Francis S Collins

List of Publications by Year
in descending order

163 papers	107,283 citations	2565 99 h-index	7234 158 g-index
168 all docs	168 docs citations	168 times ranked	96405 citing authors

#	Article	IF	Citations
1	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.	2.6	13
2	Genetic effects on liver chromatin accessibility identify disease regulatory variants. American Journal of Human Genetics, 2021, 108, 1169-1189.	2.6	22
3	Realizing the Dream of Molecularly Targeted Therapies for Cystic Fibrosis. New England Journal of Medicine, 2019, 381, 1863-1865.	13.9	34
4	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.	1.4	41
5	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	2.6	45
6	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
7	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.	1.4	30
8	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
9	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.	2.6	123
10	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.	9.4	1,331
11	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
12	The Metabolic Syndrome in Men study: a resource for studies of metabolic and cardiovascular diseases. Journal of Lipid Research, 2017, 58, 481-493.	2.0	147
13	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. American Journal of Human Genetics, 2017, 100, 428-443.	2.6	141
14	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
15	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	1.6	89
16	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
17	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.	2.9	26
18	Trans-ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the ANGPTL8 HDL-C GWAS Locus. G3: Genes, Genomes, Genetics, 2017, 7, 3217-3227.	0.8	19

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19	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
20	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
21	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.	1.5	49
22	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
23	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
24	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
25	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
26	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
27	Human Genome Project: Twenty-five years of big biology. Nature, 2015, 526, 29-31.	13.7	184
28	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.	1.5	331
29	Multiple Hepatic Regulatory Variants at the GALNT2 GWAS Locus Associated with High-Density Lipoprotein Cholesterol. American Journal of Human Genetics, 2015, 97, 801-815.	2.6	49
30	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
31	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
32	A New Initiative on Precision Medicine. New England Journal of Medicine, 2015, 372, 793-795.	13.9	4,081
33	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
34	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
35	Inheritance of rare functional GCKR variants and their contribution to triglyceride levels in families. Human Molecular Genetics, 2014, 23, 5570-5578.	1.4	21
36	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. PLoS Genetics, 2014, 10, e1004147.	1.5	50

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37	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
38	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
39	MicroRNA-27b is a regulatory hub in lipid metabolism and is altered in dyslipidemia. Hepatology, 2013, 57, 533-542.	3.6	196
40	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.	1.2	37
41	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
42	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
43	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
44	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.	1.5	112
45	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
46	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.	1.5	190
47	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.	1.5	419
48	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
49	No Interactions Between Previously Associated 2-Hour Glucose Gene Variants and Physical Activity or BMI on 2-Hour Glucose Levels. Diabetes, 2012, 61, 1291-1296.	0.3	23
50	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
51	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
52	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
53	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	9.4	762
54	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, 205-217.	3.9	41

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55	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
56	Discovery of active enhancers through bidirectional expression of short transcripts. Genome Biology, 2011, 12, R113.	13.9	120
57	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, 2624-2634.	0.3	335
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, 1608-1616.	0.3	77
59	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
60	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
61	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	9.4	591
62	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
63	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, 949-960.	9.4	836
64	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
65	Genomic Medicine â€" An Updated Primer. New England Journal of Medicine, 2010, 362, 2001-2011.	13.9	411
66	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
67	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	2.4	125
68	Finding the missing heritability of complex diseases. Nature, 2009, 461, 747-753.	13.7	7,490
69	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
70	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
71	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	9.4	1,234
72	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, 2129-2136.	0.3	161

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73	The HapMap and Genome-Wide Association Studies in Diagnosis and Therapy. Annual Review of Medicine, 2009, 60, 443-456.	5.0	191
74	The Scientific Foundation for Personal Genomics: Recommendations from a National Institutes of Healthâ€“Centers for Disease Control and Prevention Multidisciplinary Workshop. Genetics in Medicine, 2009, 11, 559-567.	1.1	207
75	Tissue-specific alternative splicing of TCF7L2. Human Molecular Genetics, 2009, 18, 3795-3804.	1.4	100
76	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, 9362-9367.	3.3	3,719
77	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
78	Common variants in the GDF5-UQCC region are associated with variation in human height. Nature Genetics, 2008, 40, 198-203.	9.4	369
79	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. Nature Genetics, 2008, 40, 161-169.	9.4	1,488
80	MicroRNA target site polymorphisms and human disease. Trends in Genetics, 2008, 24, 489-497.	2.9	318
81	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	9.4	1,683
82	Comprehensive Association Study of Type 2 Diabetes and Related Quantitative Traits With 222 Candidate Genes. Diabetes, 2008, 57, 3136-3144.	0.3	104
83	A HapMap harvest of insights into the genetics of common disease. Journal of Clinical Investigation, 2008, 118, 1590-1605.	3.9	788
84	Variations in the G6PC2/ABCB11 genomic region are associated with fasting glucose levels. Journal of Clinical Investigation, 2008, 118, 2620-8.	3.9	146
85	Validity of Reported Genetic Risk Factors for Acute Coronary Syndrome. JAMA - Journal of the American Medical Association, 2007, 298, 1757.	3.8	0
86	A Genome-Wide Association Study of Type 2 Diabetes in Finns Detects Multiple Susceptibility Variants. Science, 2007, 316, 1341-1345.	6.0	2,534
87	Replicating genotypeâ€“phenotype associations. Nature, 2007, 447, 655-660.	13.7	1,509
88	New models of collaboration in genome-wide association studies: the Genetic Association Information Network. Nature Genetics, 2007, 39, 1045-1051.	9.4	288
89	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
90	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137

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91	No Longer Just Looking under the Lamppost**Previously presented at the annual meeting of The American Society of Human Genetics, in Salt Lake City, on October 28, 2005.. American Journal of Human Genetics, 2006, 79, 421-426.	2.6	16
92	Distant conserved sequences flanking endothelial-specific promoters contain tissue-specific DNase-hypersensitive sites and over-represented motifs. Human Molecular Genetics, 2006, 15, 2098-2105.	1.4	20
93	Nurses and the Genomic Revolution. Journal of Nursing Scholarship, 2005, 37, 98-101.	1.1	36
94	Genome-wide mapping of DNase hypersensitive sites using massively parallel signature sequencing (MPSS). Genome Research, 2005, 16, 123-131.	2.4	431
95	Realizing the Promise of Genomics in Biomedical Research. JAMA - Journal of the American Medical Association, 2005, 294, 1399.	3.8	127
96	Race and ethnicity in the genome era: The complexity of the constructs.. American Psychologist, 2005, 60, 9-15.	3.8	106
97	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, 992-997.	3.3	166
98	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). Genome Research, 2004, 14, 2121-2127.	2.4	486
99	The Knockout Mouse Project. Nature Genetics, 2004, 36, 921-924.	9.4	556
100	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-S15.	9.4	249
101	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, 821-829.	0.3	73
102	A vision for the future of genomics research. Nature, 2003, 422, 835-847.	13.7	1,650
103	Welcome to the Genomic Era. New England Journal of Medicine, 2003, 349, 996-998.	13.9	251
104	Psychiatry in the Genomics Era. American Journal of Psychiatry, 2003, 160, 616-620.	4.0	71
105	Genomic Medicine â€" A Primer. New England Journal of Medicine, 2002, 347, 1512-1520.	13.9	538
106	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, 16899-16903.	3.3	1,610
107	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
108	Linkage Disequilibrium Between Microsatellite Markers Extends Beyond 1 cM on Chromosome 20 in Finns. Genome Research, 2001, 11, 1221-1226.	2.4	60

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109	The Human Genome Project and the Future of Medicine. Annals of the New York Academy of Sciences, 1999, 882, 42-55.	1.8	51
110	The Mammalian Gene Collection. Science, 1999, 286, 455-457.	6.0	266
111	A DNA Polymorphism Discovery Resource for Research on Human Genetic Variation: Table 1.. Genome Research, 1998, 8, 1229-1231.	2.4	750
112	Strategies for Mutational Analysis of the Large MultiexonATMGene Using High-Density Oligonucleotide Arrays. Genome Research, 1998, 8, 1245-1258.	2.4	116
113	Variations on a Theme: Cataloging Human DNA Sequence Variation. Science, 1997, 278, 1580-1581.	6.0	979
114	Gene Therapy for Cystic Fibrosis. Chest, 1996, 109, 241-252.	0.4	45
115	Novel missense mutation (G314R) in a cystic fibrosis patient with hepatic failure. Human Mutation, 1996, 7, 151-154.	1.1	3
116	THE GENETICIST'S APPROACH TO COMPLEX DISEASE. Annual Review of Medicine, 1996, 47, 333-353.	5.0	62
117	Transcript identification in the BRCA1 candidate region. Breast Cancer Research and Treatment, 1995, 33, 115-124.	1.1	2
118	A high-density microsatellite map of the ataxia-telangiectasia locus. Human Genetics, 1995, 95, 451-454.	1.8	56
119	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, 831-840.	13.5	372
120	A single ataxia telangiectasia gene with a product similar to PI-3 kinase. Science, 1995, 268, 1749-1753.	6.0	2,634
121	Nonsense mutations at Arg-1947 in two cases of familial neurofibromatosis type 1 in Japanese. Human Genetics, 1994, 93, 81-3.	1.8	25
122	Familial breast cancer. Approaching the isolation of a susceptibility gene. Cancer, 1994, 74, 1013-1020.	2.0	11
123	Loss of neurofibromin in adrenal gland tumors from patients with neurofibromatosis type I. Genes Chromosomes and Cancer, 1994, 10, 55-58.	1.5	67
124	A YAC Contig Spanning the Ataxia-Telangiectasia Locus (Groups A and C) at 11q22-q23. Genomics, 1994, 24, 234-242.	1.3	8
125	An African-American cystic fibrosis patient homozygous for a novel frameshift mutation associated with reduced CFTR mRNA levels. Human Mutation, 1993, 2, 148-151.	1.1	13
126	The humanNME2 gene lies within 18kb ofNME1 in chromosome 17. Genes Chromosomes and Cancer, 1993, 6, 245-248.	1.5	23

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127	Mutations in the neurofibromatosis 1 gene in sporadic malignant melanoma cell lines. Nature Genetics, 1993, 3, 118-121.	9.4	147
128	Somatic deletion of the neurofibromatosis type 1 gene in a neurofibrosarcoma supports a tumour suppressor gene hypothesis. Nature Genetics, 1993, 3, 122-126.	9.4	394
129	A cosmid contig and high resolution restriction map of the 2 megabase region containing the Huntington's disease gene. Nature Genetics, 1993, 4, 181-186.	9.4	102
130	Magnetic bead capture of expressed sequences encoded within large genomic segments. Nature, 1993, 361, 751-753.	13.7	97
131	Molecular basis of defective anion transport in L cells expressing recombinant forms of CFTR. Human Molecular Genetics, 1993, 2, 1253-1261.	1.4	83
132	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, 225-230.	1.4	100
133	Localization of the cystic fibrosis transmembrane conductance regulator in human bile duct epithelial cells. Gastroenterology, 1993, 105, 1857-1864.	0.6	330
134	Molecular Biology of Cystic Fibrosis. , 1993, 3, 33-68.		32
135	Sequencing and analysis of genomic fragments from theNF1locus. DNA Sequence, 1992, 3, 237-243.	0.7	11
136	Aberrant regulation of ras proteins in malignant tumour cells from type 1 neurofibromatosis patients. Nature, 1992, 356, 713-715.	13.7	653
137	A welcome animal model. Nature, 1992, 358, 708-709.	13.7	16
138	More from the modellers. Nature, 1992, 359, 195-196.	13.7	13
139	Positional cloning: Let's not call it reverse anymore. Nature Genetics, 1992, 1, 3-6.	9.4	456
140	The Huntington's disease candidate region exhibits many different haplotypes. Nature Genetics, 1992, 1, 99-103.	9.4	157
141	Characterization of an intron 12 splice donor mutation in the cystic fibrosis transmembrane conductance regulator (CFTR) gene. Human Mutation, 1992, 1, 380-387.	1.1	27
142	Recent progress toward understanding the molecular biology of von Recklinghausen neurofibromatosis. Annals of Neurology, 1992, 31, 555-561.	2.8	51
143	cDNA cloning of the type 1 neurofibromatosis gene: Complete sequence of the NF1 gene product. Genomics, 1991, 11, 931-940.	1.3	384
144	The Genome Project and human health. FASEB Journal, 1991, 5, 77-77.	0.2	15

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145	A de novo Alu insertion results in neurofibromatosis type 1. Nature, 1991, 353, 864-866.	13.7	444
146	Cystic Fibrosis Gene Mutation in Two Sisters with Mild Disease and Normal Sweat Electrolyte Levels. New England Journal of Medicine, 1991, 325, 1630-1634.	13.9	112
147	Molecular Genetics of von Recklinghausen Neurofibromatosis. , 1991, 20, 267-307.		9
148	The Cystic Fibrosis Gene: Isolation and Significance. Hospital Practice (1995), 1990, 25, 47-57.	0.5	32
149	A chromosome jump crosses a translocation breakpoint in the von recklinghausen neurofibromatosis region. Genes Chromosomes and Cancer, 1990, 2, 271-277.	1.5	22
150	Mutation Analysis for Heterozygote Detection and the Prenatal Diagnosis of Cystic Fibrosis. New England Journal of Medicine, 1990, 322, 291-296.	13.9	224
151	Type 1 neurofibromatosis gene: identification of a large transcript disrupted in three NF1 patients. Science, 1990, 249, 181-186.	6.0	1,433
152	Type 1 neurofibromatosis gene: correction. Science, 1990, 250, 1749-1749.	6.0	0
153	Reverse Genetics and Cystic Fibrosis. American Journal of Respiratory Cell and Molecular Biology, 1990, 2, 309-316.	1.4	10
154	Approaches to localizing disease genes as applied to cystic fibrosis. Nucleic Acids Research, 1990, 18, 345-350.	6.5	24
155	Correction of the cystic fibrosis defect in vitro by retrovirus-mediated gene transfer. Cell, 1990, 62, 1227-1233.	13.5	595
156	Response : Type 1 Neurofibromatosis Gene: Correction. Science, 1990, 250, 1749-1749.	6.0	0
157	Response : Type 1 Neurofibromatosis Gene: Correction. Science, 1990, 250, 1749-1749.	6.0	0
158	Mutations in the p53 gene occur in diverse human tumour types. Nature, 1989, 342, 705-708.	13.7	2,702
159	Identification of the cystic fibrosis gene: chromosome walking and jumping. Science, 1989, 245, 1059-1065.	6.0	3,136
160	Two patients with ring chromosome 15 syndrome. American Journal of Medical Genetics Part A, 1988, 29, 149-154.	2.4	63
161	Physical mapping of the cystic fibrosis region by pulsed-field gel electrophoresis. Genomics, 1988, 2, 346-354.	1.3	51
162	Adult Turner syndrome associated with chylous ascites and vascular anomalies. Clinical Genetics, 1987, 31, 218-223.	1.0	3

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163	Molecular Analysis of Deletion and Nondeletion Hereditary Persistence of Fetal Hemoglobin and Identification of a New Mutation Causing ?-Thalassemia. Annals of the New York Academy of Sciences, 1985, 445, 159-169.	1.8	11