Harry Ostrer

List of Publications by Year
in descending order

83 papers	5,864 citations	136885 32 h-index	79644 73 g-index
90 all docs	90 docs citations	90 times ranked	8897 citing authors

#	Article	IF	Citations
1	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
2	Familial colorectal cancer in Ashkenazim due to a hypermutable tract in APC. Nature Genetics, 1997, 17, 79-83.	9.4	630
3	Mutations in the Connexin 26 Gene (GJB2) among Ashkenazi Jews with Nonsyndromic Recessive Deafness. New England Journal of Medicine, 1998, 339, 1500-1505.	13.9	513
4	The carrier frequency of the BRCA2 6174delT mutation among Ashkenazi Jewish individuals is approximately 1%. Nature Genetics, 1996, 14, 188-190.	9.4	375
5	Genome-wide patterns of population structure and admixture among Hispanic/Latino populations. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8954-8961.	3.3	360
6	Functional variants in the LRRK2 gene confer shared effects on risk for Crohnâ€™s disease and Parkinsonâ€™s disease. Science Translational Medicine, 2018, 10, .	5.8	273
7	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	9.4	264
8	Abraham's Children in the Genome Era: Major Jewish Diaspora Populations Comprise Distinct Genetic Clusters with Shared Middle Eastern Ancestry. American Journal of Human Genetics, 2010, 86, 850-859.	2.6	217
9	A genetic profile of contemporary Jewish populations. Nature Reviews Genetics, 2001, 2, 891-898.	7.7	166
10	Sequencing an Ashkenazi reference panel supports population-targeted personal genomics and illuminates Jewish and European origins. Nature Communications, 2014, 5, 4835.	5.8	156
11	Mutations in MAP3K1 Cause 46,XY Disorders of Sex Development and Implicate a Common Signal Transduction Pathway in Human Testis Determination. American Journal of Human Genetics, 2010, 87, 898-904.	2.6	155
12	A Genome-Wide Scan of Ashkenazi Jewish Crohn's Disease Suggests Novel Susceptibility Loci. PLoS Genetics, 2012, 8, e1002559.	1.5	144
13	Loss of Mitogen-Activated Protein Kinase Kinase Kinase 4 (MAP3K4) Reveals a Requirement for MAPK Signalling in Mouse Sex Determination. PLoS Biology, 2009, 7, e1000196.	2.6	130
14	Individual patient data meta-analysis shows a significant association between the ATM rs1801516 SNP and toxicity after radiotherapy in 5456 breast and prostate cancer patients. Radiotherapy and Oncology, 2016, 121, 431-439.	0.3	98
15	Familial Sex Reversal: A Review. Journal of Clinical Endocrinology and Metabolism, 2000, 85, 483-493.	1.8	96
16	The population genetics of the Jewish people. Human Genetics, 2013, 132, 119-127.	1.8	92
17	Disorders of Sex Development (DSDs): An Update. Journal of Clinical Endocrinology and Metabolism, 2014, 99, 1503-1509.	1.8	92
18	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88

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19	Machine Learning on a Genome-wide Association Study to Predict Late Genitourinary Toxicity After Prostate Radiation Therapy. International Journal of Radiation Oncology Biology Physics, 2018, 101, 128-135.	0.4	73
20	Mutations in MAP3K1 tilt the balance from SOX9/FGF9 to WNT/Î²-catenin signaling. Human Molecular Genetics, 2014, 23, 1073-1083.	1.4	72
21	Radiogenomics Consortium Genome-Wide Association Study Meta-Analysis of Late Toxicity After Prostate Cancer Radiotherapy. Journal of the National Cancer Institute, 2020, 112, 179-190.	3.0	71
22	Genome-wide association study identifies a region on chromosome 11q14.3 associated with late rectal bleeding following radiation therapy for prostate cancer. Radiotherapy and Oncology, 2013, 107, 372-376.	0.3	70
23	Meta-analysis of Genome Wide Association Studies Identifies Genetic Markers of Late Toxicity Following Radiotherapy for Prostate Cancer. EBioMedicine, 2016, 10, 150-163.	2.7	69
24	A 2-Stage Genome-Wide Association Study to Identify Single Nucleotide Polymorphisms Associated With Development of Erectile Dysfunction Following Radiation Therapy for Prostate Cancer. International Journal of Radiation Oncology Biology Physics, 2013, 85, e21-e28.	0.4	59
25	STROGAR â€“ STrengthening the Reporting Of Genetic Association studies in Radiogenomics. Radiotherapy and Oncology, 2014, 110, 182-188.	0.3	59
26	A 2-Stage Genome-Wide Association Study to Identify Single Nucleotide Polymorphisms Associated with Development of Urinary Symptoms After Radiotherapy for Prostate Cancer. Journal of Urology, 2013, 190, 102-108.	0.2	55
27	Minor Abnormalities of Testis Development in Mice Lacking the Gene Encoding the MAPK Signalling Component, MAP3K1. PLoS ONE, 2011, 6, e19572.	1.1	55
28	A Cellular Study of Human Testis Development. Sexual Development, 2007, 1, 286-292.	1.1	54
29	The Prediction of Radiotherapy Toxicity Using Single Nucleotide Polymorphismâ€'Based Models: A Step Toward Prevention. Seminars in Radiation Oncology, 2015, 25, 281-291.	1.0	52
30	Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes. Human Molecular Genetics, 2014, 23, 4693-4702.	1.4	49
31	Cancer Risk Assessment Using Genetic Panel Testing: Considerations for Clinical Application. Journal of Genetic Counseling, 2014, 23, 604-617.	0.9	40
32	Computational methods using genome-wide association studies to predict radiotherapy complications and to identify correlative molecular processes. Scientific Reports, 2017, 7, 43381.	1.6	35
33	MAP3K1â€related gonadal dysgenesis: Six new cases and review of the literature. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2017, 175, 253-259.	0.7	35
34	Expanded genetic screening panel for the Ashkenazi Jewish population. Genetics in Medicine, 2016, 18, 522-528.	1.1	33
35	Insurance and genetic testing: where are we now?. American Journal of Human Genetics, 1993, 52, 565-77.	2.6	32
36	Human embryo and early fetus research. Clinical Genetics, 2006, 70, 98-107.	1.0	30

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37	Familial Sex Reversal: A Review. Journal of Clinical Endocrinology and Metabolism, 2000, 85, 483-493.	1.8	28
38	Genetic variants associated with breast cancer risk for Ashkenazi Jewish women with strong family histories but no identifiable BRCA1/2 mutation. Human Genetics, 2013, 132, 523-536.	1.8	26
39	How Will Big Data Improve Clinical and Basic Research in Radiation Therapy?. International Journal of Radiation Oncology Biology Physics, 2016, 95, 895-904.	0.4	25
40	Radiation biology and oncology in the genomic era. British Journal of Radiology, 2018, 91, 20170949.	1.0	25
41	High-depth whole genome sequencing of an Ashkenazi Jewish reference panel: enhancing sensitivity, accuracy, and imputation. Human Genetics, 2018, 137, 343-355.	1.8	24
42	Mutations in MAP3K1 that cause 46,XY disorders of sex development disrupt distinct structural domains in the protein. Human Molecular Genetics, 2019, 28, 1620-1628.	1.4	21
43	Novel ultra-rare exonic variants identified in a founder population implicate cadherins in schizophrenia. Neuron, 2021, 109, 1465-1478.e4.	3.8	21
44	Consumersâ€™ Desire towards Current and Prospective Reproductive Genetic Testing. Journal of Genetic Counseling, 2009, 18, 137-146.	0.9	19
45	Mapping a gene for 46,XY gonadal dysgenesis by linkage analysis. Clinical Genetics, 2003, 63, 530-535.	1.0	17
46	The Genetics of Bene Israel from India Reveals Both Substantial Jewish and Indian Ancestry. PLoS ONE, 2016, 11, e0152056.	1.1	17
47	Severe factor XI deficiency in an Arab family associated with a novel mutation in exon 11. British Journal of Haematology, 1997, 99, 575-577.	1.2	16
48	Rapidly screening variants of uncertain significance in the MAP3K1 gene for phenotypic effects. Clinical Genetics, 2012, 81, 272-277.	1.0	13
49	Sex determination: lessons from families and embryos. Clinical Genetics, 2001, 59, 207-215.	1.0	12
50	The genetic history of Cochin Jews from India. Human Genetics, 2016, 135, 1127-1143.	1.8	12
51	Robinow syndrome with developmental brain dysplasia. , 1997, 73, 98-99.		11
52	Missense mutation in the MEN1 gene discovered through whole exome sequencing co-segregates with familial hyperparathyroidism. Genetical Research, 2013, 95, 114-120.	0.3	11
53	High-Level Inducible Expression of Visual Pigments in Transfected Cells. BioTechniques, 1996, 21, 304-311.	0.8	9
54	Alterations of Sex Differentiation in Males: From Candidate Genes to Diagnosis and Treatments. Current Pharmaceutical Design, 2004, 10, 501-511.	0.9	9

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55	Glycosylation and palmitoylation are not required for the formation of the X-linked cone opsin visual pigments. Molecular Vision, 1998, 4, 28.	1.1	9
56	Changing the game with whole exome sequencing. Clinical Genetics, 2011, 80, 101-103.	1.0	8
57	Functional variant analyses (FVAs) predict pathogenicity in the BRCA1 DNA double-strand break repair pathway. Human Molecular Genetics, 2015, 24, 3030-3037.	1.4	7
58	Differential analysis of mutations in the Jewish population and their implications for diseases. Genetical Research, 2017, 99, e3.	0.3	7
59	Ectopic Otoconin 90 expression in triple negative breast cancer cell lines is associated with metastasis functions. PLoS ONE, 2019, 14, e0211737.	1.1	7
60	Robust genomic copy number predictor of pan cancer metastasis. Genes and Cancer, 2018, 9, 66-77.	0.6	7
61	Biallelic mutations in FLNB cause a skeletal dysplasia with 46,XY gonadal dysgenesis by activating Î²â€catenin. Clinical Genetics, 2018, 93, 412-416.	1.0	6
62	Identifying genes for male sex determination in humans. The Journal of Experimental Zoology, 2001, 290, 567-573.	1.4	4
63	The origin of the p.E180 growth hormone receptor gene mutation. Growth Hormone and IGF Research, 2016, 28, 51-52.	0.5	4
64	Prediction of breast cancer risk based on flow-variant analysis of circulating peripheral blood B cells. Genetics in Medicine, 2017, 19, 1071-1077.	1.1	4
65	Pathogenic Variants in <i>MAP3K1</i> Cause 46,XY Gonadal Dysgenesis: A Review. Sexual Development, 2022, 16, 92-97.	1.1	4
66	Clustering-Based Method for Developing a Genomic Copy Number Alteration Signature for Predicting the Metastatic Potential of Prostate Cancer. Journal of Probability and Statistics, 2012, 2012, 1-19.	0.3	3
67	Rapid Next-Generation Sequencing Method for Prediction of Prostate Cancer Risks. Journal of Molecular Diagnostics, 2019, 21, 49-57.	1.2	2
68	Mutation of a conserved proline disrupts the retinal-binding pocket of the X-linked cone opsins. Molecular Vision, 1997, 3, 16.	1.1	2
69	Cancer Risk C (CR-C), a functional genomics test is a sensitive and rapid test for germline mismatch repair deficiency. Genetics in Medicine, 2022, 24, 1821-1830.	1.1	2
70	US patent rulings will fuel invention. Nature, 2013, 499, 29-29.	13.7	1
71	Genetic Predictors of Cervical Dysplasia in African American HIV-Infected Women: ACTG DACS 268. HIV Clinical Trials, 2013, 14, 292-302.	2.0	1
72	Assessing risk for Mendelian disorders in a Bronx population. Molecular Genetics & Genomic Medicine, 2017, 5, 516-523.	0.6	1

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73	Survey of Radiation Oncologists to Assess Interest and Potential Use of a Genetic Test Predicting Susceptibility for the Development of Toxicities After Prostate Cancer Radiation Therapy. Advances in Radiation Oncology, 2020, 5, 897-904.	0.6	1
74	Health care professionalsâ€™ attitudes toward cancer gene panel testing. Breast Journal, 2021, 27, 499-500.	0.4	1
75	Prediction of breast cancer risk based on flow variant analysis of circulating peripheral blood mononuclear cells. Human Genetics and Genomics Advances, 2022, 3, 100085.	1.0	1
76	Response to Zlotogora and Meiner. Genetics in Medicine, 2016, 18, 530-530.	1.1	0
77	Preconditioned Random Forest Regression. , 2017, , .		0
78	Diaspora, migration, and the sciences: a new integrated perspective. European Journal of Human Genetics, 2019, 27, 509-510.	1.4	0
79	Evaluation of the melanocortin-1-receptor gene in melanoma predisposition, progression, and recurrence. Journal of Clinical Oncology, 2009, 27, 9018-9018.	0.8	0
80	Developing genetic markers for melanoma risk assessment. Journal of Clinical Oncology, 2009, 27, 9046-9046.	0.8	0
81	The unique molecular signatures of nodular and superficial spreading melanoma. Journal of Clinical Oncology, 2009, 27, 9047-9047.	0.8	0
82	SU-D-204-06: Integration of Machine Learning and Bioinformatics Methods to Analyze Genome-Wide Association Study Data for Rectal Bleeding and Erectile Dysfunction Following Radiotherapy in Prostate Cancer. Medical Physics, 2016, 43, 3333-3333.	1.6	0
83	Abstract OT2-24-03: Phase II study of a PARP inhibitor in metastatic breast cancer with somaticBRCA1/2mutations identified by cell-free DNA: Genotyping based clinical trial. Cancer Research, 2022, 82, OT2-24-03-OT2-24-03.	0.4	0