Miguel Angel Pujana

List of Publications by Year
in descending order

142	9,081	57631	48187
papers	citations	44 h-index	88 g-index

154	154	154	17334
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	3.0	19
2	Evidence for shared genetic risk factors between lymphangioleiomyomatosis and pulmonary function. ERJ Open Research, 2022, 8, 00375-2021.	1.1	0
3	CDK5RAP3, a New BRCA2 Partner That Regulates DNA Repair, Is Associated with Breast Cancer Survival. Cancers, 2022, 14, 353.	1.7	0
4	Validation of Anticorrelated TGFÎ² Signaling and Alternative End-Joining DNA Repair Signatures that Predict Response to Genotoxic Cancer Therapy. Clinical Cancer Research, 2022, 28, 1372-1382.	3.2	6
5	Modification of BRCA1-associated breast cancer risk by HMMR overexpression. Nature Communications, 2022, 13, 1895.	5.8	19
6	Pathogenic BRCA1 variants disrupt PLK1-regulation of mitotic spindle orientation. Nature Communications, 2022, 13, 2200.	5.8	3
7	A High-Throughput Screening Platform Identifies Novel Combination Treatments for Malignant Peripheral Nerve Sheath Tumors. Molecular Cancer Therapeutics, 2022, 21, 1246-1258.	1.9	2
8	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	5.8	19
9	RNF168 regulates R-loop resolution and genomic stability in BRCA1/2-deficient tumors. Journal of Clinical Investigation, 2021, 131, .	3.9	38
10	Loss of TGFÎ² signaling increases alternative end-joining DNA repair that sensitizes to genotoxic therapies across cancer types. Science Translational Medicine, 2021, 13, .	5.8	33
11	Mammary epithelial cells have lineage-rooted metabolic identities. Nature Metabolism, 2021, 3, 665-681.	5.1	24
12	Long-term results of sirolimus treatment in lymphangioleiomyomatosis: a single referral centre experience. Scientific Reports, 2021, 11, 10171.	1.6	9
13	Heterogeneity and Cancer-Related Features in Lymphangioleiomyomatosis Cells and Tissue. Molecular Cancer Research, 2021, 19, 1840-1853.	1.5	3
14	Altered regulation of BRCA1 exon 11 splicing is associated with breast cancer risk in carriers of BRCA1 pathogenic variants. Human Mutation, 2021, 42, 1488-1502.	1.1	7
15	Histamine signaling and metabolism identify potential biomarkers and therapies for lymphangioleiomyomatosis. EMBO Molecular Medicine, 2021, 13, e13929.	3.3	6
16	Tumour DDR1 promotes collagen fibre alignment to instigate immune exclusion. Nature, 2021, 599, 673-678.	13.7	139
17	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
18	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120

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19	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666.	1.1	82
20	Immune Cell Associations with Cancer Risk. IScience, 2020, 23, 101296.	1.9	6
21	NEK10 tyrosine phosphorylates p53 and controls its transcriptional activity. Oncogene, 2020, 39, 5252-5266.	2.6	12
22	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	3.4	48
23	Tumors defective in homologous recombination rely on oxidative metabolism: relevance to treatments with <scp>PARP</scp> inhibitors. EMBO Molecular Medicine, 2020, 12, e11217.	3.3	37
24	EVI1 as a Prognostic and Predictive Biomarker of Clear Cell Renal Cell Carcinoma. Cancers, 2020, 12, 300.	1.7	9
25	Looking for a Better Characterization of Triple-Negative Breast Cancer by Means of Circulating Tumor Cells. Journal of Clinical Medicine, 2020, 9, 353.	1.0	17
26	Abstract 1388: Loss of TGFÎ² signaling increases alternative end-joining and could sensitize high-grade serous ovarian cancer to PARP inhibitors. , 2020, , .		0
27	Allergy in patients with lymphangioleiomyomatosis. , 2020, , .		0
28	Abstract P4-10-17: Baseline and pharmacodynamic changes of circulating exosomal microRNAs predict early versus late progression to palbociclib plus endocrine therapy in patients with metastatic breast cancer. A sub-analysis of the PARSIFAL-1 trial. , 2020, , .		0
29	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
30	Chromosome 12p Amplification in Triple-Negative/BRCA1-Mutated Breast Cancer Associates with Emergence of Docetaxel Resistance and Carboplatin Sensitivity. Cancer Research, 2019, 79, 4258-4270.	0.4	17
31	Risk of breast cancer in patients with lymphangioleiomyomatosis. Cancer Epidemiology, 2019, 61, 154-156.	0.8	2
32	A genome-wide association study implicates NR2F2 in lymphangioleiomyomatosis pathogenesis. European Respiratory Journal, 2019, 53, 1900329.	3.1	14
33	Differential metabolic activity and discovery of therapeutic targets using summarized metabolic pathway models. Npj Systems Biology and Applications, 2019, 5, 7.	1.4	30
34	AhR controls redox homeostasis and shapes the tumor microenvironment in BRCA1-associated breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3604-3613.	3.3	96
35	Evolutionary Changes after Translational Challenges Imposed by Horizontal Gene Transfer. Genome Biology and Evolution, 2019, 11, 814-831.	1.1	23
36	Reactive oxygen species modulate macrophage immunosuppressive phenotype through the up-regulation of PD-L1. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4326-4335.	3.3	137

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37	Generalised mosaicism for TSC2 mutation in isolated lymphangioleiomyomatosis. European Respiratory Journal, 2019, 54, 1900938.	3.1	5
38	Decapping protein EDC4 regulates DNA repair and phenocopies BRCA1. Nature Communications, 2018, 9, 967.	5.8	33
39	Tumor xenograft modeling identifies TCF4/ITF2 loss associated with breast cancer chemoresistance. DMM Disease Models and Mechanisms, 2018, 11, .	1.2	15
40	Orthoxenografts of Testicular Germ Cell Tumors Demonstrate Genomic Changes Associated with Cisplatin Resistance and Identify PDMP as a Resensitizing Agent. Clinical Cancer Research, 2018, 24, 3755-3766.	3.2	17
41	ALK1 Loss Results in Vascular Hyperplasia in Mice and Humans Through PI3K Activation. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 1216-1229.	1.1	75
42	Cell Cycleâ€“Dependent Tumor Engraftment and Migration Are Enabled by Aurora-A. Molecular Cancer Research, 2018, 16, 16-31.	1.5	27
43	Disease networks identify specific conditions and pleiotropy influencing multimorbidity in the general population. Scientific Reports, 2018, 8, 15970.	1.6	22
44	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.4	54
45	Gene Expression Integration into Pathway Modules Reveals a Pan-Cancer Metabolic Landscape. Cancer Research, 2018, 78, 6059-6072.	0.4	40
46	Subjugation of TGFÎ² Signaling by Human Papilloma Virus in Head and Neck Squamous Cell Carcinoma Shifts DNA Repair from Homologous Recombination to Alternative End Joining. Clinical Cancer Research, 2018, 24, 6001-6014.	3.2	71
47	Ubiquitin ligase RNF8 suppresses Notch signaling to regulate mammary development and tumorigenesis. Journal of Clinical Investigation, 2018, 128, 4525-4542.	3.9	31
48	Abstract 2812: Status of TGFbeta signaling determines PARP inhibitor sensitivity in head and neck cancer. , 2018, , .		0
49	AURKA Overexpression Is Driven byÂFOXM1 and MAPK/ERK Activation inÂMelanoma Cells Harboring BRAF orÂNRASÂMutations: Impact on MelanomaÂPrognosis and Therapy. Journal of Investigative Dermatology, 2017, 137, 1297-1310.	0.3	40
50	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
51	Stem cell-like transcriptional reprogramming mediates metastatic resistance to mTOR inhibition. Oncogene, 2017, 36, 2737-2749.	2.6	34
52	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
53	DNA Methylomes Reveal Biological Networks Involved in Human Eye Development, Functions and Associated Disorders. Scientific Reports, 2017, 7, 11762.	1.6	44
54	Attenuation of RNA polymerase II pausing mitigates BRCA1-associated R-loop accumulation and tumorigenesis. Nature Communications, 2017, 8, 15908.	5.8	118

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55	Prediction of Breast and Prostate Cancer Risks in Male BRCA1 and BRCA2 Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	0.8	152
56	BRCA1 controls the cell division axis and governs ploidy and phenotype in human mammary cells. Oncotarget, 2017, 8, 32461-32475.	0.8	14
57	Radioresistance of mesenchymal glioblastoma initiating cells correlates with patient outcome and is associated with activation of inflammatory program. Oncotarget, 2017, 8, 73640-73653.	0.8	33
58	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS ONE, 2016, 11, e0158801.	1.1	10
59	The acetyltransferase Tip60 contributes to mammary tumorigenesis by modulating DNA repair. Cell Death and Differentiation, 2016, 23, 1198-1208.	5.0	62
60	Large-scale analysis of genome and transcriptome alterations in multiple tumors unveils novel cancer-relevant splicing networks. Genome Research, 2016, 26, 732-744.	2.4	225
61	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2016, 18, 15.	2.2	88
62	Cancer network activity associated with therapeutic response and synergism. Genome Medicine, 2016, 8, 88.	3.6	7
63	RANK Signaling Blockade Reduces Breast Cancer Recurrence by Inducing Tumor Cell Differentiation. Cancer Research, 2016, 76, 5857-5869.	0.4	47
64	RANKL/RANK control Brca1 mutation-driven mammary tumors. Cell Research, 2016, 26, 761-774.	5.7	128
65	Study of breast cancer incidence in patients of lymphangioleiomyomatosis. Breast Cancer Research and Treatment, 2016, 156, 195-201.	1.1	9
66	Rankl Impairs Lactogenic Differentiation Through Inhibition of the Prolactin/Stat5 Pathway at Midgestation. Stem Cells, 2016, 34, 1027-1039.	1.4	26
67	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
68	Cancer Stem-like Cells Act via Distinct Signaling Pathways in Promoting Late Stages of Malignant Progression. Cancer Research, 2016, 76, 1245-1259.	0.4	21
69	Analysis of Paired Primary-Metastatic Hormone-Receptor Positive Breast Tumors (HRPBC) Uncovers Potential Novel Drivers of Hormonal Resistance. PLoS ONE, 2016, 11, e0155840.	1.1	20
70	Gasdermin B expression predicts poor clinical outcome in HER2-positive breast cancer. Oncotarget, 2016, 7, 56295-56308.	0.8	83
71	Comprehensive establishment and characterization of orthoxenograft mouse models of malignant peripheral nerve sheath tumors for personalized medicine. EMBO Molecular Medicine, 2015, 7, 608-627.	3.3	36
72	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	1.1	34

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73	Lymphangioleiomyomatosis Biomarkers Linked to Lung Metastatic Potential and Cell Stemness. PLoS ONE, 2015, 10, e0132546.	1.1	15
74	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
75	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
76	Germline Mutations in FAN1 Cause Hereditary Colorectal Cancer by Impairing DNA Repair. Gastroenterology, 2015, 149, 563-566.	0.6	94
77	A validated gene regulatory network and GWAS identifies early regulators of T cellâ€“associated diseases. Science Translational Medicine, 2015, 7, 313ra178.	5.8	66
78	PKA signaling drives mammary tumorigenesis through Src. Oncogene, 2015, 34, 1160-1173.	2.6	75
79	Integrating gene expression and epidemiological data for the discovery of genetic interactions associated with cancer risk. Carcinogenesis, 2014, 35, 578-585.	1.3	1
80	Modules, networks and systems medicine for understanding disease and aiding diagnosis. Genome Medicine, 2014, 6, 82.	3.6	169
81	VAV3 mediates resistance to breast cancer endocrine therapy. Breast Cancer Research, 2014, 16, R53.	2.2	28
82	Integrated genomic and prospective clinical studies show the importance of modular pleiotropy for disease susceptibility, diagnosis and treatment. Genome Medicine, 2014, 6, 17.	3.6	27
83	Tubers from patients with tuberous sclerosis complex are characterized by changes in microtubule biology through <scp>ROCK2</scp> signalling. Journal of Pathology, 2014, 233, 247-257.	2.1	7
84	Integrating germline and somatic data towards a personalized cancer medicine. Trends in Molecular Medicine, 2014, 20, 413-415.	3.5	9
85	Linkage of DNA Methylation Quantitative Trait Loci to Human Cancer Risk. Cell Reports, 2014, 7, 331-338.	2.9	76
86	Constitutive activation of RANK disrupts mammary cell fate leading to tumorigenesis. Stem Cells, 2013, 31, 1954-1965.	1.4	40
87	Serum 25-hydroxyvitamin D3 levels and vitamin D receptor variants in melanoma patients from the Mediterranean area of Barcelona. BMC Medical Genetics, 2013, 14, 26.	2.1	24
88	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	1.5	244
89	Evaluation of <scp>PAX</scp>3 genetic variants and nevus number. Pigment Cell and Melanoma Research, 2013, 26, 666-676.	1.5	7
90	Functional and Structural Analysis of C-Terminal BRCA1 Missense Variants. PLoS ONE, 2013, 8, e61302.	1.1	16

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91	Genomic imbalance ofHMMR/RHAMMregulates the sensitivity and response of malignant peripheral nerve sheath tumour cells to aurora kinase inhibition. Oncotarget, 2013, 4, 80-93.	0.8	27
92	Lurbinectedin (PM01183), a New DNA Minor Groove Binder, Inhibits Growth of Orthotopic Primary Graft of Cisplatin-Resistant Epithelial Ovarian Cancer. Clinical Cancer Research, 2012, 18, 5399-5411.	3.2	86
93	Cancer develops, progresses and responds to therapies through restricted perturbation of the proteinâ€“protein interaction network. Integrative Biology (United Kingdom), 2012, 4, 1038.	0.6	10
94	DNA Methylation Plasticity of Human Adipose-Derived Stem Cells in Lineage Commitment. American Journal of Pathology, 2012, 181, 2079-2093.	1.9	36
95	Distinct DNA methylomes of newborns and centenarians. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10522-10527.	3.3	687
96	Analysis of SLX4/FANCP in non-BRCA1/2-mutated breast cancer families. BMC Cancer, 2012, 12, 84.	1.1	14
97	Tools for protein-protein interaction network analysis in cancer research. Clinical and Translational Oncology, 2012, 14, 3-14.	1.2	35
98	Abstract 2608: Interplay between BRCA1 and RHAMM regulates epithelial apicobasal polarization and may influence risk of breast cancer. , 2012, , .		0
99	Exploring the link between MORF4L1 and risk of breast cancer. Breast Cancer Research, 2011, 13, R40.	2.2	23
100	Evidence for a link between TNFRSF11A and risk of breast cancer. Breast Cancer Research and Treatment, 2011, 129, 947-954.	1.1	12
101	Validation of a DNA methylation microarray for 450,000 CpG sites in the human genome. Epigenetics, 2011, 6, 692-702.	1.3	908
102	Gene Expression Differences between Colon and Rectum Tumors. Clinical Cancer Research, 2011, 17, 7303-7312.	3.2	69
103	Interplay between BRCA1 and RHAMM Regulates Epithelial Apicobasal Polarization and May Influence Risk of Breast Cancer. PLoS Biology, 2011, 9, e1001199.	2.6	91
104	Biological reprogramming in acquired resistance to endocrine therapy of breast cancer. Oncogene, 2010, 29, 6071-6083.	2.6	59
105	Exploring the Link between Germline and Somatic Genetic Alterations in Breast Carcinogenesis. PLoS ONE, 2010, 5, e14078.	1.1	33
106	TACC3-TSC2 maintains nuclear envelope structure and controls cell division. Cell Cycle, 2010, 9, 1143-1155.	1.3	46
107	Gene set-based analysis of polymorphisms: finding pathways or biological processes associated to traits in genome-wide association studies. Nucleic Acids Research, 2009, 37, W340-W344.	6.5	64
108	Gene expression profiling integrated into network modelling reveals heterogeneity in the mechanisms of BRCA1 tumorigenesis. British Journal of Cancer, 2009, 101, 1469-1480.	2.9	13

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109	Biological Convergence of Cancer Signatures. PLoS ONE, 2009, 4, e4544.	1.1	20
110	Biological processes, properties and molecular wiring diagrams of candidate low-penetrance breast cancer susceptibility genes. BMC Medical Genomics, 2008, 1, 62.	0.7	13
111	Genetic and genomic analysis modeling of germline c-MYC overexpression and cancer susceptibility. BMC Genomics, 2008, 9, 12.	1.2	27
112	CLEAR-test: Combining inference for differential expression and variability in microarray data analysis. Journal of Biomedical Informatics, 2008, 41, 33-45.	2.5	8
113	Genetic interactions: the missing links for a better understanding of cancer susceptibility, progression and treatment. Molecular Cancer, 2008, 7, 4.	7.9	10
114	Genetic Variants in Apoptosis and Immunoregulation-Related Genes Are Associated with Risk of Chronic Lymphocytic Leukemia. Cancer Research, 2008, 68, 10178-10186.	0.4	67
115	Fas-activated serine/threonine phosphoprotein (FAST) is a regulator of alternative splicing. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11370-11375.	3.3	32
116	Integrative analysis of a cancer somatic mutome. Molecular Cancer, 2007, 6, 13.	7.9	28
117	Molecular characterization of a t(9;12)(p21;q13) balanced chromosome translocation in combination with integrative genomics analysis identifiesC9orf14as a candidate tumor-suppressor. Genes Chromosomes and Cancer, 2007, 46, 155-162.	1.5	10
118	Network modeling links breast cancer susceptibility and centrosome dysfunction. Nature Genetics, 2007, 39, 1338-1349.	9.4	602
119	Evidence for systems-level molecular mechanisms of tumorigenesis. BMC Genomics, 2007, 8, 185.	1.2	31
120	Geminin is bound to chromatin in G2/M phase to promote proper cytokinesis. International Journal of Biochemistry and Cell Biology, 2006, 38, 1207-1220.	1.2	15
121	Transgenic mice overexpressing the full-length neurotrophin receptor TrkC exhibit increased catecholaminergic neuron density in specific brain areas and increased anxiety-like behavior and panic reaction. Neurobiology of Disease, 2006, 24, 403-418.	2.1	50
122	Novel Pheochromocytoma Susceptibility Loci Identified by Integrative Genomics. Cancer Research, 2005, 65, 9651-9658.	0.4	88
123	Enrichment of segmental duplications in regions of breaks of synteny between the human and mouse genomes suggest their involvement in evolutionary rearrangements. Human Molecular Genetics, 2003, 12, 2201-2208.	1.4	121
124	Human Chromosome 7: DNA Sequence and Biology. Science, 2003, 300, 767-772.	6.0	185
125	Genomic inversions of human chromosome 15q11-q13 in mothers of Angelman syndrome patients with class II (BP2/3) deletions. Human Molecular Genetics, 2003, 12, 849-858.	1.4	131
126	Human chromosome 15q11-q14 regions of rearrangements contain clusters of LCR15 duplicons. European Journal of Human Genetics, 2002, 10, 26-35.	1.4	92

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127	Chromosomal regions containing high-density and ambiguously mapped putative single nucleotide polymorphisms (SNPs) correlate with segmental duplications in the human genome. Human Molecular Genetics, 2002, 11, 1987-1995.	1.4	80
128	Cloning of S4D-SRCRB, a new soluble member of the group B scavenger receptor cysteine-rich family (SRCR-SF) mapping to human Chromosome 7q11.23. Immunogenetics, 2002, 54, 621-634.	1.2	13
129	5â€² UTR-region SNP in the NTRK3 gene is associated with panic disorder. Molecular Psychiatry, 2002, 7, 928-930.	4.1	28
130	A Polymorphic Genomic Duplication on Human Chromosome 15 Is a Susceptibility Factor for Panic and Phobic Disorders. Cell, 2001, 106, 367-379.	13.5	219
131	Additional Complexity on Human Chromosome 15q: Identification of a Set of Newly Recognized Duplicons (LCR15) on 15q11-q13, 15q24, and 15q26. Genome Research, 2001, 11, 98-111.	2.4	60
132	Isolation and characterisation of a novel human gene (C9orf11) on chromosome 9p21, a region frequently deleted in human cancer. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2000, 1517, 128-134.	2.4	6
133	Genomic organization of the human CD5 gene. Immunogenetics, 2000, 51, 993-1001.	1.2	40
134	HMG20A and HMG20B map to human chromosomes 15q24 and 19p13.3 and constitute a distinct class of HMG-box genes with ubiquitous expression. Cytogenetic and Genome Research, 2000, 88, 62-67.	0.6	36
135	Spinocerebellar ataxias in Spanish patients: genetic analysis of familial and sporadic cases. Human Genetics, 1999, 104, 516-522.	1.8	140
136	Anticipation is not associated with CAG repeat expansion in parent-offspring pairs of patients affected with schizophrenia. , 1999, 88, 50-56.		13
137	Uncloned expanded CAG/CTG repeat sequences in autosomal dominant cerebellar ataxia (ADCA) detected by the repeat expansion detection (RED) method.. Journal of Medical Genetics, 1998, 35, 99-102.	1.5	6
138	Large CAG/CTG repeat templates produced by PCR, usefulness for the DIRECT method of cloning genes with CAG/CTG repeat expansions. Nucleic Acids Research, 1998, 26, 1352-1353.	6.5	13
139	Analysis of amino-acid and nucleotide variants in the spinocerebellar ataxia type 1 (SCA1) gene in schizophrenic patients. Human Genetics, 1997, 99, 772-775.	1.8	6
140	Polymorphisms at 13 expressed human sequences containing CAG/CTG repeats and analysis in autosomal dominant cerebellar ataxia (ADCA) patients. Human Genetics, 1997, 101, 18-21.	1.8	3
141	The repeat expansion detection method in the analysis of diseases with CAG/CTG repeat expansion: Usefulness and limitations. Human Mutation, 1997, 10, 486-488.	1.1	9
142	Cloning (CAG/GTC)n STSs by an Alu-(CAG/GTC)n PCR method: an approach to human chromosome 12 and spinocerebellar ataxia 2 (SCA2). Nucleic Acids Research, 1996, 24, 3651-3652.	6.5	2