

Peter K Rogan

List of Publications by Year in descending order

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166
papers

5,257
citations

109321

35
h-index

106344

65
g-index

203
all docs

203
docs citations

203
times ranked

6372
citing authors

#	ARTICLE	IF	CITATIONS
1	Hepatic CYP2B6 Expression: Gender and Ethnic Differences and Relationship to CYP2B6 Genotype and CAR (Constitutive Androstane Receptor) Expression. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2003, 307, 906-922.	2.5	367
2	ENIGMA-Evidence-based network for the interpretation of germline mutant alleles: An international initiative to evaluate risk and clinical significance associated with sequence variation in BRCA1 and BRCA2 genes. <i>Human Mutation</i> , 2012, 33, 2-7.	2.5	269
3	Imprinting-Mutation Mechanisms in Prader-Willi Syndrome. <i>American Journal of Human Genetics</i> , 1999, 64, 397-413.	6.2	262
4	The Frequency of Uniparental Disomy in Prader-Willi Syndrome. <i>New England Journal of Medicine</i> , 1992, 326, 1599-1607.	27.0	257
5	Chromosome Breakage in the Prader-Willi and Angelman Syndromes Involves Recombination between Large, Transcribed Repeats at Proximal and Distal Breakpoints. <i>American Journal of Human Genetics</i> , 1999, 65, 370-386.	6.2	254
6	Predicting responses to platin chemotherapy agents with biochemically-inspired machine learning. <i>Signal Transduction and Targeted Therapy</i> , 2019, 4, 1.	17.1	202
7	Information analysis of human splice site mutations. <i>Human Mutation</i> , 1998, 12, 153-171.	2.5	187
8	Minimal definition of the imprinting center and fixation of chromosome 15q11-q13 epigenotype by imprinting mutations.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 7811-7815.	7.1	168
9	Automated splicing mutation analysis by information theory. <i>Human Mutation</i> , 2005, 25, 334-342.	2.5	146
10	Nondisjunction of human acrocentric chromosomes: studies of 432 trisomic fetuses and liveborns. <i>Human Genetics</i> , 1994, 94, 411-7.	3.8	104
11	Mutations that alter RNA splicing of the human HPRT gene: a review of the spectrum. <i>Mutation Research - Reviews in Mutation Research</i> , 1998, 411, 179-214.	5.5	102
12	Genomic signatures for paclitaxel and gemcitabine resistance in breast cancer derived by machine learning. <i>Molecular Oncology</i> , 2016, 10, 85-100.	4.6	99
13	<i>FANCM</i> c.5791C>T nonsense mutation (rs144567652) induces exon skipping, affects DNA repair activity and is a familial breast cancer risk factor. <i>Human Molecular Genetics</i> , 2015, 24, 5345-5355.	2.9	91
14	Interpretation of mRNA splicing mutations in genetic disease: review of the literature and guidelines for information-theoretical analysis. <i>F1000Research</i> , 2014, 3, 282.	1.6	85
15	Clinical spectrum and molecular diagnosis of Angelman and Prader-Willi syndrome patients with an imprinting mutation. , 1997, 68, 195-206.		84
16	Human SP-A locus: allele frequencies and linkage disequilibrium between the two surfactant protein A genes.. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 1996, 15, 489-498.	2.9	70
17	Relationship of sleep abnormalities to patient genotypes in Prader-Willi syndrome. , 1996, 67, 478-482.		69
18	Identification and characterization of novel sequence variations in the cytochrome P4502D6 (CYP2D6) gene in African Americans. <i>Pharmacogenomics Journal</i> , 2005, 5, 173-182.	2.0	67

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19	Daytime Sleepiness and REM Abnormalities in Prader-Willi Syndrome: Evidence of Generalized Hypoarousal. <i>International Journal of Neuroscience</i> , 1996, 87, 127-139.	1.6	66
20	Information theory-based analysis of CYP2C19, CYP2D6 and CYP3A5 splicing mutations. <i>Pharmacogenetics and Genomics</i> , 2003, 13, 207-218.	5.7	66
21	Full length article. <i>Gene</i> , 1998, 215, 111-122.	2.2	62
22	Study of nucleic acids isolated from ancient remains. <i>American Journal of Physical Anthropology</i> , 1990, 33, 195-214.	2.1	57
23	Exon Skipping in IVD RNA Processing in Isovaleric Acidemia Caused by Point Mutations in the Coding Region of the IVD Gene. <i>American Journal of Human Genetics</i> , 2000, 66, 356-367.	6.2	57
24	Using information content and base frequencies to distinguish mutations from genetic polymorphisms in splice junction recognition sites. <i>Human Mutation</i> , 1995, 6, 74-76.	2.5	55
25	Absence of linkage of apparently single gene mediated ADHD with the human syntenic region of the mouse mutant <i>Coloboma</i> . <i>American Journal of Medical Genetics Part A</i> , 1995, 60, 573-579.	2.4	51
26	Loss of Heterozygosity and Microsatellite Instability at the Retinoblastoma Locus in Osteosarcomas. <i>Diagnostic Molecular Pathology</i> , 1996, 5, 214-219.	2.1	50
27	Hydration in purple membrane as a function of relative humidity. <i>Journal of Molecular Biology</i> , 1981, 145, 281-284.	4.2	47
28	A new missense mutation, Arg719Gln, in the β -cardiac heavy chain myosin gene of patients with familial hypertrophic cardiomyopathy. <i>Human Molecular Genetics</i> , 1994, 3, 1025-1026.	2.9	47
29	Bloom syndrome and maternal uniparental disomy for chromosome 15. <i>American Journal of Human Genetics</i> , 1994, 55, 74-80.	6.2	47
30	Clinical and molecular analyses of deletion 3p25-pter syndrome. <i>American Journal of Medical Genetics Part A</i> , 1993, 46, 623-629.	2.4	46
31	Microsatellite "Centromere Mapping in the Zebrafish (<i>Danio rerio</i>). <i>Genomics</i> , 1995, 30, 337-341.	2.9	46
32	Association of a mosaic chromosomal 22q 11 deletion with hypoplastic left heart syndrome. <i>American Journal of Cardiology</i> , 1996, 77, 1023-1025.	1.6	46
33	Prediction of Mutant mRNA Splice Isoforms by Information Theory-Based Exon Definition. <i>Human Mutation</i> , 2013, 34, n/a-n/a.	2.5	46
34	Distinct 15q genotypes in Russell-Silver and ring 15 syndromes. <i>American Journal of Medical Genetics Part A</i> , 1996, 62, 10-15.	2.4	45
35	Splicing mutation analysis reveals previously unrecognized pathways in lymph node-invasive breast cancer. <i>Scientific Reports</i> , 2014, 4, 7063.	3.3	41
36	Racial Differences in Allelic Distribution at the Human Pulmonary Surfactant Protein B Gene Locus (SP-B). <i>Experimental Lung Research</i> , 1996, 22, 489-494.	1.2	39

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37	Prioritizing Variants in Complete Hereditary Breast and Ovarian Cancer Genes in Patients Lacking Known BRCA Mutations. <i>Human Mutation</i> , 2016, 37, 640-652.	2.5	39
38	Development and Refinement of Pregnane X Receptor (PXR) DNA Binding Site Model Using Information Theory. <i>Journal of Biological Chemistry</i> , 2004, 279, 46779-46786.	3.4	38
39	Sequence-Based Design of Single-Copy Genomic DNA Probes for Fluorescence In Situ Hybridization. <i>Genome Research</i> , 2001, 11, 1086-1094.	5.5	37
40	Splice variants but not mutations of DNA polymerase beta are common in bladder cancer. <i>Cancer Research</i> , 2002, 62, 3251-6.	0.9	35
41	Bipartite pattern discovery by entropy minimization-based multiple local alignment. <i>Nucleic Acids Research</i> , 2004, 32, 4979-4991.	14.5	33
42	Comprehensive prediction of mRNA splicing effects of BRCA1 and BRCA2 variants. <i>Human Mutation</i> , 2011, 32, 735-742.	2.5	30
43	Automated discrimination of dicentric and monocentric chromosomes by machine learning-based image processing. <i>Microscopy Research and Technique</i> , 2016, 79, 393-402.	2.2	30
44	Normal and abnormal mechanisms of gene splicing and relevance to inherited skin diseases. <i>Journal of Dermatological Science</i> , 2005, 40, 73-84.	1.9	29
45	Nasal epithelial cells are a reliable source to study splicing variants in Usher syndrome. <i>Human Mutation</i> , 2010, 31, 734-741.	2.5	29
46	Interpretation, Stratification and Evidence for Sequence Variants Affecting mRNA Splicing in Complete Human Genome Sequences. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 77-85.	6.9	29
47	Radiation Dose Estimation by Automated Cytogenetic Biodosimetry. <i>Radiation Protection Dosimetry</i> , 2016, 172, 207-217.	0.8	29
48	Predicting Outcomes of Hormone and Chemotherapy in the Molecular Taxonomy of Breast Cancer International Consortium (METABRIC) Study by Biochemically-inspired Machine Learning. <i>F1000Research</i> , 2016, 5, 2124.	1.6	29
49	L1 repeat elements in the human epsilon-G gamma-globin gene intergenic region: sequence analysis and concerted evolution within this family.. <i>Molecular Biology and Evolution</i> , 1987, 4, 327-42.	8.9	28
50	Maternal uniparental disomy of chromosome 21 in a normal child. , 1999, 83, 69-71.		28
51	A unified analytic framework for prioritization of non-coding variants of uncertain significance in heritable breast and ovarian cancer. <i>BMC Medical Genomics</i> , 2016, 9, 19.	1.5	28
52	Discovery and validation of information theory-based transcription factor and cofactor binding site motifs. <i>Nucleic Acids Research</i> , 2017, 45, e27-e27.	14.5	28
53	Splice-site contribution in alternative splicing of PLP1 and DM20: molecular studies in oligodendrocytes. <i>Human Mutation</i> , 2006, 27, 69-77.	2.5	27
54	Splice-Site Mutations in Atherosclerosis Candidate Genes. <i>Circulation</i> , 1999, 100, 693-699.	1.6	26

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55	Prevalence and spectrum of germline rare variants in BRCA1/2 and PALB2 among breast cancer cases in Sarawak, Malaysia. <i>Breast Cancer Research and Treatment</i> , 2017, 165, 687-697.	2.5	26
56	Collaborative, Multidisciplinary Evaluation of Cancer Variants Through Virtual Molecular Tumor Boards Informs Local Clinical Practices. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 602-613.	2.1	26
57	Transmission of mitochondrial DNA heteroplasmy in normal pedigrees. <i>Human Genetics</i> , 1998, 102, 182-186.	3.8	25
58	Sequence-Based, in situ detection of chromosomal abnormalities at high resolution. <i>American Journal of Medical Genetics Part A</i> , 2003, 121A, 245-257.	2.4	25
59	Automating dicentric chromosome detection from cytogenetic biodosimetry data. <i>Radiation Protection Dosimetry</i> , 2014, 159, 95-104.	0.8	25
60	Accurate cytogenetic biodosimetry through automated dicentric chromosome curation and metaphase cell selection. <i>F1000Research</i> , 2017, 6, 1396.	1.6	23
61	Intensity Integrated Laplacian-Based Thickness Measurement for Detecting Human Metaphase Chromosome Centromere Location. <i>IEEE Transactions on Biomedical Engineering</i> , 2013, 60, 2005-2013.	4.2	21
62	Validation of predicted mRNA splicing mutations using high-throughput transcriptome data. <i>F1000Research</i> , 2014, 3, 8.	1.6	21
63	Klinefelter and trisomy X syndromes in patients with Prader-Willi syndrome and uniparental maternal disomy of chromosome 15—a coincidence?. <i>American Journal of Medical Genetics Part A</i> , 1997, 72, 111-114.	2.4	20
64	Predicting Outcomes of Hormone and Chemotherapy in the Molecular Taxonomy of Breast Cancer International Consortium (METABRIC) Study by Biochemically-inspired Machine Learning. <i>F1000Research</i> , 2016, 5, 2124.	1.6	20
65	Conservation in the 5' region of the long interspersed mouse L1 repeat: implications of comparative sequence analysis. <i>Nucleic Acids Research</i> , 1986, 14, 3119-3136.	14.5	19
66	Assessment of the functional impact of germline BRCA1/2 variants located in non-coding regions in families with breast and/or ovarian cancer predisposition. <i>Breast Cancer Research and Treatment</i> , 2018, 168, 311-325.	2.5	19
67	Expression Changes Confirm Genomic Variants Predicted to Result in Allele-Specific, Alternative mRNA Splicing. <i>Frontiers in Genetics</i> , 2020, 11, 109.	2.3	19
68	Predicting ionizing radiation exposure using biochemically-inspired genomic machine learning. <i>F1000Research</i> , 2018, 7, 233.	1.6	19
69	Genome-wide prediction, display and refinement of binding sites with information theory-based models. <i>BMC Bioinformatics</i> , 2003, 4, 38.	2.6	18
70	An image processing algorithm for accurate extraction of the centerline from human metaphase chromosomes. , 2010, , .		18
71	Duplication and loss of chromosome 21 in two children with Down syndrome and acute leukemia. <i>American Journal of Medical Genetics Part A</i> , 1995, 59, 174-181.	2.4	17
72	Predicting severity of haemophilia A and B splicing mutations by information analysis. <i>Haemophilia</i> , 2006, 12, 258-262.	2.1	17

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73	Expedited Radiation Biodosimetry by Automated Dicentric Chromosome Identification (ADCI) and Dose Estimation. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	16
74	Survival Outcome Differences Based on Treatments Used and Knowledge of the Primary Tumour Site for Patients with Cancer of Unknown and Known Primary in Ontario. <i>Current Oncology</i> , 2018, 25, 307-316.	2.2	16
75	Relaxation of imprinting in Prader-Willi syndrome. <i>Human Genetics</i> , 1998, 103, 694.	3.8	15
76	Structural and genic characterization of stable genomic regions in breast cancer: Relevance to chemotherapy. <i>Molecular Oncology</i> , 2012, 6, 347-359.	4.6	15
77	<i>BRCA1</i> and <i>BRCA2</i> 5' noncoding region variants identified in breast cancer patients alter promoter activity and protein binding. <i>Human Mutation</i> , 2018, 39, 2025-2039.	2.5	15
78	Validation of predicted mRNA splicing mutations using high-throughput transcriptome data. <i>F1000Research</i> , 2014, 3, 8.	1.6	14
79	RADIATION DOSE ESTIMATION BY COMPLETELY AUTOMATED INTERPRETATION OF THE DICENTRIC CHROMOSOME ASSAY. <i>Radiation Protection Dosimetry</i> , 2019, 186, 42-47.	0.8	14
80	Estimating partial-body ionizing radiation exposure by automated cytogenetic biodosimetry. <i>International Journal of Radiation Biology</i> , 2020, 96, 1492-1503.	1.8	14
81	Transcription factor binding site clusters identify target genes with similar tissue-wide expression and buffer against mutations. <i>F1000Research</i> , 2018, 7, 1933.	1.6	14
82	BIPAD: a web server for modeling bipartite sequence elements. <i>BMC Bioinformatics</i> , 2006, 7, 76.	2.6	13
83	Gene expression for biodosimetry and effect prediction purposes: promises, pitfalls and future directions – key session ConRad 2021. <i>International Journal of Radiation Biology</i> , 2022, 98, 843-854.	1.8	13
84	Expanding probe repertoire and improving reproducibility in human genomic hybridization. <i>Nucleic Acids Research</i> , 2013, 41, e81-e81.	14.5	12
85	Congenital contractures, ectodermal dysplasia, cleft lip/palate, and developmental impairment: A distinct syndrome. <i>American Journal of Medical Genetics Part A</i> , 1993, 47, 550-555.	2.4	11
86	Distortion of quantitative genomic and expression hybridization by Cot-1 DNA: mitigation of this effect. <i>Nucleic Acids Research</i> , 2005, 33, e191-e191.	14.5	11
87	A proposed molecular mechanism for pathogenesis of severe RNA-viral pulmonary infections. <i>F1000Research</i> , 2020, 9, 943.	1.6	11
88	Pan-cancer repository of validated natural and cryptic mRNA splicing mutations. <i>F1000Research</i> , 2018, 7, 1908.	1.6	11
89	Identification of mosaicism in Prader-Willi syndrome using fluorescent in situ hybridization. , 1996, 66, 403-412.		10
90	Context-based FISH localization of genomic rearrangements within chromosome 15q11.2q13 duplicons. <i>Molecular Cytogenetics</i> , 2011, 4, 15.	0.9	10

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91	The Potential Clinical and Economic Value of Primary Tumour Identification in Metastatic Cancer of Unknown Primary Tumour: A Population-Based Retrospective Matched Cohort Study. <i>Pharmacoeconomics - Open</i> , 2018, 2, 255-270.	1.8	10
92	Transcription factor binding site clusters identify target genes with similar tissue-wide expression and buffer against mutations. <i>F1000Research</i> , 2018, 7, 1933.	1.6	10
93	Information analysis of human splice site mutations. <i>Human Mutation</i> , 1998, 12, 153-171.	2.5	10
94	Identical twins with Weissenbacher-Zweymüller syndrome and neural tube defect. <i>American Journal of Medical Genetics Part A</i> , 1993, 45, 614-618.	2.4	9
95	Cost-effectiveness of using a gene expression profiling test to aid in identifying the primary tumour in patients with cancer of unknown primary. <i>Pharmacogenomics Journal</i> , 2017, 17, 286-300.	2.0	9
96	Predicting ionizing radiation exposure using biochemically-inspired genomic machine learning. <i>F1000Research</i> , 2018, 7, 233.	1.6	9
97	Pan-cancer repository of validated natural and cryptic mRNA splicing mutations. <i>F1000Research</i> , 2018, 7, 1908.	1.6	9
98	Mosaicism in Prader-Willi syndrome. , 2000, 90, 175-176.		8
99	Redundant designations of BRCA1 intron 11 splicing mutation; c. 4216-2A>G; IVS11-2A>G; L78833, 37698, A>G. <i>Human Mutation</i> , 2000, 16, 264-264.	2.5	8
100	Tandem machine learning for the identification of genes regulated by transcription factors. <i>BMC Bioinformatics</i> , 2005, 6, 204.	2.6	8
101	Best Practices for Evaluating Mutation Prediction Methods. <i>Human Mutation</i> , 2013, 34, 1581-1582.	2.5	8
102	Localized, non-random differences in chromatin accessibility between homologous metaphase chromosomes. <i>Molecular Cytogenetics</i> , 2014, 7, 70.	0.9	8
103	Identification and survival outcomes of a cohort of patients with cancer of unknown primary in Ontario, Canada. <i>Acta Oncologica</i> , 2015, 54, 1781-1787.	1.8	8
104	Multigene signatures of responses to chemotherapy derived by biochemically-inspired machine learning. <i>Molecular Genetics and Metabolism</i> , 2019, 128, 45-52.	1.1	8
105	Meeting radiation dosimetry capacity requirements of population-scale exposures by geostatistical sampling. <i>PLoS ONE</i> , 2020, 15, e0232008.	2.5	8
106	Interpretation of mRNA splicing mutations in genetic disease: review of the literature and guidelines for information-theoretical analysis. <i>F1000Research</i> , 0, 3, 282.	1.6	8
107	Dendrimer FISH detection of single-copy intervals in acute promyelocytic leukemia. <i>Molecular and Cellular Probes</i> , 2006, 20, 114-120.	2.1	7
108	Determination of genomic copy number with quantitative microsphere hybridization. <i>Human Mutation</i> , 2006, 27, 376-386.	2.5	7

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109	Pathway-extended gene expression signatures integrate novel biomarkers that improve predictions of patient responses to kinase inhibitors. <i>MedComm</i> , 2020, 1, 311-327.	7.2	7
110	Centromere detection of human metaphase chromosome images using a candidate based method. <i>FL1000Research</i> , 0, 5, 1565.	1.6	7
111	A common insertion/deletion polymorphism in the Prader-Willi syndrome minimal critical region. <i>Human Molecular Genetics</i> , 1994, 3, 1912-1912.	2.9	6
112	Reversing chromatin accessibility differences that distinguish homologous mitotic metaphase chromosomes. <i>Molecular Cytogenetics</i> , 2015, 8, 65.	0.9	6
113	An Accurate Image Processing Algorithm for Detecting FISH Probe Locations Relative to Chromosome Landmarks on DAPI Stained Metaphase Chromosome Images. , 2010, , .		5
114	Relating Centromeric Topography in Fixed Human Chromosomes to $\hat{\pm}$ -Satellite DNA and CENP-B Distribution. <i>Cytogenetic and Genome Research</i> , 2013, 139, 234-242.	1.1	5
115	The Structure and Magnetic and Electrical Conductivity Properties of the Charge Transfer Compound 1,1'-Dimethylferrocenium Bis-(Tetracyanoquinodimethane), $[(CH_3)_2C_5H_4]_2Fe[TcNQ]_2$. , 1979, , 407-414.		5
116	Two-dimensional agarose gel electrophoresis of restriction-digested genomic DNA. <i>Methods</i> , 1991, 3, 91-97.	3.8	4
117	A proposed molecular mechanism for pathogenesis of severe RNA-viral pulmonary infections. <i>FL1000Research</i> , 2020, 9, 943.	1.6	4
118	Towards large scale automated interpretation of cytogenetic biodosimetry data. , 2012, , .		3
119	Intensity integrated Laplacian algorithm for human metaphase chromosome centromere detection. , 2012, , .		3
120	Visual analytics for supporting evidence-based interpretation of molecular cytogenomic findings. , 2015, , .		3
121	Automated Cytogenetic Biodosimetry at Population-Scale. <i>Radiation</i> , 2021, 1, 79-94.	1.4	3
122	High-Fidelity Amplification of Ribosomal Gene Sequences from South American Mummies. , 1994, , 182-194.		3
123	The Clinical Significance of Occult Gastrointestinal Primary Tumours in Metastatic Cancer: A Population Retrospective Cohort Study. <i>Cancer Research and Treatment</i> , 2018, 50, 183-194.	3.0	3
124	The structure of the dihydrofolate reductase inhibitor 2,4,6-triamino-5-chloroquinazoline. <i>Acta Crystallographica Section B: Structural Crystallography and Crystal Chemistry</i> , 1980, 36, 2358-2362.	0.4	2
125	Deeper understanding of unclassified intronic variants and ESEs. <i>Human Mutation</i> , 2010, 31, V-V.	2.5	2
126	Clinical spectrum and molecular diagnosis of Angelman and Prader-Willi syndrome patients with an imprinting mutation. <i>American Journal of Medical Genetics Part A</i> , 1997, 68, 195-206.	2.4	2

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127	Improved radiation expression profiling in blood by sequential application of sensitive and specific gene signatures. <i>International Journal of Radiation Biology</i> , 2022, 98, 924-941.	1.8	2
128	Distinct 15q genotypes in Russell-Silver and ring 15 syndromes. <i>American Journal of Medical Genetics Part A</i> , 1996, 62, 10-15.	2.4	2
129	Phylogenetic Inference Based on Information Theory-Based PCR Amplification. <i>Journal of Phytopathology</i> , 1998, 146, 427-430.	1.0	1
130	Information theory as a model of genomic sequences. , 2005, , .		1
131	Ab initio exon definition using an information theory-based approach. , 2009, , .		1
132	Proffered Papers and Posters Submitted to the Fifth International Symposium on Hereditary Breast and Ovarian Cancer, BRCA: Twenty Years of Advances. <i>Current Oncology</i> , 2014, 21, 358-391.	2.2	1
133	Visual Display of Sequence Conservation as an Aid to Taxonomic Classification Using PCR Amplification. , 1995, , 21-32.		1
134	Predicting Outcomes of Hormone and Chemotherapy in the Molecular Taxonomy of Breast Cancer International Consortium (METABRIC) Study by Biochemically-inspired Machine Learning. <i>F1000Research</i> , 0, 5, 2124.	1.6	1
135	High resolution definition of chromosome abnormalities with probes designed from genome sequences. <i>Discovery Medicine</i> , 2004, 4, 99-101.	0.5	1
136	Likely community transmission of COVID-19 infections between neighboring, persistent hotspots in Ontario, Canada. <i>F1000Research</i> , 0, 10, 1312.	1.6	1
137	Restriction mapping by preferential ligation of adjacent digestion fragments. <i>Nucleic Acids Research</i> , 1986, 14, 9219-9219.	14.5	0
138	A new missense mutation, Arg719Gln, in the β -cardiac heavy chain myosin gene of patients with familial hypertrophic cardiomyopathy. <i>Human Molecular Genetics</i> , 1994, 3, 1716-1716.	2.9	0
139	Development of a directory of genetic probes as a shared institutional resource. <i>Computer Methods and Programs in Biomedicine</i> , 1995, 46, 35-39.	4.7	0
140	Reply to letter to the editor by Nicholls??mosaicism in Prader-Willi syndrome?. , 2000, 90, 177-177.		0
141	Characterization of an African American (AA) subject carrying two novel functional CYP2D6 alleles.. <i>Clinical Pharmacology and Therapeutics</i> , 2003, 73, P12-P12.	4.7	0
142	High resolution detection of chromosome abnormalities with single copy fluorescence in situ hybridization. , 0, , .		0
143	Bipartite pattern discovery by entropy minimization-based multiple local alignment. <i>Nucleic Acids Research</i> , 2004, 32, 5320-5320.	14.5	0
144	Extensive alternative splicing of cytochrome P4502D6 (CYP2D6) mRNA: explanation for variability among subjects with identical genotypes?. <i>Clinical Pharmacology and Therapeutics</i> , 2004, 75, P52.	4.7	0

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145	Usher Syndrome Splicing Variants Evaluated in Nasal Epithelial Cells. <i>Human Mutation</i> , 2010, 31, v-v.	2.5	0
146	Nanoscale Imaging of Fish Probe Binding to Metaphase Chromosomes. <i>Biophysical Journal</i> , 2011, 100, 356a.	0.5	0
147	Web-service Available for the Shannon Human Splicing Pipeline for mRNA Splicing Mutation Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 151.	6.9	0
148	The Clinical Significance of Occult Gynecologic Primary Tumours in Metastatic Cancer. <i>Current Oncology</i> , 2017, 24, 368-378.	2.2	0
149	Differentially accessible, single copy sequences form contiguous domains along metaphase chromosomes that are conserved among multiple tissues. <i>Molecular Cytogenetics</i> , 2021, 14, 49.	0.9	0
150	Automated Phenotype-Genotype Table Understanding. <i>Studies in Computational Intelligence</i> , 2013, , 47-52.	0.9	0
151	Abstract 4172: Noncoding mutation analysis reveals previously unrecognized pathways in lymph node-invasive breast cancer. , 2014, , .		0
152	Pan-cancer repository of validated natural and cryptic mRNA splicing mutations. <i>F1000Research</i> , 0, 7, 1908.	1.6	0
153	Abstract 3222: The Virtual Molecular Tumor Board of the Variant Interpretation for Cancer Consortium: A systematic gateway connecting cancer genome interpretation and progress in genomic knowledgebases in cancer. , 2020, , .		0
154	Atypical Clinical Findings in Prader-Willi Syndrome Patients: Analysis of Survey Data. <i>Prader-Willi Perspectives</i> , 1996, 4, 3-6.	0.0	0
155	Title is missing!. , 2020, 15, e0232008.		0
156	Title is missing!. , 2020, 15, e0232008.		0
157	Title is missing!. , 2020, 15, e0232008.		0
158	Title is missing!. , 2020, 15, e0232008.		0
159	Title is missing!. , 2020, 15, e0232008.		0
160	Title is missing!. , 2020, 15, e0232008.		0
161	Title is missing!. , 2020, 15, e0232008.		0
162	Title is missing!. , 2020, 15, e0232008.		0

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163	Title is missing!. , 2020, 15, e0232008.		0
164	Title is missing!. , 2020, 15, e0232008.		0
165	Klinefelter and trisomy X syndromes in patients with Prader-Willi syndrome and uniparental maternal disomy of chromosome 15—a coincidence?. American Journal of Medical Genetics Part A, 1997, 72, 111-114.	2.4	0
166	Redundant designations of BRCA1 intron 11 splicing mutation; c. 4216-2A>G; IVS11-2A>G; L78833, 37698, A>G. Human Mutation, 2000, 16, 264.	2.5	0