Jan P Dumanski

List of Publications by Year
in descending order

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117 papers	9,076 citations	76031 42 h-index	49824 91 g-index
127 all docs	127 docs citations	127 times ranked	10163 citing authors

#	Article	IF	Citations
1	Loss of Y and clonal hematopoiesis in bloodâ€”two sides of the same coin?. Leukemia, 2022, 36, 889-891.	3.3	21
2	Comprehensive cancer-oriented biobanking resource of human samples for studies of post-zygotic genetic variation involved in cancer predisposition. PLoS ONE, 2022, 17, e0266111.	1.1	4
3	High prevalence of somatic PIK3CA and TP53 pathogenic variants in the normal mammary gland tissue of sporadic breast cancer patients revealed by duplex sequencing. Npj Breast Cancer, 2022, 8, .	2.3	8
4	Immune cells lacking Y chromosome show dysregulation of autosomal gene expression. Cellular and Molecular Life Sciences, 2021, 78, 4019-4033.	2.4	54
5	Leukocytes with chromosome Y loss have reduced abundance of the cell surface immunoprotein CD99. Scientific Reports, 2021, 11, 15160.	1.6	23
6	Variable degree of mosaicism for tetrasomy 18p in phenotypically discordant monozygotic twinsâ€”Diagnostic implications. Molecular Genetics & Genomic Medicine, 2021, 9, e1526.	0.6	7
7	Longitudinal changes in the frequency of mosaic chromosome Y loss in peripheral blood cells of aging men varies profoundly between individuals. European Journal of Human Genetics, 2020, 28, 349-357.	1.4	47
8	The level of myeloid derived-suppressor cells in peripheral blood of patients with prostate cancerafter various types of therapy. Polish Journal of Pathology, 2020, 71, 46-54.	0.1	5
9	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
10	PRR14L mutations are associated with chromosome 22 acquired uniparental disomy, age-related clonal hematopoiesis and myeloid neoplasia. Leukemia, 2019, 33, 1184-1194.	3.3	11
11	Mosaic loss of chromosome Y in leukocytes matters. Nature Genetics, 2019, 51, 4-7.	9.4	47
12	A MUTYH germline mutation is associated with small intestinal neuroendocrine tumors. Endocrine-Related Cancer, 2017, 24, 427-443.	1.6	49
13	Mosaicism in health and disease â€” clones picking up speed. Nature Reviews Genetics, 2017, 18, 128-142.	7.7	200
14	Loss of Chromosome Y in Leukocytes and Major Cardiovascular Events. Circulation: Cardiovascular Genetics, 2017, 10, e001820.	5.1	5
15	Biobanking multifocal breast carcinomas: sample adequacy with regard to histology and <scp>DNA</scp> content. Histopathology, 2016, 68, 411-421.	1.6	5
16	Mosaic Loss of Chromosome Y in Blood Is Associated with Alzheimer Disease. American Journal of Human Genetics, 2016, 98, 1208-1219.	2.6	164
17	Concurrent DNA Copy-Number Alterations and Mutations in Genes Related to Maintenance of Genome Stability in Uninvolved Mammary Glandular Tissue from Breast Cancer Patients. Human Mutation, 2015, 36, 1088-1099.	1.1	11
18	Signatures of post-zygotic structural genetic aberrations in the cells of histologically normal breast tissue that can predispose to sporadic breast cancer. Genome Research, 2015, 25, 1521-1535.	2.4	25

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19	Smoking is associated with mosaic loss of chromosome Y. Science, 2015, 347, 81-83.	6.0	163
20	Mosaic loss of chromosome Y in peripheral blood is associated with shorter survival and higher risk of cancer. Nature Genetics, 2014, 46, 624-628.	9.4	320
21	Age dependence of tumor genetics in unfavorable neuroblastoma: arrayCGH profiles of 34 consecutive cases, using a Swedish 25-year neuroblastoma cohort for validation. BMC Cancer, 2013, 13, 231.	1.1	9
22	Non-heritable genetics of human disease: spotlight on post-zygotic genetic variation acquired during lifetime. Journal of Medical Genetics, 2013, 50, 1-10.	1.5	38
23	Republished: Non-heritable genetics of human disease: spotlight on post-zygotic genetic variation acquired during lifetime. Postgraduate Medical Journal, 2013, 89, 417-426.	0.9	7
24	Post-Zygotic and Inter-Individual Structural Genetic Variation in a Presumptive Enhancer Element of the Locus between the IL10RÎ² and IFNAR1 Genes. PLoS ONE, 2013, 8, e67752.	1.1	2
25	Procoagulant activity in patients with sickle cell trait. Blood Coagulation and Fibrinolysis, 2012, 23, 268-270.	0.5	8
26	Structural Genetic Variation in the Context of Somatic Mosaicism. Methods in Molecular Biology, 2012, 838, 249-272.	0.4	34
27	Age-Related Somatic Structural Changes in the Nuclear Genome of Human Blood Cells. American Journal of Human Genetics, 2012, 90, 217-228.	2.6	168
28	Common pathogenetic mechanism involving human chromosome 18 in familial and sporadic ileal carcinoid tumors. Genes Chromosomes and Cancer, 2011, 50, 82-94.	1.5	79
29	Focal amplifications are associated with high grade and recurrences in stage Ta bladder carcinoma. International Journal of Cancer, 2010, 126, 1390-1402.	2.3	54
30	Somatic mosaicism for chromosome X and Y aneuploidies in monozygotic twins heterozygous for sickle cell disease mutation. American Journal of Medical Genetics, Part A, 2010, 152A, 2595-2598.	0.7	19
31	Frequent genetic differences between matched primary and metastatic breast cancer provide an approach to identification of biomarkers for disease progression. European Journal of Human Genetics, 2010, 18, 560-568.	1.4	42
32	Recurrent genomic alterations in benign and malignant pheochromocytomas and paragangliomas revealed by whole-genome array comparative genomic hybridization analysis. Endocrine-Related Cancer, 2010, 17, 561-579.	1.6	29
33	Integrative epigenomic and genomic analysis of malignant pheochromocytoma. Experimental and Molecular Medicine, 2010, 42, 484.	3.2	32
34	Genome-wide microarray-based comparative genomic hybridization analysis of lymphoplasmacytic lymphomas reveals heterogeneous aberrations. Leukemia and Lymphoma, 2009, 50, 1528-1534.	0.6	8
35	Characterization of novel and complex genomic aberrations in glioblastoma using a 32K BAC array. Neuro-Oncology, 2009, 11, 803-818.	0.6	43
36	Genomeâ€wide highâ€resolution analysis of DNA copy number alterations in NF1â€associated malignant peripheral nerve sheath tumors using 32K BAC array. Genes Chromosomes and Cancer, 2009, 48, 897-907.	1.5	50

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37	Tissue-specific variation in DNA methylation levels along human chromosome 1. Epigenetics and Chromatin, 2009, 2, 7.	1.8	54
38	Phenotypic and Genetic Discordance in Monozygotic Twins with Sickle Anemia and Ã°-Thalassemia.. Blood, 2009, 114, 5084-5084.	0.6	0
39	Profiling of copy number variations (CNVs) in healthy individuals from three ethnic groups using a human genome 32â€‰K BAC-clone-based array. Human Mutation, 2008, 29, 398-408.	1.1	46
40	Somatic mosaicism for copy number variation in differentiated human tissues. Human Mutation, 2008, 29, 1118-1124.	1.1	184
41	Distal 22q11.2 microduplication encompassing the BCR gene. American Journal of Medical Genetics, Part A, 2008, 146A, 3075-3081.	0.7	30
42	Phenotypically Concordant and Discordant Monozygotic Twins Display Different DNA Copy-Number-Variation Profiles. American Journal of Human Genetics, 2008, 82, 763-771.	2.6	533
43	Autoantibodies to glutathione S-transferase theta 1 in patients with primary sclerosing cholangitis and other autoimmune diseases. Journal of Autoimmunity, 2008, 30, 273-282.	3.0	16
44	A segmental maximum a posteriori approach to genome-wide copy number profiling. Bioinformatics, 2008, 24, 751-758.	1.8	29
45	The Mechanism of Cystic Fibrosis Transmembrane Conductance Regulator Transcriptional Repression during the Unfolded Protein Response. Journal of Biological Chemistry, 2008, 283, 12154-12165.	1.6	66
46	High-Resolution DNA Copy Number Profiling of Malignant Peripheral Nerve Sheath Tumors Using Targeted Microarray-Based Comparative Genomic Hybridization. Clinical Cancer Research, 2008, 14, 1015-1024.	3.2	119
47	A previously unrecognized microdeletion syndrome on chromosome 22 band q11.2 encompassing the BCR gene. American Journal of Medical Genetics, Part A, 2007, 143A, 2178-2184.	0.7	42
48	Comprehensive genetic and epigenetic analysis of sporadic meningioma for macro-mutations on 22q and micro-mutations within the NF2 locus. BMC Genomics, 2007, 8, 16.	1.2	67
49	Analysis of copy number variation in the normal human population within a region containing complex segmental duplications on 22q11 using high-resolution array-CGH. Genomics, 2006, 88, 152-162.	1.3	13
50	Chromosome 22 array-CGH profiling of breast cancer delimited minimal common regions of genomic imbalances and revealed frequent intra-tumoral genetic heterogeneity. International Journal of Oncology, 2006, 29, 935.	1.4	5
51	Microarray-based survey of CpG islands identifies concurrent hyper- and hypomethylation patterns in tissues derived from patients with breast cancer. Genes Chromosomes and Cancer, 2006, 45, 656-667.	1.5	40
52	Detailed assessment of chromosome 22 aberrations in sporadic pheochromocytoma using array-CGH. International Journal of Cancer, 2006, 118, 1159-1164.	2.3	24
53	Identification of limited regions of genetic aberrations in patients affected with Wilms' tumor using a tiling-path chromosome 22 array. International Journal of Cancer, 2006, 119, 571-578.	2.3	10
54	Chromosome 22 array-CGH profiling of breast cancer delimited minimal common regions of genomic imbalances and revealed frequent intra-tumoral genetic heterogeneity. International Journal of Oncology, 2006, 29, 935-45.	1.4	15

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55	Copy-number polymorphisms: mining the tip of an iceberg. Trends in Genetics, 2005, 21, 315-317.	2.9	45
56	High-resolution gene copy number and expression profiling of human chromosome 22 in ovarian carcinomas. Genes Chromosomes and Cancer, 2005, 42, 228-237.	1.5	21
57	Localization of a putative low-penetrance ependymoma susceptibility locus to 22q11 using a chromosome 22 tiling-path genomic microarray. Genes Chromosomes and Cancer, 2005, 43, 329-338.	1.5	25
58	Chromosome 22 tiling-path array-CGH analysis identifies germ-line- and tumor-specific aberrations in patients with glioblastoma multiforme. Genes Chromosomes and Cancer, 2005, 44, 161-169.	1.5	30
59	Identification of genetic aberrations on chromosome 22 outside theNF2locus in schwannomatosis and neurofibromatosis type 2. Human Mutation, 2005, 26, 540-549.	1.1	29
60	High-resolution array-CGH profiling of germline and tumor-specific copy number alterations on chromosome 22 in patients affected with schwannomas. Human Genetics, 2005, 118, 35-44.	1.8	19
61	Comprehensive DNA Copy Number Profiling of Meningioma Using a Chromosome 1 Tiling Path Microarray Identifies Novel Candidate Tumor Suppressor Loci. Cancer Research, 2005, 65, 2653-2661.	0.4	42
62	Exon Array CGH: Detection of Copy-Number Changes at the Resolution of Individual Exons in the Human Genome. American Journal of Human Genetics, 2005, 76, 750-762.	2.6	132
63	DNA copy-number analysis of the 22q11 deletion-syndrome region using array-CGH with genomic and PCR-based targets. International Journal of Molecular Medicine, 2004, 13, 273.	1.8	15
64	LARGE can functionally bypass Î±-dystroglycan glycosylation defects in distinct congenital muscular dystrophies. Nature Medicine, 2004, 10, 696-703.	15.2	253
65	Genomic microarrays in the spotlight. Trends in Genetics, 2004, 20, 87-94.	2.9	155
66	Molecular Recognition by LARGE Is Essential for Expression of Functional Dystroglycan. Cell, 2004, 117, 953-964.	13.5	243
67	DNA copy-number analysis of the 22q11 deletion-syndrome region using array-CGH with genomic and PCR-based targets. International Journal of Molecular Medicine, 2004, 13, 273-9.	1.8	43
68	NF2 Tumor Suppressor Gene: A Comprehensive and Efficient Detection of Somatic Mutations by Denaturing HPLC and Microarray-CGH. NeuroMolecular Medicine, 2003, 3, 41-52.	1.8	12
69	Development of NF2 gene specific, strictly sequence defined diagnostic microarray for deletion detection. Journal of Molecular Medicine, 2003, 81, 443-451.	1.7	31
70	Strong conservation of the human NF2 locus based on sequence comparison in five species. Mammalian Genome, 2003, 14, 526-536.	1.0	7
71	Does chromosome 22 have anything to do with sex determination: Further studies on a 46,XX,22q11.2 del male. American Journal of Medical Genetics Part A, 2003, 123A, 64-67.	2.4	10
72	Coincidence of synteny breakpoints with malignancy-related deletions on human chromosome 3. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6622-6627.	3.3	14

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73	The transcriptional map of the common eliminated region 1 (C3CER1) in 3p21.3. European Journal of Human Genetics, 2002, 10, 52-61.	1.4	37
74	A full-coverage, high-resolution human chromosome 22 genomic microarray for clinical and research applications. Human Molecular Genetics, 2002, 11, 3221-3229.	1.4	129
75	Mouse cytosolic and mitochondrial deoxyribonucleotidases: cDNA cloning of the mitochondrial enzyme, gene structures, chromosomal mapping and comparison with the human orthologs. Gene, 2002, 294, 109-117.	1.0	10
76	Comparative human/murine sequence analysis of the common eliminated region 1 from human 3p21.3. Mammalian Genome, 2002, 13, 646-655.	1.0	16
77	FISH-mapping of a 100-kb terminal 22q13 deletion. Human Genetics, 2002, 110, 439-443.	1.8	78
78	A region close to Tp53 shows LOH in familial breast cancer. International Journal of Molecular Medicine, 2002, 9, 405-9.	1.8	2
79	The LZTFL1 Gene Is a Part of a Transcriptional Map Covering 250 kb within the Common Eliminated Region 1 (C3CER1) in 3p21.3. Genomics, 2001, 73, 10-19.	1.3	33
80	Analysis of short stature homeobox-containing gene (SHOX) and auxological phenotype in dyschondrosteosis and isolated Madelung deformity. Human Genetics, 2001, 109, 551-558.	1.8	60
81	High resolution deletion analysis of constitutional DNA from neurofibromatosis type 2 (NF2) patients using microarray-CGH. Human Molecular Genetics, 2001, 10, 271-282.	1.4	147
82	A case of dermatofibrosarcoma protuberans of the vulva with a COL1A1/PDGFB fusion identical to a case of giant cell fibroblastoma. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2000, 437, 95-100.	1.4	42
83	Fine mapping of the constitutional translocation t(11;22)(q23;q11). Human Genetics, 2000, 106, 506-516.	1.8	20
84	Mutations in short stature homeobox containing gene (SHOX) in dyschondrosteosis but not in hypochondroplasia. Human Genetics, 2000, 107, 145-149.	1.8	37
85	Characterization of Five Novel Human Genes in the 11q13-q22 Region. Biochemical and Biophysical Research Communications, 2000, 273, 90-94.	1.0	13
86	Duplications on Human Chromosome 22 Reveal a Novel Ret Finger Protein-Like Gene Family with Sense and Endogenous Antisense Transcripts. Genome Research, 1999, 9, 803-814.	2.4	32
87	Psoriasis Upregulated Phorbolin-1 Shares Structural but not Functional Similarity to the mRNA-Editing Protein Apobec-1. Journal of Investigative Dermatology, 1999, 113, 162-169.	0.3	51
88	FMIP, a novel Fms-interacting protein, affects granulocyte/macrophage differentiation. Oncogene, 1999, 18, 6488-6495.	2.6	47
89	Severe phenotype of neurofibromatosis type 2 in a patient with a 7.4-MB constitutional deletion on chromosome 22: Possible localization of a neurofibromatosis type 2 modifier gene?. , 1999, 25, 184-190.		37
90	TOM1Genes Map to Human Chromosome 22q13.1 and Mouse Chromosome 8C1 and Encode Proteins Similar to the Endosomal Proteins HGS and STAM. Genomics, 1999, 57, 380-388.	1.3	26

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91	A 1-Mb PAC Contig Spanning the Common Eliminated Region 1 (CER1) in Microcell Hybrid-Derived SCID Tumors. Genomics, 1999, 62, 147-155.	1.3	28
92	Genomic Structure, 5â€² Flanking Sequences, and Precise Localization in 1P31.1 of the Human Prostaglandin F Receptor Gene. Biochemical and Biophysical Research Communications, 1999, 254, 413-416.	1.0	17
93	The Mouse Ortholog of the HumanSMARCB1Gene Encodes Two Splice Forms. Biochemical and Biophysical Research Communications, 1999, 257, 886-890.	1.0	27
94	Characterization of the MEN1 Ortholog in Zebrafish. Biochemical and Biophysical Research Communications, 1999, 264, 404-408.	1.0	30
95	Various regions within the alpha-helical domain of theCOL1A1 gene are fused to the second exon of thePDGFB gene in dermatofibrosarcomas and giant-cell fibroblastomas. , 1998, 23, 187-193.		158
96	Characterization of the human NIPSNAP1 gene from 22q12: a member of a novel gene family. Gene, 1998, 212, 13-20.	1.0	48
97	A case of dermatofibrosarcoma protuberans with a ring chromosome 5 and a rearranged chromosome 22 containing amplified COL1A1 and PDGFB sequences. Cancer Letters, 1998, 133, 129-134.	3.2	35
98	Cloning, Expression Pattern, and Chromosomal Assignment to 16q23 of the Human Î³-Adaptin Gene (ADTG). Genomics, 1998, 50, 275-280.	1.3	7
99	Deregulation of the platelet-derived growth factor Î²-chain gene via fusion with collagen gene COL1A1 in dermatof ibrosarcoma protuberans and giant-cell fibroblastoma. Nature Genetics, 1997, 15, 95-98.	9.4	510
100	Characterization of the mouse beta-prime adaptin gene; cDNA sequence, genomic structure, and chromosomal localization. Mammalian Genome, 1997, 8, 651-656.	1.0	7
101	1p and 3p deletions in meningiomas without detectable aberrations of chromosome 22 identified by comparative genomic hybridization. , 1997, 20, 419-424.		29
102	Regional Localization of over 300 Loci on Human Chromosome 22 Using a Somatic Cell Hybrid Mapping Panel. Genomics, 1996, 35, 275-288.	1.3	28
103	Structure of the Promoter and Genomic Organization of the Human Î²â€²-Adaptin Gene (BAM22) from Chromosome 22q12. Genomics, 1996, 36, 112-117.	1.3	27
104	Sequence and Expression of the Mouse Homologue to Human Phospholipase C Î²3 Neighboring Gene. Biochemical and Biophysical Research Communications, 1996, 223, 335-340.	1.0	8
105	Characterization of a second human clathrin heavy chain polypeptide gene (CLH-22) from chromosome 22q11. Human Molecular Genetics, 1996, 5, 625-631.	1.4	54
106	Isolation and mapping of cosmid markers on human chromosome 22, including one within the submicroscopically deleted region of DiGeorge syndrome. Human Genetics, 1994, 93, 248-254.	1.8	30
107	Deletions on chromosome 22 in sporadic meningioma. Genes Chromosomes and Cancer, 1994, 10, 122-130.	1.5	115
108	Chromosomal deletions in anaplastic meningiomas suggest multiple regions outside chromosome 22 as important in tumor progression. International Journal of Cancer, 1994, 56, 354-357.	2.3	90

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109	Evidence for the complete inactivation of the NF2 gene in the majority of sporadic meningiomas. Nature Genetics, 1994, 6, 180-184.	9.4	514
110	Physical Mapping of the NF2/Meningioma Region on Human Chromosome 22q12. Genomics, 1994, 19, 52-59.	1.3	18
111	Regional fine mapping of the Î² crystallin genes on chromosome 22 excludes these genes as physically linked markers for neurofibromatosis type 2. Genes Chromosomes and Cancer, 1993, 8, 112-118.	1.5	10
112	Alteration in a new gene encoding a putative membrane-organizing protein causes neuro-fibromatosis type 2. Nature, 1993, 363, 515-521.	13.7	1,351
113	The Genes for Oncostatin M (OSM) and Leukemia Inhibitory Factor (LIF) Are Tightly Linked on Human Chromosome 22. Genomics, 1993, 17, 136-140.	1.3	52
114	Microdeletions within 22q11 associated with sporadic and familial DiGeorge syndrome. Genomics, 1991, 10, 201-206.	1.3	241
115	A map of 22 loci on human chromosome 22. Genomics, 1991, 11, 709-719.	1.3	30
116	The Molecular Genetics of Meningiomas. Brain Pathology, 1990, 1, 19-24.	2.1	55
117	Isolation of anonymous, polymorphic DNA fragments from human chromosome 22q12-qter. Human Genetics, 1990, 84, 219-222.	1.8	26