A Cecile J W Janssens

List of Publications by Year
in descending order

159	13,778	41258 49	22764 112
papers	citations	h-index	g-index

168	168	168	22637
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
2	Genome-wide Analysis of Genetic Loci Associated With Alzheimer Disease. JAMA - Journal of the American Medical Association, 2010, 303, 1832.	3.8	1,064
3	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. Nature Genetics, 2009, 41, 47-55.	9.4	776
4	Simple Risk Model Predicts Incidence of Atrial Fibrillation in a Racially and Geographically Diverse Population: the CHARGEâ€AF Consortium. Journal of the American Heart Association, 2013, 2, e000102.	1.6	601
5	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
6	Interpreting Incremental Value of Markers Added to Risk Prediction Models. American Journal of Epidemiology, 2012, 176, 473-481.	1.6	397
7	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	9.4	303
8	Genome-based prediction of common diseases: advances and prospects. Human Molecular Genetics, 2008, 17, R166-R173.	1.4	287
9	Predicting Type 2 Diabetes Based on Polymorphisms From Genome-Wide Association Studies. Diabetes, 2008, 57, 3122-3128.	0.3	265
10	Improving reporting standards for polygenic scores in risk prediction studies. Nature, 2021, 591, 211-219.	13.7	265
11	A Critical Appraisal of the Scientific Basis of Commercial Genomic Profiles Used to Assess Health Risks and Personalize Health Interventions. American Journal of Human Genetics, 2008, 82, 593-599.	2.6	258
12	PredictABEL: an R package for the assessment of risk prediction models. European Journal of Epidemiology, 2011, 26, 261-264.	2.5	231
13	Eye color and the prediction of complex phenotypes from genotypes. Current Biology, 2009, 19, R192-R193.	1.8	226
14	Three Genome-wide Association Studies and a Linkage Analysis Identify HERC2 as a Human Iris Color Gene. American Journal of Human Genetics, 2008, 82, 411-423.	2.6	220
15	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
16	Predictive testing for complex diseases using multiple genes: Fact or fiction?. Genetics in Medicine, 2006, 8, 395-400.	1.1	202
17	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	1.5	181
18	Reflection on modern methods: Revisiting the area under the ROC Curve. International Journal of Epidemiology, 2020, 49, 1397-1403.	0.9	165

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19	B-type natriuretic peptide and C-reactive protein in the prediction of atrial fibrillation risk: the CHARGE-AF Consortium of community-based cohort studies. Europace, 2014, 16, 1426-1433.	0.7	144
20	Genome-based prediction of common diseases: methodological considerations for future research. Genome Medicine, 2009, 1, 20.	3.6	133
21	The impact of genotype frequencies on the clinical validity of genomic profiling for predicting common chronic diseases. Genetics in Medicine, 2007, 9, 528-535.	1.1	128
22	Predicting human height by Victorian and genomic methods. European Journal of Human Genetics, 2009, 17, 1070-1075.	1.4	108
23	Family history and the natural history of colorectal cancer: systematic review. Genetics in Medicine, 2015, 17, 702-712.	1.1	107
24	Survival in Elderly Persons with Down Syndrome. Journal of the American Geriatrics Society, 2008, 56, 2311-2316.	1.3	103
25	Prenatal exposure to the 1944â€“45 Dutch â€˜hunger winterâ€™ and addiction later in life. Addiction, 2008, 103, 433-438.	1.7	96
26	A tiered-layered-staged model for informed consent in personal genome testing. European Journal of Human Genetics, 2013, 21, 596-601.	1.4	96
27	Using family history information to promote healthy lifestyles and prevent diseases; a discussion of the evidence. BMC Public Health, 2010, 10, 248.	1.2	89
28	Personal utility in genomic testing: is there such a thing?. Journal of Medical Ethics, 2015, 41, 322-326.	1.0	89
29	Meta-analysis of genome-wide association for migraine in six population-based European cohorts. European Journal of Human Genetics, 2011, 19, 901-907.	1.4	87
30	Predicting Polygenic Obesity Using Genetic Information. Cell Metabolism, 2017, 25, 535-543.	7.2	86
31	Prediction of Age-related Macular Degeneration in the General Population. Ophthalmology, 2013, 120, 2644-2655.	2.5	84
32	Genetic testing and common disorders in a public health framework: how to assess relevance and possibilities. European Journal of Human Genetics, 2011, 19, S6-S44.	1.4	75
33	Validity of polygenic risk scores: are we measuring what we think we are?. Human Molecular Genetics, 2019, 28, R143-R150.	1.4	75
34	Plasma Î² amyloid and the risk of Alzheimer's disease in Down syndrome. Neurobiology of Aging, 2012, 33, 1988-1994.	1.5	73
35	Revisiting the Clinical Validity of Multiplex Genetic Testing in Complex Diseases. American Journal of Human Genetics, 2004, 74, 585-588.	2.6	72
36	Evaluation of risk prediction updates from commercial genome-wide scans. Genetics in Medicine, 2009, 11, 588-594.	1.1	69

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37	Impact of Communicating Familial Risk of Diabetes on Illness Perceptions and Self-Reported Behavioral Outcomes. Diabetes Care, 2009, 32, 597-599.	4.3	65
38	Replication of CD58 and CLEC16A as genome-wide significant risk genes for multiple sclerosis. Journal of Human Genetics, 2009, 54, 676-680.	1.1	65
39	Variations in predicted risks in personal genome testing for common complex diseases. Genetics in Medicine, 2014, 16, 85-91.	1.1	63
40	Improvement of Risk Prediction by Genomic Profiling: Reclassification Measures Versus the Area Under the Receiver Operating Characteristic Curve. American Journal of Epidemiology, 2010, 172, 353-361.	1.6	61
41	The apolipoprotein E gene and its age-specific effects on cognitive function. Neurobiology of Aging, 2010, 31, 1831-1833.	1.5	60
42	Personal genome testing: Test characteristics to clarify the discourse on ethical, legal and societal issues. BMC Medical Ethics, 2011, 12, 11.	1.0	59
43	Migraine is not associated with enhanced atherosclerosis. Cephalalgia, 2013, 33, 228-235.	1.8	57
44	Strengthening the Reporting of Genetic Risk Prediction Studies: The GRIPS Statement. PLoS Medicine, 2011, 8, e1000420.	3.9	57
45	Early Age at Menopause is Associated with Increased risk of Dementia and Mortality in Women with Down Syndrome. Journal of Alzheimer's Disease, 2010, 19, 545-550.	1.2	56
46	Fatigue: an important feature of late-onset Pompe disease. Journal of Neurology, 2007, 254, 941-945.	1.8	55
47	Research Conducted Using Data Obtained through Online Communities: Ethical Implications of Methodological Limitations. PLoS Medicine, 2012, 9, e1001328.	3.9	54
48	Racial/Ethnic Variation in the Association of Lipid-Related Genetic Variants With Blood Lipids in the US Adult Population. Circulation: Cardiovascular Genetics, 2011, 4, 523-533.	5.1	53
49	Cox proportional hazards models have more statistical power than logistic regression models in cross-sectional genetic association studies. European Journal of Human Genetics, 2008, 16, 1111-1116.	1.4	50
50	Perception of prognostic risk in patients with multiple sclerosis: the relationship with anxiety, depression, and disease-related distress. Journal of Clinical Epidemiology, 2004, 57, 180-186.	2.4	47
51	A New Logistic Regression Approach for the Evaluation of Diagnostic Test Results. Medical Decision Making, 2005, 25, 168-177.	1.2	45
52	How can polygenic inheritance be used in population screening for common diseases?. Genetics in Medicine, 2013, 15, 437-443.	1.1	45
53	â€˜It might happen or it might notâ€™: how patients with multiple sclerosis explain their perception of prognostic risk. Social Science and Medicine, 2004, 59, 861-868.	1.8	44
54	Value of genetic profiling for the prediction of coronary heart disease. American Heart Journal, 2009, 158, 105-110.	1.2	44

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55	Predictive genetic testing for type 2 diabetes. BMJ: British Medical Journal, 2006, 333, 509-510.	2.4	41
56	A systematic review and critical assessment of 11 discordant meta-analyses on reduced-function CYP2C19 genotype and risk of adverse clinical outcomes in clopidogrel users. Genetics in Medicine, 2015, 17, 3-11.	1.1	40
57	A collaborative translational research framework for evaluating and implementing the appropriate use of human genome sequencing to improve health. PLoS Medicine, 2018, 15, e1002631.	3.9	40
58	Polygenic Risk Scores That Predict Common Diseases Using Millions of Single Nucleotide Polymorphisms: Is More, Better?. Clinical Chemistry, 2019, 65, 609-611.	1.5	40
59	Cost-Effectiveness of Risk-Stratified Colorectal Cancer Screening Based on Polygenic Risk: Current Status and Future Potential. JNCI Cancer Spectrum, 2020, 4, pkz086.	1.4	39
60	An epidemiological perspective on the future of direct-to-consumer personal genome testing. Investigative Genetics, 2010, 1, 10.	3.3	38
61	Novel citation-based search method for scientific literature: a validation study. BMC Medical Research Methodology, 2020, 20, 25.	1.4	37
62	A Study of the SORL1 Gene in Alzheimer's Disease and Cognitive Function. Journal of Alzheimer's Disease, 2009, 18, 51-64.	1.2	36
63	Clinical Implications of Old and New Genes for Open-Angle Glaucoma. Ophthalmology, 2011, 118, 2389-2397.	2.5	34
64	Novel citation-based search method for scientific literature: application to meta-analyses. BMC Medical Research Methodology, 2015, 15, 84.	1.4	34
65	Personalizing Breast Cancer Screening Based on Polygenic Risk and Family History. Journal of the National Cancer Institute, 2021, 113, 434-442.	3.0	34
66	A critical evaluation of the algorithm behind the Relative Citation Ratio (RCR). PLoS Biology, 2017, 15, e2002536.	2.6	34
67	Use of genomic profiling to assess risk for cardiovascular disease and identify individualized prevention strategiesâ€"A targeted evidence-based review. Genetics in Medicine, 2010, 12, 772-784.	1.1	32
68	Usefulness of Genetic Polymorphisms and Conventional Risk Factors to Predict Coronary Heart Disease in Patients With Familial Hypercholesterolemia. American Journal of Cardiology, 2009, 103, 375-380.	0.7	31
69	Comparison of participant information and informed consent forms of five European studies in genetic isolated populations. European Journal of Human Genetics, 2010, 18, 296-302.	1.4	31
70	Genome-Wide Profiling of Blood Pressure in Adults and Children. Hypertension, 2012, 59, 241-247.	1.3	31
71	Genetic risk profiling for prediction of type 2 diabetes. PLOS Currents, 2011, 3, RRN1208.	1.4	31
72	Does Genetic Testing Really Improve the Prediction of Future Type 2 Diabetes?. PLoS Medicine, 2006, 3, e114.	3.9	30

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73	Strengthening the reporting of genetic risk prediction studies (GRIPS): explanation and elaboration. European Journal of Clinical Investigation, 2011, 41, 1010-1035.	1.7	30
74	Informed Consent in Directâ€toâ€Consumer Personal Genome Testing: The Outline of A Model between Specific and Generic Consent. Bioethics, 2014, 28, 343-351.	0.7	30
75	Genome-Based Prediction of Breast Cancer Risk in the General Population: A Modeling Study Based on Meta-Analyses of Genetic Associations. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 9-22.	1.1	29
76	A Methodological Perspective on Genetic Risk Prediction Studies in Type 2 Diabetes: Recommendations for Future Research. Current Diabetes Reports, 2011, 11, 511-518.	1.7	28
77	Patients with Barrett's esophagus perceive their risk of developing esophageal adenocarcinoma as low. Gastrointestinal Endoscopy, 2007, 65, 26-30.	0.5	27
78	A Genome-Wide Screen for Depression in Two Independent Dutch Populations. Biological Psychiatry, 2010, 68, 187-196.	0.7	27
79	Strengthening the reporting of genetic risk prediction studies: the GRIPS statement. European Journal of Clinical Investigation, 2011, 41, 1004-1009.	1.7	27
80	The role of disease characteristics in the ethical debate on personal genome testing. BMC Medical Genomics, 2012, 5, 4.	0.7	26
81	Cost Effectiveness of Age-Specific Screening Intervals for People With Family Histories of Colorectal Cancer. Gastroenterology, 2018, 154, 105-116.e20.	0.6	26
82	Assessment of Improved Prediction Beyond Traditional Risk Factors. Circulation: Cardiovascular Genetics, 2010, 3, 3-5.	5.1	24
83	Accuracy of self-reported family history is strongly influenced by the accuracy of self-reported personal health status of relatives. Journal of Clinical Epidemiology, 2012, 65, 82-89.	2.4	24
84	Refining genome-wide linkage intervals using a meta-analysis of genome-wide association studies identifies loci influencing personality dimensions. European Journal of Human Genetics, 2013, 21, 876-882.	1.4	24
85	Genetic architecture of circulating lipid levels. European Journal of Human Genetics, 2011, 19, 813-819.	1.4	23
86	Genetic Scoring Analysis: a way forward in Genome Wide Association Studies?. European Journal of Epidemiology, 2009, 24, 585-587.	2.5	22
87	Genetic architecture of open angle glaucoma and related determinants. Journal of Medical Genetics, 2011, 48, 190-196.	1.5	21
88	Strengthening the reporting of genetic risk prediction studies: the GRIPS statement. BMJ: British Medical Journal, 2011, 342, d631-d631.	2.4	20
89	Predictive Value of Multiple Genetic Testing for Age-Related Macular Degeneration. JAMA Ophthalmology, 2007, 125, 1270.	2.6	19
90	Shared genetic factors in the co-occurrence of symptoms of depression and cardiovascular risk factors. Journal of Affective Disorders, 2010, 122, 247-252.	2.0	19

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91	Evaluation of polygenic risk models using multiple performance measures: a critical assessment of discordant results. Genetics in Medicine, 2019, 21, 391-397.	1.1	19
92	Critical examination of current response shift methods and proposal for advancing new methods. Quality of Life Research, 2021, 30, 3325-3342.	1.5	19
93	Heritability of dietary food intake patterns. Acta Diabetologica, 2013, 50, 721-726.	1.2	18
94	An Electrocardiogram-Based Risk Equation for Incident Cardiovascular Disease From the National Health and Nutrition Examination Survey. JAMA Cardiology, 2016, 1, 779.	3.0	18
95	Perspectives on the Use of Multiple Sclerosis Risk Genes for Prediction. PLoS ONE, 2011, 6, e26493.	1.1	17
96	Role of shared genetic and environmental factors in symptoms of depression and body composition. Psychiatric Genetics, 2009, 19, 32-38.	0.6	16
97	Translational Research in Genomics of Alzheimer's Disease: A Review of Current Practice and Future Perspectives. Journal of Alzheimer's Disease, 2010, 20, 967-980.	1.2	16
98	Ethnic differences and parental beliefs are important for overweight prevention and management in children: a cross-sectional study in the Netherlands. BMC Public Health, 2012, 12, 867.	1.2	16
99	Is the time right for translation research in genomics?. European Journal of Epidemiology, 2008, 23, 707-710.	2.5	14
100	Strengthening the reporting of genetic risk prediction studies (GRIPS): explanation and elaboration. European Journal of Epidemiology, 2011, 26, 313-337.	2.5	14
101	The hidden harm behind the return of results from personal genome services: a need for rigorous and responsible evaluation. Genetics in Medicine, 2015, 17, 621-622.	1.1	14
102	No association between the angiotensin-converting enzyme gene and major depression: a caseâ€“control study and meta-analysis. Psychiatric Genetics, 2006, 16, 225-226.	0.6	13
103	Angiotensinogen M235T polymorphism and symptoms of depression in a population-based study and a family-based study. Psychiatric Genetics, 2008, 18, 162-166.	0.6	13
104	Strengthening the reporting of genetic risk prediction studies: the GRIPS statement. European Journal of Epidemiology, 2011, 26, 255-259.	2.5	13
105	Strengthening the reporting of Genetic Risk Prediction Studies: The GRIPS statement. Genetics in Medicine, 2011, 13, 453-456.	1.1	13
106	Small improvement in the area under the receiver operating characteristic curve indicated small changes in predicted risks. Journal of Clinical Epidemiology, 2016, 79, 159-164.	2.4	13
107	Towards predictive genetic testing of complex diseases. European Journal of Epidemiology, 2006, 21, 869-870.	2.5	12
108	Strengthening the reporting of genetic risk prediction studies (GRIPS): explanation and elaboration. European Journal of Human Genetics, 2011, 19, 615-615.	1.4	12

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109	Longevity candidate genes and their association with personality traits in the elderly. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 192-200.	1.1	12
110	Constructing Hypothetical Risk Data from the Area under the ROC Curve: Modelling Distributions of Polygenic Risk. PLoS ONE, 2016, 11, e0152359.	1.1	12
111	An empirical comparison of meta-analyses of published gene-disease associations versus consortium analyses. Genetics in Medicine, 2009, 11, 153-162.	1.1	11
112	HFE gene mutations increase the risk of coronary heart disease in women. European Journal of Epidemiology, 2010, 25, 643-649.	2.5	11
113	Predictive genetic testing for the identification of high-risk groups: a simulation study on the impact of predictive ability. Genome Medicine, 2011, 3, 51.	3.6	11
114	Strengthening the reporting of Genetic RIsk Prediction Studies: the GRIPS Statement. Journal of Clinical Epidemiology, 2011, 64, 843-847.	2.4	11
115	Discriminative accuracy of genomic profiling comparing multiplicative and additive risk models. European Journal of Human Genetics, 2011, 19, 180-185.	1.4	11
116	Predictive ability of direct-to-consumer pharmacogenetic testing: when is lack of evidence really lack of evidence?. Pharmacogenomics, 2013, 14, 341-344.	0.6	11
117	Estimating the predictive ability of genetic risk models in simulated data based on published results from genome-wide association studies. Frontiers in Genetics, 2014, 5, 179.	1.1	11
118	Genetic Factors Influence the Clustering of Depression among Individuals with Lower Socioeconomic Status. PLoS ONE, 2009, 4, e5069.	1.1	11
119	Apolipoprotein E gene is related to mortality only in normal weight individuals: The Rotterdam study. European Journal of Epidemiology, 2008, 23, 135-142.	2.5	10
120	Strengthening the reporting of genetic risk prediction studies: the GRIPS statement. Genome Medicine, 2011, 3, 16.	3.6	10
121	Incremental value of rare genetic variants for the prediction of multifactorial diseases. Genome Medicine, 2013, 5, 76.	3.6	10
122	Designing babies through gene editing: science or science fiction?. Genetics in Medicine, 2016, 18, 1186-1187.	1.1	10
123	Strengthening the reporting of Genetic RIsk Prediction Studies (GRIPS): explanation and elaboration. Journal of Clinical Epidemiology, 2011, 64, e1-e22.	2.4	9
124	Strengthening the reporting of genetic risk prediction studies: the GRIPS statement. European Journal of Human Genetics, 2011, 19, 833-836.	1.4	9
125	How Attitudes Research Contributes to Overoptimistic Expectations of Personal Genome Testing. American Journal of Bioethics, 2009, 9, 23-25.	0.5	8
126	Prediction impact curve is a new measure integrating intervention effects in the evaluation of risk models. Journal of Clinical Epidemiology, 2016, 69, 89-95.	2.4	8

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127	Proprietary Algorithms for Polygenic Risk: Protecting Scientific Innovation or Hiding the Lack of It?. Genes, 2019, 10, 448.	1.0	8
128	Scientific reporting is suboptimal for aspects that characterize genetic risk prediction studies: a review of published articles based on the Genetic RIsk Prediction Studies statement. Journal of Clinical Epidemiology, 2014, 67, 487-499.	2.4	7
129	External validation is only needed when prediction models are worth it (Letter commenting on: J Clin) Tj ETQq1 1 0.784314 rgBT /Ove	2.4	7
130	Value of the HLA-DRB1 shared epitope for predicting radiographic damage in rheumatoid arthritis depends on the individual patient risk profile. Journal of Rheumatology, 2006, 33, 2383-9.	1.0	7
131	Quality criteria for health checks: Development of a European consensus agreement. Preventive Medicine, 2014, 67, 238-241.	1.6	5
132	Returning pharmacogenetic secondary findings from genome sequencing: letâ€™s not put the cart before the horse. Genetics in Medicine, 2015, 17, 854-856.	1.1	5
133	How the Intended Use of Polygenic Risk Scores Guides the Design and Evaluation of Prediction Studies. Current Epidemiology Reports, 2019, 6, 184-190.	1.1	5
134	ROC curves for clinical prediction models part 2. The ROC plot: the picture that could be worth a 1000 words. Journal of Clinical Epidemiology, 2020, 126, 217-219.	2.4	5
135	Three Genome-wide Association Studies and a Linkage Analysis Identify HERC2 as a Human Iris Color Gene. American Journal of Human Genetics, 2008, 82, 801.	2.6	4
136	Carriage of Reduced-Function CYP2C19 Allele Among Patients Treated With Clopidogrel. JAMA - Journal of the American Medical Association, 2011, 305, 467.	3.8	4
137	Analytical and simulation methods for estimating the potential predictive ability of genetic profiling: a comparison of methods and results. European Journal of Human Genetics, 2012, 20, 1270-1274.	1.4	4
138	Ethnicity, educational level and attitudes contribute to parental intentions about genetic testing for child obesity. Journal of Community Genetics, 2013, 4, 243-250.	0.5	4
139	Uninformed consent in nutrigenomic research. European Journal of Human Genetics, 2017, 25, 789-790.	1.4	4
140	Five genetic variants associated with prostate cancer. New England Journal of Medicine, 2008, 358, 2739; author reply 2741.	13.9	4
141	Letter to the editor. Multiple Sclerosis Journal, 2004, 10, 716-716.	1.4	3
142	CHOLESTERYL ESTER TRANSFER PROTEIN GENE AND CORONARY HEART DISEASE MORTALITY: THE ROTTERDAM STUDY. Journal of the American Geriatrics Society, 2007, 55, 1483-1484.	1.3	2
143	Reply to Stephan etÂal.. American Journal of Human Genetics, 2008, 83, 131.	2.6	2
144	Strengthening the Reporting of Genetic Risk Prediction Studies: The GRIPS Statement. Circulation: Cardiovascular Genetics, 2011, 4, 206-209.	5.1	2

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145	Raw Data: Access to Inaccuracy. Science, 2014, 343, 968-968.	6.0	2
146	Naming and framing in genomic testing. Trends in Molecular Medicine, 2014, 20, 63-65.	3.5	2
147	Finding Wealth in Waste: Irreplicability Re-Examined. BioEssays, 2018, 40, 1800173.	1.2	2
148	Two Authors Reply. American Journal of Epidemiology, 2011, 173, 714-715.	1.6	1
149	Predictive or not predictive: understanding the mixed messages from the patient's <scp>DNA</scp> sequence. Journal of Clinical Nursing, 2015, 24, 3730-3735.	1.4	1
150	The Value of Genetic Variation in the Prediction of Obesity. , 2016, , 441-462.		1
151	Risk Analysis of Prostate Cancer in PRACTICAL Consortiumâ€"Letter. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 222-222.	1.1	1
152	Lowering the P Value Threshold. JAMA - Journal of the American Medical Association, 2018, 320, 936.	3.8	1
153	Direct-to-Consumer Genetic Testing. , 2019, , 89-101.		1
154	ROC curves for clinical prediction models part 4. Selection of the risk thresholdâ€"once chosen, always the same?. Journal of Clinical Epidemiology, 2020, 126, 224-225.	2.4	1
155	Do we measure or compute polygenic risk scores? Why language matters. Human Genetics, 2021, , 1.	1.8	1
156	It is time to get real when trying to predict educational performance. ELife, 2020, 9, .	2.8	1
157	Reply to â€œDisease risks derived from genetic variants need clinical contextâ€• Genetics in Medicine, 2010, 12, 56-57.	1.1	0
158	Response to letter Dr Gail. Journal of Clinical Epidemiology, 2017, 85, 70-71.	2.4	0
159	Defining Evidence for Precision Medicine. Epidemiology, 2019, 30, 342-344.	1.2	0