide Association Study Links Vitamin D-Binding Protein With Autoantigenicity in Type 1 Diabetes. <i>Diabetes</i> , 2016 , 65, 1341-9	0.9	20
81	NF- κ B signaling dynamics is controlled by a dose-sensing autoregulatory loop. <i>Science Signaling</i> , 2019 , 12,	8.8	19
80	Heterogeneity in recent-onset type 1 diabetes - a clinical trial perspective. <i>Diabetes/Metabolism Research and Reviews</i> , 2015 , 31, 588-94	7.5	19
79	Precision annotation of digital samples in NCBI's gene expression omnibus. <i>Scientific Data</i> , 2017 , 4, 170185	18.5	19
78	Single-cell and population NF- κ B dynamic responses depend on lipopolysaccharide preparation. <i>PLoS ONE</i> , 2013 , 8, e53222	3.7	18
77	Meta-Analysis of Vaginal Microbiome Data Provides New Insights Into Preterm Birth. <i>Frontiers in Microbiology</i> , 2020 , 11, 476	5.7	18
76	Reanalysis of the Rituximab in ANCA-Associated Vasculitis trial identifies granulocyte subsets as a novel early marker of successful treatment. <i>Arthritis Research and Therapy</i> , 2015 , 17, 262	5.7	17
75	Self-reported dietary adherence, disease-specific symptoms, and quality of life are associated with healthcare provider follow-up in celiac disease. <i>BMC Gastroenterology</i> , 2017 , 17, 156	3	16
74	Digitally deconvolving the tumor microenvironment. <i>Genome Biology</i> , 2016 , 17, 175	18.3	16
73	Improving the phenotype risk score as a scalable approach to identifying patients with Mendelian disease. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2019 , 26, 1437-1447	8.6	15
72	The microfluidic multitrap nanophysiometer for hematologic cancer cell characterization reveals temporal sensitivity of the calcein-AM efflux assay. <i>Scientific Reports</i> , 2014 , 4, 5117	4.9	15
71	Heterogeneity in HIV and cellular transcription profiles in cell line models of latent and productive infection: implications for HIV latency. <i>Retrovirology</i> , 2019 , 16, 32	3.6	14
70	A robust and interpretable end-to-end deep learning model for cytometry data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 21373-21380	11.5	14
69	Comparing Ethnicity-Specific Reference Intervals for Clinical Laboratory Tests from EHR Data. <i>Journal of Applied Laboratory Medicine</i> , 2018 , 3, 366-377	2	14
68	Eating breakfast and avoiding late-evening snacking sustains lipid oxidation. <i>PLoS Biology</i> , 2020 , 18, e300622	9.622	12
67	PatientExploreR: an extensible application for dynamic visualization of patient clinical history from electronic health records in the OMOP common data model. <i>Bioinformatics</i> , 2019 , 35, 4515-4518	7.2	10
66	Big data opens a window onto wellness. <i>Nature Biotechnology</i> , 2017 , 35, 720-721	44.5	10

65	Risky Business: Meeting the Structural Needs of Transdisciplinary Science. <i>Journal of Pediatrics</i> , 2017 , 191, 255-258	3.6	10
64	Protected Health Information filter (Philter): accurately and securely de-identifying free-text clinical notes. <i>Npj Digital Medicine</i> , 2020 , 3, 57	15.7	10
63	Cox regression increases power to detect genotype-phenotype associations in genomic studies using the electronic health record. <i>BMC Genomics</i> , 2019 , 20, 805	4.5	10
62	Robust prediction of clinical outcomes using cytometry data. <i>Bioinformatics</i> , 2019 , 35, 1197-1203	7.2	10
61	Comparison of automated and human assignment of MeSH terms on publicly-available molecular datasets. <i>Journal of Biomedical Informatics</i> , 2011 , 44 Suppl 1, S39-S43	10.2	9
60	Discovering Cross-Reactivity in Urine Drug Screening Immunoassays through Large-Scale Analysis of Electronic Health Records. <i>Clinical Chemistry</i> , 2019 , 65, 1522-1531	5.5	7
59	Combinatorial processing of bacterial and host-derived innate immune stimuli at the single-cell level. <i>Molecular Biology of the Cell</i> , 2019 , 30, 282-292	3.5	7
58	CovidCounties is an interactive real time tracker of the COVID19 pandemic at the level of US counties. <i>Scientific Data</i> , 2020 , 7, 405	8.2	7
57	Assessment of Postdonation Outcomes in US Living Kidney Donors Using Publicly Available Data Sets. <i>JAMA Network Open</i> , 2019 , 2, e191851	10.4	6
56	Is the crowd better as an assistant or a replacement in ontology engineering? An exploration through the lens of the Gene Ontology. <i>Journal of Biomedical Informatics</i> , 2016 , 60, 199-209	10.2	6
55	Cancer Cell-Autonomous Parainflammation Mimics Immune Cell Infiltration. <i>Cancer Research</i> , 2017 , 77, 3740-3744	10.1	6
54	CHARACTERISTICS OF DRUG COMBINATION THERAPY IN ONCOLOGY BY ANALYZING CLINICAL TRIAL DATA ON CLINICALTRIALS.GOV 2014 ,		6
53	Validating pathophysiological models of aging using clinical electronic medical records. <i>Journal of Biomedical Informatics</i> , 2010 , 43, 358-64	10.2	6
52	Enabling precision medicine in neonatology, an integrated repository for preterm birth research. <i>Scientific Data</i> , 2018 , 5, 180219	8.2	6
51	Distinct Components of Photoperiodic Light Are Differentially Encoded by the Mammalian Circadian Clock. <i>Journal of Biological Rhythms</i> , 2020 , 35, 353-367	3.2	5
50	Tracing diagnosis trajectories over millions of patients reveal an unexpected risk in schizophrenia. <i>Scientific Data</i> , 2019 , 6, 201	8.2	5
49	Symphony: simulating large-scale, rhythmic data. <i>PeerJ</i> , 2019 , 7, e6985	3.1	5
48	The risks of using the chi-square periodogram to estimate the period of biological rhythms. <i>PLoS Computational Biology</i> , 2021 , 17, e1008567	5	5

47	Age- and Sex-Associated Variations in the Sensitivity of Serological Tests Among Individuals Infected With SARS-CoV-2. <i>JAMA Network Open</i> , 2021 , 4, e210337	10.4	5
46	Recent Advances in Systems and Network Medicine: Meeting Report from the First International Conference in Systems and Network Medicine. <i>Systems Medicine (New Rochelle, N Y)</i> , 2020 , 3, 22-35	1.6	4
45	Open data informatics and data repurposing for IBD. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018 , 15, 715-716	24.2	4
44	Gene expression deconvolution in linear space. <i>Nature Methods</i> , 2012 , 9, 9-9	21.6	4
43	Application of Machine Learning for Cytometry Data.. <i>Frontiers in Immunology</i> , 2021 , 12, 787574	8.4	4
42	Automated quality control and cell identification of droplet-based single-cell data using dropkick. <i>Genome Research</i> , 2021 , 31, 1742-1752	9.7	4
41	Trials and Tribulations-11 Reasons Why We Need to Promote Clinical Trials Data Sharing. <i>JAMA Network Open</i> , 2021 , 4, e2035043	10.4	4
40	It takes a genome to understand a village: Population scale precision medicine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 12344-12346	11.5	3
39	Rethinking PICO in the Machine Learning Era: ML-PICO. <i>Applied Clinical Informatics</i> , 2021 , 12, 407-416	3.1	3
38	Tau-independent Phase Analysis: A Novel Method for Accurately Determining Phase Shifts. <i>Journal of Biological Rhythms</i> , 2018 , 33, 223-232	3.2	2
37	IDENTIFICATION OF DISCRIMINATING BIOMARKERS FOR HUMAN DISEASE USING INTEGRATIVE NETWORK BIOLOGY 2008 ,		2
36	2007 ,		2
35	Open challenges in developing digital therapeutics in the United States 2022 , 1, e0000008		2
34	NOVEL INTEGRATION OF HOSPITAL ELECTRONIC MEDICAL RECORDS AND GENE EXPRESSION MEASUREMENTS TO IDENTIFY GENETIC MARKERS OF MATURATION 2007 ,		2
33	Releasing a preprint is associated with more attention and citations for the peer-reviewed article		2
32	Accuracy of medical billing data against the electronic health record in the measurement of colorectal cancer screening rates. <i>BMJ Open Quality</i> , 2020 , 9,	1.9	2
31	Genetic analysis in a patient with nine primary malignant neoplasms: a rare case of Li-Fraumeni syndrome. <i>Oncology Reports</i> , 2016 , 35, 1519-28	3.5	2
30	Immune modulators in disease: integrating knowledge from the biomedical literature and gene expression. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2016 , 23, 617-26	8.6	2

29	Quantifying Variation in Treatment Utilization for Type 2 Diabetes Across Five Major University of California Health Systems. <i>Diabetes Care</i> , 2021 , 44, 908-914	14.6	2
28	Pulling the covers in electronic health records for an association study with self-reported sleep behaviors. <i>Chronobiology International</i> , 2018 , 35, 1702-1712	3.6	2
27	The Role of Electronic Health Records in Advancing Genomic Medicine. <i>Annual Review of Genomics and Human Genetics</i> , 2021 , 22, 219-238	9.7	2
26	Serological targeted analysis of an ITIH4 peptide isoform: a preterm birth biomarker and its associated SNP implications. <i>Journal of Genetics and Genomics</i> , 2015 , 42, 507-10	4	1
25	RImmPort 2014 ,		1
24	Towards the characterization of normal peripheral immune cells with data from ImmPort 2014 ,		1
23	Allogeneic Antibodies Identify GVL Targets CHAF1b and NuSAP1 in AML Patients.. <i>Blood</i> , 2007 , 110, 1682-1688	168	1
22	Case-control study of the association of chronic acid suppression and social determinants of health with COVID-19 infection. <i>Scientific Reports</i> , 2021 , 11, 20987	4.9	1
21	Population level rhythms in human skin: implications for circadian medicine		1
20	Cox regression increases power to detect genotype-phenotype associations in genomic studies using the electronic health record		1
19	CovidCounties - an interactive, real-time tracker of the COVID-19 pandemic at the level of US counties 2020 ,		1
18	The 10,000 Immunomes Project: A resource for human immunology		1
17	Monitoring the circadian clock in human blood using personalized machine learning		1
16	pmparser and PMDB: resources for large-scale, open studies of the biomedical literature. <i>PeerJ</i> , 2021 , 9, e11071	3.1	1
15	Five-year pediatric use of a digital wearable fitness device: lessons from a pilot case study. <i>JAMIA Open</i> , 2021 , 4, ooab054	2.9	1
14	Assessing Clinical Outcomes in a Data-Rich World-A Reality Check on Real-World Data. <i>JAMA Network Open</i> , 2021 , 4, e2117826	10.4	1
13	A Computational Approach to Identify Interfering Medications on Urine Drug Screening Assays without Data from Confirmatory Testing. <i>Journal of Analytical Toxicology</i> , 2021 , 45, 325-330	2.9	1
12	Individualized Constellation of Killer Cell Immunoglobulin-Like Receptors and Cognate HLA Class I Ligands that Controls Natural Killer Cell Antiviral Immunity Predisposes COVID-19.. <i>Frontiers in Genetics</i> , 2022 , 13, 845474	4.5	1

11	Deep learning from multiple experts improves identification of amyloid neuropathologies.. <i>Acta Neuropathologica Communications</i> , 2022 , 10, 66	7.3	1
10	Systematic identification of ACE2 expression modulators reveals cardiomyopathy as a risk factor for mortality in COVID-19 patients.. <i>Genome Biology</i> , 2022 , 23, 15	18.3	0
9	Opportunities and Challenges in Democratizing Immunology Datasets. <i>Frontiers in Immunology</i> , 2021 , 12, 647536	8.4	0
8	Big Data in Nephrology. <i>Nature Reviews Nephrology</i> , 2021 , 17, 676-687	14.9	0
7	Algorithmic Stewardship in Health Care-Reply. <i>JAMA - Journal of the American Medical Association</i> , 2021 , 325, 588-589	27.4	0
6	Optogenetic stimulation of VIPergic SCN neurons induces photoperiodic-like changes in the mammalian circadian clock. <i>European Journal of Neuroscience</i> , 2021 , 54, 7063-7071	3.5	0
5	Selected proceedings of the First Summit on Translational Bioinformatics 2008. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 2, 11	3.6	
4	Eating breakfast and avoiding late-evening snacking sustains lipid oxidation 2020 , 18, e3000622		
3	Eating breakfast and avoiding late-evening snacking sustains lipid oxidation 2020 , 18, e3000622		
2	Eating breakfast and avoiding late-evening snacking sustains lipid oxidation 2020 , 18, e3000622		
1	Eating breakfast and avoiding late-evening snacking sustains lipid oxidation 2020 , 18, e3000622		