Nancy J Cox

List of Publications by Year
in descending order

112	23,627	108046	33145
papers	citations	37 h-index	104 g-index

126	126	126	44532
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Analyses of biomarker traits in diverse UK biobank participants identify associations missed by European-centric analysis strategies. Journal of Human Genetics, 2022, 67, 87-93.	1.1	27
2	TPMT and NUDT15 Variants Predict Discontinuation of Azathioprine for Myelotoxicity in Patients with Inflammatory Disease: Realâ€World Clinical Results. Clinical Pharmacology and Therapeutics, 2022, 111, 263-271.	2.3	14
3	A transcriptomeâ€wide association study identifies novel candidate susceptibility genes for prostate cancer risk. International Journal of Cancer, 2022, 150, 80-90.	2.3	9
4	Integration of DNA sequencing with population pharmacokinetics to improve the prediction of irinotecan exposure in cancer patients. British Journal of Cancer, 2022, 126, 640-651.	2.9	7
5	Polygenic transcriptome risk scores (PTRS) can improve portability of polygenic risk scores across ancestries. Genome Biology, 2022, 23, 23.	3.8	42
6	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
7	Integrating gene expression and clinical data to identify drug repurposing candidates for hyperlipidemia and hypertension. Nature Communications, 2022, 13, 46.	5.8	19
8	Brief Report: Predicted Expression of Genes Involved in the Thiopurine Metabolic Pathway and Azathioprine Discontinuation Due to Myelotoxicity. Clinical and Translational Science, 2022, , .	1.5	3
9	Leveraging electronic health records to inform genetic counseling practice surrounding psychiatric disorders. Journal of Genetic Counseling, 2022, , .	0.9	1
10	Pharmacogenomics of <scp>cisplatinâ€induced</scp> neurotoxicities: Hearing loss, tinnitus, and peripheral sensory neuropathy. Cancer Medicine, 2022, 11, 2801-2816.	1.3	14
11	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traitsâ€"The Hispanic/Latino Anthropometry Consortium. Human Genetics and Genomics Advances, 2022, 3, 100099.	1.0	3
12	Two polymorphic gene loci associated with treprostinil dose in pulmonary arterial hypertension. Pharmacogenetics and Genomics, 2022, Publish Ahead of Print, .	0.7	1
13	Sex differences in the genetic architecture of cognitive resilience to Alzheimerâ€™s disease. Brain, 2022, 145, 2541-2554.	3.7	26
14	Race, Genotype, and Azathioprine Discontinuation. Annals of Internal Medicine, 2022, 175, 1092-1099.	2.0	14
15	Improving the computation efficiency of polygenic risk score modeling: faster in Julia. Life Science Alliance, 2022, 5, e202201382.	1.3	0
16	Genetic risk for major depressive disorder and loneliness in sex-specific associations with coronary artery disease. Molecular Psychiatry, 2021, 26, 4254-4264.	4.1	26
17	A retrospective approach to evaluating potential adverse outcomes associated with delay of procedures for cardiovascular and cancer-related diagnoses in the context of COVID-19. Journal of Biomedical Informatics, 2021, 113, 103657.	2.5	20
18	Host genetic effects in pneumonia. American Journal of Human Genetics, 2021, 108, 194-201.	2.6	17

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19	Synaptic processes and immune-related pathways implicated in Tourette syndrome. Translational Psychiatry, 2021, 11, 56.	2.4	31
20	DDIWAS: High-throughput electronic health record-based screening of drug-drug interactions. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1421-1430.	2.2	10
21	Alcohol and cigarette smoking consumption as genetic proxies for alcohol misuse and nicotine dependence. Drug and Alcohol Dependence, 2021, 221, 108612.	1.6	11
22	Haploinsufficiency of PRR12 causes a spectrum of neurodevelopmental, eye, and multisystem abnormalities. Genetics in Medicine, 2021, 23, 1234-1245.	1.1	6
23	Phenotypic signatures in clinical data enable systematic identification of patients for genetic testing. Nature Medicine, 2021, 27, 1097-1104.	15.2	21
24	High-throughput framework forÂgenetic analyses of adverse drug reactions using electronic health records. PLoS Genetics, 2021, 17, e1009593.	1.5	5
25	Association Between a Common, Benign Genotype and Unnecessary Bone Marrow Biopsies Among African American Patients. JAMA Internal Medicine, 2021, 181, 1100.	2.6	18
26	Three dimensional modeling of biologically relevant fluid shear stress in human renal tubule cells mimics in vivo transcriptional profiles. Scientific Reports, 2021, 11, 14053.	1.6	22
27	Recommendations for Statistical Reporting in Cardiovascular Medicine: A Special Report From the American Heart Association. Circulation, 2021, 144, e70-e91.	1.6	36
28	Linking the genomic signatures of human beat synchronization and learned song in birds. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200329.	1.8	5
29	A transcriptome-wide association study identifies novel blood-based gene biomarker candidates for Alzheimerâ€™s disease risk. Human Molecular Genetics, 2021, 31, 289-299.	1.4	7
30	A transcriptome-wide association study of Alzheimerâ€™s disease using prediction models of relevant tissues identifies novel candidate susceptibility genes. Genome Medicine, 2021, 13, 141.	3.6	25
31	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	2.6	14
32	Discovery and implications of polygenicity of common diseases. Science, 2021, 373, 1468-1473.	6.0	80
33	Integration of genetic, transcriptomic, and clinical data provides insight into 16p11.2 and 22q11.2 CNV genes. Genome Medicine, 2021, 13, 172.	3.6	16
34	Soluble Urokinase Plasminogen Activator Receptor: Genetic Variation and Cardiovascular Disease Risk in Black Adults. Circulation Genomic and Precision Medicine, 2021, 14, CIRCGEN121003421.	1.6	7
35	VEGF-family brain protein abundance: Associations with Alzheimer's disease pathology and cognitive decline.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e052984.	0.4	0
36	Sex differences in the genetic architecture underlying resilience in AD.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e055010.	0.4	0

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37	APOE Îµ4-specific associations of VEGF gene family expression with cognitive aging and Alzheimer's disease. Neurobiology of Aging, 2020, 87, 18-25.	1.5	24
38	A brief history of human disease genetics. Nature, 2020, 577, 179-189.	13.7	441
39	PheMap: a multi-resource knowledge base for high-throughput phenotyping within electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1675-1687.	2.2	28
40	A unified framework for joint-tissue transcriptome-wide association and Mendelian randomization analysis. Nature Genetics, 2020, 52, 1239-1246.	9.4	134
41	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. Cell Reports, 2020, 31, 107716.	2.9	44
42	Genetic variants and functional pathways associated with resilience to Alzheimerâ€™s disease. Brain, 2020, 143, 2561-2575.	3.7	93
43	A Transcriptome-Wide Association Study Identifies Candidate Susceptibility Genes for Pancreatic Cancer Risk. Cancer Research, 2020, 80, 4346-4354.	0.4	28
44	Single nucleus and bulk homogenate RNAâ€sequencing comparison of vascular endothelial growth factor family associations with Alzheimer's disease. Alzheimer's and Dementia, 2020, 16, e046170.	0.4	0
45	Combining clinical and candidate gene data into a risk score for azathioprine-associated leukopenia in routine clinical practice. Pharmacogenomics Journal, 2020, 20, 736-745.	0.9	6
46	Phenome-based approach identifies RIC1-linked Mendelian syndrome through zebrafish models, biobank associations and clinical studies. Nature Medicine, 2020, 26, 98-109.	15.2	32
47	Electronic health record phenotypes associated with genetically regulated expression of CFTR and application to cystic fibrosis. Genetics in Medicine, 2020, 22, 1191-1200.	1.1	6
48	Automated Phenotyping Tool for Identifying Developmental Language Disorder Cases in Health Systems Data (APT-DLD): A New Research Algorithm for Deployment in Large-Scale Electronic Health Record Systems. Journal of Speech, Language, and Hearing Research, 2020, 63, 3019-3035.	0.7	7
49	Sex differences in the genetic predictors of Alzheimerâ€™s pathology. Brain, 2019, 142, 2581-2589.	3.7	65
50	Inferred divergent gene regulation in archaic hominins reveals potential phenotypic differences. Nature Ecology and Evolution, 2019, 3, 1598-1606.	3.4	45
51	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
52	Multi-tissue transcriptome analyses identify genetic mechanisms underlying neuropsychiatric traits. Nature Genetics, 2019, 51, 933-940.	9.4	77
53	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	9.4	154
54	Clinical and Genome-wide Analysis of Cisplatin-induced Tinnitus Implicates Novel Ototoxic Mechanisms. Clinical Cancer Research, 2019, 25, 4104-4116.	3.2	27

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55	Complex Simplicity and Hirschsprungâ€™s Disease. New England Journal of Medicine, 2019, 380, 1478-1479.	13.9	7
56	A Bayesian framework that integrates multi-omics data and gene networks predicts risk genes from schizophrenia GWAS data. Nature Neuroscience, 2019, 22, 691-699.	7.1	118
57	GRIK5 Genetically Regulated Expression Associated with Eye and Vascular Phenomes: Discovery through Iteration among Biobanks, Electronic Health Records, and Zebrafish. American Journal of Human Genetics, 2019, 104, 503-519.	2.6	21
58	Diagnostic Algorithms to Study Post-Concussion Syndrome Using Electronic Health Records: Validating a Method to Capture an Important Patient Population. Journal of Neurotrauma, 2019, 36, 2167-2177.	1.7	8
59	Estimating heritability and genetic correlations from large health datasets in the absence of genetic data. Nature Communications, 2019, 10, 5508.	5.8	17
60	De novopattern discovery enables robust assessment of functional consequences of non-coding variants. Bioinformatics, 2019, 35, 1453-1460.	1.8	15
61	2017 Presidential Address: Checking, Balancing, and Celebrating Diversity: Celebrating Some of the Women Who Paved the Way. American Journal of Human Genetics, 2018, 102, 342-349.	2.6	1
62	Critical Evaluation of Data Requires Rigorous but Broadly Based Statistical Inference. Circulation Research, 2018, 122, 1049-1051.	2.0	0
63	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849.	1.6	64
64	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. Science, 2018, 359, 1233-1239.	6.0	164
65	Shared Genetic Control of Brain Activity During Sleep and Insulin Secretion: A Laboratory-Based Family Study. Diabetes, 2018, 67, 155-164.	0.3	1
66	P1â€139: THE CONTRIBUTION OF SEXâ€SPECIFIC ASSOCIATIONS IN GENETIC STUDIES OF ALZHEIMER'S DISEASE PATHOLOGY. Alzheimer's and Dementia, 2018, 14, P327.	0.4	0
67	Relationship between very low low-density lipoprotein cholesterol concentrations not due to statin therapy and risk of type 2 diabetes: A US-based cross-sectional observational study using electronic health records. PLoS Medicine, 2018, 15, e1002642.	3.9	22
68	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. Nature Genetics, 2018, 50, 956-967.	9.4	389
69	Sex-specific genetic predictors of Alzheimerâ€™s disease biomarkers. Acta Neuropathologica, 2018, 136, 857-872.	3.9	87
70	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	5.8	748
71	Variants in WFS1 and Other Mendelian Deafness Genes Are Associated with Cisplatin-Associated Ototoxicity. Clinical Cancer Research, 2017, 23, 3325-3333.	3.2	65
72	Clinical and Genome-Wide Analysis of Cisplatin-Induced Peripheral Neuropathy in Survivors of Adult-Onset Cancer. Clinical Cancer Research, 2017, 23, 5757-5768.	3.2	63

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73	Rare Copy Number Variants in NRXN1 and CNTN6 Increase Risk for Tourette Syndrome. Neuron, 2017, 94, 1101-1111.e7.	3.8	137
74	Bedside Back to Bench: Building Bridges between Basic and Clinical Genomic Research. Cell, 2017, 169, 6-12.	13.5	103
75	Leveraging blood serotonin as an endophenotype to identify de novo and rare variants involved in autism. Molecular Autism, 2017, 8, 14.	2.6	50
76	Reaching for the next branch on the biobank tree of knowledge. Nature Genetics, 2017, 49, 1295-1296.	9.4	5
77	Evidence of selection on splicing-associated loci in human populations and relevance to disease loci mapping. Scientific Reports, 2017, 7, 5980.	1.6	10
78	Classification of common human diseases derived from shared genetic and environmental determinants. Nature Genetics, 2017, 49, 1319-1325.	9.4	181
79	Genetic resilience to amyloid related cognitive decline. Brain Imaging and Behavior, 2017, 11, 401-409.	1.1	32
80	Up For A Challenge (U4C): Stimulating innovation in breast cancer genetic epidemiology. PLoS Genetics, 2017, 13, e1006945.	1.5	3
81	Admixture mapping in two Mexican samples identifies significant associations of locus ancestry with triglyceride levels in the BUD13/ZNF259/APOA5 region and fine mapping points to rs964184 as the main driver of the association signal. PLoS ONE, 2017, 12, e0172880.	1.1	16
82	Evaluating phecodes, clinical classification software, and ICD-9-CM codes for phenome-wide association studies in the electronic health record. PLoS ONE, 2017, 12, e0175508.	1.1	268
83	Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. PLoS Genetics, 2016, 12, e1006423.	1.5	143
84	Cancer biomarker discovery is improved by accounting for variability in general levels of drug sensitivity in pre-clinical models. Genome Biology, 2016, 17, 190.	3.8	35
85	A variant at 9p21.3 functionally implicates CDKN2B in paediatric B-cell precursor acute lymphoblastic leukaemia aetiology. Nature Communications, 2016, 7, 10635.	5.8	44
86	Genome-wide association studies in women of African ancestry identified 3q26.21 as a novel susceptibility locus for oestrogen receptor negative breast cancer. Human Molecular Genetics, 2016, 25, ddw305.	1.4	50
87	Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects and tissue-specific enrichment of eQTLs. Scientific Reports, 2016, 6, 19429.	1.6	63
88	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	1.4	21
89	SCAN database: facilitating integrative analyses of cytosine modification and expression QTL. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav025-bav025.	1.4	19
90	Consensus Genotyper for Exome Sequencing (CGES): improving the quality of exome variant genotypes. Bioinformatics, 2015, 31, 187-193.	1.8	18

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91	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. Bioinformatics, 2015, 31, 1452-1459.	1.8	14
92	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
93	A gene-based association method for mapping traits using reference transcriptome data. Nature Genetics, 2015, 47, 1091-1098.	9.4	1,473
94	Loss of Heterozygosity at the CYP2D6 Locus in Breast Cancer: Implications for Germline Pharmacogenetic Studies. Journal of the National Cancer Institute, 2015, 107, .	3.0	37
95	Identification of a Variant in KDR Associated with Serum VEGFR2 and Pharmacodynamics of Pazopanib. Clinical Cancer Research, 2015, 21, 365-372.	3.2	29
96	pRRophetic: An R Package for Prediction of Clinical Chemotherapeutic Response from Tumor Gene Expression Levels. PLoS ONE, 2014, 9, e107468.	1.1	1,363
97	Obesity-associated variants within FTO form long-range functional connections with IRX3. Nature, 2014, 507, 371-375.	13.7	1,079
98	Cross-Tissue and Tissue-Specific eQTLs: Partitioning the Heritability of a Complex Trait. American Journal of Human Genetics, 2014, 95, 521-534.	2.6	82
99	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
100	Genetic Variation Is the Major Determinant of Individual Differences in Leukocyte Endothelial Adhesion. PLoS ONE, 2014, 9, e87883.	1.1	5
101	A Nondegenerate Code of Deleterious Variants in Mendelian Loci Contributes to Complex Disease Risk. Cell, 2013, 155, 70-80.	13.5	209
102	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	9.4	6,815
103	Genome-Wide Association Study Identifies Germline Polymorphisms Associated with Relapse of Childhood Acute Lymphoblastic Leukemia. Blood, 2012, 120, 878-878.	0.6	0
104	Trait-Associated SNPs Are More Likely to Be eQTLs: Annotation to Enhance Discovery from GWAS. PLoS Genetics, 2010, 6, e1000888.	1.5	1,161
105	Genetic inheritance of body mass index in African-American and African families. Genetic Epidemiology, 2000, 18, 360-376.	0.6	18
106	A second-generation screen of the human genome for susceptibility to insulin-dependent diabetes mellitus. Nature Genetics, 1998, 19, 292-296.	9.4	330
107	Diabetes, dependence, asymptotics, selection and significance. Nature Genetics, 1997, 17, 148-148.	9.4	8
108	A gene defect that causes conduction system disease and dilated cardiomyopathy maps to chromosome 1p1â€“1q1. Nature Genetics, 1994, 7, 546-551.	9.4	187

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109	Stuttering: A complex behavioral disorder for our times?. American Journal of Medical Genetics Part A, 1993, 48, 177-178.	2.4	4
110	Sequential imputation and multipoint linkage analysis. Genetic Epidemiology, 1993, 10, 483-488.	0.6	18
111	Genetic Aspects of Early Childhood Stuttering. Journal of Speech, Language, and Hearing Research, 1993, 36, 701-706.	0.7	88
112	Analysis of Genetically Regulated Gene Expression Identifies a Trauma Type Specific PTSD Gene, SNRNP35. SSRN Electronic Journal, 0, , .	0.4	0