Peter K Rogan

List of Publications by Year
in descending order

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163 papers	5,257 citations	109137 35 h-index	106150 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. Journal of Pharmacology and Experimental Therapeutics, 2003, 307, 906-922.	1.3	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. Human Mutation, 2012, 33, 2-7.	1.1	269
3	Imprinting-Mutation Mechanisms in Prader-Willi Syndrome. American Journal of Human Genetics, 1999, 64, 397-413.	2.6	262
4	The Frequency of Uniparental Disomy in Prader-Willi Syndrome. New England Journal of Medicine, 1992, 326, 1599-1607.	13.9	257
5	Chromosome Breakage in the Prader-Willi and Angelman Syndromes Involves Recombination between Large, Transcribed Repeats at Proximal and Distal Breakpoints. American Journal of Human Genetics, 1999, 65, 370-386.	2.6	254
6	Predicting responses to platin chemotherapy agents with biochemically-inspired machine learning. Signal Transduction and Targeted Therapy, 2019, 4, 1.	7.1	202
7	Information analysis of human splice site mutations. Human Mutation, 1998, 12, 153-171.	1.1	187
8	Minimal definition of the imprinting center and fixation of chromosome 15q11-q13 epigenotype by imprinting mutations.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 7811-7815.	3.3	168
9	Automated splicing mutation analysis by information theory. Human Mutation, 2005, 25, 334-342.	1.1	146
10	Nondisjunction of human acrocentric chromosomes: studies of 432 trisomic fetuses and liveborns. Human Genetics, 1994, 94, 411-7.	1.8	104
11	Mutations that alter RNA splicing of the human HPRT gene: a review of the spectrum. Mutation Research - Reviews in Mutation Research, 1998, 411, 179-214.	2.4	102
12	Genomic signatures for paclitaxel and gemcitabine resistance in breast cancer derived by machine learning. Molecular Oncology, 2016, 10, 85-100.	2.1	99
13	FANCMc.5791C>T nonsense mutation (rs144567652) induces exon skipping, affects DNA repair activity and is a familial breast cancer risk factor. Human Molecular Genetics, 2015, 24, 5345-5355.	1.4	91
14	Interpretation of mRNA splicing mutations in genetic disease: review of the literature and guidelines for information-theoretical analysis. F1000Research, 2014, 3, 282.	0.8	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.. American Journal of Respiratory Cell and Molecular Biology, 1996, 15, 489-498.	1.4	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. Pharmacogenomics Journal, 2005, 5, 173-182.	0.9	67

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19	Daytime Sleepines and Rem Abormalities in Prader-Willi Syndrome: Evidence of Generalized Hypoarousal. International Journal of Neuroscience, 1996, 87, 127-139.	0.8	66
20	Information theory-based analysis of CYP2C19, CYP2D6 and CYP3A5 splicing mutations. Pharmacogenetics and Genomics, 2003, 13, 207-218.	5.7	66
21	Full length article. Gene, 1998, 215, 111-122.	1.0	62
22	Study of nucleic acids isolated from ancient remains. American Journal of Physical Anthropology, 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. American Journal of Human Genetics, 2000, 66, 356-367.	2.6	57
24	Using information content and base frequencies to distinguish mutations from genetic polymorphisms in splice junction recognition sites. Human Mutation, 1995, 6, 74-76.	1.1	55
25	Absence of linkage of apparently single gene mediated ADHD with the human syntenic region of the mouse mutantColoboma. American Journal of Medical Genetics Part A, 1995, 60, 573-579.	2.4	51
26	Loss of Heterozygosity and Microsatellite Instability at the Retinoblastoma Locus in Osteosarcomas. Diagnostic Molecular Pathology, 1996, 5, 214-219.	2.1	50
27	Hydration in purple membrane as a function of relative humidity. Journal of Molecular Biology, 1981, 145, 281-284.	2.0	47
28	A new missense mutation, Arg719Gln, in the Î²-cardiac heavy chain myosin gene of patients with familial hypertrophic cardiomyopathy. Human Molecular Genetics, 1994, 3, 1025-1026.	1.4	47
29	Bloom syndrome and maternal uniparental disomy for chromosome 15. American Journal of Human Genetics, 1994, 55, 74-80.	2.6	47
30	Clinical and molecular analyses of deletion 3p25-pter syndrome. American Journal of Medical Genetics Part A, 1993, 46, 623-629.	2.4	46
31	Microsatelliteâ€“Centromere Mapping in the Zebrafish (Danio rerio). Genomics, 1995, 30, 337-341.	1.3	46
32	Association of a mosaic chromosomal 22q 11 deletion with hypoplastic left heart syndrome. American Journal of Cardiology, 1996, 77, 1023-1025.	0.7	46
33	Prediction of Mutant mRNA Splice Isoforms by Information Theory-Based Exon Definition. Human Mutation, 2013, 34, n/a-n/a.	1.1	46
34	Distinct 15q genotypes in Russell-Silver and ring 15 syndromes. American Journal of Medical Genetics Part A, 1996, 62, 10-15.	2.4	45
35	Splicing mutation analysis reveals previously unrecognized pathways in lymph node-invasive breast cancer. Scientific Reports, 2014, 4, 7063.	1.6	41
36	Racial Differences in Allelic Distribution at the Human Pulmonary Surfactant Protein B Gene Locus (SP-B). Experimental Lung Research, 1996, 22, 489-494.	0.5	39

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37	Prioritizing Variants in Complete Hereditary Breast and Ovarian Cancer Genes in Patients Lacking KnownBRCAMutations. Human Mutation, 2016, 37, 640-652.	1.1	39
38	Development and Refinement of Pregnane X Receptor (PXR) DNA Binding Site Model Using Information Theory. Journal of Biological Chemistry, 2004, 279, 46779-46786.	1.6	38
39	Sequence-Based Design of Single-Copy Genomic DNA Probes for Fluorescence In Situ Hybridization. Genome Research, 2001, 11, 1086-1094.	2.4	37
40	Splice variants but not mutations of DNA polymerase beta are common in bladder cancer. Cancer Research, 2002, 62, 3251-6.	0.4	35
41	Bipartite pattern discovery by entropy minimization-based multiple local alignment. Nucleic Acids Research, 2004, 32, 4979-4991.	6.5	33
42	Comprehensive prediction of mRNA splicing effects of BRCA1 and BRCA2 variants. Human Mutation, 2011, 32, 735-742.	1.1	30
43	Automated discrimination of dicentric and monocentric chromosomes by machine learning-based image processing. Microscopy Research and Technique, 2016, 79, 393-402.	1.2	30
44	Normal and abnormal mechanisms of gene splicing and relevance to inherited skin diseases. Journal of Dermatological Science, 2005, 40, 73-84.	1.0	29
45	Nasal epithelial cells are a reliable source to study splicing variants in Usher syndrome. Human Mutation, 2010, 31, 734-741.	1.1	29
46	Interpretation, Stratification and Evidence for Sequence Variants Affecting mRNA Splicing in Complete Human Genome Sequences. Genomics, Proteomics and Bioinformatics, 2013, 11, 77-85.	3.0	29
47	Radiation Dose Estimation by Automated Cytogenetic Biodosimetry. Radiation Protection Dosimetry, 2016, 172, 207-217.	0.4	29
48	Predicting Outcomes of Hormone and Chemotherapy in the MolecularÂTaxonomy ofÂBreast CancerÂInternationalÂConsortium (METABRIC) Study by Biochemically-inspired Machine Learning. F1000Research, 2016, 5, 2124.	0.8	29
49	L1 repeat elements in the human epsilon-G gamma-globin gene intergenic region: sequence analysis and concerted evolution within this family.. Molecular Biology and Evolution, 1987, 4, 327-42.	3.5	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. BMC Medical Genomics, 2016, 9, 19.	0.7	28
52	Discovery and validation of information theory-based transcription factor and cofactor binding site motifs. Nucleic Acids Research, 2017, 45, e27-e27.	6.5	28
53	Splice-site contribution in alternative splicing ofPLP1 andDM20: molecular studies in oligodendrocytes. Human Mutation, 2006, 27, 69-77.	1.1	27
54	Splice-Site Mutations in Atherosclerosis Candidate Genes. Circulation, 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. Breast Cancer Research and Treatment, 2017, 165, 687-697.	1.1	26
56	Collaborative, Multidisciplinary Evaluation of Cancer Variants Through Virtual Molecular Tumor Boards Informs Local Clinical Practices. JCO Clinical Cancer Informatics, 2020, 4, 602-613.	1.0	26
57	Transmission of mitochondrial DNA heteroplasmy in normal pedigrees. Human Genetics, 1998, 102, 182-186.	1.8	25
58	Sequence-Based, in situ detection of chromosomal abnormalities at high resolution. American Journal of Medical Genetics Part A, 2003, 121A, 245-257.	2.4	25
59	Automating dicentric chromosome detection from cytogenetic biodosimetry data. Radiation Protection Dosimetry, 2014, 159, 95-104.	0.4	25
60	Accurate cytogenetic biodosimetry through automated dicentric chromosome curation and metaphase cell selection. F1000Research, 2017, 6, 1396.	0.8	23
61	Intensity Integrated Laplacian-Based Thickness Measurement for Detecting Human Metaphase Chromosome Centromere Location. IEEE Transactions on Biomedical Engineering, 2013, 60, 2005-2013.	2.5	21
62	Validation of predicted mRNA splicing mutations using high-throughput transcriptome data. F1000Research, 2014, 3, 8.	0.8	21
63	Klinefelter and trisomy X syndromes in patients with Prader-Willi syndrome and uniparental maternal disomy of chromosome 15â€”A coincidence?. American Journal of Medical Genetics Part A, 1997, 72, 111-114.	2.4	20
64	Predicting Outcomes of Hormone and Chemotherapy in the MolecularÂTaxonomy ofÂBreast CancerÂInternationalÂConsortium (METABRIC) Study by Biochemically-inspired Machine Learning. F1000Research, 2016, 5, 2124.	0.8	20
65	Conservation in the 5' region of the long interspersed mouse L1 repeat: implications of comparative sequence analysis. Nucleic Acids Research, 1986, 14, 3119-3136.	6.5	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. Breast Cancer Research and Treatment, 2018, 168, 311-325.	1.1	19
67	Expression Changes Confirm Genomic Variants Predicted to Result in Allele-Specific, Alternative mRNA Splicing. Frontiers in Genetics, 2020, 11, 109.	1.1	19
68	Predicting ionizing radiation exposure using biochemically-inspired genomic machine learning. F1000Research, 2018, 7, 233.	0.8	19
69	Genome-wide prediction, display and refinement of binding sites with information theory-based models. BMC Bioinformatics, 2003, 4, 38.	1.2	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. American Journal of Medical Genetics Part A, 1995, 59, 174-181.	2.4	17
72	Predicting severity of haemophilia A and B splicing mutations by information analysis. Haemophilia, 2006, 12, 258-262.	1.0	17

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73	Expedited Radiation Biodosimetry by Automated Dicentric Chromosome Identification (ADCI) and Dose Estimation. Journal of Visualized Experiments, 2017, , .	0.2	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. Current Oncology, 2018, 25, 307-316.	0.9	16
75	Relaxation of imprinting in Prader-Willi syndrome. Human Genetics, 1998, 103, 694.	1.8	15
76	Structural and genic characterization of stable genomic regions in breast cancer: Relevance to chemotherapy. Molecular Oncology, 2012, 6, 347-359.	2.1	15
77	BRCA1 and BRCA2 5â€² noncoding region variants identified in breast cancer patients alter promoter activity and protein binding. Human Mutation, 2018, 39, 2025-2039.	1.1	15
78	Validation of predicted mRNA splicing mutations using high-throughput transcriptome data. F1000Research, 2014, 3, 8.	0.8	14
79	RADIATION DOSE ESTIMATION BY COMPLETELY AUTOMATED INTERPRETATION OF THE DICENTRIC CHROMOSOME ASSAY. Radiation Protection Dosimetry, 2019, 186, 42-47.	0.4	14
80	Estimating partial-body ionizing radiation exposure by automated cytogenetic biodosimetry. International Journal of Radiation Biology, 2020, 96, 1492-1503.	1.0	14
81	Transcription factor binding site clusters identify target genes with similar tissue-wide expression and buffer against mutations. F1000Research, 2018, 7, 1933.	0.8	14
82	BIPAD: a web server for modeling bipartite sequence elements. BMC Bioinformatics, 2006, 7, 76.	1.2	13
83	Gene expression for biodosimetry and effect prediction purposes: promises, pitfalls and future directions â€“ key session ConRad 2021. International Journal of Radiation Biology, 2022, 98, 843-854.	1.0	13
84	Expanding probe repertoire and improving reproducibility in human genomic hybridization. Nucleic Acids Research, 2013, 41, e81-e81.	6.5	12
85	Congenital contractures, ectodermal dysplasia, cleft lip/palate, and developmental impairment: A distinct syndrome. American Journal of Medical Genetics Part A, 1993, 47, 550-555.	2.4	11
86	Distortion of quantitative genomic and expression hybridization by Cot-1 DNA: mitigation of this effect. Nucleic Acids Research, 2005, 33, e191-e191.	6.5	11
87	A proposed molecular mechanism for pathogenesis of severe RNA-viral pulmonary infections. F1000Research, 2020, 9, 943.	0.8	11
88	Pan-cancer repository of validated natural and cryptic mRNA splicing mutations. F1000Research, 2018, 7, 1908.	0.8	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. Molecular Cytogenetics, 2011, 4, 15.	0.4	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. PharmacoEconomics - Open, 2018, 2, 255-270.	0.9	10
92	Transcription factor binding site clusters identify target genes with similar tissue-wide expression and buffer against mutations. F1000Research, 2018, 7, 1933.	0.8	10
93	Information analysis of human splice site mutations. Human Mutation, 1998, 12, 153-171.	1.1	10
94	Identical twins with Weissenbacher-ZweymÃ¼ller syndrome and neural tube defect. American Journal of Medical Genetics Part A, 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. Pharmacogenomics Journal, 2017, 17, 286-300.	0.9	9
96	Predicting ionizing radiation exposure using biochemically-inspired genomic machine learning. F1000Research, 2018, 7, 233.	0.8	9
97	Pan-cancer repository of validated natural and cryptic mRNA splicing mutations. F1000Research, 2018, 7, 1908.	0.8	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. Human Mutation, 2000, 16, 264-264.	1.1	8
100	Tandem machine learning for the identification of genes regulated by transcription factors. BMC Bioinformatics, 2005, 6, 204.	1.2	8
101	Best Practices for Evaluating Mutation Prediction Methods. Human Mutation, 2013, 34, 1581-1582.	1.1	8
102	Localized, non-random differences in chromatin accessibility between homologous metaphase chromosomes. Molecular Cytogenetics, 2014, 7, 70.	0.4	8
103	Identification and survival outcomes of a cohort of patients with cancer of unknown primary in Ontario, Canada. Acta OncolÃ³gica, 2015, 54, 1781-1787.	0.8	8
104	Multigene signatures of responses to chemotherapy derived by biochemically-inspired machine learning. Molecular Genetics and Metabolism, 2019, 128, 45-52.	0.5	8
105	Meeting radiation dosimetry capacity requirements of population-scale exposures by geostatistical sampling. PLoS ONE, 2020, 15, e0232008.	1.1	8
106	Interpretation of mRNA splicing mutations in genetic disease: review of the literature and guidelines for information-theoretical analysis. F1000Research, 0, 3, 282.	0.8	8
107	Dendrimer FISH detection of single-copy intervals in acute promyelocytic leukemia. Molecular and Cellular Probes, 2006, 20, 114-120.	0.9	7
108	Determination of genomic copy number with quantitative microsphere hybridization. Human Mutation, 2006, 27, 376-386.	1.1	7

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109	Pathwayâ€extended gene expression signatures integrate novel biomarkers that improve predictions of patient responses to kinase inhibitors. MedComm, 2020, 1, 311-327.	3.1	7
110	Centromere detection of human metaphase chromosomeÂimages using a candidate based method. F1000Research, 0, 5, 1565.	0.8	7
111	A common insertion/deletion polymorphism in the Praderâ€"Willi syndrome minimal critical region. Human Molecular Genetics, 1994, 3, 1912-1912.	1.4	6
112	Reversing chromatin accessibility differences that distinguish homologous mitotic metaphase chromosomes. Molecular Cytogenetics, 2015, 8, 65.	0.4	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 Î±-Satellite DNA and CENP-B Distribution. Cytogenetic and Genome Research, 2013, 139, 234-242.	0.6	5
115	The Structure and Magnetic and Electrical Conductivity Properties of the Charge Transfer Compound 1,1â€²-Dimethylferrocenium Bis-(Tetracyanoquinodimethane), [(CH3C5H4)2Fe][TCNQ]2. , 1979, , 407-414.		5
116	Two-dimensional agarose gel electrophoresis of restriction-digested genomic DNA. Methods, 1991, 3, 91-97.	1.9	4
117	A proposed molecular mechanism for pathogenesis of severe RNA-viral pulmonary infections. F1000Research, 2020, 9, 943.	0.8	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. Radiation, 2021, 1, 79-94.	0.6	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. Cancer Research and Treatment, 2018, 50, 183-194.	1.3	3
124	The structure of the dihydrofolate reductase inhibitor 2,4,6-triamino-5-chloroquinazoline. Acta Crystallographica Section B: Structural Crystallography and Crystal Chemistry, 1980, 36, 2358-2362.	0.4	2
125	Deeper understanding of unclassified intronic variants and ESEs. Human Mutation, 2010, 31, V-V.	1.1	2
126	Clinical spectrum and molecular diagnosis of Angelman and Prader-Willi syndrome patients with an imprinting mutation. , 1997, 68, 195.		2

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127	Improved radiation expression profiling in blood by sequential application of sensitive and specific gene signatures. International Journal of Radiation Biology, 2022, 98, 924-941.	1.0	2
128	Phylogenetic Inference Based on Information Theory-Based PCR Amplification. Journal of Phytopathology, 1998, 146, 427-430.	0.5	1
129	Information theory as a model of genomic sequences. , 2005, , .		1
130	Ab initio exon definition using an information theory-based approach. , 2009, , .		1
131	Proffered Papers and Posters Submitted to the Fifth International Symposium on Hereditary Breast and Ovarian Cancer, BRCA: Twenty Years of Advances. Current Oncology, 2014, 21, 358-391.	0.9	1
132	Visual Display of Sequence Conservation as an Aid to Taxonomic Classification Using PCR Amplification. , 1995, , 21-32.		1
133	Predicting Outcomes of Hormone and Chemotherapy in the MolecularÂTaxonomy ofÂBreast CancerÂInternationalÂConsortium (METABRIC) Study by Biochemically-inspired Machine Learning. F1000Research, 0, 5, 2124.	0.8	1
134	High resolution definition of chromosome abnormalities with probes designed from genome sequences. Discovery Medicine, 2004, 4, 99-101.	0.5	1
135	Likely community transmission of COVID-19 infections between neighboring, persistent hotspots in Ontario, Canada. F1000Research, 0, 10, 1312.	0.8	1
136	Restriction mapping by preferential ligatlon of adjacent digestion fragments. Nucleic Acids Research, 1986, 14, 9219-9219.	6.5	0
137	A new missense mutation, Arg719Gln, in the Î²-cardiac heavy chain myosin gene of patients with familial hypertrophic cardiomyopathy. Human Molecular Genetics, 1994, 3, 1716-1716.	1.4	0
138	Development of a directory of genetic probes as a shared institutional resource. Computer Methods and Programs in Biomedicine, 1995, 46, 35-39.	2.6	0
139	Reply to letter to the editor by Nicholls??mosaicism in Praeder-Willi syndrome?. , 2000, 90, 177-177.		0
140	Characterization of an African American (AA) subject carrying two novel functional CYP2D6 alleles.. Clinical Pharmacology and Therapeutics, 2003, 73, P12-P12.	2.3	0
141	High resolution detection of chromosome abnormalities with single copy fluorescence in situ hybridization. , 0, , .		0
142	Bipartite pattern discovery by entropy minimization-based multiple local alignment. Nucleic Acids Research, 2004, 32, 5320-5320.	6.5	0
143	Extensive alternative splicing of cytochrome P4502D6 (CYP2D6) mRNA: explanation for variability among subjects with identical genotypes?. Clinical Pharmacology and Therapeutics, 2004, 75, P52.	2.3	0
144	Usher Syndrome Splicing Variants Evaluated in Nasal Epithelial Cells. Human Mutation, 2010, 31, v-v.	1.1	0

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145	Nanoscale Imaging of Fish Probe Binding to Metaphase Chromosomes. Biophysical Journal, 2011, 100, 356a.	0.2	0
146	The Clinical Significance of Occult Gynecologic Primary Tumours in Metastatic Cancer. Current Oncology, 2017, 24, 368-378.	0.9	0
147	Differentially accessible, single copy sequences form contiguous domains along metaphase chromosomes that are conserved among multiple tissues. Molecular Cytogenetics, 2021, 14, 49.	0.4	0
148	Automated Phenotype-Genotype Table Understanding. Studies in Computational Intelligence, 2013, , 47-52.	0.7	0
149	Abstract 4172: Noncoding mutation analysis reveals previously unrecognized pathways in lymph node-invasive breast cancer. , 2014, , .		0
150	Pan-cancer repository of validated natural and cryptic mRNA splicing mutations. F1000Research, 0, 7, 1908.	0.8	0
151	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
152	Atypical Clinical Findings in Prader-Willi Syndrome Patients: Analysis of Survey Data. Prader-Willi Perspectives, 1996, 4, 3-6.	0.0	0
153	Title is missing!. , 2020, 15, e0232008.		0
154	Title is missing!. , 2020, 15, e0232008.		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	Redundant designations of BRCA1 intron 11 splicing mutation; c. 4216-2A>G; IVS11-2A>G; L78833, 37698, A>G. Human Mutation, 2000, 16, 264.	1.1	0