Janet E Olson

List of Publications by Citations

130 papers	9,693 citations	40 h-index	98 g-index
143 ext. papers	11,802 ext. citations	8.8 avg, IF	4.38 L-index

#	Paper	IF	Citations
130	Genome-wide association study identifies novel breast cancer susceptibility loci. *Nature*, **2007**, 447, 1087-93	50.4	1957
129	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
128	A common coding variant in CASP8 is associated with breast cancer risk. *Nature Genetics*, **2007**, 39, 352-8	36.3	557
127	Inherited mutations in 17 breast cancer susceptibility genes among a large triple-negative breast cancer cohort unselected for family history of breast cancer. *Journal of Clinical Oncology*, **2015**, 33, 304-11	2.2	435
126	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. *Nature Genetics*, **2013**, 45, 371-84, 384e1-2	36.3	422
125	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. *Nature Genetics*, **2015**, 47, 373-80	36.3	406
124	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, **2019**, 104, 21-34	11	363
123	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nature Genetics*, **2013**, 45, 392-8, 398e1-2	36.3	327
122	Prediction of breast cancer risk based on profiling with common genetic variants. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	324
121	Heterogeneity of breast cancer associations with five susceptibility loci by clinical and pathological characteristics. *PLoS Genetics*, **2008**, 4, e1000054	6	280
120	The continuing increase in the incidence of primary central nervous system non-Hodgkin lymphoma: a surveillance, epidemiology, and end results analysis. *Cancer*, **2002**, 95, 1504-10	6.4	251
119	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
118	Preemptive genotyping for personalized medicine: design of the right drug, right dose, right time-using genomic data to individualize treatment protocol. *Mayo Clinic Proceedings*, **2014**, 89, 25-33	6.4	213
117	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
116	The Mayo Clinic Biobank: a building block for individualized medicine. *Mayo Clinic Proceedings*, **2013**, 88, 952-62	6.4	144
115	Incorporating a Genetic Risk Score Into Coronary Heart Disease Risk Estimates: Effect on Low-Density Lipoprotein Cholesterol Levels (the MI-GENES Clinical Trial). *Circulation*, **2016**, 133, 1181-8	16.7	138
114	CHEK2*1100delC heterozygosity in women with breast cancer associated with early death, breast cancer-specific death, and increased risk of a second breast cancer. *Journal of Clinical Oncology*, **2012**, 30, 4308-16	2.2	134

113	The contributions of breast density and common genetic variation to breast cancer risk. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	128
112	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
111	A Population-Based Study of Genes Previously Implicated in Breast Cancer. *New England Journal of Medicine*, **2021**, 384, 440-451	59.2	115
110	Postmenopausal cancer risk after self-reported endometriosis diagnosis in the Iowa Women's Health Study. *Cancer*, **2002**, 94, 1612-8	6.4	105
109	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. *Nature Genetics*, **2018**, 50, 968-978	36.3	101
108	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. *Nature Genetics*, **2016**, 48, 374-86	36.3	93
107	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nature Communications*, **2014**, 4, 4999	17.4	87
106	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. *Breast Cancer Research* , **2014**, 16, 3419	8.3	82
105	Fine-scale mapping of the FGFR2 breast cancer risk locus: putative functional variants differentially bind FOXA1 and E2F1. *American Journal of Human Genetics*, **2013**, 93, 1046-60	11	80
104	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. *PLoS Medicine*, **2016**, 13, e1002105	11.6	80
103	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	74
102	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375	17.4	64
101	Aspirin use and the risk of cholangiocarcinoma. *Hepatology*, **2016**, 64, 785-96	11.2	63
100	Fine-scale mapping of the 5q11.2 breast cancer locus reveals at least three independent risk variants regulating MAP3K1. *American Journal of Human Genetics*, **2015**, 96, 5-20	11	59
99	Combined genetic and splicing analysis of BRCA1 c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. *Human Molecular Genetics*, **2016**, 25, 2256-2268	5.6	55
98	Multidisciplinary model to implement pharmacogenomics at the point of care. *Genetics in Medicine*, **2017**, 19, 421-429	8.1	54
97	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
96	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. *Genetics in Medicine*, **2017**, 19, 599-603	8.1	51

95	Impact of demographics on human gut microbial diversity in a US Midwest population. *PeerJ*, **2016**, 4, e1514	3.1	51
94	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
93	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. *Human Molecular Genetics*, **2014**, 23, 6096-111	5.6	48
92	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. *Cancer Research*, **2015**, 75, 2457-67	10.1	45
91	Integrating Pharmacogenomics into Clinical Practice: Promise vs Reality. *American Journal of Medicine*, **2016**, 129, 1093-1099.e1	2.4	42
90	Identification of novel genetic markers of breast cancer survival. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	38
89	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. *BMC Medicine*, **2015**, 13, 156	11.4	37
88	MicroRNA related polymorphisms and breast cancer risk. *PLoS ONE*, **2014**, 9, e109973	3.7	37
87	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. *Human Molecular Genetics*, **2015**, 24, 2966-84	5.6	36
86	Participant-perceived understanding and perspectives on pharmacogenomics: the Mayo Clinic RIGHT protocol (Right Drug, Right Dose, Right Time). *Genetics in Medicine*, **2017**, 19, 819-825	8.1	35
85	Ethical Considerations Related to Return of Results from Genomic Medicine Projects: The eMERGE Network (Phase III) Experience. *Journal of Personalized Medicine*, **2018**, 8,	3.6	32
84	Genetic predisposition to ductal carcinoma in situ of the breast. *Breast Cancer Research*, **2016**, 18, 22	8.3	31
83	A novel housing-based socioeconomic measure predicts hospitalisation and multiple chronic conditions in a community population. *Journal of Epidemiology and Community Health*, **2016**, 70, 286-91	5.1	29
82	Evaluation of Germline Genetic Testing Criteria in a Hospital-Based Series of Women With Breast Cancer. *Journal of Clinical Oncology*, **2020**, 38, 1409-1418	2.2	28
81	Improvement in Cardiovascular Risk Prediction with Electronic Health Records. *Journal of Cardiovascular Translational Research*, **2016**, 9, 214-222	3.3	27
80	Body mass index and breast cancer survival: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2017**, 46, 1814-1822	7.8	27
79	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. *International Journal of Cancer*, **2016**, 139, 1303-1317	7.5	26
78	A Robust e-Epidemiology Tool in Phenotyping Heart Failure with Differentiation for Preserved and Reduced Ejection Fraction: the Electronic Medical Records and Genomics (eMERGE) Network. *Journal of Cardiovascular Translational Research*, **2015**, 8, 475-83	3.3	25

77	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. *Human Molecular Genetics*, **2016**, 25, 3863-3876	5.6	24
76	Individual housing-based socioeconomic status predicts risk of accidental falls among adults. *Annals of Epidemiology*, **2017**, 27, 415-420.e2	6.4	24
75	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nature Communications*, **2020**, 11, 312	17.4	20
74	The Return of Actionable Variants Empirical (RAVE) Study, a Mayo Clinic Genomic Medicine Implementation Study: Design and Initial Results. *Mayo Clinic Proceedings*, **2018**, 93, 1600-1610	6.4	20
73	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. *Scientific Reports*, **2018**, 8, 6574	4.9	19
72	SNP-SNP interaction analysis of NF-B signaling pathway on breast cancer survival. *Oncotarget*, **2015**, 6, 37979-94	3.3	19
71	Cohort Profile: The Right Drug, Right Dose, Right Time: Using Genomic Data to Individualize Treatment Protocol (RIGHT Protocol). *International Journal of Epidemiology*, **2020**, 49, 23-24k	7.8	19
70	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. *Breast Cancer Research*, **2019**, 21, 68	8.3	18
69	RAD51B in Familial Breast Cancer. *PLoS ONE*, **2016**, 11, e0153788	3.7	18
68	Fine-scale mapping of the 4q24 locus identifies two independent loci associated with breast cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 1680-91	4	17
67	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. *Breast Cancer Research and Treatment*, **2016**, 157, 117-31	4.4	17
66	The BRCA2 c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. *Human Mutation*, **2018**, 39, 729-741	4.7	16
65	Does a family history of cancer increase the risk for postmenopausal endometrial carcinoma? **1999**, 85, 2444-2449		16
64	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. *Gynecologic Oncology*, **2016**, 141, 386-401	4.9	15
63	Personalizing Aspirin Use for Targeted Breast Cancer Chemoprevention in Postmenopausal Women. *Mayo Clinic Proceedings*, **2016**, 91, 71-80	6.4	15
62	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. *Cancer Causes and Control*, **2016**, 27, 679-93	2.8	15
61	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. *Oncotarget*, **2015**, 6, 7390-407	3.3	14
60	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. *Journal of the National Cancer Institute*, **2021**, 113, 329-337	9.7	14

59	Developing a Process for Returning Medically Actionable Genomic Variants to Latino Patients in a Federally Qualified Health Center. *Public Health Genomics*, **2018**, 21, 77-84	1.9	14
58	Design of a randomized controlled trial of disclosing genomic risk of coronary heart disease: the Myocardial Infarction Genes (MI-GENES) study. *BMC Medical Genomics*, **2015**, 8, 51	3.7	13
57	Inferring multimodal latent topics from electronic health records. *Nature Communications*, **2020**, 11, 2536	17.4	13
56	Germline Rare Coding Variants and Risk of Pancreatic Cancer in Minority Populations. *Cancer Epidemiology Biomarkers and Prevention*, **2018**, 27, 1364-1370	4	13
55	A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. *Breast Cancer Research*, **2015**, 17, 110	8.3	13
54	Zoledronic acid for treatment of osteopenia and osteoporosis in women with primary breast cancer undergoing adjuvant aromatase inhibitor therapy: a 5-year follow-up. *Supportive Care in Cancer*, **2016**, 24, 1219-26	3.9	12
53	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. *Carcinogenesis*, **2015**, 36, 256-71	4.6	12
52	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. *Breast Cancer Research*, **2014**, 16, R51	8.3	12
51	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. *American Journal of Human Genetics*, **2020**, 107, 837-848	11	12
50	Risk of Breast Cancer Among Carriers of Pathogenic Variants in Breast Cancer Predisposition Genes Varies by Polygenic Risk Score. *Journal of Clinical Oncology*, **2021**, 39, 2564-2573	2.2	12
49	Characteristics and utilisation of the Mayo Clinic Biobank, a clinic-based prospective collection in the USA: cohort profile. *BMJ Open*, **2019**, 9, e032707	3	9
48	How well do whole exome sequencing results correlate with medical findings? A study of 89 Mayo Clinic Biobank samples. *Frontiers in Genetics*, **2015**, 6, 244	4.5	8
47	Variability in assigning pathogenicity to incidental findings: insights from LDLR sequence linked to the electronic health record in 1013 individuals. *European Journal of Human Genetics*, **2017**, 25, 410-415	5.3	7
46	Perception of genetic risk among genetic counselors. *Journal of Genetic Counseling*, **2000**, 9, 47-59	2.5	7
45	Risk of serious infection among individuals with and without low count monoclonal B-cell lymphocytosis (MBL). *Leukemia*, **2021**, 35, 239-244	10.7	7
44	Association between Alcohol Consumption, Folate Intake, and Risk of Pancreatic Cancer: A Case-Control Study. *Nutrients*, **2017**, 9,	6.7	6
43	Genetic Predictors of Chemotherapy-Induced Peripheral Neuropathy from Paclitaxel, Carboplatin and Oxaliplatin: NCCTG/Alliance N08C1, N08CA and N08CB Study. *Cancers*, **2021**, 13,	6.6	6
42	Association between an individual housing-based socioeconomic index and inconsistent self-reporting of health conditions: a prospective cohort study in the Mayo Clinic Biobank. *BMJ Open*, **2018**, 8, e020054	3	6

41	Assessing the stability of biobank donor preferences regarding sample use: evidence supporting the value of dynamic consent. *European Journal of Human Genetics*, **2020**, 28, 1168-1177	5.3	5
40	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. *British Journal of Cancer*, **2016**, 114, 298-304	8.7	5
39	Association of mitochondrial DNA copy number with self-rated health status. *The Application of Clinical Genetics*, **2018**, 11, 121-127	3.1	5
38	Managing the Unimaginable: Biobank Participant Views on Reconsent for Whole Genome Sequencing of Stored Biospecimens. *Biopreservation and Biobanking*, **2019**, 17, 296-302	2.1	4
37	Genetic basis of hypercholesterolemia in adults. *Npj Genomic Medicine*, **2021**, 6, 28	6.2	4
36	Real-World Experiences With Yoga on Cancer-Related Symptoms in Women With Breast Cancer. *Global Advances in Health and Medicine*, **2021**, 10, 2164956120984140	1.9	4
35	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. *Nature Communications*, **2021**, 12, 1078	17.4	4
34	Ascertainment of delirium status using natural language processing from electronic health records. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2020**,	6.4	3
33	Colorectal cancer outcomes after screening with the multi-target stool DNA assay: protocol for a large-scale, prospective cohort study (the Voyage study). *BMJ Open Gastroenterology*, **2020**, 7, e000353	3.9	3
32	An assessment of patient perspectives on pharmacogenomics educational materials. *Pharmacogenomics*, **2020**, 21, 347-358	2.6	3
31	Real-world experiences with acupuncture among breast cancer survivors: a cross-sectional survey study. *Supportive Care in Cancer*, **2020**, 28, 5833-5838	3.9	3
30	An investigation of the biological basis of an interaction of abdominal fat distribution and family history of breast cancer. A nested study of sisters in the Iowa Women's Health Study (United States). *Cancer Causes and Control*, **2000**, 11, 941-54	2.8	3
29	Association of Genetic Variants at With Chemotherapy-Related Heart Failure. *Frontiers in Cardiovascular Medicine*, **2020**, 7, 142	5.4	3
28	Two truncating variants in FANCC and breast cancer risk. *Scientific Reports*, **2019**, 9, 12524	4.9	2
27	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. *Scientific Reports*, **2020**, 10, 9688	4.9	2
26	Characteristics Associated With Recruitment and Re-contact in Mayo Clinic Biobank. *Frontiers in Public Health*, **2020**, 8, 9	6	2
25	Challenges in returning results in a genomic medicine implementation study: the Return of Actionable Variants Empirical (RAVE) study. *Npj Genomic Medicine*, **2020**, 5, 19	6.2	2
24	Longitudinal cohorts for harnessing the electronic health record for disease prediction in a US population. *BMJ Open*, **2021**, 11, e044353	3	2

23	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. *British Journal of Cancer*, **2021**, 124, 842-854	8.7	2
22	No Association Between Pharmacogenomics Variants and Hospital and Emergency Department Utilization: A Mayo Clinic Biobank Retrospective Study. *Pharmacogenomics and Personalized Medicine*, **2021**, 14, 229-237	2.1	2
21	Does a family history of cancer increase the risk for postmenopausal endometrial carcinoma? **1999**, 85, 2444		2
20	Impact of Diverse Data Sources on Computational Phenotyping. *Frontiers in Genetics*, **2020**, 11, 556	4.5	1
19	Mini-Review of Laboratory Operations in Biobanking: Building Biobanking Resources for Translational Research. *Frontiers in Public Health*, **2020**, 8, 362	6	1
18	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. *American Journal of Human Genetics*, **2021**, 108, 1190-1203	11	1
17	Genetic Variations and Health-Related Quality of Life (HRQOL): A Genome-Wide Study Approach. *Cancers*, **2021**, 13,	6.6	1
16	Impact of Pharmacogenomic Information on Values of Care and Quality of Life Associated with Codeine and Tramadol-Related Adverse Drug Events. *Mayo Clinic Proceedings Innovations, Quality & Outcomes*, **2021**, 5, 35-45	3.1	1
15	Polygenic risk score and risk of monoclonal B-cell lymphocytosis in caucasians and risk of chronic lymphocytic leukemia (CLL) in African Americans. *Leukemia*, **2021**,	10.7	1
14	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium **2014**, n/a-n/a		1
13	A hybrid model to identify fall occurrence from electronic health records.. *International Journal of Medical Informatics*, **2022**, 162, 104736	5.3	1
12	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci.. *Breast Cancer Research*, **2022**, 24, 27	8.3	1
11	Rare germline copy number variants (CNVs) and breast cancer risk.. *Communications Biology*, **2022**, 5, 65	6.7	0
10	Prevalence and Overall Survival of Low Count Monoclonal B-Cell Lymphocytosis (LC-MBL): A Screening Study of 8,297 Individuals from the Mayo Clinic Biobank. *Blood*, **2021**, 138, 2632-2632	2.2	0
9	Long-term neurotoxicity in women with breast cancer.. *Journal of Clinical Oncology*, **2019**, 37, e23089-e23089	2.8	0
8	Validation of a population coronary disease predictive system: the CASSANDRA model. *Journal of Epidemiology and Community Health*, **2014**, 68, 1009	5.1	
7	Polygenic Risk Score and Risk of Chronic Lymphocytic Leukemia, Monoclonal B-Cell Lymphocytosis (MBL), and MBL Subtypes. *Blood*, **2020**, 136, 35-36	2.2	
6	Relationship and Susceptibility to Serious Infections Among Monoclonal B-Cell Lymphocytosis (MBL), Monoclonal Gammopathy of Undetermined Significance (MGUS), and Clonal Hematopoiesis (CH) Premalignant Conditions. *Blood*, **2021**, 138, 3739-3739	2.2	

5	Association between the Risk of Low/High-Count Monoclonal B-Cell Lymphocytosis (MBL) and the Chronic Lymphocytic Leukemia (CLL) Polygenic Risk Score (PRS). *Blood*, **2018**, 132, 5538-5538	2.2
4	Acupuncture: Real-world patient-reported outcomes of treatment-related symptoms in breast cancer survivors.. *Journal of Clinical Oncology*, **2019**, 37, e23111-e23111	2.2
3	N-terminal pro-brain natriuretic peptide levels after receipt of anthracycline for breast cancer.. *Journal of Clinical Oncology*, **2020**, 38, e24103-e24103	2.2
2	Pathway to Ascertain the Role of Pharmacogenomics in Healthcare Utilization Outcomes [Response to Letter]. *Pharmacogenomics and Personalized Medicine*, **2021**, 14, 545-546	2.1
1	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women.. *Scientific Reports*, **2022**, 12, 6199	4.9