Ola Myklebost

List of Publications by Year
in descending order

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183	13,833	25423	26792
papers	citations	59 h-index	111 g-index

190	190	190	20669
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	miR-486-5p expression is regulated by DNA methylation in osteosarcoma. BMC Genomics, 2022, 23, 142.	1.2	8
2	Clonal evolution after treatment pressure in multiple myeloma: heterogenous genomic aberrations and transcriptomic convergence. Leukemia, 2022, 36, 1887-1897.	3.3	23
3	Discovery of novel candidates for anti-liposarcoma therapies by medium-scale high-throughput drug screening. PLoS ONE, 2021, 16, e0248140.	1.1	6
4	Multimodal analysis of cell-free DNA whole-genome sequencing for pediatric cancers with low mutational burden. Nature Communications, 2021, 12, 3230.	5.8	95
5	Methylation-dependent SUMOylation of the architectural transcription factor HMGA2. Biochemical and Biophysical Research Communications, 2021, 552, 91-97.	1.0	4
6	Cancer Predisposition Sequencing Reporter (<scp>CPSR</scp>): A flexible variant report engine for highâ€throughput germline screening in cancer. International Journal of Cancer, 2021, 149, 1955-1960.	2.3	12
7	The expressed mutational landscape of microsatellite stable colorectal cancers. Genome Medicine, 2021, 13, 142.	3.6	4
8	Clinical and molecular implications of NAB2-STAT6 fusion variants in solitary fibrous tumour. Pathology, 2021, 53, 713-719.	0.3	29
9	Cell Fusion of Mesenchymal Stem/Stromal Cells and Breast Cancer Cells Leads to the Formation of Hybrid Cells Exhibiting Diverse and Individual (Stem Cell) Characteristics. International Journal of Molecular Sciences, 2020, 21, 9636.	1.8	15
10	Mutational dynamics and immune evasion in diffuse large B-cell lymphoma explored in a relapse-enriched patient series. Blood Advances, 2020, 4, 1859-1866.	2.5	7
11	Accurate 3-gene-signature for early diagnosis of liposarcoma progression. Clinical Sarcoma Research, 2020, 10, 4.	2.3	4
12	Preclinical Evaluation of the Pan-FGFR Inhibitor LY2874455 in FRS2-Amplified Liposarcoma. Cells, 2019, 8, 189.	1.8	16
13	Multifocal Primary Prostate Cancer Exhibits High Degree of Genomic Heterogeneity. European Urology, 2019, 75, 498-505.	0.9	108
14	Personal Cancer Genome Reporter: variant interpretation report for precision oncology. Bioinformatics, 2018, 34, 1778-1780.	1.8	33
15	Sample-Index Misassignment Impacts Tumour Exome Sequencing. Scientific Reports, 2018, 8, 5307.	1.6	17
16	Report from the 4th European Bone Sarcoma Networking meeting: focus on osteosarcoma. Clinical Sarcoma Research, 2018, 8, .	2.3	3
17	Real-Time Vital Mineralization Detection and Quantification during In Vitro Osteoblast Differentiation. Biological Procedures Online, 2018, 20, 14.	1.4	19
18	Preclinical Evaluation of Vemurafenib as Therapy for BRAFV600E Mutated Sarcomas. International Journal of Molecular Sciences, 2018, 19, 969.	1.8	12

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19	Patterns of genomic evolution in advanced melanoma. Nature Communications, 2018, 9, 2665.	5.8	62
20	Noninvasive Detection of ctDNA Reveals Intratumor Heterogeneity and Is Associated with Tumor Burden in Gastrointestinal Stromal Tumor. Molecular Cancer Therapeutics, 2018, 17, 2473-2480.	1.9	61
21	Evaluation of commercial DNA and RNA extraction methods for high-throughput sequencing of FFPE samples. PLoS ONE, 2018, 13, e0197456.	1.1	46
22	Whole-Exome and mRNA Sequencing of Multiple Myeloma Reveal Transformation to a More High-Risk and Proliferative Tumor at Relapse. Blood, 2018, 132, 3157-3157.	0.6	0
23	Use of liquid biopsies to monitor disease progression in a sarcoma patient: a case report. BMC Cancer, 2017, 17, 29.	1.1	21
24	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. Nature Communications, 2017, 8, 15936.	5.8	179
25	Monitoring multiple myeloma by quantification of recurrent mutations in serum. Haematologica, 2017, 102, 1266-1272.	1.7	51
26	High number of kinomeâ€mutations in nonâ€small cell lung cancer is associated with reduced immune response and poor relapseâ€free survival. International Journal of Cancer, 2017, 141, 184-190.	2.3	14
27	Analysis of the miR-34 family functions in breast cancer reveals annotation error of miR-34b. Scientific Reports, 2017, 7, 9655.	1.6	31
28	PP2A Regulatory Subunit B55Î³ is a Gatekeeper of Osteoblast Maturation and Lineage Maintenance. Stem Cells and Development, 2017, 26, 1375-1383.	1.1	6
29	Multilevel genomics of colorectal cancers with microsatellite instabilityâ€"clinical impact of JAK1 mutations and consensus molecular subtype 1. Genome Medicine, 2017, 9, 46.	3.6	71
30	Multi-omics of 34 colorectal cancer cell lines - a resource for biomedical studies. Molecular Cancer, 2017, 16, 116.	7.9	232
31	Preclinical evaluation of potential therapeutic targets in dedifferentiated liposarcoma. Oncotarget, 2016, 7, 54583-54595.	0.8	23
32	TP53 Mutation Spectrum in Smokers and Never Smoking Lung Cancer Patients. Frontiers in Genetics, 2016, 07, 85.	1.1	76
33	Monogenic and polygenic determinants of sarcoma risk: an international genetic study. Lancet Oncology, The, 2016, 17, 1261-1271.	5.1	161
34	The Genomic Landscape of Pancreatic and Periampullary Adenocarcinoma. Cancer Research, 2016, 76, 5092-5102.	0.4	33
35	The ENCCA-WP7/EuroSarc/EEC/PROVABES/EURAMOS 3rd European Bone Sarcoma Networking Meeting/Joint Workshop of EU Bone Sarcoma Translational Research Networks; Vienna, Austria, September 24â€"25, 2015. Workshop Report. Clinical Sarcoma Research, 2016, 6, 3.	2.3	14
36	Genome Analysis of Osteosarcoma Progression Samples Identifies FGFR1 Overexpression as a Potential Treatment Target and CHM as a Candidate Tumor Suppressor Gene. PLoS ONE, 2016, 11, e0163859.	1.1	13

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37	HSP90 inhibition blocks ERBB3 and RET phosphorylation in myxoid/round cell liposarcoma and causes massive cell deathin vitroandin vivo. Oncotarget, 2016, 7, 433-445.	0.8	12
38	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
39	Personalized cancer therapy for soft tissue sarcomas: progress and pitfalls. Personalized Medicine, 2015, 12, 593-602.	0.8	0
40	Norwegian Cancer Genomics Consortium: a platform for research on personalized cancer medicine in a public health system. Drug Discovery Today, 2015, 20, 1419-1421.	3.2	3
41	Bone marrow stroma-derived PGE2 protects BCP-ALL cells from DNA damage-induced p53 accumulation and cell death. Molecular Cancer, 2015, 14, 14.	7.9	52
42	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	2.4	69
43	BRAF V600E mutation in early-stage multiple myeloma: good response to broad acting drugs and no relation to prognosis. Blood Cancer Journal, 2015, 5, e299-e299.	2.8	36
44	Discovery of Recurrent Mutations Associated with Chemo-Immunotherapy Relapse in Diffuse Large B-Cell Lymphoma. Blood, 2015, 126, 110-110.	0.6	1
45	Metabolic reprogramming of metastatic breast cancer and melanoma by let-7a microRNA. Oncotarget, 2015, 6, 2451-2465.	0.8	68
46	Genomic landscape of liposarcoma. Oncotarget, 2015, 6, 42429-42444.	0.8	94
47	Generation and Characterisation of Novel Pancreatic Adenocarcinoma Xenograft Models and Corresponding Primary Cell Lines. PLoS ONE, 2014, 9, e103873.	1.1	17
48	The tankyraseâ€specific inhibitor <scp>JW</scp>74 affects cell cycle progression and induces apoptosis and differentiation in osteosarcoma cell lines. Cancer Medicine, 2014, 3, 36-46.	1.3	47
49	The Architecture and Evolution of Cancer Neochromosomes. Cancer Cell, 2014, 26, 653-667.	7.7	161
50	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	6.0	348
51	Performance comparison of four exome capture systems for deep sequencing. BMC Genomics, 2014, 15, 449.	1.2	152
52	Reexpression of LSAMP inhibits tumor growth in a preclinical osteosarcoma model. Molecular Cancer, 2014, 13, 93.	7.9	25
53	The Regulatory Landscape of Osteogenic Differentiation. Stem Cells, 2014, 32, 2780-2793.	1.4	85
54	Generation and Characterization of an Immortalized Human Mesenchymal Stromal Cell Line. Stem Cells and Development, 2014, 23, 2377-2389.	1.1	38

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55	Clinical and Biological Implications of BRAF V600E Mutation in Multiple Myeloma. Blood, 2014, 124, 5685-5685.	0.6	1
56	IR/IGF1R signaling as potential target for treatment of high-grade osteosarcoma. BMC Cancer, 2013, 13, 245.	1.1	73
57	Comparison of glioma stem cells to neural stem cells from the adult human brain identifies dysregulated Wnt- signaling and a fingerprint associated with clinical outcome. Experimental Cell Research, 2013, 319, 2230-2243.	1.2	92
58	Functional characterisation of osteosarcoma cell lines and identification of mRNAs and miRNAs associated with aggressive cancer phenotypes. British Journal of Cancer, 2013, 109, 2228-2236.	2.9	188
59	Correlation of TP53 and MDM2 genotypes with response to therapy in sarcoma. Cancer, 2013, 119, 1013-1022.	2.0	36
60	Identification of PPAP2B as a novel recurrent translocation partner gene of HMGA2 in lipomas. Genes Chromosomes and Cancer, 2013, 52, 580-590.	1.5	24
61	Common Fusion Transcripts Identified in Colorectal Cancer Cell Lines by High-Throughput RNA Sequencing. Translational Oncology, 2013, 6, 546-IN5.	1.7	29
62	Distinct H3F3A and H3F3B driver mutations define chondroblastoma and giant cell tumor of bone. Nature Genetics, 2013, 45, 1479-1482.	9.4	667
63	Epigenetic Regulation and Functional Characterization of MicroRNA-142 in Mesenchymal Cells. PLoS ONE, 2013, 8, e79231.	1.1	20
64	Characterization of Liposarcoma Cell Lines for Preclinical and Biological Studies. Sarcoma, 2012, 2012, 1-9.	0.7	33
65	Global Gene Expression Profiling of Human Osteosarcomas Reveals Metastasis-Associated Chemokine Pattern. Sarcoma, 2012, 2012, 1-12.	0.7	33
66	508 Identification of Fusion Transcripts in Colorectal Cancer by Combined RNA-seq and Exon Microarray Analyses. European Journal of Cancer, 2012, 48, S121.	1.3	0
67	Adipocyte Differentiation of Human Bone Marrow-Derived Stromal Cells Is Modulated by MicroRNA-155, MicroRNA-221, and MicroRNA-222. Stem Cells and Development, 2012, 21, 873-883.	1.1	87
68	Modulation of the Osteosarcoma Expression Phenotype by MicroRNAs. PLoS ONE, 2012, 7, e48086.	1.1	253
69	Identification of osteosarcoma driver genes by integrative analysis of copy number and gene expression data. Genes Chromosomes and Cancer, 2012, 51, 696-706.	1.5	108
70	Preclinical xenograft models of human sarcoma show nonrandom loss of aberrations. Cancer, 2012, 118, 558-570.	2.0	40
71	Integrative Analysis Reveals Relationships of Genetic and Epigenetic Alterations in Osteosarcoma. PLoS ONE, 2012, 7, e48262.	1.1	87
72	Abstract 5128: Identification of osteosarcoma driver genes by integrative analysis of copy number and gene expression data. , 2012, , .		0

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73	Genome wide single cell analysis of chemotherapy resistant metastatic cells in a case of gastroesophageal adenocarcinoma. BMC Cancer, 2011, 11, 455.	1.1	10
74	MDM2 antagonist Nutlin-3a potentiates antitumour activity of cytotoxic drugs in sarcoma cell lines. BMC Cancer, 2011, 11, 211:1-11.	1.1	48
75	mRNA expression profiles of primary high-grade central osteosarcoma are preserved in cell lines and xenografts. BMC Medical Genomics, 2011, 4, 66.	0.7	30
76	Liposarcoma cells with aldefluor and CD133 activity have a cancer stem cell potential. Clinical Sarcoma Research, 2011, 1, 8.	2.3	22
77	Workshop Report on the European Bone Sarcoma Networking Meeting: Integration of Clinical Trials with Tumor Biology. Journal of Adolescent and Young Adult Oncology, 2011, 1, 118-123.	0.7	2
78	Tumor-Infiltrating Macrophages Are Associated with Metastasis Suppression in High-Grade Osteosarcoma: A Rationale for Treatment with Macrophage Activating Agents. Clinical Cancer Research, 2011, 17, 2110-2119.	3.2	365
79	Genomic alterations reveal potential for higher grade transformation in follicular lymphoma and confirm parallel evolution of tumor cell clones. Blood, 2010, 116, 1489-1497.	0.6	58
80	Identification of target genes for wild type and truncated HMGA2 in mesenchymal stem-like cells. BMC Cancer, 2010, 10, 329.	1.1	25
81	Evaluation of high-resolution microarray platforms for genomic profiling of bone tumours. BMC Research Notes, 2010, 3, 223.	0.6	12
82	Molecular characterization of commonly used cell lines for bone tumor research: A transâ€European EuroBoNet effort. Genes Chromosomes and Cancer, 2010, 49, 40-51.	1.5	141
83	DNA Copy Number Changes in Human Malignant Fibrous Histiocytomas by Array Comparative Genomic Hybridisation. PLoS ONE, 2010, 5, e15378.	1.1	12
84	670 Characterisation of LSAMP, a novel candidate tumour suppressor gene in osteosarcomas. European Journal of Cancer, Supplement, 2010, 8, 169.	2.2	0
85	795 Integrative analysis of genome-wide genetic and epigenetic changes in human osteosarcomas. European Journal of Cancer, Supplement, 2010, 8, 200.	2.2	0
86	819 Integrated analysis reveals overexpression of miRNA clusters in osteosarcomas. European Journal of Cancer, Supplement, 2010, 8, 206-207.	2.2	0
87	Extensive adipogenic and osteogenic differentiation of patterned human mesenchymal stem cells in a microfluidic device. Lab on A Chip, 2010, 10, 1401.	3.1	24
88	A Tissue Microarray Study of Osteosarcoma: Histopathologic and Immunohistochemical Validation of Xenotransplanted Tumors as Preclinical Models. Applied Immunohistochemistry and Molecular Morphology, 2010, 18, 453-461.	0.6	28
89	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
90	Upregulation of stem cell genes in multidrug resistant K562 leukemia cells. Leukemia Research, 2009, 33, 1379-1385.	0.4	23

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91	Highâ€resolution analysis of genetic stability of human adipose tissue stem cells cultured to senescence. Journal of Cellular and Molecular Medicine, 2008, 12, 553-563.	1.6	148
92	DNA copy number changes in high-grade malignant peripheral nerve sheath tumors by array CGH. Molecular Cancer, 2008, 7, 48.	7.9	41
93	GeneCount: genome-wide calculation of absolute tumor DNA copy numbers from array comparative genomic hybridization data. Genome Biology, 2008, 9, R86.	13.9	14
94	Gene expression profiles of primary colorectal carcinomas, liver metastases, and carcinomatoses. Molecular Cancer, 2007, 6, 2.	7.9	61
95	Potential for treatment of liposarcomas with the MDM2 antagonist Nutlin-3A. International Journal of Cancer, 2007, 121, 199-205.	2.3	106
96	Diagnostic and prognostic gene expression signatures in 177 soft tissue sarcomas: hypoxia-induced transcription profile signifies metastatic potential. BMC Genomics, 2007, 8, 73.	1.2	144
97	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. Nature Biotechnology, 2006, 24, 1151-1161.	9.4	1,927
98	Gain of chromosome 6p is an infrequent cause of increased PIM1 expression in B-cell non-Hodgkin's lymphomas. Leukemia, 2006, 20, 539-542.	3.3	15
99	Small-molecule MDM2 antagonists reveal aberrant p53 signaling in cancer: Implications for therapy. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1888-1893.	3.3	632
100	Array Comparative Genomic Hybridization Reveals Distinct DNA Copy Number Differences between Gastrointestinal Stromal Tumors and Leiomyosarcomas. Cancer Research, 2006, 66, 8984-8993.	0.4	97
101	Expression Patterns of Cell Cycle Components in Sporadic and Neurofibromatosis Type 1-Related Malignant Peripheral Nerve Sheath Tumors. Journal of Neuropathology and Experimental Neurology, 2005, 64, 74-81.	0.9	36
102	Translocation t(14;18) and gain of chromosome 18/BCL2: effects on BCL2 expression and apoptosis in B-cell non-Hodgkin's lymphomas. Leukemia, 2005, 19, 2313-2323.	3.3	27
103	Limitations of mRNA amplification from small-size cell samples. BMC Genomics, 2005, 6, 147.	1.2	35
104	Response of malignant B lymphocytes to ionizing radiation: Gene expression and genotype. International Journal of Cancer, 2005, 115, 935-942.	2.3	21
105	Mapping and characterization of the amplicon near APOA2 in 1q23 in human sarcomas by FISH and array CGH. Molecular Cancer, 2005, 4, 39.	7.9	25
106	Lessons from genetic profiling in soft tissue sarcomas. Acta Orthopaedica, 2004, 75, 35-50.	1.4	8
107	Putting Norway on the gene-therapy map. Nature, 2004, 429, 129-129.	13.7	0
108	M-CGH: analysing microarray-based CGH experiments. BMC Bioinformatics, 2004, 5, 74.	1.2	41

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109	Profound influence of microarray scanner characteristics on gene expression ratios: analysis and procedure for correction. BMC Genomics, 2004, 5, 10.	1.2	63
110	Analysis of the humoral immune response to immunoselected phage-displayed peptides by a microarray-based method. Proteomics, 2004, 4, 2572-2582.	1.3	36
111	Amplification of chromosome 1 sequences in lipomatous tumors and other sarcomas. International Journal of Cancer, 2004, 109, 363-369.	2.3	55
112	Constitutive Expression of the AP-1 Transcription Factors c-jun, junD, junB, and c-fos and the Marginal Zone B-Cell Transcription Factor Notch2 in Splenic Marginal Zone Lymphoma. Journal of Molecular Diagnostics, 2004, 6, 297-307.	1.2	45
113	Tumor classification and marker gene prediction by feature selection and fuzzy c-means clustering using microarray data. BMC Bioinformatics, 2003, 4, 60.	1.2	80
114	Effects of mRNA amplification on gene expression ratios in cDNA experiments estimated by analysis of variance. BMC Genomics, 2003, 4, 11.	1.2	66
115	11q13 Alterations in two cases of hibernoma: Large heterozygous deletions and rearrangement breakpoints nearGARPin 11q13.5. Genes Chromosomes and Cancer, 2003, 37, 389-395.	1.5	49
116	Amplification and overexpression of COPS3 in osteosarcomas potentially target TP53 for proteasome-mediated degradation. Oncogene, 2003, 22, 5358-5361.	2.6	62
117	MGraph: graphical models for microarray data analysis. Bioinformatics, 2003, 19, 2210-2211.	1.8	29
118	Interferon-Î³ suppresses S100A4 transcription independently of apoptosis or cell cycle arrest. British Journal of Cancer, 2003, 88, 1995-2001.	2.9	20
119	MArray: analysing single, replicated or reversed microarray experiments. Bioinformatics, 2002, 18, 1139-1140.	1.8	30
120	Analysis of repeatability in spotted cDNA microarrays. Nucleic Acids Research, 2002, 30, 3235-3244.	6.5	49
121	Clustering of the SOM easily reveals distinct gene expression patterns: results of a reanalysis of lymphoma study. BMC Bioinformatics, 2002, 3, 36.	1.2	99
122	Positional cloning identifies a novel cyclophilin as a candidate amplified oncogene in 1q21. Oncogene, 2002, 21, 2261-2269.	2.6	52
123	The SYT-SSX1 fusion type of synovial sarcoma is associated with increased expression of cyclin A and D1. A link between t(X;18)(p11.2; q11.2) and the cell cycle machinery. Oncogene, 2002, 21, 5791-5796.	2.6	42
124	Ectopic sequences from truncatedHMGIC in liposarcomas are derived from various amplified chromosomal regions. Genes Chromosomes and Cancer, 2001, 31, 264-273.	1.5	37
125	Amplification and overexpression of PRUNE in human sarcomas and breast carcinomasâ€“a possible mechanism for altering the nm23-H1 activity. Oncogene, 2001, 20, 6881-6890.	2.6	52
126	Dedifferentiation of a well-differentiated liposarcoma to a highly malignant metastatic osteosarcoma:. Cancer Genetics and Cytogenetics, 2001, 125, 100-111.	1.0	54

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127	A well-differentiated liposarcoma with a new type of chromosome 12-derived markers. Cancer Genetics and Cytogenetics, 2001, 131, 13-18.	1.0	26
128	Characterization of centromere alterations in liposarcomas. Genes Chromosomes and Cancer, 2000, 29, 117-129.	1.5	73
129	Frequent Loss of 9p21 (p16INK4A) and Other Genomic Imbalances in Human Malignant Fibrous Histiocytoma. Cancer Genetics and Cytogenetics, 2000, 118, 89-98.	1.0	63
130	Structure of the supernumerary ring and giant rod chromosomes in adipose tissue tumors. Genes Chromosomes and Cancer, 1999, 24, 30-41.	1.5	247
131	A novel chromosomal region of allelic loss, 4q32-q34, in human osteosarcomas revealed by representational difference analysis. Genes Chromosomes and Cancer, 1999, 26, 115-124.	1.5	17
132	Chromosome band 9p21 is frequently altered in malignant peripheral nerve sheath tumors: Studies ofCDKN2A and other genes of the pRB pathway. Genes Chromosomes and Cancer, 1999, 26, 151-160.	1.5	76
133	Characterization of the 17p amplicon in human sarcomas: Microsatellite marker analysis. , 1999, 82, 329-333.		23
134	Sensitive fluorescent in situ hybridisation method for the characterisation of breast cancer cells in bone marrow aspirates. Journal of Clinical Pathology, 1999, 52, 68-74.	2.1	16
135	Structure of the supernumerary ring and giant rod chromosomes in adipose tissue tumors. , 1999, 24, 30.		3
136	Structure of the supernumerary ring and giant rod chromosomes in adipose tissue tumors. Genes Chromosomes and Cancer, 1999, 24, 30-41.	1.5	91
137	Chromosome band 9p21 is frequently altered in malignant peripheral nerve sheath tumors: studies of CDKN2A and other genes of the pRB pathway. Genes Chromosomes and Cancer, 1999, 26, 151-60.	1.5	22
138	GLI gene and rhabdomyosarcoma. Nature Medicine, 1998, 4, 869-869.	15.2	1
139	Molecular characterization of a novel amplicon at 1q21-q22 frequently observed in human sarcomas. British Journal of Cancer, 1998, 78, 495-503.	2.9	69
140	HMGIC, the gene for an architectural transcription factor, is amplified and rearranged in a subset of human sarcomas. Oncogene, 1997, 14, 2935-2941.	2.6	89
141	Recurrent gains of 1q, 8 and 12 in the Ewing family of tumours by comparative genomic hybridization. British Journal of Cancer, 1997, 75, 1403-1409.	2.9	109
142	Molecular cytogenetics of bone and soft tissue tumors. Cancer Genetics and Cytogenetics, 1997, 95, 67-73.	1.0	23
143	Complexity of 12q13â€“22 amplicon in liposarcoma: Microsatellite repeat analysis. , 1997, 18, 66-79.		34
144	Separate amplified regions encompassingCDK4 andMDM2 in human sarcomas. , 1996, 17, 254-259.		102

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145	First for biotech. Nature, 1996, 384, 208-208.	13.7	1
146	Reversal of the in vivo metastatic phenotype of human tumor cells by an anti-CAPL (mts1) ribozyme. Cancer Research, 1996, 56, 5490-8.	0.4	102
147	Homozygous deletion frequency and expression levels of the CDKN2 gene in human sarcomas - relationship to amplification and mRNA levels of CDK4 and CCND1. British Journal of Cancer, 1995, 72, 393-398.	2.9	97
148	Comparative genomic hybridization analysis of human sarcomas: I. Occurrence of genomic imbalances and identification of a novel major amplicon at 1q21â€“q22 in soft tissue sarcomas. Genes Chromosomes and Cancer, 1995, 14, 8-14.	1.5	128
149	Comparative genomic hybridization analysis of human sarcomas: II. Identification of novel amplicons at 6p and 17p in osteosarcomas. Genes Chromosomes and Cancer, 1995, 14, 15-21.	1.5	130
150	Identification of two distinct chromosome 12-derived amplification units in neuroblastoma cell line NGP. Cancer Genetics and Cytogenetics, 1995, 82, 151-154.	1.0	43
151	Cloning and Characterization of Two Forms of Bovine Polymeric Immunoglobulin Receptor cDNA. DNA and Cell Biology, 1995, 14, 251-256.	0.9	52
152	MDM2 Gene Amplification and Transcript Levels in Human Sarcomas: Relationship to TP53 Gene Status. Journal of the National Cancer Institute, 1994, 86, 1297-1302.	3.0	184
153	A long range restriction map spanning the myxoid liposarcoma breakpoint in the q13-14 region of human chromosome 12. Human Genetics, 1994, 94, 259-264.	1.8	6
154	Comparative genomic hybridization as a tool to define two distinct chromosome 12-derived amplification units in well-differentiated liposarcomas. Genes Chromosomes and Cancer, 1994, 9, 292-295.	1.5	67
155	The protooncogene CHOP/GADD153, involved in growth arrest and DNA damage response, is amplified in a subset of human sarcomas. Cancer Genetics and Cytogenetics, 1994, 78, 165-171.	1.0	52
156	Amplification of the GLI and LRP/A2MR Loci in Tumor Cells: Is GLI only by Chance Coamplified Together with Another Gene Related to Tumor Progression?. , 1994, , 151-161.		0
157	Expression of the neuroectodermal intermediate filament nestin in human melanomas. Cancer Research, 1994, 54, 354-6.	0.4	76
158	Isolation, sequencing, and expression analysis of a bovine apolipoprotein E (APOE) cDNA and chromosomal localization of the APOE locus. Mammalian Genome, 1993, 4, 53-57.	1.0	10
159	Mapping of amplification units in the q13-14 region of chromosome 12 in human sarcomas: some amplica do not include MDM2. Cell Growth & Differentiation: the Molecular Biology Journal of the American Association for Cancer Research, 1993, 4, 1065-70.	0.8	34
160	p53 abnormalities in different subtypes of human sarcomas. Cancer Research, 1993, 53, 468-71.	0.4	114
161	Uptake of chylomicron remnant retinyl esters in human leukocytes in vivo. European Journal of Clinical Investigation, 1992, 22, 229-234.	1.7	22
162	A physical map of a 1.3-Mb region on the long arm of chromosome 12, spanning the GLI and LRP loci. Genomics, 1992, 14, 117-120.	1.3	14

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163	Levels of nm23 messenger RNA in metastatic malignant melanomas: inverse correlation to disease progression. Cancer Research, 1992, 52, 6088-91.	0.4	153
164	The human genes for complement components 6 (C6) and 9 (C9) are closely linked on chromosome 5.. Journal of Medical Genetics, 1991, 28, 587-590.	1.5	17
165	Association analysis of lipid levels and apolipoprotein restriction fragment length polymorphisms. Human Genetics, 1990, 86, 209-14.	1.8	13
166	Multiple RFLPs of human complement component nine (C9) detected by TaqI. Nucleic Acids Research, 1990, 18, 3112-3112.	6.5	4
167	The gene for the human putative apoE receptor is on chromosome 12 in the segment q13â€“14. Genomics, 1989, 5, 65-69.	1.3	29
168	The genes for apolipoprotein AII (APOA2) and the Duffy blood group (FY) are linked on chromosome 1 in man. Genomics, 1989, 4, 169-173.	1.3	11
169	The gene for human complement C9 is on chromosome 5. Genomics, 1989, 5, 149-152.	1.3	18
170	Low-density-lipoprotein receptors in different rabbit liver cells. Biochemical Journal, 1989, 261, 587-593.	1.7	7
171	A physical map of the apolipoprotein gene cluster on human chromosome 19. Human Genetics, 1988, 78, 244-247.	1.8	62
172	Surface location and high affinity for calcium of a 500-kd liver membrane protein closely related to the LDL-receptor suggest a physiological role as lipoprotein receptor.. EMBO Journal, 1988, 7, 4119-4127.	3.5	859
173	Surface location and high affinity for calcium of a 500-kd liver membrane protein closely related to the LDL-receptor suggest a physiological role as lipoprotein receptor. EMBO Journal, 1988, 7, 4119-27.	3.5	260
174	The isolation and characterisation of a cDNA clone for human lecithin:cholesterol acyl transferase and its use to analyse the genes in patients with LCAT deficiency and fish eye disease. Biochemical and Biophysical Research Communications, 1987, 148, 161-169.	1.0	35
175	Confirmation of the close linkage between the loci for human apolipoproteins AI and AIV by the use of a cloned cDNA probe and two restriction site polymorphisms. Human Genetics, 1986, 72, 68-71.	1.8	10
176	The gene for human apolipoprotein CI is located 4.3 kilobases away from the apolipoprotein E gene on chromosome 19. Human Genetics, 1986, 73, 286-289.	1.8	24
177	The apolipoprotein CII gene: Subchromosomal localisation and linkage to the myotonic dystrophy locus. Human Genetics, 1985, 70, 271-3.	1.8	71
178	Cell cycle traverse and protein metabolism in human NHIK 3025 cells: The role of anchorage. Journal of Cellular Physiology, 1985, 125, 528-532.	2.0	8
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