Steven N Hart

List of Publications by Year in descending order

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139	9,106	66343	45317
papers	citations	42 h-index	90 g-index

148	148	148	14507
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mapping molecular subtype specific alterations in breast cancer brain metastases identifies clinically relevant vulnerabilities. Nature Communications, 2022, 13, 514.	12.8	38
2	Breast Cancer Screening Strategies for Women With ATM, CHEK2, and PALB2 Pathogenic Variants. JAMA Oncology, 2022, 8, 587.	7.1	36
3	An integrative model for the comprehensive classification of BRCA1 and BRCA2 variants of uncertain clinical significance. Npj Genomic Medicine, 2022, 7, .	3.8	4
4	Classification of BRCA2 Variants of Uncertain Significance (VUS) Using an ACMG/AMP Model Incorporating a Homology-Directed Repair (HDR) Functional Assay. Clinical Cancer Research, 2022, 28, 3742-3751.	7.0	7
5	Genetic Risk of Second Primary Cancer in Breast Cancer Survivors: The Multiethnic Cohort Study. Cancer Research, 2022, 82, 3201-3208.	0.9	2
6	Wholeâ€exome sequencing of nonâ€•BRCA1/BRCA2 mutation carrier cases at highâ€risk for hereditary breast/ovarian cancer. Human Mutation, 2021, 42, 290-299.	2.5	32
7	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.	6.4	5
8	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	12.8	19
9	A Population-Based Study of Genes Previously Implicated in Breast Cancer. New England Journal of Medicine, 2021, 384, 440-451.	27.0	414
10	Abstract PD13-01: Homologous recombination deficiency represents a new therapeutic strategy for breast cancer brain metastases. , 2021, , .		0
11	Strong functional data for pathogenicity or neutrality classify BRCA2 DNA-binding-domain variants of uncertain significance. American Journal of Human Genetics, 2021, 108, 458-468.	6.2	31
12	Mutations in BRCA1/2 and Other Panel Genes in Patients With Metastatic Breast Cancer â€"Association With Patient and Disease Characteristics and Effect on Prognosis. Journal of Clinical Oncology, 2021, 39, 1619-1630.	1.6	39
13	Risk of Late-Onset Breast Cancer in Genetically Predisposed Women. Journal of Clinical Oncology, 2021, 39, 3430-3440.	1.6	21
14	Comparison of the Prevalence of Pathogenic Variants in Cancer Susceptibility Genes in Black Women and Non-Hispanic White Women With Breast Cancer in the United States. JAMA Oncology, 2021, 7, 1045.	7.1	21
15	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	5.0	7
16	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.	1.6	47
17	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
18	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	2.5	19

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19	Racial and Ethnic Differences in Multigene Hereditary Cancer Panel Test Results for Women With Breast Cancer. Journal of the National Cancer Institute, 2021, 113, 1429-1433.	6.3	18
20	Germline Pathogenic Variants in Cancer Predisposition Genes Among Women With Invasive Lobular Carcinoma of the Breast. Journal of Clinical Oncology, 2021, 39, 3918-3926.	1.6	22
21	Design considerations for workflow management systems use in production genomics research and the clinic. Scientific Reports, 2021, 11, 21680.	3.3	7
22	A clinical guide to hereditary cancer panel testing: evaluation of gene-specific cancer associations and sensitivity of genetic testing criteria in a cohort of 165,000 high-risk patients. Genetics in Medicine, 2020, 22, 407-415.	2.4	136
23	Classification of variants of uncertain significance in BRCA1 and BRCA2 using personal and family history of cancer from individuals in a large hereditary cancer multigene panel testing cohort. Genetics in Medicine, 2020, 22, 701-708.	2.4	28
24	Effect of Germline Mutations in Homologous Recombination Repair Genes on Overall Survival of Patients with Pancreatic Adenocarcinoma. Clinical Cancer Research, 2020, 26, 6505-6512.	7.0	24
25	Mutation Rates in Cancer Susceptibility Genes in Patients With Breast Cancer With Multiple Primary Cancers. JCO Precision Oncology, 2020, 4, 916-925.	3.0	9
26	Contribution of Germline Predisposition Gene Mutations to Breast Cancer Risk in African American Women. Journal of the National Cancer Institute, 2020, 112, 1213-1221.	6.3	51
27	Prediction of the functional impact of missense variants in BRCA1 and BRCA2 with BRCA-ML. Npj Breast Cancer, 2020, 6, 13.	5.2	21
28	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2
29	Evaluation of Germline Genetic Testing Criteria in a Hospital-Based Series of Women With Breast Cancer. Journal of Clinical Oncology, 2020, 38, 1409-1418.	1.6	64
30	The Contribution of Germline Predisposition Gene Mutations to Clinical Subtypes of Invasive Breast Cancer From a Clinical Genetic Testing Cohort. Journal of the National Cancer Institute, 2020, 112, 1231-1241.	6.3	61
31	Pathogenic Variants in Cancer Predisposition Genes and Prostate Cancer Risk in Men of African Ancestry. JCO Precision Oncology, 2020, 4, 32-43.	3.0	30
32	Mutation prevalence tables for hereditary cancer derived from multigene panel testing. Human Mutation, 2020, 41, e1-e6.	2.5	19
33	Abstract PD3-02: Polygenic risk scores provide clinically meaningful risk stratification among women carrying moderate penetrance pathogenic variants in breast cancer predisposition genes: Results from the CARRIERS study. , 2020, , .		0
34	Abstract PD3-01: Population-based breast cancer risk estimates for predisposition gene mutations: Results from the CARRIERS study. , 2020, , .		0
35	Abstract P6-08-01: Comparison of recommendations for germline genetic testing in an unselected cohort of patients with breast cancer. , 2020, , .		0
36	Image-to-image translation for automatic ink removal in whole slide images. Journal of Medical Imaging, 2020, 7, 057502.	1.5	5

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37	Comprehensive annotation of BRCA1 and BRCA2 missense variants by functionally validated sequence-based computational prediction models. Genetics in Medicine, 2019, 21, 71-80.	2.4	52
38	Risk of Different Cancers Among First-degree Relatives of Pancreatic Cancer Patients: Influence of Probandsâ€™ Susceptibility Gene Mutation Status. Journal of the National Cancer Institute, 2019, 111, 264-271.	6.3	10
39	Robust hierarchical density estimation and regression for re-stained histological whole slide image co-registration. PLoS ONE, 2019, 14, e0220074.	2.5	18
40	Sentieon DNASeq Variant Calling Workflow Demonstrates Strong Computational Performance and Accuracy. Frontiers in Genetics, 2019, 10, 736.	2.3	131
41	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
42	Recommendations for performance optimizations when using GATK3.8 and GATK4. BMC Bioinformatics, 2019, 20, 557.	2.6	25
43	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
44	Cancer susceptibility gene mutations in type I and II endometrial cancer. Gynecologic Oncology, 2019, 152, 20-25.	1.4	32
45	Germline BRCA1and BRCA2 mutations in patients with HER2-negative metastatic breast cancer (mBC) treated with first-line chemotherapy: Data from the German PRAEGNANT registry.. Journal of Clinical Oncology, 2019, 37, 1048-1048.	1.6	3
46	Racial and ethnic differences in the results of multigene panel testing of inherited cancer predisposition genes in breast cancer patients.. Journal of Clinical Oncology, 2019, 37, 1514-1514.	1.6	4
47	Contribution of Inherited DNA-Repair Gene Mutations to Hormone-Sensitive and Castrate-Resistant Metastatic Prostate Cancer and Implications for Clinical Outcome. JCO Precision Oncology, 2019, 3, 1-12.	3.0	13
48	Classification of Melanocytic Lesions in Selected and Whole-Slide Images via Convolutional Neural Networks. Journal of Pathology Informatics, 2019, 10, 5.	1.7	45
49	Genetic predisposition to breast cancer among African American women.. Journal of Clinical Oncology, 2019, 37, 104-104.	1.6	0
50	Abstract 4169: Population-based breast cancer risk estimates associated with cancer predisposition gene mutations from 32,298 breast cancer patients and 31,869 matched unaffected controls from the CARRIERS study. , 2019, , .		0
51	Abstract 4177: The joint effects of polygenic risk scores and pathogenic variants in cancer predisposition genes on breast cancer risk in the general population: results from the CARRIERS study. , 2019, , .		0
52	BRCA1/2 Mutations and Bevacizumab in the Neoadjuvant Treatment of Breast Cancer: Response and Prognosis Results in Patients With Triple-Negative Breast Cancer From the GeparQuinto Study. Journal of Clinical Oncology, 2018, 36, 2281-2287.	1.6	86
53	Multigene Hereditary Cancer Panels Reveal High-Risk Pancreatic Cancer Susceptibility Genes. JCO Precision Oncology, 2018, 2, 1-28.	3.0	23
54	Triple-Negative Breast Cancer Risk Genes Identified by Multigene Hereditary Cancer Panel Testing. Journal of the National Cancer Institute, 2018, 110, 855-862.	6.3	225

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55	Association Between Inherited Germline Mutations in Cancer Predisposition Genes and Risk of Pancreatic Cancer. JAMA - Journal of the American Medical Association, 2018, 319, 2401.	7.4	375
56	Will digital pathology be as disruptive as genomics?. Journal of Pathology Informatics, 2018, 9, 27.	1.7	3
57	Prognostic impact of DNA repair germline variants in hormone sensitive prostate cancer stage.. Journal of Clinical Oncology, 2018, 36, 262-262.	1.6	0
58	Germline BRCA1/2, PALB2, and ATM mutations in 3,030 patients with pancreatic adenocarcinoma: Survival analysis of carriers and noncarriers.. Journal of Clinical Oncology, 2018, 36, 280-280.	1.6	0
59	Inherited mutations in breast cancer patients with and without multiple primary cancers.. Journal of Clinical Oncology, 2018, 36, 1503-1503.	1.6	0
60	Expanding BRCA1/2 testing criteria to include other confirmed breast and ovarian cancer susceptibility genes.. Journal of Clinical Oncology, 2018, 36, 1524-1524.	1.6	0
61	Associations Between Cancer Predisposition Testing Panel Genes and Breast Cancer. JAMA Oncology, 2017, 3, 1190.	7.1	472
62	The contribution of pathogenic variants in breast cancer susceptibility genes to familial breast cancer risk. Npj Breast Cancer, 2017, 3, 22.	5.2	108
63	HARNESSING BIG DATA FOR PRECISION MEDICINE: INFRASTRUCTURES AND APPLICATIONS. , 2017, 22, 635-639.		1
64	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
65	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
66	Tumor Sequencing and Patient-Derived Xenografts in the Neoadjuvant Treatment of Breast Cancer. Journal of the National Cancer Institute, 2017, 109, .	6.3	61
67	Frequency of mutations in a large series of clinically ascertained ovarian cancer cases tested on multi-gene panels compared to reference controls. Gynecologic Oncology, 2017, 147, 375-380.	1.4	105
68	Predicting Triple-Negative Breast Cancer Subtype Using Multiple Single Nucleotide Polymorphisms for Breast Cancer Risk and Several Variable Selection Methods. Geburtshilfe Und Frauenheilkunde, 2017, 77, 667-678.	1.8	21
69	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. Breast Cancer Research and Treatment, 2017, 161, 117-134.	2.5	18
70	Empowering Mayo Clinic Individualized Medicine with Genomic Data Warehousing. Journal of Personalized Medicine, 2017, 7, 7.	2.5	12
71	Abstract 1287: Multigene panel testing and risk estimates in 10,233 ovarian cancer cases. , 2017, , .		0
72	Abstract 4265: Risks of familial breast cancer associated with known and proposed breast cancer susceptibility genes. , 2017, , .		0

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73	Patient survival and tumor characteristics associated with CHEK2:p.I157T â€“ findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	5.0	39
74	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	5.0	31
75	Determining the frequency of pathogenic germline variants from exome sequencing in patients with castrate-resistant prostate cancer. BMJ Open, 2016, 6, e010332.	1.9	32
76	Evaluation of ACMG-Guideline-Based Variant Classification of Cancer Susceptibility and Non-Cancer-Associated Genes in Families Affected by Breast Cancer. American Journal of Human Genetics, 2016, 98, 801-817.	6.2	113
77	A Recurrent ERCC3 Truncating Mutation Confers Moderate Risk for Breast Cancer. Cancer Discovery, 2016, 6, 1267-1275.	9.4	41
78	rs2735383, located at a microRNA binding site in the 3â€™UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	3.3	2
79	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
80	Novel patient-derived xenograft mouse model for pancreatic acinar cell carcinoma demonstrates single agent activity of oxaliplatin. Journal of Translational Medicine, 2016, 14, 129.	4.4	13
81	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
82	Integrated Genomic Analysis of Pancreatic Ductal Adenocarcinomas Reveals Genomic Rearrangement Events as Significant Drivers of Disease. Cancer Research, 2016, 76, 749-761.	0.9	27
83	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
84	Collaborative science in the next-generation sequencing era: a viewpoint on how to combine exome sequencing data across sites to identify novel disease susceptibility genes. Briefings in Bioinformatics, 2016, 17, 672-677.	6.5	6
85	Prevalence of Pathogenic Mutations in Cancer Predisposition Genes among Pancreatic Cancer Patients. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 207-211.	2.5	116
86	VCF-Miner: GUI-based application for mining variants and annotations stored in VCF files. Briefings in Bioinformatics, 2016, 17, 346-351.	6.5	54
87	Cancer susceptibility mutations in individuals with breast and ovarian cancer using next-generation sequencing.. Journal of Clinical Oncology, 2016, 34, 1515-1515.	1.6	2
88	Risks of triple negative breast cancer associated with cancer predisposition gene mutations.. Journal of Clinical Oncology, 2016, 34, 1513-1513.	1.6	0
89	Abstract 796: ERCC3 R109X is a moderate risk breast cancer risk variant in Ashkenazi Jews. , 2016, , .		0
90	Abstract 5220: Evaluation of ACMG guideline classified variants in 180 cancer and incidental non-cancer genes in families with breast/ovarian cancer. , 2016, , .		0

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91	Abstract 810: The CARRIERS consortium: Establishing refined breast cancer risk estimates in known predisposition genes. , 2016, , .		0
92	Abstract 2597: Breast and ovarian cancer risks associated with cancer predisposition gene mutations identified by multigene panel testing. , 2016, , .		1
93	Mutational Landscapes of Sequential Prostate Metastases and Matched Patient Derived Xenografts during Enzalutamide Therapy. PLoS ONE, 2015, 10, e0145176.	2.5	26
94	Transcriptomic and Immunohistochemical Profiling of SLC6A14 in Pancreatic Ductal Adenocarcinoma. BioMed Research International, 2015, 2015, 1-10.	1.9	22
95	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, 304-311.	1.6	521
96	TP53mutations, tetraploidy and homologous recombination repair defects in early stage high-grade serous ovarian cancer. Nucleic Acids Research, 2015, 43, 6945-6958.	14.5	46
97	Exome sequencing reveals frequent deleterious germline variants in cancer susceptibility genes in women with invasive breast cancer undergoing neoadjuvant chemotherapy. Breast Cancer Research and Treatment, 2015, 153, 435-443.	2.5	26
98	Bioinformatics for Clinical Next Generation Sequencing. Clinical Chemistry, 2015, 61, 124-135.	3.2	114
99	PANDA: pathway and annotation explorer for visualizing and interpreting gene-centric data. PeerJ, 2015, 3, e970.	2.0	3
100	Abstract P4-12-03: Triple-negative breast cancer: Frequency of inherited mutations in breast cancer susceptibility genes. , 2015, , .		0
101	Abstract PD3-3: Impact of neoadjuvant chemotherapy on the clonal composition of breast cancer. , 2015, , .		0
102	Activation of TAK1 by MYD88 L265P drives malignant B-cell Growth in non-Hodgkin lymphoma. Blood Cancer Journal, 2014, 4, e183-e183.	6.2	67
103	Pregnancy-associated plasma protein-A expression in human breast cancer. Growth Hormone and IGF Research, 2014, 24, 264-267.	1.1	31
104	The Biological Reference Repository (BioR): a rapid and flexible system for genomics annotation. Bioinformatics, 2014, 30, 1920-1922.	4.1	67
105	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2014, 16, 3416.	5.0	57
106	Somatic expression of ENRAGE is associated with obesity status among patients with clear cell renal cell carcinoma. Carcinogenesis, 2014, 35, 822-827.	2.8	18
107	Exome sequencing identifies FANCM as a susceptibility gene for triple-negative breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15172-15177.	7.1	162
108	PatternCNV: a versatile tool for detecting copy number changes from exome sequencing data. Bioinformatics, 2014, 30, 2678-2680.	4.1	43

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109	Fibroblast growth factor receptor 2 translocations in intrahepatic cholangiocarcinoma. Human Pathology, 2014, 45, 1630-1638.	2.0	235
110	From Days to Hours: Reporting Clinically Actionable Variants from Whole Genome Sequencing. PLoS ONE, 2014, 9, e86803.	2.5	4
111	Abstract 1291: High and moderate penetrance germline mutations in a number of genes are responsible for a small proportion of familial breast cancer risk in BRCAx families. , 2014, , .		0
112	Abstract 4185: Analysis of sequencing data to identify potential drug targets for an individual newly diagnosed with basal breast cancer who failed to respond to current standard neoadjuvant chemotherapy. , 2014, , .		0
113	Abstract 2378: Harmonization of next generation sequencing data within consortia for gene discovery in familial breast cancer. , 2014, , .		0
114	Abstract 3282: Determination of cancer susceptibility in probands with breast and ovarian cancer. , 2014, , .		0
115	Abstract 5592: Molecular classification of triple negative breast cancer via RNA-sequencing data. , 2014, , .		0
116	Hepatocyte Nuclear Factor 4 Alpha and Farnesoid X Receptor Co-regulates Gene Transcription in Mouse Livers on a Genome-Wide Scale. Pharmaceutical Research, 2013, 30, 2188-2198.	3.5	27
117	Genetic Alterations Associated With Progression From Pancreatic Intraepithelial Neoplasia to Invasive Pancreatic Tumor. Gastroenterology, 2013, 145, 1098-1109.e1.	1.3	166
118	APOBEC3B Upregulation and Genomic Mutation Patterns in Serous Ovarian Carcinoma. Cancer Research, 2013, 73, 7222-7231.	0.9	153
119	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	3.5	244
120	Calculating Sample Size Estimates for RNA Sequencing Data. Journal of Computational Biology, 2013, 20, 970-978.	1.6	238
121	SoftSearch: Integration of Multiple Sequence Features to Identify Breakpoints of Structural Variations. PLoS ONE, 2013, 8, e83356.	2.5	37
122	Abstract B42: Overexpression of ENRAGE is an obesity-related alteration in clear cell renal cell carcinoma. , 2013, , .		0
123	Activation Of TAK1 By MYD88 L265P Drives Malignant B Cell Growth In Non-Hodgkin Lymphomas. Blood, 2013, 122, 245-245.	1.4	1
124	The Role of CYP3A4 mRNA Transcript with Shortened 3â€²-Untranslated Region in Hepatocyte Differentiation, Liver Development, and Response to Drug Induction. Molecular Pharmacology, 2012, 81, 86-96.	2.3	10
125	Deep Sequence Analysis of Non-Small Cell Lung Cancer: Integrated Analysis of Gene Expression, Alternative Splicing, and Single Nucleotide Variations in Lung Adenocarcinomas with and without Oncogenic KRAS Mutations. Frontiers in Oncology, 2012, 2, 12.	2.8	46
126	A high-throughput-sequence analysis infrastructure technology investigation framework for the evaluation of next-generation sequencing software. Genome Biology, 2011, 12, .	9.6	0

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127	Farnesoid X Receptor and Hepatocyte Nuclear Factor 4 alpha Interact to Regulate Gene Transcription in the Liver. FASEB Journal, 2011, 25, 1018.7.	0.5	0
128	Genome-wide tissue-specific farnesoid X receptor binding in mouse liver and intestine. Hepatology, 2010, 51, 1410-1419.	7.3	173
129	Farnesoid X Receptor Activation Mediates Head-to-Tail Chromatin Looping in theNr0b2Gene Encoding Small Heterodimer Partner. Molecular Endocrinology, 2010, 24, 1404-1412.	3.7	38
130	A Comparison of Whole Genome Gene Expression Profiles of HepaRG Cells and HepG2 Cells to Primary Human Hepatocytes and Human Liver Tissues. Drug Metabolism and Disposition, 2010, 38, 988-994.	3.3	222
131	Three Patterns of Cytochrome P450 Gene Expression during Liver Maturation in Mice. Drug Metabolism and Disposition, 2009, 37, 116-121.	3.3	91
132	Dynamic Patterns of Histone Methylation Are Associated with Ontogenic Expression of the Cyp3a Genes during Mouse Liver Maturation. Molecular Pharmacology, 2009, 75, 1171-1179.	2.3	67
133	Dynamic DNA and histone methylation influences the ontogeny of xenobiotic metabolizing genes during postnatal mouse liver maturation. FASEB Journal, 2009, 23, 752.4.	0.5	0
134	Microarray analysis of the in vivo sequence preferences of a minor groove binding drug. BMC Genomics, 2008, 9, 32.	2.8	4
135	P450 oxidoreductase: genetic polymorphisms and implications for drug metabolism and toxicity. Expert Opinion on Drug Metabolism and Toxicology, 2008, 4, 439-452.	3.3	51
136	Genetic polymorphisms in cytochrome P450 oxidoreductase influence microsomal P450-catalyzed drug metabolism. Pharmacogenetics and Genomics, 2008, 18, 11-24.	1.5	84
137	Assessment of Allelic Variation Among Massasauga Rattlesnake Populations via Microsatellite Analysis. Transactions of the Missouri Academy of Science, 2008, 42, 30-38.	0.2	1
138	Genetic polymorphisms in the RNA polymerase II core promoter and enhancer elements of the UGT1A1 promoter influence activation of its gene transcription. FASEB Journal, 2008, 22, 921.16.	0.5	0
139	Novel SNPs in Cytochrome P450 Oxidoreductase. Drug Metabolism and Pharmacokinetics, 2007, 22, 322-326.	2.2	15