Peter K Rogan

List of Publications by Year
in descending order

166	5,257	109321	106344
papers	citations	35 h-index	65 g-index

203	203	203	6372
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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.	1.8	13
2	Improved radiation expression profiling in blood by sequential application of sensitive and specific gene signatures. International Journal of Radiation Biology, 2022, 98, 924-941.	1.8	2
3	Automated Cytogenetic Biodosimetry at Population-Scale. Radiation, 2021, 1, 79-94.	1.4	3
4	Differentially accessible, single copy sequences form contiguous domains along metaphase chromosomes that are conserved among multiple tissues. Molecular Cytogenetics, 2021, 14, 49.	0.9	0
5	Collaborative, Multidisciplinary Evaluation of Cancer Variants Through Virtual Molecular Tumor Boards Informs Local Clinical Practices. JCO Clinical Cancer Informatics, 2020, 4, 602-613.	2.1	26
6	Estimating partial-body ionizing radiation exposure by automated cytogenetic biodosimetry. International Journal of Radiation Biology, 2020, 96, 1492-1503.	1.8	14
7	Pathwayâ€extended gene expression signatures integrate novel biomarkers that improve predictions of patient responses to kinase inhibitors. MedComm, 2020, 1, 311-327.	7.2	7
8	Expression Changes Confirm Genomic Variants Predicted to Result in Allele-Specific, Alternative mRNA Splicing. Frontiers in Genetics, 2020, 11, 109.	2.3	19
9	Meeting radiation dosimetry capacity requirements of population-scale exposures by geostatistical sampling. PLoS ONE, 2020, 15, e0232008.	2.5	8
10	A proposed molecular mechanism for pathogenesis of severe RNA-viral pulmonary infections. F1000Research, 2020, 9, 943.	1.6	11
11	A proposed molecular mechanism for pathogenesis of severe RNA-viral pulmonary infections. F1000Research, 2020, 9, 943.	1.6	4
12	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
13	Title is missing!. , 2020, 15, e0232008.		0
14	Title is missing!. , 2020, 15, e0232008.		0
15	Title is missing!. , 2020, 15, e0232008.		0
16	Title is missing!. , 2020, 15, e0232008.		0
17	Title is missing!. , 2020, 15, e0232008.		0
18	Title is missing!. , 2020, 15, e0232008.		0

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19	Title is missing!. , 2020, 15, e0232008.		0
20	Title is missing!. , 2020, 15, e0232008.		0
21	Title is missing!. , 2020, 15, e0232008.		0
22	Title is missing!. , 2020, 15, e0232008.		0
23	Multigene signatures of responses to chemotherapy derived by biochemically-inspired machine learning. Molecular Genetics and Metabolism, 2019, 128, 45-52.	1.1	8
24	Predicting responses to platin chemotherapy agents with biochemically-inspired machine learning. Signal Transduction and Targeted Therapy, 2019, 4, 1.	17.1	202
25	RADIATION DOSE ESTIMATION BY COMPLETELY AUTOMATED INTERPRETATION OF THE DICENTRIC CHROMOSOME ASSAY. Radiation Protection Dosimetry, 2019, 186, 42-47.	0.8	14
26	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.	1.8	10
27	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.	2.5	19
28	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.	2.2	16
29	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.	2.5	15
30	Predicting ionizing radiation exposure using biochemically-inspired genomic machine learning. F1000Research, 2018, 7, 233.	1.6	9
31	Predicting ionizing radiation exposure using biochemically-inspired genomic machine learning. F1000Research, 2018, 7, 233.	1.6	19
32	Pan-cancer repository of validated natural and cryptic mRNA splicing mutations. F1000Research, 2018, 7, 1908.	1.6	9
33	Pan-cancer repository of validated natural and cryptic mRNA splicing mutations. F1000Research, 2018, 7, 1908.	1.6	11
34	Transcription factor binding site clusters identify target genes with similar tissue-wide expression and buffer against mutations. F1000Research, 2018, 7, 1933.	1.6	10
35	Transcription factor binding site clusters identify target genes with similar tissue-wide expression and buffer against mutations. F1000Research, 2018, 7, 1933.	1.6	14
36	The Clinical Significance of Occult Gastrointestinal Primary Tumours in Metastatic Cancer: A Population Retrospective Cohort Study. Cancer Research and Treatment, 2018, 50, 183-194.	3.0	3

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37	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.	2.0	9
38	Expedited Radiation Biodosimetry by Automated Dicentric Chromosome Identification (ADCI) and Dose Estimation. Journal of Visualized Experiments, 2017, , .	0.3	16
39	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.	2.5	26
40	The Clinical Significance of Occult Gynecologic Primary Tumours in Metastatic Cancer. Current Oncology, 2017, 24, 368-378.	2.2	0
41	Discovery and validation of information theory-based transcription factor and cofactor binding site motifs. Nucleic Acids Research, 2017, 45, e27-e27.	14.5	28
42	Accurate cytogenetic biodosimetry through automated dicentric chromosome curation and metaphase cell selection. F1000Research, 2017, 6, 1396.	1.6	23
43	Automated discrimination of dicentric and monocentric chromosomes by machine learning-based image processing. Microscopy Research and Technique, 2016, 79, 393-402.	2.2	30
44	Prioritizing Variants in Complete Hereditary Breast and Ovarian Cancer Genes in Patients Lacking KnownBRCAMutations. Human Mutation, 2016, 37, 640-652.	2.5	39
45	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.	1.5	28
46	Radiation Dose Estimation by Automated Cytogenetic Biodosimetry. Radiation Protection Dosimetry, 2016, 172, 207-217.	0.8	29
47	Genomic signatures for paclitaxel and gemcitabine resistance in breast cancer derived by machine learning. Molecular Oncology, 2016, 10, 85-100.	4.6	99
48	Predicting Outcomes of Hormone and Chemotherapy in the MolecularÂTaxonomy ofÂBreast CancerÂInternationalÂConsortium (METABRIC) Study by Biochemically-inspired Machine Learning. F1000Research, 2016, 5, 2124.	1.6	20
49	Predicting Outcomes of Hormone and Chemotherapy in the MolecularÂTaxonomy ofÂBreast CancerÂInternationalÂConsortium (METABRIC) Study by Biochemically-inspired Machine Learning. F1000Research, 2016, 5, 2124.	1.6	29
50	Visual analytics for supporting evidence-based interpretation of molecular cytogenomic findings. , 2015, , .		3
51	Reversing chromatin accessibility differences that distinguish homologous mitotic metaphase chromosomes. Molecular Cytogenetics, 2015, 8, 65.	0.9	6
52	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.	2.9	91
53	Identification and survival outcomes of a cohort of patients with cancer of unknown primary in Ontario, Canada. Acta OncolÃ³gica, 2015, 54, 1781-1787.	1.8	8
54	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.	2.2	1

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55	Automating dicentric chromosome detection from cytogenetic biodosimetry data. Radiation Protection Dosimetry, 2014, 159, 95-104.	0.8	25
56	Localized, non-random differences in chromatin accessibility between homologous metaphase chromosomes. Molecular Cytogenetics, 2014, 7, 70.	0.9	8
57	Web-service Available for the Shannon Human Splicing Pipeline for mRNA Splicing Mutation Analysis. Genomics, Proteomics and Bioinformatics, 2014, 12, 151.	6.9	0
58	Validation of predicted mRNA splicing mutations using high-throughput transcriptome data. F1000Research, 2014, 3, 8.	1.6	14
59	Splicing mutation analysis reveals previously unrecognized pathways in lymph node-invasive breast cancer. Scientific Reports, 2014, 4, 7063.	3.3	41
60	Validation of predicted mRNA splicing mutations using high-throughput transcriptome data. F1000Research, 2014, 3, 8.	1.6	21
61	Interpretation of mRNA splicing mutations in genetic disease: review of the literature and guidelines for information-theoretical analysis. F1000Research, 2014, 3, 282.	1.6	85
62	Abstract 4172: Noncoding mutation analysis reveals previously unrecognized pathways in lymph node-invasive breast cancer. , 2014, , .		0
63	Intensity Integrated Laplacian-Based Thickness Measurement for Detecting Human Metaphase Chromosome Centromere Location. IEEE Transactions on Biomedical Engineering, 2013, 60, 2005-2013.	4.2	21
64	Best Practices for Evaluating Mutation Prediction Methods. Human Mutation, 2013, 34, 1581-1582.	2.5	8
65	Prediction of Mutant mRNA Splice Isoforms by Information Theory-Based Exon Definition. Human Mutation, 2013, 34, n/a-n/a.	2.5	46
66	Interpretation, Stratification and Evidence for Sequence Variants Affecting mRNA Splicing in Complete Human Genome Sequences. Genomics, Proteomics and Bioinformatics, 2013, 11, 77-85.	6.9	29
67	Relating Centromeric Topography in Fixed Human Chromosomes to Î±-Satellite DNA and CENP-B Distribution. Cytogenetic and Genome Research, 2013, 139, 234-242.	1.1	5
68	Expanding probe repertoire and improving reproducibility in human genomic hybridization. Nucleic Acids Research, 2013, 41, e81-e81.	14.5	12
69	Automated Phenotype-Genotype Table Understanding. Studies in Computational Intelligence, 2013, , 47-52.	0.9	0
70	Towards large scale automated interpretation of cytogenetic biodosimetry data. , 2012, , .		3
71	Intensity integrated Laplacian algorithm for human metaphase chromosome centromere detection. , 2012, , .		3
72	Structural and genic characterization of stable genomic regions in breast cancer: Relevance to chemotherapy. Molecular Oncology, 2012, 6, 347-359.	4.6	15

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73	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.	2.5	269
74	Nanoscale Imaging of Fish Probe Binding to Metaphase Chromosomes. Biophysical Journal, 2011, 100, 356a.	0.5	0
75	Context-based FISH localization of genomic rearrangements within chromosome 15q11.2q13 duplicons. Molecular Cytogenetics, 2011, 4, 15.	0.9	10
76	Comprehensive prediction of mRNA splicing effects of BRCA1 and BRCA2 variants. Human Mutation, 2011, 32, 735-742.	2.5	30
77	Deeper understanding of unclassified intronic variants and ESEs. Human Mutation, 2010, 31, V-V.	2.5	2
78	Nasal epithelial cells are a reliable source to study splicing variants in Usher syndrome. Human Mutation, 2010, 31, 734-741.	2.5	29
79	Usher Syndrome Splicing Variants Evaluated in Nasal Epithelial Cells. Human Mutation, 2010, 31, v-v.	2.5	0
80	An Accurate Image Processing Algorithm for Detecting FISH Probe Locations Relative to Chromosome Landmarks on DAPI Stained Metaphase Chromosome Images. , 2010, , .		5
81	An image processing algorithm for accurate extraction of the centerline from human metaphase chromosomes. , 2010, , .		18
82	Ab initio exon definition using an information theory-based approach. , 2009, , .		1
83	Dendrimer FISH detection of single-copy intervals in acute promyelocytic leukemia. Molecular and Cellular Probes, 2006, 20, 114-120.	2.1	7
84	Predicting severity of haemophilia A and B splicing mutations by information analysis. Haemophilia, 2006, 12, 258-262.	2.1	17
85	BIPAD: a web server for modeling bipartite sequence elements. BMC Bioinformatics, 2006, 7, 76.	2.6	13
86	Splice-site contribution in alternative splicing ofPLP1 andDM20: molecular studies in oligodendrocytes. Human Mutation, 2006, 27, 69-77.	2.5	27
87	Determination of genomic copy number with quantitative microsphere hybridization. Human Mutation, 2006, 27, 376-386.	2.5	7
88	Identification and characterization of novel sequence variations in the cytochrome P4502D6 (CYP2D6) gene in African Americans. Pharmacogenomics Journal, 2005, 5, 173-182.	2.0	67
89	Tandem machine learning for the identification of genes regulated by transcription factors. BMC Bioinformatics, 2005, 6, 204.	2.6	8
90	Automated splicing mutation analysis by information theory. Human Mutation, 2005, 25, 334-342.	2.5	146

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91	Information theory as a model of genomic sequences. , 2005, , .		1
92	Distortion of quantitative genomic and expression hybridization by Cot-1 DNA: mitigation of this effect. Nucleic Acids Research, 2005, 33, e191-e191.	14.5	11
93	Normal and abnormal mechanisms of gene splicing and relevance to inherited skin diseases. Journal of Dermatological Science, 2005, 40, 73-84.	1.9	29
94	Bipartite pattern discovery by entropy minimization-based multiple local alignment. Nucleic Acids Research, 2004, 32, 5320-5320.	14.5	0
95	Bipartite pattern discovery by entropy minimization-based multiple local alignment. Nucleic Acids Research, 2004, 32, 4979-4991.	14.5	33
96	Development and Refinement of Pregnane X Receptor (PXR) DNA Binding Site Model Using Information Theory. Journal of Biological Chemistry, 2004, 279, 46779-46786.	3.4	38
97	Extensive alternative splicing of cytochrome P4502D6 (CYP2D6) mRNA: explanation for variability among subjects with identical genotypes?. Clinical Pharmacology and Therapeutics, 2004, 75, P52.	4.7	0
98	High resolution definition of chromosome abnormalities with probes designed from genome sequences. Discovery Medicine, 2004, 4, 99-101.	0.5	1
99	Genome-wide prediction, display and refinement of binding sites with information theory-based models. BMC Bioinformatics, 2003, 4, 38.	2.6	18
100	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
101	Characterization of an African American (AA) subject carrying two novel functional CYP2D6 alleles.. Clinical Pharmacology and Therapeutics, 2003, 73, P12-P12.	4.7	0
102	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.	2.5	367
103	Information theory-based analysis of CYP2C19, CYP2D6 and CYP3A5 splicing mutations. Pharmacogenetics and Genomics, 2003, 13, 207-218.	5.7	66
104	Splice variants but not mutations of DNA polymerase beta are common in bladder cancer. Cancer Research, 2002, 62, 3251-6.	0.9	35
105	Sequence-Based Design of Single-Copy Genomic DNA Probes for Fluorescence In Situ Hybridization. Genome Research, 2001, 11, 1086-1094.	5.5	37
106	Mosaicism in Prader-Willi syndrome. , 2000, 90, 175-176.		8
107	Reply to letter to the editor by Nicholls??mosaicism in Praeder-Willi syndrome?. , 2000, 90, 177-177.		0
108	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.	2.5	8

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109	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.	6.2	57
110	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
111	Splice-Site Mutations in Atherosclerosis Candidate Genes. Circulation, 1999, 100, 693-699.	1.6	26
112	Maternal uniparental disomy of chromosome 21 in a normal child. , 1999, 83, 69-71.		28
113	Imprinting-Mutation Mechanisms in Prader-Willi Syndrome. American Journal of Human Genetics, 1999, 64, 397-413.	6.2	262
114	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.	6.2	254
115	Phylogenetic Inference Based on Information Theory-Based PCR Amplification. Journal of Phytopathology, 1998, 146, 427-430.	1.0	1
116	Information analysis of human splice site mutations. Human Mutation, 1998, 12, 153-171.	2.5	187
117	Transmission of mitochondrial DNA heteroplasmy in normal pedigrees. Human Genetics, 1998, 102, 182-186.	3.8	25
118	Relaxation of imprinting in Prader-Willi syndrome. Human Genetics, 1998, 103, 694.	3.8	15
119	Full length article. Gene, 1998, 215, 111-122.	2.2	62
120	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.	5.5	102
121	Information analysis of human splice site mutations. Human Mutation, 1998, 12, 153-171.	2.5	10
122	Clinical spectrum and molecular diagnosis of Angelman and Prader-Willi syndrome patients with an imprinting mutation. , 1997, 68, 195-206.		84
123	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
124	Clinical spectrum and molecular diagnosis of Angelman and Praderâ€Willi syndrome patients with an imprinting mutation. American Journal of Medical Genetics Part A, 1997, 68, 195-206.	2.4	2
125	Klinefelter and trisomy X syndromes in patients with Praderâ€Willi syndrome and uniparental maternal disomy of chromosome 15â€”A coincidence?. American Journal of Medical Genetics Part A, 1997, 72, 111-114.	2.4	0
126	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.	7.1	168

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127	Loss of Heterozygosity and Microsatellite Instability at the Retinoblastoma Locus in Osteosarcomas. Diagnostic Molecular Pathology, 1996, 5, 214-219.	2.1	50
128	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.	2.9	70
129	Association of a mosaic chromosomal 22q 11 deletion with hypoplastic left heart syndrome. American Journal of Cardiology, 1996, 77, 1023-1025.	1.6	46
130	Distinct 15q genotypes in Russell-Silver and ring 15 syndromes. American Journal of Medical Genetics Part A, 1996, 62, 10-15.	2.4	45
131	Relationship of sleep abnormalities to patient genotypes in Prader-Willi syndrome. , 1996, 67, 478-482.		69
132	Identification of mosaicism in Prader-Willi syndrome using fluorescent in situ hybridization. , 1996, 66, 403-412.		10
133	Daytime Sleepines and Rem Abrormalities in Prader-Willi Syndrome: Evidence of Generalized Hypoarousal. International Journal of Neuroscience, 1996, 87, 127-139.	1.6	66
134	Racial Differences in Allelic Distribution at the Human Pulmonary Surfactant Protein B Gene Locus (SP-B). Experimental Lung Research, 1996, 22, 489-494.	1.2	39
135	Atypical Clinical Findings in Prader-Willi Syndrome Patients: Analysis of Survey Data. Prader-Willi Perspectives, 1996, 4, 3-6.	0.0	0
136	Distinct 15q genotypes in Russellâ€Silver and ring 15 syndromes. American Journal of Medical Genetics Part A, 1996, 62, 10-15.	2.4	2
137	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
138	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
139	Using information content and base frequencies to distinguish mutations from genetic polymorphisms in splice junction recognition sites. Human Mutation, 1995, 6, 74-76.	2.5	55
140	Development of a directory of genetic probes as a shared institutional resource. Computer Methods and Programs in Biomedicine, 1995, 46, 35-39.	4.7	0
141	Microsatelliteâ€“Centromere Mapping in the Zebrafish (Danio rerio). Genomics, 1995, 30, 337-341.	2.9	46
142	Visual Display of Sequence Conservation as an Aid to Taxonomic Classification Using PCR Amplification. , 1995, , 21-32.		1
143	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.	2.9	47
144	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.	2.9	0

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145	A common insertion/deletion polymorphism in the Praderâ€"Willi syndrome minimal critical region. Human Molecular Genetics, 1994, 3, 1912-1912.	2.9	6
146	Nondisjunction of human acrocentric chromosomes: studies of 432 trisomic fetuses and liveborns. Human Genetics, 1994, 94, 411-7.	3.8	104
147	High-Fidelity Amplification of Ribosomal Gene Sequences from South American Mummies. , 1994, , 182-194.		3
148	Bloom syndrome and maternal uniparental disomy for chromosome 15. American Journal of Human Genetics, 1994, 55, 74-80.	6.2	47
149	Identical twins with Weissenbacher-ZweymÃ¼ller syndrome and neural tube defect. American Journal of Medical Genetics Part A, 1993, 45, 614-618.	2.4	9
150	Clinical and molecular analyses of deletion 3p25-pter syndrome. American Journal of Medical Genetics Part A, 1993, 46, 623-629.	2.4	46
151	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
152	The Frequency of Uniparental Disomy in Prader-Willi Syndrome. New England Journal of Medicine, 1992, 326, 1599-1607.	27.0	257
153	Two-dimensional agarose gel electrophoresis of restriction-digested genomic DNA. Methods, 1991, 3, 91-97.	3.8	4
154	Study of nucleic acids isolated from ancient remains. American Journal of Physical Anthropology, 1990, 33, 195-214.	2.1	57
155	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.	8.9	28
156	Restriction mapping by preferential ligatlon of adjacent digestion fragments. Nucleic Acids Research, 1986, 14, 9219-9219.	14.5	0
157	Conservation in the 5' region of the long interspersed mouse L1 repeat: implications of comparative sequence analysis. Nucleic Acids Research, 1986, 14, 3119-3136.	14.5	19
158	Hydration in purple membrane as a function of relative humidity. Journal of Molecular Biology, 1981, 145, 281-284.	4.2	47
159	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
160	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
161	High resolution detection of chromosome abnormalities with single copy fluorescence in situ hybridization. , 0, , .		0
162	Interpretation of mRNA splicing mutations in genetic disease: review of the literature and guidelines for information-theoretical analysis. F1000Research, 0, 3, 282.	1.6	8

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163	Centromere detection of human metaphase chromosomeÂimages using a candidate based method. F1000Research, 0, 5, 1565.	1.6	7
164	Predicting Outcomes of Hormone and Chemotherapy in the MolecularÂTaxonomy ofÂBreast CancerÂInternationalÂConsortium (METABRIC) Study by Biochemically-inspired Machine Learning. F1000Research, 0, 5, 2124.	1.6	1
165	Pan-cancer repository of validated natural and cryptic mRNA splicing mutations. F1000Research, 0, 7, 1908.	1.6	0
166	Likely community transmission of COVID-19 infections between neighboring, persistent hotspots in Ontario, Canada. F1000Research, 0, 10, 1312.	1.6	1