Karoly Szuhai

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2983216/publications.pdf

Version: 2024-02-01

214	10,635	30551	46524
papers	citations	56 h-index	93 g-index

222	222	222	15610
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Sarcoma Derived from Cultured Mesenchymal Stem Cells. Stem Cells, 2007, 25, 371-379.	1.4	601
2	Chromosome Segregation Errors as a Cause of DNA Damage and Structural Chromosome Aberrations. Science, 2011, 333, 1895-1898.	6.0	491
3	Somatic mosaic IDH1 and IDH2 mutations are associated with enchondroma and spindle cell hemangioma in Ollier disease and Maffucci syndrome. Nature Genetics, 2011, 43, 1256-1261.	9.4	488
4	Osteosarcoma originates from mesenchymal stem cells in consequence of aneuploidization and genomic loss of Cdkn2. Journal of Pathology, 2009, 219, 294-305.	2.1	234
5	EWSR1-CREB1 and EWSR1-ATF1 Fusion Genes in Angiomatoid Fibrous Histiocytoma. Clinical Cancer Research, 2007, 13, 7322-7328.	3.2	207
6	Array-CGH detection of micro rearrangements in mentally retarded individuals: clinical significance of imbalances present both in affected children and normal parents. Journal of Medical Genetics, 2005, 43, 180-186.	1.5	190
7	Oncogenomic analysis of mycosis fungoides reveals major differences with SÃ©zary syndrome. Blood, 2009, 113, 127-136.	0.6	188
8	The NFATc2 Gene Is Involved in a Novel Cloned Translocation in a Ewing Sarcoma Variant That Couples Its Function in Immunology to Oncology. Clinical Cancer Research, 2009, 15, 2259-2268.	3.2	180
9	Peters Plus Syndrome Is Caused by Mutations in B3GALTL, a Putative Glycosyltransferase. American Journal of Human Genetics, 2006, 79, 562-566.	2.6	178
10	Opening the archives for state of the art tumour genetic research: sample processing for array-CGH using decalcified, formalin-fixed, paraffin-embedded tissue-derived DNA samples. BMC Research Notes, 2011, 4, 1.	0.6	177
11	Novel and Highly Recurrent Chromosomal Alterations in Sèzary Syndrome. Cancer Research, 2008, 68, 2689-2698.	0.4	176
12	Role of the transcription factor T (brachyury) in the pathogenesis of sporadic chordoma: a genetic and functionalâ€based study. Journal of Pathology, 2011, 223, 327-335.	2.1	174
13	Mutation Analysis of H3F3A and H3F3B as a Diagnostic Tool for Giant Cell Tumor of Bone and Chondroblastoma. American Journal of Surgical Pathology, 2015, 39, 1576-1583.	2.1	174
14	Human cardiomyocyte progenitor cell transplantation preserves long-term function of the infarcted mouse myocardium. Cardiovascular Research, 2009, 83, 527-535.	1.8	158
15	Guidelines for molecular karyotyping in constitutional genetic diagnosis. European Journal of Human Genetics, 2007, 15, 1105-1114.	1.4	144
16	Gene-expression profiling and array-based CGH classify CD4+CD56+ hematodermic neoplasm and cutaneous myelomonocytic leukemia as distinct disease entities. Blood, 2007, 109, 1720-1727.	0.6	137
17	Local recurrence of myxofibrosarcoma is associated with increase in tumour grade and cytogenetic aberrations, suggesting a multistep tumour progression model. Modern Pathology, 2006, 19, 407-416.	2.9	130
18	Array-Based Comparative Genomic Hybridization Analysis Reveals Recurrent Chromosomal Alterations and Prognostic Parameters in Primary Cutaneous Large B-Cell Lymphoma. Journal of Clinical Oncology, 2006, 24, 296-305.	0.8	125

#	Article	IF	Citations
19	Cathepsin K Is the Principal Protease in Giant Cell Tumor of Bone. American Journal of Pathology, 2004, 165, 593-600.	1.9	113
20	A common single-nucleotide variant in T is strongly associated with chordoma. Nature Genetics, 2012, 44, 1185-1187.	9.4	112
21	Transactivating mutation of theMYOD1gene is a frequent event in adult spindle cell rhabdomyosarcoma. Journal of Pathology, 2014, 232, 300-307.	2.1	111
22	Real-time monitoring of rolling-circle amplification using a modified molecular beacon design. Nucleic Acids Research, 2002, 30, 66e-66.	6.5	110
23	Genomic imbalances associated with mullerian aplasia. Journal of Medical Genetics, 2007, 45, 228-232.	1.5	110
24	Selective resistance to the PARP inhibitor olaparib in a mouse model for BRCA1-deficient metaplastic breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8409-8414.	3.3	106
25	Frequent deletion of the CDKN2A locus in chordoma: analysis of chromosomal imbalances using array comparative genomic hybridisation. British Journal of Cancer, 2008, 98, 434-442.	2.9	104
26	Whole-genome array-CGH screening in undiagnosed syndromic patients: old syndromes revisited and new alterations. Cytogenetic and Genome Research, 2006, 115, 254-261.	0.6	103
27	The Role of EXT1 in Nonhereditary Osteochondroma: Identification of Homozygous Deletions. Journal of the National Cancer Institute, 2007, 99, 396-406.	3.0	101
28	Genomic alterations and gene expression in primary diffuse large Bâ€cell lymphomas of immuneâ€privileged sites: the importance of apoptosis and immunomodulatory pathways. Journal of Pathology, 2008, 216, 209-217.	2.1	100
29	Anti-EGFR Antibody Cetuximab Enhances the Cytolytic Activity of Natural Killer Cells toward Osteosarcoma. Clinical Cancer Research, 2012, 18, 432-441.	3.2	97
30	Genetic characterization of mesenchymal, clear cell, and dedifferentiated chondrosarcoma. Genes Chromosomes and Cancer, 2012, 51, 899-909.	1.5	95
31	Presence of a high amount of stroma and downregulation of SMAD4 predict for worse survival for stage I-II colon cancer patients. Cellular Oncology, 2009, 31, 169-78.	1.9	92
32	1q gain and CDT2 overexpression underlie an aggressive and highly proliferative form of Ewing sarcoma. Oncogene, 2012, 31, 1287-1298.	2.6	91
33	PRAME as a Potential Target for Immunotherapy in Metastatic Uveal Melanoma. JAMA Ophthalmology, 2017, 135, 541.	1.4	87
34	Actomyosin drives cancer cell nuclear dysmorphia and threatens genome stability. Nature Communications, 2017, 8, 16013.	5.8	87
35	Molecular Analysis of Gene Fusions in Bone and Soft Tissue Tumors by Anchored Multiplex PCRâ€“Based Targeted Next-Generation Sequencing. Journal of Molecular Diagnostics, 2018, 20, 653-663.	1.2	85
36	Simultaneous A8344G heteroplasmy and mitochondrial DNA copy number quantification in Myoclonus Epilepsy and Ragged-Red Fibers (MERRF) syndrome by a multiplex Molecular Beacon based real-time fluorescence PCR. Nucleic Acids Research, 2001, 29, 13e-13.	6.5	84

#	Article	IF	Citations
37	LSAMP, a novel candidate tumor suppressor gene in human osteosarcomas, identified by array comparative genomic hybridization. Genes Chromosomes and Cancer, 2009, 48, 679-693.	1.5	84
38	Molecular pathology and its diagnostic use in bone tumors. Cancer Genetics, 2012, 205, 193-204.	0.2	80
39	Malignant fibrous histiocytoma and fibrosarcoma of bone: a re-assessment in the light of currently employed morphological, immunohistochemical and molecular approaches. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2012, 461, 561-570.	1.4	78
40	Chemotherapy-resistant osteosarcoma is highly susceptible to IL-15-activated allogeneic and autologous NK cells. Cancer Immunology, Immunotherapy, 2011, 60, 575-586.	2.0	76
41	Sleeping Beauty transposon-based system for cellular reprogramming and targeted gene insertion in induced pluripotent stem cells. Nucleic Acids Research, 2013, 41, 1829-1847.	6.5	75
42	GRM1 is upregulated through gene fusion and promoter swapping in chondromyxoid fibroma. Nature Genetics, 2014, 46, 474-477.	9.4	75
43	Machine learning analysis of gene expression data reveals novel diagnostic and prognostic biomarkers and identifies therapeutic targets for soft tissue sarcomas. PLoS Computational Biology, 2019, 15, e1006826.	1.5	75
44	Ring chromosome formation as a novel escape mechanism in patients with inverted duplication and terminal deletion. European Journal of Human Genetics, 2007, 15, 548-555.	1.4	73
45	No genomic aberrations in Langerhans cell histiocytosis as assessed by diverse molecular technologies. Genes Chromosomes and Cancer, 2009, 48, 239-249.	1.5	71
46	COBRA: combined binary ratio labeling of nucleic-acid probes for multi-color fluorescence in situ hybridization karyotyping. Nature Protocols, 2006, 1, 264-275.	5.5	70
47	Fusion events lead to truncation of FOS in epithelioid hemangioma of bone. Genes Chromosomes and Cancer, 2015, 54, 565-574.	1.5	69
48	Connexin 26 mutations in cases of sensorineural deafness in eastern Austria. European Journal of Human Genetics, 2002, 10, 427-432.	1.4	68
49	No Haploinsufficiency but Loss of Heterozygosity for EXT in Multiple Osteochondromas. American Journal of Pathology, 2010, 177, 1946-1957.	1.9	67
50	Combined array-comparative genomic hybridization and single-nucleotide polymorphism-loss of heterozygosity analysis reveals complex genetic alterations in cervical cancer. BMC Genomics, 2007, 8, 53.	1.2	66
51	Secondary peripheral chondrosarcoma evolving from osteochondroma as a result of outgrowth of cells with functional EXT. Oncogene, 2012, 31, 1095-1104.	2.6	66
52	Cellular/intramuscular myxoma and grade I myxofibrosarcoma are characterized by distinct genetic alterations and specific composition of their extracellular matrix. Journal of Cellular and Molecular Medicine, 2009, 13, 1291-1301.	1.6	65
53	Report of a del22q11 in a patient with Mayer-Rokitansky-KÃ¼ster-Hauser (MRKH) anomaly and exclusion ofWNT-4,RAR-gamma, andRXR-alpha as major genes determining MRKH anomaly in a study of 25 affected women. American Journal of Medical Genetics, Part A, 2006, 140A, 1339-1342.	0.7	64
54	Cutaneous Anaplastic Large Cell Lymphoma and Peripheral T-Cell Lymphoma NOS Show Distinct Chromosomal Alterations and Differential Expression of Chemokine Receptors and Apoptosis Regulators. Journal of Investigative Dermatology, 2010, 130, 563-575.	0.3	62

#	Article	IF	Citations
55	Copy number variation in regions flanked (or unflanked) by duplicons among patients with developmental delay and/or congenital malformations; detection of reciprocal and partial Williams-Beuren duplications. European Journal of Human Genetics, 2006, 14, 180-189.	1.4	60
56	High-resolution copy number analysis of paraffin-embedded archival tissue using SNP BeadArrays. Genome Research, 2007, 17, 368-376.	2.4	60
57	Unscrambling the genomic chaos of osteosarcoma reveals extensive transcript fusion, recurrent rearrangements and frequent novel TP53 aberrations. Oncotarget, 2016, 7, 5273-5288.	0.8	60
58	Genomic analysis reveals recurrent deletion of JAKâ€STAT signaling inhibitors HNRNPK and SOCS1 in mycosis fungoides. Genes Chromosomes and Cancer, 2018, 57, 653-664.	1.5	56
59	The second European interdisciplinary Ewing sarcoma research summit - A joint effort to deconstructing the multiple layers of a complex disease. Oncotarget, 2016, 7, 8613-8624.	0.8	55
60	Simultaneous molecular karyotyping and mapping of viral DNA integration sites by 25-color COBRA-FISH. , 2000, 28, 92-97.		54
61	Longâ€“term culture of primary human lymphoblastic leukemia cells in the absence of serum or hematopoietic growth factors. Experimental Hematology, 2009, 37, 376-385.	0.2	54
62	A short-term in vivo model for giant cell tumor of bone. BMC Cancer, 2011, 11, 241.	1.1	54
63	Sequencing Overview of Ewing Sarcoma: A Journey across Genomic, Epigenomic and Transcriptomic Landscapes. International Journal of Molecular Sciences, 2015, 16, 16176-16215.	1.8	54
64	DNA methylation and transcriptional trajectories during human development and reprogramming of isogenic pluripotent stem cells. Nature Communications, 2017, 8, 908.	5.8	53
65	A Novel Strategy for Human Papillomavirus Detection and Genotyping with SybrGreen and Molecular Beacon Polymerase Chain Reaction. American Journal of Pathology, 2001, 159, 1651-1660.	1.9	52
66	Insights from genomic microarrays into structural chromosome rearrangements. American Journal of Medical Genetics, Part A, 2005, 132A, 36-40.	0.7	52
67	Small deletions but not methylation underlie CDKN2A/p16 loss of expression in conventional osteosarcoma. Genes Chromosomes and Cancer, 2010, 49, 1095-1103.	1.5	52
68	Array-comparative genomic hybridization of central chondrosarcoma. Cancer, 2006, 107, 380-388.	2.0	51
69	A homozygous deletion of a normal variation locus in a patient with hearing loss from non-consanguineous parents. Journal of Medical Genetics, 2009, 46, 412-417.	1.5	51
70	Mediator complex subunit 12 exon 2 mutation analysis in different subtypes of smooth muscle tumors confirms genetic heterogeneity. Human Pathology, 2013, 44, 1597-1604.	1.1	51
71	Tiling resolution array-CGH shows that somatic mosaic deletion of the EXT gene is causative in EXT gene mutation negative multiple osteochondromas patients. Human Mutation, 2011, 32, E2036-E2049.	1.1	50
72	DNA methylation profiling distinguishes Ewing-like sarcoma with EWSR1â€“NFATc2 fusion from Ewing sarcoma. Journal of Cancer Research and Clinical Oncology, 2019, 145, 1273-1281.	1.2	50

#	Article	IF	Citations
73	A 17q21.31 microdeletion encompassing the MAPT gene in a mentally impaired patient. Cytogenetic and Genome Research, 2006, 114, 89-92.	0.6	45
74	Genomic instability in giant cell tumor of bone. A study of 52 cases using DNA ploidy, relocalization FISH, and arrayâ€CGH analysis. Genes Chromosomes and Cancer, 2009, 48, 468-479.	1.5	45
75	Utility of FOS as diagnostic marker for osteoid osteoma and osteoblastoma. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2020, 476, 455-463.	1.4	44
76	Molecular and clinical characterization of de novo and familial cases with microduplication 3q29: guidelines for copy number variation case reporting. Cytogenetic and Genome Research, 2008, 123, 65-78.	0.6	43
77	Two distinct regions in 2q24.2â€q24.3 associated with idiopathic epilepsy. Epilepsia, 2010, 51, 2457-2460.	2.6	43
78	Generation of induced pluripotent stem cells from human foetal fibroblasts using the Sleeping Beauty transposon gene delivery system. Differentiation, 2013, 86, 30-37.	1.0	43
79	Aberrant Heparan Sulfate Proteoglycan Localization, Despite Normal Exostosin, in Central Chondrosarcoma. American Journal of Pathology, 2009, 174, 979-988.	1.9	42
80	Ewing sarcoma inhibition by disruption of <scp>EWSR1â€“FLI1</scp> transcriptional activity and reactivation of p53. Journal of Pathology, 2014, 233, 415-424.	2.1	42
81	Loss of p53 partially rescues embryonic development of Palb2 knockout mice but does not foster haploinsufficiency of Palb2 in tumour suppression. Journal of Pathology, 2011, 224, 10-21.	2.1	41
82	Human Extravillous Trophoblasts Penetrate Decidual Veins and Lymphatics before Remodeling Spiral Arteries during Early Pregnancy. PLoS ONE, 2017, 12, e0169849.	1.1	41
83	Single nucleotide polymorphism array analysis of chromosomal instability patterns discriminates rectal adenomas from carcinomas. Journal of Pathology, 2007, 212, 269-277.	2.1	39
84	Positioning of cervical carcinoma and Burkitt lymphoma translocation breakpoints with respect to the human papillomavirus integration cluster in FRA8C at 8q24.13. Cancer Genetics and Cytogenetics, 2004, 154, 1-9.	1.0	38
85	Genome-wide analysis of Ollier disease: Is it all in the genes?. Orphanet Journal of Rare Diseases, 2011, 6, 2.	1.2	36
86	Three new chondrosarcoma cell lines: one grade III conventional central chondrosarcoma and two dedifferentiated chondrosarcomas of bone. BMC Cancer, 2012, 12, 375.	1.1	36
87	Primary synovial sarcoma of the heart: a cytogenetic and molecular genetic analysis combining RT-PCR and COBRA-FISH of a case with a complex karyotype. Modern Pathology, 2004, 17, 1434-1439.	2.9	35
88	Disruption of Drosophila Rad50 causes pupal lethality, the accumulation of DNA double-strand breaks and the induction of apoptosis in third instar larvae. DNA Repair, 2004, 3, 603-615.	1.3	35
89	Distinct nuclear gene expression profiles in cells with mtDNA depletion and homoplasmic A3243G mutation. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2005, 578, 43-52.	0.4	35
90	Expression analysis of candidate breast tumour suppressor genes on chromosome 16q. Breast Cancer Research, 2005, 7, R998-1004.	2.2	35

#	Article	IF	Citations
91	Functional analyses of a human vascular tumor FOS variant identify a novel degradation mechanism and a link to tumorigenesis. Journal of Biological Chemistry, 2017, 292, 21282-21290.	1.6	35
92	Telatinib Is an Effective Targeted Therapy for Pseudomyogenic Hemangioendothelioma. Clinical Cancer Research, 2018, 24, 2678-2687.	3.2	35
93	Molecular cytogenetic characterization of four previously established and two newly established Ewing sarcoma cell lines. Cancer Genetics and Cytogenetics, 2006, 166, 173-179.	1.0	34
94	Establishment and detailed functional and molecular genetic characterisation of a novel sacral chordoma cell line, MUG-Chor1. International Journal of Oncology, 2012, 40, 443-51.	1.4	33
95	Heterogeneous and Complex Rearrangements of Chromosome Arm 6q in Chondromyxoid Fibroma. American Journal of Pathology, 2010, 177, 1365-1376.	1.9	32
96	Array CGH detection of a cryptic deletion in a complex chromosome rearrangement. Human Genetics, 2005, 116, 390-394.	1.8	31
97	Inhibition of Bcl-2 family members sensitizes mesenchymal chondrosarcoma to conventional chemotherapy: report on a novel mesenchymal chondrosarcoma cell line. Laboratory Investigation, 2016, 96, 1128-1137.	1.7	31
98	A novel t(6;14)(q25â¼q27;q32) in acute myelocytic leukemia involves the BCL11B gene. Cancer Genetics and Cytogenetics, 2004, 149, 72-76.	1.0	30
99	Hypoparathyroidism-retardation-dysmorphism syndrome in a girl: A new variant not caused by aTBCEmutation-clinical report and review. American Journal of Medical Genetics, Part A, 2006, 140A, 611-617.	0.7	30
100	CXCL14, CXCR7 expression and CXCR4 splice variant ratio associate with survival and metastases in Ewing sarcoma patients. European Journal of Cancer, 2015, 51, 2624-2633.	1.3	30
101	Recurrent Chromosome 22 Deletions in Osteoblastoma Affect Inhibitors of the Wnt/Beta-Catenin Signaling Pathway. PLoS ONE, 2013, 8, e80725.	1.1	29
102	PRAME and HLA Class I expression patterns make synovial sarcoma a suitable target for PRAME specific T-cell receptor gene therapy. OncoImmunology, 2018, 7, e1507600.	2.1	28
103	Does <scp>CSF</scp>1 overexpression or rearrangement influenceÂbiological behaviour in tenosynovial giant cellÂtumours of the knee?. Histopathology, 2019, 74, 332-340.	1.6	28
104	Chromosomal and Microsatellite Instability of Adenocarcinomas and Dysplastic Lesions (DALM) in Ulcerative Colitis. Diagnostic Molecular Pathology, 2006, 15, 216-222.	2.1	27
105	Array CGH analysis identifies two distinct subgroups of primary angiosarcoma of bone. Genes Chromosomes and Cancer, 2015, 54, 72-81.	1.5	27
106	BMP-SMAD Signaling Regulates Lineage Priming, but Is Dispensable for Self-Renewal in Mouse Embryonic Stem Cells. Stem Cell Reports, 2016, 6, 85-94.	2.3	27
107	Breakpoint characterization of large deletions in EXT1 or EXT2 in 10 Multiple Osteochondromas families. BMC Medical Genetics, 2011, 12, 85.	2.1	26
108	Simultaneous mapping of human papillomavirus integration sites and molecular karyotyping in short-term cultures of cervical carcinomas by using 49-color combined binary ratio labeling fluorescence in situ hybridization. Cancer Genetics and Cytogenetics, 2002, 134, 145-150.	1.0	25

#	Article	IF	Citations
109	Genomic array and expression analysis of frequent high-level amplifications in adenocarcinomas of the gastro-esophageal junction. Cancer Genetics and Cytogenetics, 2006, 166, 157-162.	1.0	25
110	Detection and molecular cytogenetic characterization of a novel ring chromosome in a histological variant of Ewing sarcoma. Cancer Genetics and Cytogenetics, 2007, 172, 12-22.	1.0	25
111	Kinome profiling of myxoid liposarcoma reveals NF-kappaB-pathway kinase activity and Casein Kinase II inhibition as a potential treatment option. Molecular Cancer, 2010, 9, 257.	7.9	25
112	Notochordal Tumors. Surgical Pathology Clinics, 2017, 10, 637-656.	0.7	25
113	Expanding the editable genome and CRISPRâ€“Cas9 versatility using DNA cutting-free gene targeting based on in trans paired nicking. Nucleic Acids Research, 2020, 48, 974-995.	6.5	25
114	Familial Adenomatous Polyposis-Associated Desmoids Display Significantly More Genetic Changes than Sporadic Desmoids. PLoS ONE, 2011, 6, e24354.	1.1	24
115	Expanding the Spectrum of EWSR1-NFATC2-rearranged Benign Tumors. American Journal of Surgical Pathology, 2021, 45, 1669-1681.	2.1	24
116	Diagnosis of genetic abnormalities in developmentally delayed patients: A new strategy combining MLPA and array-CGH. American Journal of Medical Genetics, Part A, 2007, 143A, 610-614.	0.7	22
117	Differences in telomerase expression by the CD1a+ cells in Langerhans cell histiocytosis reflect the diverse clinical presentation of the disease. Journal of Pathology, 2007, 212, 188-197.	2.1	22
118	GJB2 Mutations in Hearing Impairment: Identification of a Broad Clinical Spectrum for Improved Genetic Counseling. Laryngoscope, 2005, 115, 461-465.	1.1	21
119	Non-Random mtDNA Segregation Patterns Indicate a Metastable Heteroplasmic Segregation Unit in m.3243A>G Cybrid Cells. PLoS ONE, 2012, 7, e52080.	1.1	21
120	Osteosarcoma Derived from Cultured Mesenchymal Stem Cells.. Blood, 2006, 108, 2554-2554.	0.6	21
121	Analysis of stromal cells in osteofibrous dysplasia and adamantinoma of long bones. Modern Pathology, 2012, 25, 56-64.	2.9	20
122	<scp>CD</scp>99â€positive undifferentiated round cell sarcoma diagnosed on fine needle aspiration cytology, later found to harbour a <scp>CIC</scp>â€<scp>DUX</scp>4 translocation: a recently described entity. Cytopathology, 2014, 25, 129-132.	0.4	20
123	Expression of the immune regulation antigen CD70 in osteosarcoma. Cancer Cell International, 2015, 15, 31.	1.8	20
124	Optimized amplification and fluorescent labeling of small cell samples for genomic array-CGH. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2007, 71A, 585-591.	1.1	19
125	Multiplex ligationâ€dependent probe amplification and fluorescence in situ hybridization are complementary techniques to detect cytogenetic abnormalities in multiple myeloma. Genes Chromosomes and Cancer, 2013, 52, 785-793.	1.5	19
126	Coronaviruses and arteriviruses display striking differences in their cyclophilin A-dependence during replication in cell culture. Virology, 2018, 517, 148-156.	1.1	19

#	Article	IF	Citations
127	Nodular fasciitis: a comprehensive, time-correlated investigation of 17 cases. Modern Pathology, 2021, 34, 2192-2199.	2.9	19
128	A balanced t(5;17) (p15;q22-23) in chondroblastoma: frequency of the re-arrangement and analysis of the candidate genes. BMC Cancer, 2009, 9, 393.	1.1	18
129	Multicolor fluorescence in situ hybridization analysis of a synovial sarcoma of the larynx with a t(X;18)(p11.2;q11.2) and trisomies 2 and 8. Cancer Genetics and Cytogenetics, 2004, 153, 48-52.	1.0	17
130	Establishment and cytogenetic characterization of a human acute lymphoblastic leukemia cell line (ALL-VG) with ETV6/ABL1 rearrangement. Cancer Genetics and Cytogenetics, 2008, 185, 37-42.	1.0	17
131	p120-catenin prevents multinucleation through control of MKLP1-dependent RhoA activity during cytokinesis. Nature Communications, 2016, 7, 13874.	5.8	17
132	Establishment and characterization of a new human myxoid liposarcoma cell line (DL-221) with the FUS-DDIT3 translocation. Laboratory Investigation, 2016, 96, 885-894.	1.7	17
133	Interstitial deletion of 6q without phenotypic effect. American Journal of Medical Genetics, Part A, 2007, 143A, 1354-1357.	0.7	16
134	Array-based comparative genomic hybridisation analysis reveals recurrent chromosomal alterations in primary diffuse large B cell lymphoma of bone. Journal of Clinical Pathology, 2010, 63, 1095-1100.	1.0	16
135	Molecular Pathology of Bone Tumors. Journal of Molecular Diagnostics, 2019, 21, 171-182.	1.2	16
136	Translocase of the outer mitochondrial membrane complex subunit 20 (TOMM20) facilitates cancer aggressiveness and therapeutic resistance in chondrosarcoma. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165962.	1.8	16
137	BRCA2 heterozygosity delays cytokinesis in primary human fibroblasts. Cellular Oncology, 2009, 31, 191-201.	1.9	16
138	Genomic analysis of early adenocarcinoma of the esophagus or gastroesophageal junction: Tumor progression is associated with alteration of 1q and 8p sequences. Genes Chromosomes and Cancer, 2006, 45, 516-525.	1.5	15
139	Characterization of a New Human Cell Line (CH-3573) Derived from a Grade II Chondrosarcoma with Matrix Production. Pathology and Oncology Research, 2012, 18, 793-802.	0.9	15
140	Intronic deletion and duplication proximal of the EXT1 gene: A novel causative mechanism for multiple osteochondromas. Genes Chromosomes and Cancer, 2013, 52, 431-436.	1.5	15
141	Expression of CCL21 in Ewing sarcoma shows an inverse correlation with metastases and is a candidate target for immunotherapy. Cancer Immunology, Immunotherapy, 2016, 65, 995-1002.	2.0	15
142	Mutation-driven epigenetic alterations as a defining hallmark of central cartilaginous tumours, giant cell tumour of bone and chondroblastoma. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2020, 476, 135-146.	1.4	15
143	Unraveling the Resistance of IGF-Pathway Inhibition in Ewing Sarcoma. Cancers, 2020, 12, 3568.	1.7	15
144	Rapid detection of genomic imbalances using micro-arrays consisting of pooled BACs covering all human chromosome arms. Nucleic Acids Research, 2005, 33, e159-e159.	6.5	14

#	Article	IF	Citations
145	Physical status of multiple human papillomavirus genotypes in flow-sorted cervical cancer cells. Cancer Genetics and Cytogenetics, 2007, 175, 132-137.	1.0	14
146	Deletions encompassing 1q41q42.1 and clinical features of autosomal dominant Robinow syndrome. Clinical Genetics, 2010, 77, 404-407.	1.0	14
147	Activation of the vitamin D receptor selectively interferes with calcineurin-mediated inflammation: a clinical evaluation in the abdominal aortic aneurysm. Laboratory Investigation, 2016, 96, 784-790.	1.7	14
148	Oncogenic functions of hMDMX in in vitro transformation of primary human fibroblasts and embryonic retinoblasts. Molecular Cancer, 2011, 10, 111.	7.9	13
149	Maternally inherited partial monosomy 9p (pterâ€‰â†'â€‰p24.1) and partial trisomy 20p (pterâ€‰â†'â€‰p12.1) characterized by microarray comparative genomic hybridization. American Journal of Medical Genetics, Part A, 2011, 155, 2754-2761.	0.7	13
150	MLPA is a powerful tool for detecting lymphoblastic transformation in chronic myeloid leukemia and revealing the clonal origin of relapse in pediatric acute lymphoblastic leukemia. Cancer Genetics, 2012, 205, 465-469.	0.2	13
151	<scp>DOG</scp>1 expression in giantâ€cellâ€containing bone tumours. Histopathology, 2016, 68, 942-945.	1.6	13
152	More Cases of Benign Testicular Teratomas are Detected in Adults than in Children. A Clinicopathological Study of 543 Testicular Germ Cell Tumor Cases. Pathology and Oncology Research, 2017, 23, 513-517.	0.9	13
153	High-Throughput Copy Number Profiling by Digital Multiplex Ligation-Dependent Probe Amplification in Multiple Myeloma. Journal of Molecular Diagnostics, 2018, 20, 777-788.	1.2	13
154	Presence of a High Amount of Stroma and Downregulation of SMAD4 Predict for Worse Survival for Stage Iâ€“II Colon Cancer Patients. Analytical Cellular Pathology, 2009, 31, 169-178.	0.7	13
155	Evaluation of high-resolution microarray platforms for genomic profiling of bone tumours. BMC Research Notes, 2010, 3, 223.	0.6	12
156	Centriole movements in mammalian epithelial cells during cytokinesis. BMC Cell Biology, 2010, 11, 34.	3.0	12
157	Paratesticular desmoplastic small round cell tumour: an unusual tumour with an unusual fusion; cytogenetic and molecular genetic analysis combining RT-PCR and COBRA-FISH. Clinical Sarcoma Research, 2012, 2, 3.	2.3	12
158	Array-CGH Analysis of Cutaneous Anaplastic Large Cell Lymphoma. Methods in Molecular Biology, 2013, 973, 197-212.	0.4	12
159	No TP63 rearrangements in a selected group of primary cutaneous CD30+ lymphoproliferative disorders with aggressive clinical course. Blood, 2016, 128, 141-143.	0.6	12
160	FOS Rearrangement and Expression in Cementoblastoma. American Journal of Surgical Pathology, 2021, 45, 690-693.	2.1	12
161	Chromosome abnormalities in two patients with features of autosomal dominant Robinow syndrome. American Journal of Medical Genetics, Part A, 2007, 143A, 1790-1795.	0.7	11
162	â€˜The chicken or the egg?â€™ dilemma strikes back for the controlling mechanism in chordoma[#]. Journal of Pathology, 2012, 228, 261-265.	2.1	11

#	ARTICLE	IF	CITATIONS
163	Human melanoma brain metastases cell line MUG-Mel1, isolated clones and their detailed characterization. Scientific Reports, 2019, 9, 4096.	1.6	11
164	Loss of <scp>NF2</scp> defines a genetic subgroup of <scp>nonâ€FOS</scp>â€rearranged osteoblastoma. Journal of Pathology: Clinical Research, 2020, 6, 231-237.	1.3	11
165	The impact of monosomies, trisomies and segmental aneuploidies on chromosomal stability. PLoS ONE, 2022, 17, e0268579.	1.1	11
166	Sequential and hierarchical chromosomal changes and chromosome instability are distinct features of high hyperdiploid pediatric acute lymphoblastic leukemia. Pediatric Blood and Cancer, 2014, 61, 2208-2214.	0.8	10
167	Further Evidence of the Existence of Benign Teratomas of the Postpubertal Testis. American Journal of Surgical Pathology, 2014, 38, 580-581.	2.1	10
168	Novel splice variants of CXCR4 identified by transcriptome sequencing. Biochemical and Biophysical Research Communications, 2015, 466, 89-94.	1.0	10
169	Comprehensive profiling of disease-relevant copy number aberrations for advanced clinical diagnostics of pediatric acute lymphoblastic leukemia. Modern Pathology, 2020, 33, 812-824.	2.9	10
170	GRM1 Immunohistochemistry Distinguishes Chondromyxoid Fibroma From its Histologic Mimics. American Journal of Surgical Pathology, 2022, 46, 1407-1414.	2.1	10
171	A Rett syndrome patient with a ring X chromosome: further evidence for skewing of X inactivation and heterogeneity in the aetiology of the disease. European Journal of Human Genetics, 2001, 9, 171-177.	1.4	9
172	A complex rearrangement on chromosome 22 affecting both homologues; haplo-insufficiency of the Cat eye syndrome region may have no clinical relevance. Human Genetics, 2006, 120, 77-84.	1.8	9
173	Angiomatoid Fibrous Histiocytoma: Pleomorphic Variant Associated with Multiplication of EWSR1-CREB1 Fusion Gene. Pathology and Oncology Research, 2012, 18, 545-548.	0.9	9
174	Breast cancer dormancy is associated with a 4NG1 state and not senescence. Npj Breast Cancer, 2021, 7, 140.	2.3	9
175	Large-scale genome editing based on high-capacity adenovectors andÂCRISPR-Cas9 nucleases rescues full-length dystrophin synthesis in DMD muscle cells. Nucleic Acids Research, 2022, 50, 7761-7782.	6.5	9
176	Mesenchymal stromal cells of osteosarcoma patients do not show evidence of neoplastic changes during long-term culture. Clinical Sarcoma Research, 2015, 5, 16.	2.3	8
177	Bioorthogonally Applicable Fluorescence Deactivation Strategy for Receptor Kinetics Study and Theranostic Pretargeting Approaches. ChemBioChem, 2018, 19, 1758-1765.	1.3	8
178	Attenuated isolated 3â€™ signal: A highly challenging therapy relevant ALK FISH pattern in NSCLC. Lung Cancer, 2020, 143, 80-85.	0.9	8
179	Gene fusions in vascular tumors and their underlying molecular mechanisms. Expert Review of Molecular Diagnostics, 2021, 21, 897-909.	1.5	8
180	Transcriptional progression during meiotic prophase I reveals sex-specific features and X chromosome dynamics in human fetal female germline. PLoS Genetics, 2021, 17, e1009773.	1.5	8

#	Article	IF	Citations
181	Generation of Fibrodysplasia ossificans progressiva and control integration free iPSC lines from periodontal ligament fibroblasts. Stem Cell Research, 2019, 41, 101639.	0.3	7
182	Vascular Tumor Recapitulated in Endothelial Cells from hiPSCs Engineered to Express the SERPINE1-FOSB Translocation. Cell Reports Medicine, 2020, 1, 100153.	3.3	7
183	Tenosynovial giant cell tumors (TGCT): molecular biology, drug targets and non-surgical pharmacological approaches. Expert Opinion on Therapeutic Targets, 2022, 26, 333-345.	1.5	7
184	Maffucci syndrome: A genomeâ€wide analysis using high resolution single nucleotide polymorphism and expression arrays on four cases. Genes Chromosomes and Cancer, 2011, 50, 673-679.	1.5	6
185	Microarray Techniques to Analyze Copy-Number Alterations in Genomic DNA: Array Comparative Genomic Hybridization and Single-Nucleotide Polymorphism Array. Journal of Investigative Dermatology, 2015, 135, 1-5.	0.3	6
186	A translocation t(6;14) in two cases of leiomyosarcoma: Molecular cytogenetic and array-based comparative genomic hybridization characterization. Cancer Genetics, 2015, 208, 537-544.	0.2	6
187	Clonal T- and natural killer-cell large granular lymphocyte proliferations in a single patient established by array-based comparative genomic hybridization analysis. Leukemia, 2006, 20, 2212-2214.	3.3	5
188	Fluorescent CXCR4 targeting peptide as alternative for antibody staining in Ewing sarcoma. BMC Cancer, 2017, 17, 383.	1.1	5
189	Tissue Damage Caused by Myeloablative, but Not Non-Myeloablative, Conditioning before Allogeneic Stem Cell Transplantation Results in Dermal Macrophage Recruitment without Active T-Cell Interaction. Frontiers in Immunology, 2018, 9, 331.	2.2	5
190	Transformed Canine and Murine Mesenchymal Stem Cells as a Model for Sarcoma with Complex Genomics. Cancers, 2021, 13, 1126.	1.7	5
191	Higher cMET dependence of sacral compared to clival chordoma cells: contributing to a better understanding of cMET in chordoma. Scientific Reports, 2021, 11, 12466.	1.6	5
192	A murine mesenchymal stem cell model for initiating events in osteosarcomagenesis points to CDK4/CDK6 inhibition as a therapeutic target. Laboratory Investigation, 2022, 102, 391-400.	1.7	5
193	Does parosteal liposarcoma differ from other atypical lipomatous tumors/well-differentiated liposarcomas? A molecular cytogenetic study using combined multicolor COBRA-FISH karyotyping and array-based comparative genomic hybridization. Cancer Genetics and Cytogenetics, 2007, 176, 115-120.	1.0	4
194	Silent Philadelphia Chromosome. Cancer Genetics and Cytogenetics, 2000, 118, 14-19.	1.0	3
195	Identification of a SNP in a Regulatory Region of GJB2 Associated With Idiopathic Nonsyndromic Autosomal Recessive Hearing Loss in a Multicenter Study. Otology and Neurotology, 2013, 34, 650-656.	0.7	3
196	Conserved hierarchical gain of chromosome 4 is an independent prognostic factor in high hyperdiploid pediatric acute lymphoblastic leukemia. Leukemia Research, 2017, 52, 28-33.	0.4	3
197	Insulin-Like Growth Factor 2 in Physiology, Cancer, and Cancer Treatment. OBM Genetics, 2019, 3, 1-1.	0.2	3
198	CTâ€guided, COBRAâ€FISHâ€assisted diagnosis of wellâ€differentiated liposarcoma (inflammatory subtype) of the retroperitoneum. Histopathology, 2007, 51, 422-426.	1.6	2

#	ARTICLE	IF	CITATIONS
199	Multiple genomic aberrations in a patient with mental retardation and hypogonadism: 45,X/46,X,psu dic(Y) karyotype, thyroid hormone receptor beta (THRB) mutation and heterozygosity for Wilson disease. American Journal of Medical Genetics, Part A, 2009, 149A, 2231-2235.	0.7	2
200	Widening the clinical spectrum of Pitt-Rogers-Danks/Wolf-Hirschhorn syndromes. Genetics and Molecular Biology, 2007, 30, 339-342.	0.6	2
201	Array-based genomic analysis of screen-detected Gleason score 6 and 7 prostatic adenocarcinomas. Anticancer Research, 2006, 26, 1193-200.	0.5	2
202	Multiple Tumor Case: Report and Analysis of an Autopsy Case. Tumori, 1997, 83, 715-717.	0.6	1
203	BRCA2 Heterozygosity Delays Cytokinesis in Primary Human Fibroblasts. Analytical Cellular Pathology, 2009, 31, 191-201.	0.7	1
204	P63: Molecular karyotyping ofÂaÂchondroblastoma toÂidentify theÂnew formed chimera-gene. European Journal of Medical Genetics, 2005, 48, 523.	0.7	0
205	Multiplex Capabilities for Serological Immunoassays Using Luminex xMAPÂ® Technology. Clinical Immunology, 2007, 123, S50.	1.4	0
206	Novel translocation variant in ewing sarcoma involving the NFATc2 gene. Cancer Genetics and Cytogenetics, 2010, 203, 47.	1.0	0
207	878 Novel Eight-target FISH Approach for Profiling Clonality of High-hyperdiploid Paediatric Acute Lymphoblastic Leukemia (HHD-pALL). European Journal of Cancer, 2012, 48, S212.	1.3	0
208	Genomic analysis reveals recurrent deletion of HNRNPK and SOCS1 in mycosis fungoides. European Journal of Cancer, 2018, 101, S7.	1.3	0
209	Non-Hodgkin lymphoma of bone of the femur and humerus: a case report and review of the literature. Oxford Medical Case Reports, 2021, 2021, omab024.	0.2	0
210	Establishment and Characterization of a tel/abl Rearrangement Responsible for Imatinib Sensitivity in bcr/abl Negative Acute Lymphoblastic Leukemia.. Blood, 2007, 110, 4280-4280.	0.6	0
211	Focal Deletion of Genes Involved in the Control of Cell Cycle Progression Contributes to Growth Factor Independence in Acute Lymphoblastic Leukemia Cells. Blood, 2008, 112, 789-789.	0.6	0
212	Array-CGH and SNP-Arrays, the New Karyotype. , 2012, , 39-52.		0
213	Abstract 3108: Modeling translocation driven tumors with human induced pluripotent stem cells (hiPSCs) using CRISPR-Cas9: Pseudomyogenic hemangioendothelioma as a proof of principle. , 2018, , .		0
214	Comprehensive Profiling of Disease-Relevant Copy Number Aberrations Improves Risk Assessment and Unveils the Clonal Origin of Relapse in Pediatric Acute Lymphoblastic Leukemia. Blood, 2019, 134, 1474-1474.	0.6	0