Francis S Collins

List of Publications by Citations

Source: https://exaly.com/author-pdf/11326341/francis-s-collins-publications-by-citations.pdf
Version: 2024-04-10

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.

162 papers	88,881 citations	94 h-index	168 g-index
168 ext. papers	100,142 ext. citations	23.2 avg, IF	7.22 L-index

#	Paper	IF	Citations
162	Finding the missing heritability of complex diseases. *Nature*, **2009**, 461, 747-53	50.4	6084
161	Initial sequencing and comparative analysis of the mouse genome. *Nature*, **2002**, 420, 520-62	50.4	5376
160	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
159	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
158	Potential etiologic and functional implications of genome-wide association loci for human diseases and traits. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 9362-7	11.5	3120
157	A new initiative on precision medicine. *New England Journal of Medicine*, **2015**, 372, 793-5	59.2	3119
156	Identification of the cystic fibrosis gene: chromosome walking and jumping. *Science*, **1989**, 245, 1059-65	33.3	2745
155	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
154	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
153	Mutations in the p53 gene occur in diverse human tumour types. *Nature*, **1989**, 342, 705-8	50.4	2418
152	A single ataxia telangiectasia gene with a product similar to PI-3 kinase. *Science*, **1995**, 268, 1749-53	33.3	2334
151	A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants. *Science*, **2007**, 316, 1341-5	33.3	2269
150	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
149	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
148	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
147	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
146	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nature Genetics*, **2008**, 40, 638-45	36.3	1496

145	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
144	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 16899-903	11.5	1457
143	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
142	A vision for the future of genomics research. *Nature*, **2003**, 422, 835-47	50.4	1390
141	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics*, **2009**, 41, 25-34	36.3	1368
140	Replicating genotype-phenotype associations. *Nature*, **2007**, 447, 655-60	50.4	1363
139	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
138	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. *Nature Genetics*, **2008**, 40, 161-9	36.3	1304
137	Type 1 neurofibromatosis gene: identification of a large transcript disrupted in three NF1 patients. *Science*, **1990**, 249, 181-6	33.3	1279
136	Common variants at 30 loci contribute to polygenic dyslipidemia. *Nature Genetics*, **2009**, 41, 56-65	36.3	1095
135	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
134	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
133	Variations on a theme: cataloging human DNA sequence variation. *Science*, **1997**, 278, 1580-1	33.3	849
132	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
131	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nature Genetics*, **2010**, 42, 949-60	36.3	724
130	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
129	A HapMap harvest of insights into the genetics of common disease. *Journal of Clinical Investigation*, **2008**, 118, 1590-605	15.9	683
128	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. *Nature Genetics*, **2018**, 50, 1505-1513	36.3	675

127	A DNA polymorphism discovery resource for research on human genetic variation. *Genome Research*, **1998**, 8, 1229-31	9.7	627
126	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
125	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nature Genetics*, **2012**, 44, 659-69	36.3	615
124	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
123	Aberrant regulation of ras proteins in malignant tumour cells from type 1 neurofibromatosis patients. *Nature*, **1992**, 356, 713-5	50.4	589
122	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584
121	Correction of the cystic fibrosis defect in vitro by retrovirus-mediated gene transfer. *Cell*, **1990**, 62, 1227-33	30.2	528
120	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527
119	The knockout mouse project. *Nature Genetics*, **2004**, 36, 921-4	36.3	490
118	Genomic medicine--a primer. *New England Journal of Medicine*, **2002**, 347, 1512-20	59.2	468
117	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
116	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	39	414
115	The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC). *Genome Research*, **2004**, 14, 2121-7	9.7	404
114	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393
113	A de novo Alu insertion results in neurofibromatosis type 1. *Nature*, **1991**, 353, 864-6	50.4	390
112	Genome-wide mapping of DNase hypersensitive sites using massively parallel signature sequencing (MPSS). *Genome Research*, **2006**, 16, 123-31	9.7	363
111	Genomic medicine--an updated primer. *New England Journal of Medicine*, **2010**, 362, 2001-11	59.2	354
110	cDNA cloning of the type 1 neurofibromatosis gene: complete sequence of the NF1 gene product. *Genomics*, **1991**, 11, 931-40	4.3	350

109	Somatic deletion of the neurofibromatosis type 1 gene in a neurofibrosarcoma supports a tumour suppressor gene hypothesis. *Nature Genetics*, **1993**, 3, 122-6	36.3	347
108	TEL1, an S. cerevisiae homolog of the human gene mutated in ataxia telangiectasia, is functionally related to the yeast checkpoint gene MEC1. *Cell*, **1995**, 82, 831-40	56.2	331
107	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. *PLoS Genetics*, **2012**, 8, e1002607	6	326
106	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325
105	Common variants in the GDF5-UQCC region are associated with variation in human height. *Nature Genetics*, **2008**, 40, 198-203	36.3	315
104	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
103	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
102	Localization of the cystic fibrosis transmembrane conductance regulator in human bile duct epithelial cells. *Gastroenterology*, **1993**, 105, 1857-64	13.3	289
101	Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. *Diabetes*, **2011**, 60, 2624-34	0.9	285
100	MicroRNA target site polymorphisms and human disease. *Trends in Genetics*, **2008**, 24, 489-97	8.5	285
99	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
98	New models of collaboration in genome-wide association studies: the Genetic Association Information Network. *Nature Genetics*, **2007**, 39, 1045-51	36.3	258
97	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
96	The mammalian gene collection. *Science*, **1999**, 286, 455-7	33.3	237
95	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
94	Welcome to the genomic era. *New England Journal of Medicine*, **2003**, 349, 996-8	59.2	221
93	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
92	Mutation analysis for heterozygote detection and the prenatal diagnosis of cystic fibrosis. *New England Journal of Medicine*, **1990**, 322, 291-6	59.2	197

91	What we do and don't know about 'race', 'ethnicity', genetics and health at the dawn of the genome era. *Nature Genetics*, **2004**, 36, S13-5	36.3	193
90	The Scientific Foundation for personal genomics: recommendations from a National Institutes of Health-Centers for Disease Control and Prevention multidisciplinary workshop. *Genetics in Medicine*, **2009**, 11, 559-67	8.1	186
89	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
88	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
87	MicroRNA-27b is a regulatory hub in lipid metabolism and is altered in dyslipidemia. *Hepatology*, **2013**, 57, 533-42	11.2	164
86	Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. *PLoS Genetics*, **2012**, 8, e1002741	6	162
85	The HapMap and genome-wide association studies in diagnosis and therapy. *Annual Review of Medicine*, **2009**, 60, 443-56	17.4	155
84	Identifying gene regulatory elements by genome-wide recovery of DNase hypersensitive sites. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 992-7	11.5	150
83	Association of 18 confirmed susceptibility loci for type 2 diabetes with indices of insulin release, proinsulin conversion, and insulin sensitivity in 5,327 nondiabetic Finnish men. *Diabetes*, **2009**, 58, 2129-36	9.9	149
82	The Huntington's disease candidate region exhibits many different haplotypes. *Nature Genetics*, **1992**, 1, 99-103	36.3	142
81	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
80	Mutations in the neurofibromatosis 1 gene in sporadic malignant melanoma cell lines. *Nature Genetics*, **1993**, 3, 118-21	36.3	133
79	Variations in the G6PC2/ABCB11 genomic region are associated with fasting glucose levels. *Journal of Clinical Investigation*, **2008**, 118, 2620-8	15.9	127
78	Human Genome Project: Twenty-five years of big biology. *Nature*, **2015**, 526, 29-31	50.4	122
77	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
76	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
75	Realizing the promise of genomics in biomedical research. *JAMA - Journal of the American Medical Association*, **2005**, 294, 1399-402	27.4	105
74	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103

73	Strategies for mutational analysis of the large multiexon ATM gene using high-density oligonucleotide arrays. *Genome Research*, **1998**, 8, 1245-58	9.7	99
72	The completion of the Mammalian Gene Collection (MGC). *Genome Research*, **2009**, 19, 2324-33	9.7	98
71	Cystic fibrosis gene mutation in two sisters with mild disease and normal sweat electrolyte levels. *New England Journal of Medicine*, **1991**, 325, 1630-4	59.2	97
70	Trans-ethnic fine-mapping of lipid loci identifies population-specific signals and allelic heterogeneity that increases the trait variance explained. *PLoS Genetics*, **2013**, 9, e1003379	6	94
69	A cosmid contig and high resolution restriction map of the 2 megabase region containing the Huntington's disease gene. *Nature Genetics*, **1993**, 4, 181-6	36.3	93
68	Magnetic bead capture of expressed sequences encoded within large genomic segments. *Nature*, **1993**, 361, 751-3	50.4	92
67	Discovery of active enhancers through bidirectional expression of short transcripts. *Genome Biology* , **2011**, 12, R113	18.3	91
66	Tissue-specific alternative splicing of TCF7L2. *Human Molecular Genetics*, **2009**, 18, 3795-804	5.6	89
65	Expression of an abundant alternatively spliced form of the cystic fibrosis transmembrane conductance regulator (CFTR) gene is not associated with a cAMP-activated chloride conductance. *Human Molecular Genetics*, **1993**, 2, 225-30	5.6	88
64	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. *American Journal of Human Genetics*, **2017**, 100, 428-443	11	87
63	Comprehensive association study of type 2 diabetes and related quantitative traits with 222 candidate genes. *Diabetes*, **2008**, 57, 3136-44	0.9	82
62	The Metabolic Syndrome in Men study: a resource for studies of metabolic and cardiovascular diseases. *Journal of Lipid Research*, **2017**, 58, 481-493	6.3	77
61	Race and ethnicity in the genome era: the complexity of the constructs. *American Psychologist*, **2005**, 60, 9-15	9.5	77
60	Molecular basis of defective anion transport in L cells expressing recombinant forms of CFTR. *Human Molecular Genetics*, **1993**, 2, 1253-61	5.6	76
59	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. *Journal of the American Heart Association*, **2017**, 6,	6	65
58	Effects of 34 risk loci for type 2 diabetes or hyperglycemia on lipoprotein subclasses and their composition in 6,580 nondiabetic Finnish men. *Diabetes*, **2011**, 60, 1608-16	0.9	65
57	A large set of Finnish affected sibling pair families with type 2 diabetes suggests susceptibility loci on chromosomes 6, 11, and 14. *Diabetes*, **2004**, 53, 821-9	0.9	64
56	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. *American Journal of Human Genetics*, **2018**, 102, 375-400	11	59

55	Psychiatry in the genomics era. *American Journal of Psychiatry*, **2003**, 160, 616-20	11.9	57
54	Loss of neurofibromin in adrenal gland tumors from patients with neurofibromatosis type I. *Genes Chromosomes and Cancer*, **1994**, 10, 55-8	5	57
53	The geneticist's approach to complex disease. *Annual Review of Medicine*, **1996**, 47, 333-53	17.4	55
52	A high-density microsatellite map of the ataxia-telangiectasia locus. *Human Genetics*, **1995**, 95, 451-4	6.3	54
51	Two patients with ring chromosome 15 syndrome. *American Journal of Medical Genetics Part A*, **1988**, 29, 149-54		53
50	Linkage disequilibrium between microsatellite markers extends beyond 1 cM on chromosome 20 in Finns. *Genome Research*, **2001**, 11, 1221-6	9.7	51
49	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
48	Recent progress toward understanding the molecular biology of von Recklinghausen neurofibromatosis. *Annals of Neurology*, **1992**, 31, 555-61	9.4	44
47	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
46	Physical mapping of the cystic fibrosis region by pulsed-field gel electrophoresis. *Genomics*, **1988**, 2, 346-54	4.3	43
45	Re-sequencing expands our understanding of the phenotypic impact of variants at GWAS loci. *PLoS Genetics*, **2014**, 10, e1004147	6	42
44	Multiple Hepatic Regulatory Variants at the GALNT2 GWAS Locus Associated with High-Density Lipoprotein Cholesterol. *American Journal of Human Genetics*, **2015**, 97, 801-15	11	40
43	The human genome project and the future of medicine. *Annals of the New York Academy of Sciences* , **1999**, 882, 42-55; discussion 56-65	6.5	39
42	Gene therapy for cystic fibrosis. *Chest*, **1996**, 109, 241-52	5.3	39
41	Common, low-frequency, and rare genetic variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. *PLoS Genetics*, **2017**, 13, e1007079	6	33
40	Nurses and the genomic revolution. *Journal of Nursing Scholarship*, **2005**, 37, 98-101	3.6	32
39	Correlation of rare coding variants in the gene encoding human glucokinase regulatory protein with phenotypic, cellular, and kinetic outcomes. *Journal of Clinical Investigation*, **2012**, 122, 205-17	15.9	31
38	A Drosophila functional evaluation of candidates from human genome-wide association studies of type 2 diabetes and related metabolic traits identifies tissue-specific roles for dHHEX. *BMC Genomics*, **2013**, 14, 136	4.5	27

37	Molecular biology of cystic fibrosis. *Molecular Genetic Medicine*, **1993**, 3, 33-68		26
36	Characterization of an intron 12 splice donor mutation in the cystic fibrosis transmembrane conductance regulator (CFTR) gene. *Human Mutation*, **1992**, 1, 380-7	4.7	25
35	The cystic fibrosis gene: isolation and significance. *Hospital Practice (1995)*, **1990**, 25, 47-57	2.2	24
34	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
33	No interactions between previously associated 2-hour glucose gene variants and physical activity or BMI on 2-hour glucose levels. *Diabetes*, **2012**, 61, 1291-6	0.9	21
32	The human NME2 gene lies within 18kb of NME1 in chromosome 17. *Genes Chromosomes and Cancer*, **1993**, 6, 245-8	5	21
31	Approaches to localizing disease genes as applied to cystic fibrosis. *Nucleic Acids Research*, **1990**, 18, 345-50	20.1	21
30	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. *American Journal of Human Genetics*, **2019**, 105, 773-787	11	20
29	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. *Human Molecular Genetics*, **2018**, 27, 1664-1674	5.6	20
28	Nonsense mutations at Arg-1947 in two cases of familial neurofibromatosis type 1 in Japanese. *Human Genetics*, **1994**, 93, 81-3	6.3	20
27	A chromosome jump crosses a translocation breakpoint in the von Recklinghausen neurofibromatosis region. *Genes Chromosomes and Cancer*, **1990**, 2, 271-7	5	20
26	Inheritance of rare functional GCKR variants and their contribution to triglyceride levels in families. *Human Molecular Genetics*, **2014**, 23, 5570-8	5.6	18
25	Fine-mapping of an expanded set of type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps		18
24	Distant conserved sequences flanking endothelial-specific promoters contain tissue-specific DNase-hypersensitive sites and over-represented motifs. *Human Molecular Genetics*, **2006**, 15, 2098-105	5.6	17
23	Genetic risk scores in the prediction of plasma glucose, impaired insulin secretion, insulin resistance and incident type 2 diabetes in the METSIM study. *Diabetologia*, **2017**, 60, 1722-1730	10.3	15
22	-ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the HDL-C GWAS Locus. *G3: Genes, Genomes, Genetics*, **2017**, 7, 3217-3227	3.2	14
21	Colocalization of GWAS and eQTL signals at loci with multiple signals identifies additional candidate genes for body fat distribution. *Human Molecular Genetics*, **2019**, 28, 4161-4172	5.6	12
20	Sequencing and analysis of genomic fragments from the NF1 locus. *DNA Sequence*, **1992**, 3, 237-43		11

19	2005 William Allan Award address. No longer just looking under the lamppost. *American Journal of Human Genetics*, **2006**, 79, 421-6	11	10
18	Familial breast cancer. Approaching the isolation of a susceptibility gene. *Cancer*, **1994**, 74, 1013-20	6.4	10
17	The Genome Project and human health. *FASEB Journal*, **1991**, 5, 77	0.9	10
16	Reverse genetics and cystic fibrosis. *American Journal of Respiratory Cell and Molecular Biology*, **1990**, 2, 309-16	5.7	9
15	Molecular genetics of von Recklinghausen neurofibromatosis. *Advances in Human Genetics*, **1991**, 20, 267-307		9
14	An African-American cystic fibrosis patient homozygous for a novel frameshift mutation associated with reduced CFTR mRNA levels. *Human Mutation*, **1993**, 2, 148-51	4.7	8
13	Molecular analysis of deletion and nondeletion hereditary persistence of fetal hemoglobin and identification of a new mutation causing beta-thalassemia. *Annals of the New York Academy of Sciences*, **1985**, 445, 159-69	6.5	8
12	A YAC contig spanning the ataxia-telangiectasia locus (groups A and C) at 11q22-q23. *Genomics*, **1994**, 24, 234-42	4.3	7
11	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
10	Genetic effects on liver chromatin accessibility identify disease regulatory variants. *American Journal of Human Genetics*, **2021**, 108, 1169-1189	11	3
9	Transcript identification in the BRCA1 candidate region. *Breast Cancer Research and Treatment*, **1995**, 33, 115-24	4.4	2
8	Novel missense mutation (G314R) in a cystic fibrosis patient with hepatic failure. *Human Mutation*, **1996**, 7, 151-4	4.7	2
7	Adult Turner syndrome associated with chylous ascites and vascular anomalies. *Clinical Genetics*, **1987**, 31, 218-23	4	1
6	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1
5	Subcutaneous adipose tissue splice quantitative trait loci reveal differences in isoform usage associated with cardiometabolic traits.. *American Journal of Human Genetics*, **2022**, 109, 66-80	11	0
4	Validity of reported genetic risk factors for acute coronary syndrome. *JAMA - Journal of the American Medical Association*, **2007**, 298, 1757; author reply 1759	27.4	
3	Type 1 neurofibromatosis gene: correction. *Science*, **1990**, 250, 1749-1749	33.3	
2	Response : Type 1 Neurofibromatosis Gene: Correction. *Science*, **1990**, 250, 1749-1749	33.3	

1 Response : Type 1 Neurofibromatosis Gene: Correction. *Science*, **1990**, 250, 1749-1749 33.3