Eivind Hovig

List of Publications by Year in descending order

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Version: 2024-02-01

254 papers	12,496 citations	38742 50 h-index	30922 102 g-index
284 all docs	284 docs citations	284 times ranked	17266 citing authors

#	Article	IF	Citations
1	A literature network of human genes for high-throughput analysis of gene expression. Nature Genetics, 2001, 28, 21-28.	21.4	655
2	Database of p53 gene somatic mutations in human tumors and cell lines. Nucleic Acids Research, 1994, 22, 3551-5.	14.5	646
3	Ten Simple Rules for Reproducible Computational Research. PLoS Computational Biology, 2013, 9, e1003285.	3.2	509
4	Title is missing!. Nature Genetics, 2001, 28, 21-28.	21.4	482
5	A Uniform System for the Annotation of Vertebrate microRNA Genes and the Evolution of the Human microRNAome. Annual Review of Genetics, 2015, 49, 213-242.	7.6	467
6	Somatic point mutations in the p53 gene of human tumors and cell lines: updated compilation. Nucleic Acids Research, 1996, 24, 141-146.	14.5	422
7	Cancer incidence and survival in Lynch syndrome patients receiving colonoscopic and gynaecological surveillance: first report from the prospective Lynch syndrome database. Gut, 2017, 66, 464-472.	12.1	411
8	Cancer risk and survival in path_MMR carriers by gene and gender up to 75 years of age: a report from the Prospective Lynch Syndrome Database. Gut, 2018, 67, 1306-1316.	12.1	410
9	Cancer risks by gene, age, and gender in 6350 carriers of pathogenic mismatch repair variants: findings from the Prospective Lynch Syndrome Database. Genetics in Medicine, 2020, 22, 15-25.	2.4	365
10	Database of p53 gene somatic mutations in human tumors and cell lines: updated compilation and future prospects. Nucleic Acids Research, 1997, 25, 151-157.	14.5	301
11	Methods that remove batch effects while retaining group differences may lead to exaggerated confidence in downstream analyses. Biostatistics, 2016, 17, 29-39.	1.5	268
12	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
13	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
14	MirGeneDB 2.0: the metazoan microRNA complement. Nucleic Acids Research, 2020, 48, D132-D141.	14.5	194
15	Constant denaturant gel electrophoresis as a rapid screening technique for p53 mutations.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 8405-8409.	7.1	177
16	Differential expression patterns ofS100a2, S100a4 andS100a6 during progression of human malignant melanoma. , 1997, 74, 464-469.		155
17	TP53 mutations and breast cancer prognosis: Particularly poor survival rates for cases with mutations in the zinc-binding domains. Genes Chromosomes and Cancer, 1995, 14, 71-75.	2.8	154
18	Performance comparison of four exome capture systems for deep sequencing. BMC Genomics, 2014, 15, 449.	2.8	152

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19	Identification of a novel cytokeratin 19 pseudogene that may interfere with reverse transcriptase-polymerase chain reaction assays used to detect micrometastatic tumor cells. International Journal of Cancer, 1999, 80, 119-125.	5.1	151
20	A sequence-oriented comparison of gene expression measurements across different hybridization-based technologies. Nature Biotechnology, 2006, 24, 832-840.	17.5	144
21	Screening for germ line TP53 mutations in breast cancer patients. Cancer Research, 1992, 52, 3234-6.	0.9	139
22	S100A4 involvement in metastasis: deregulation of matrix metalloproteinases and tissue inhibitors of matrix metalloproteinases in osteosarcoma cells transfected with an anti-S100A4 ribozyme. Cancer Research, 1999, 59, 4702-8.	0.9	136
23	Deep Sequencing the MicroRNA Transcriptome in Colorectal Cancer. PLoS ONE, 2013, 8, e66165.	2.5	132
24	Incidence of and survival after subsequent cancers in carriers of pathogenic MMR variants with previous cancer: a report from the prospective Lynch syndrome database. Gut, 2017, 66, 1657-1664.	12.1	127
25	Involvement of the pRb/p16/cdk4/cyclin D1 pathway in the tumorigenesis of sporadic malignant melanomas. British Journal of Cancer, 1996, 73, 909-916.	6.4	125
26	Gene Expression Analysis in Blood Cells in Response to Unmodified and 2â€²-Modified siRNAs Reveals TLR-dependent and Independent Effects. Journal of Molecular Biology, 2007, 365, 90-108.	4.2	123
27	Real-Time Nucleic Acid Sequence-Based Amplification in Nanoliter Volumes. Analytical Chemistry, 2004, 76, 9-14.	6.5	122
28	Options available for profiling small samples: a review of sample amplification technology when combined with microarray profiling. Nucleic Acids Research, 2006, 34, 996-1014.	14.5	116
29	Constant denaturant gel electrophoresis, a modification of denaturing gradient gel electrophoresis, in mutation detection. Mutation Research-Fundamental and Molecular Mechanisms of Mutagenesis, 1991, 262, 63-71.	1.1	112
30	Genetic epidemiology of BRCA mutations â€“ family history detects less than 50% of the mutation carriers. European Journal of Cancer, 2007, 43, 1713-1717.	2.8	106
31	Reversal of the in vivo metastatic phenotype of human tumor cells by an anti-CAPL (mts1) ribozyme. Cancer Research, 1996, 56, 5490-8.	0.9	102
32	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.	6.4	97
33	Parallel nanoliter detection of cancer markers using polymer microchips. Lab on A Chip, 2005, 5, 416-420.	6.0	91
34	Integrative Analysis Reveals Relationships of Genetic and Epigenetic Alterations in Osteosarcoma. PLoS ONE, 2012, 7, e48262.	2.5	87
35	Substantial Loss of Conserved and Gain of Novel MicroRNA Families in Flatworms. Molecular Biology and Evolution, 2013, 30, 2619-2628.	8.9	84
36	CDKN2A (p16INK4A) somatic and germline mutations. Human Mutation, 1996, 7, 294-303.	2.5	83

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37	Tumor classification and marker gene prediction by feature selection and fuzzy c-means clustering using microarray data. BMC Bioinformatics, 2003, 4, 60.	2.6	80
38	Associations between gene expressions in breast cancer and patient survival. Human Genetics, 2002, 111, 411-420.	3.8	78
39	Activation of NFâ€ºB by extracellular S100A4: Analysis of signal transduction mechanisms and identification of target genes. International Journal of Cancer, 2008, 123, 1301-1310.	5.1	78
40	The Genomic HyperBrowser: inferential genomics at the sequence level. Genome Biology, 2010, 11, R121.	9.6	78
41	TP53 Mutation Spectrum in Smokers and Never Smoking Lung Cancer Patients. Frontiers in Genetics, 2016, 07, 85.	2.3	76
42	The Majority of Viral-Cellular Fusion Transcripts in Cervical Carcinomas Cotranscribe Cellular Sequences of Known or Predicted Genes. Cancer Research, 2008, 68, 2514-2522.	0.9	74
43	Hi-C-constrained physical models of human chromosomes recover functionally-related properties of genome organization. Scientific Reports, 2016, 6, 35985.	3.3	72
44	Effects of mRNA amplification on gene expression ratios in cDNA experiments estimated by analysis of variance. BMC Genomics, 2003, 4, 11.	2.8	66
45	Profound influence of microarray scanner characteristics on gene expression ratios: analysis and procedure for correction. BMC Genomics, 2004, 5, 10.	2.8	63
46	MirGeneDB 2.1: toward a complete sampling of all major animal phyla. Nucleic Acids Research, 2022, 50, D204-D210.	14.5	63
47	Ancient genomes from Iceland reveal the making of a human population. Science, 2018, 360, 1028-1032.	12.6	62
48	Patterns of genomic evolution in advanced melanoma. Nature Communications, 2018, 9, 2665.	12.8	62
49	Comparison of hybridization-based and sequencing-based gene expression technologies on biological replicates. BMC Genomics, 2007, 8, 153.	2.8	61
50	Accuracy and efficiency of germline variant calling pipelines for human genome data. Scientific Reports, 2020, 10, 20222.	3.3	61
51	The disruptive positions in human G-quadruplex motifs are less polymorphic and more conserved than their neutral counterparts. Nucleic Acids Research, 2009, 37, 5749-5756.	14.5	58
52	Somatic spectrum of cancer-associated single basepair substitutions in the TP53 gene is determined mainly by endogenous mechanisms of mutation and by selection. Human Mutation, 1995, 5, 48-57.	2.5	56
53	S100A4 regulates membrane induced activation of matrix metalloproteinase-2 in osteosarcoma cells. Clinical and Experimental Metastasis, 2003, 20, 701-711.	3.3	55
54	Subtypeâ€specific microâ€RNA expression signatures in breast cancer progression. International Journal of Cancer, 2016, 139, 1117-1128.	5.1	53

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55	Colocalization analyses of genomic elements: approaches, recommendations and challenges. Bioinformatics, 2019, 35, 1615-1624.	4.1	53
56	A statistical model of ChIA-PET data for accurate detection of chromatin 3D interactions. Nucleic Acids Research, 2014, 42, e143-e143.	14.5	50
57	Analysis of repeatability in spotted cDNA microarrays. Nucleic Acids Research, 2002, 30, 3235-3244.	14.5	49
58	Colorectal cancer incidence in path_MLH1 carriers subjected to different follow-up protocols: a Prospective Lynch Syndrome Database report. Hereditary Cancer in Clinical Practice, 2017, 15, 18.	1.5	49
59	Genetic epidemiology of BRCA1 mutations in Norway. European Journal of Cancer, 2001, 37, 2428-2434.	2.8	47
60	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.	2.8	45
61	The Human Genomic Melting Map. PLoS Computational Biology, 2007, 3, e93.	3.2	44
62	BRCA1 mutations in ovarian cancer and borderline tumours in Norway: a nested caseâ€“control study. British Journal of Cancer, 2004, 91, 1829-1834.	6.4	43
63	Lack of association between screening interval and cancer stage in Lynch syndrome may be accounted for by over-diagnosis; a prospective Lynch syndrome database report. Hereditary Cancer in Clinical Practice, 2019, 17, 8.	1.5	42
64	Computational approaches in cancer multidrug resistance research: Identification of potential biomarkers, drug targets and drug-target interactions. Drug Resistance Updates, 2020, 48, 100662.	14.4	42
65	Three per cent of Norwegian Ovarian Cancers are caused by BRCA1 1675delA or 1135insA. European Journal of Cancer, 1999, 35, 779-781.	2.8	41
66	Ectopic expression of target genes may represent an inherent limitation of RT-PCR assays used for micrometastasis detection: studies on the epithelial glycoprotein geneEGP-2. , 1997, 72, 191-196.		40
67	CLC and IFNAR1 are differentially expressed and a global immunity score is distinct between early- and late-onset colorectal cancer. Genes and Immunity, 2011, 12, 653-662.	4.1	40
68	A survey of the clinicopathological and molecular characteristics of patients with suspected Lynch syndrome in Latin America. BMC Cancer, 2017, 17, 623.	2.6	40
69	Detection of base mutations in genomic DNA using denaturing gradient gel electrophoresis (DGGE) followed by transfer and hybridization with gene-specific probes. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1988, 202, 77-83.	1.0	39
70	Melanoma brain colonization involves the emergence of a brain-adaptive phenotype. Oncoscience, 2014, 1, 82-94.	2.2	39
71	HiBrowse: multi-purpose statistical analysis of genome-wide chromatin 3D organization. Bioinformatics, 2014, 30, 1620-1622.	4.1	37
72	Analysis of the humoral immune response to immunoselected phage-displayed peptides by a microarray-based method. Proteomics, 2004, 4, 2572-2582.	2.2	36

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73	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.	6.2	36
74	Transcriptionally Active Regions Are the Preferred Targets for Chromosomal HPV Integration in Cervical Carcinogenesis. PLoS ONE, 2015, 10, e0119566.	2.5	36
75	Limitations of mRNA amplification from small-size cell samples. BMC Genomics, 2005, 6, 147.	2.8	35
76	From proteomes to complexomes in the era of systems biology. Proteomics, 2014, 14, 24-41.	2.2	35
77	Naive Donor NK Cell Repertoires Associated with Less Leukemia Relapse after Allogeneic Hematopoietic Stem Cell Transplantation. Journal of Immunology, 2016, 196, 1400-1411.	0.8	35
78	Gene-expression profiling in breast cancer. Lancet, The, 2005, 365, 634-635.	13.7	34
79	Personal Cancer Genome Reporter: variant interpretation report for precision oncology. Bioinformatics, 2018, 34, 1778-1780.	4.1	33
80	The Genomic HyperBrowser: an analysis web server for genome-scale data. Nucleic Acids Research, 2013, 41, W133-W141.	14.5	32
81	Photochemically Induced Gene Silencing Using Small Interfering RNA Molecules in Combination with Lipid Carriers. Oligonucleotides, 2007, 17, 166-173.	2.7	31
82	BRCA1 1675delA and 1135insA Account for One Third of Norwegian Familial Breast-Ovarian Cancer and Are Associated with Later Disease Onset than Less Frequent Mutations. Disease Markers, 1999, 15, 79-84.	1.3	30
83	MArray: analysing single, replicated or reversed microarray experiments. Bioinformatics, 2002, 18, 1139-1140.	4.1	30
84	MGraph: graphical models for microarray data analysis. Bioinformatics, 2003, 19, 2210-2211.	4.1	29
85	Evaluation of Various Polyethylenimine Formulations for Light-Controlled Gene Silencing using Small Interfering RNA Molecules. Oligonucleotides, 2008, 18, 123-132.	2.7	29
86	Penetrances of BRCA1 1675delA and 1135insA with Respect to Breast Cancer and Ovarian Cancer. American Journal of Human Genetics, 1999, 65, 671-679.	6.2	28
87	The BRCA1 syndrome and other inherited breast or breastâ€“ovarian cancers in a Norwegian prospective series. European Journal of Cancer, 2001, 37, 1027-1032.	2.8	28
88	Risk-reducing hysterectomy and bilateral salpingo-oophorectomy in female heterozygotes of pathogenic mismatch repair variants: a Prospective Lynch Syndrome Database report. Genetics in Medicine, 2021, 23, 705-712.	2.4	28
89	Survival by colon cancer stage and screening interval in Lynch syndrome: a prospective Lynch syndrome database report. Hereditary Cancer in Clinical Practice, 2019, 17, 28.	1.5	27
90	Tankyrase inhibition sensitizes melanoma to PD-1 immune checkpoint blockade in syngeneic mouse models. Communications Biology, 2020, 3, 196.	4.4	27

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91	A BRCA1 founder mutation, identified with haplotype analysis, allowing genotype/phenotype determination and predictive testing. European Journal of Cancer, 1997, 33, 2390-2392.	2.8	26
92	Profiling networks of distinct immune-cells in tumors. BMC Bioinformatics, 2016, 17, 263.	2.6	26
93	Understanding the Melanocyte Distribution in Human Epidermis: An Agent-Based Computational Model Approach. PLoS ONE, 2012, 7, e40377.	2.5	26
94	FigSearch: a figure legend indexing and classification system. Bioinformatics, 2004, 20, 2880-2882.	4.1	25
95	Photochemically Induced Gene Silencing Using PNA-Peptide Conjugates. Oligonucleotides, 2006, 16, 145-157.	2.7	25
96	Cyclodextrin-Containing Polymer Delivery System for Light-Directed siRNA Gene Silencing. Oligonucleotides, 2010, 20, 175-182.	2.7	25
97	Increased expression of IRF4 and ETS1 in CD4⁺ cells from patients with intermittent allergic rhinitis. Allergy: European Journal of Allergy and Clinical Immunology, 2012, 67, 33-40.	5.7	25
98	Upregulation of stem cell genes in multidrug resistant K562 leukemia cells. Leukemia Research, 2009, 33, 1379-1385.	0.8	23
99	Clonal evolution after treatment pressure in multiple myeloma: heterogenous genomic aberrations and transcriptomic convergence. Leukemia, 2022, 36, 1887-1897.	7.2	23
100	Speed-up of DNA melting algorithm with complete nearest neighbor properties. Biopolymers, 2003, 70, 364-376.	2.4	22
101	Handling realistic assumptions in hypothesis testing of 3D co-localization of genomic elements. Nucleic Acids Research, 2013, 41, 5164-5174.	14.5	22
102	GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. GigaScience, 2017, 6, 1-12.	6.4	22
103	Roadmap for a precision-medicine initiative in the Nordic region. Nature Genetics, 2019, 51, 924-930.	21.4	22
104	The CRCbiome study: a large prospective cohort study examining the role of lifestyle and the gut microbiome in colorectal cancer screening participants. BMC Cancer, 2021, 21, 930.	2.6	22
105	Gene-expression profiling in breast cancer. Lancet, The, 2005, 365, 634-635.	13.7	22
106	Response of malignant B lymphocytes to ionizing radiation: Gene expression and genotype. International Journal of Cancer, 2005, 115, 935-942.	5.1	21
107	Mapping of oxidative stress responses of human tumor cells following photodynamic therapy using hexaminolevulinate. BMC Genomics, 2007, 8, 273.	2.8	21
108	Combining Network Modeling and Gene Expression Microarray Analysis to Explore the Dynamics of Th1 and Th2 Cell Regulation. PLoS Computational Biology, 2010, 6, e1001032.	3.2	21

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109	Predicting Physical Interactions between Protein Complexes. Molecular and Cellular Proteomics, 2013, 12, 1723-1734.	3.8	21
110	Use of liquid biopsies to monitor disease progression in a sarcoma patient: a case report. BMC Cancer, 2017, 17, 29.	2.6	21
111	Interferon-Î³ suppresses S100A4 transcription independently of apoptosis or cell cycle arrest. British Journal of Cancer, 2003, 88, 1995-2001.	6.4	20
112	Identifying elemental genomic track types and representing them uniformly. BMC Bioinformatics, 2011, 12, 494.	2.6	20
113	c-Myb Binding Sites in Haematopoietic Chromatin Landscapes. PLoS ONE, 2015, 10, e0133280.	2.5	20
114	Genome Scanning of Human Breast Carcinomas Using Micro- and Minisatellite Core Probes. Genomics, 1993, 17, 66-75.	2.9	19
115	Stitchprofiles.uio.no: analysis of partly melted DNA conformations using stitch profiles. Nucleic Acids Research, 2005, 33, W573-W576.	14.5	19
116	Loss of Snord116 impacts lateral hypothalamus, sleep, and food-related behaviors. JCI Insight, 2020, 5, .	5.0	19
117	Methods for quantitation of gene expression. Frontiers in Bioscience - Landmark, 2009, Volume, 552.	3.0	19
118	Protein Arrays: A Versatile Toolbox for Target Identification and Monitoring of Patient Immune Responses. , 2007, 360, 335-348.		18
119	Identification of genetic variants for clinical management of familial colorectal tumors. BMC Medical Genetics, 2018, 19, 26.	2.1	18
120	Immunological network signatures of cancer progression and survival. BMC Medical Genomics, 2011, 4, 28.	1.5	17
121	Enhancing nucleic acid delivery by photochemical internalization. Therapeutic Delivery, 2013, 4, 1125-1140.	2.2	17
122	Sample-Index Misassignment Impacts Tumour Exome Sequencing. Scientific Reports, 2018, 8, 5307.	3.3	17
123	Combining a Universal Telomerase Based Cancer Vaccine With Ipilimumab in Patients With Metastatic Melanoma - Five-Year Follow Up of a Phase I/IIa Trial. Frontiers in Immunology, 2021, 12, 663865.	4.8	17
124	Screening for mutations in human HPRT cDNA using the polymerase chain reaction (PCR) in combination with constant denaturant gel electrophoresis (CDGE). Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1992, 269, 41-53.	1.0	16
125	Disentangling the perturbational effects of amino acid substitutions in the DNA-binding domain of p53. Human Genetics, 1999, 104, 15-22.	3.8	16
126	Light-Induced Gene Expression Using Messenger RNA Molecules. Oligonucleotides, 2010, 20, 1-6.	2.7	16

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127	CD14 and Complement Crosstalk and Largely Mediate the Transcriptional Response to Escherichia coli in Human Whole Blood as Revealed by DNA Microarray. PLoS ONE, 2015, 10, e0117261.	2.5	16
128	T-cell receptor tau delta +/CD3+4-8-T- cell acute lymphoblastic leukemias: a distinct subgroup of leukemias in children. A report of five cases. Blood, 1991, 77, 2023-2030.	1.4	15
129	Differential display analysis of breast carcinoma cells enriched by immunomagnetic target cell selection: Gene expression profiles in bone marrow target cells. International Journal of Cancer, 2002, 97, 28-33.	5.1	15
130	Transcriptome changes in a colon adenocarcinoma cell line in response to photochemical treatment as used in photochemical internalisation (PCI). FEBS Letters, 2006, 580, 5739-5746.	2.8	15
131	Investigation of Established Genetic Risk Variants for Glioma in Prediagnostic Samples from a Population-Based Nested Caseâ€“Control Study. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 810-816.	2.5	15
132	GeneCount: genome-wide calculation of absolute tumor DNA copy numbers from array comparative genomic hybridization data. Genome Biology, 2008, 9, R86.	9.6	14
133	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.	5.1	14
134	From colorectal cancer pattern to the characterization of individuals at risk: Picture for genetic research in Latin America. International Journal of Cancer, 2019, 145, 318-326.	5.1	14
135	Detection of DNA variation in cancer. Pharmacogenetics and Genomics, 1992, 2, 317-328.	5.7	13
136	Intracellular metabolism of a 2'-O-methyl-stabilized ribozyme after uptake by DOTAP transfection or asfree ribozyme. A study by capillary electrophoresis. Nucleic Acids Research, 1998, 26, 4241-4248.	14.5	13
137	Determination of Hereditary Mutations in the BRCA1 Gene Using Archived Serum Samples and Capillary Electrophoresis. Analytical Chemistry, 2004, 76, 4406-4409.	6.5	13
138	Performance Comparison of Multiple Microarray Platforms for Gene Expression Profiling. Methods in Molecular Biology, 2012, 802, 141-155.	0.9	13
139	Pathway analysis of genetic markers associated with a functional MRI faces paradigm implicates polymorphisms in calcium responsive pathways. NeuroImage, 2013, 70, 143-149.	4.2	13
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145	Risk-Reducing Gynecological Surgery in Lynch Syndrome: Results of an International Survey from the Prospective Lynch Syndrome Database. Journal of Clinical Medicine, 2020, 9, 2290.	2.4	12
146	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.	5.1	12
147	A Primer on the Current State of Microarray Technologies. Methods in Molecular Biology, 2012, 802, 3-17.	0.9	12
148	CA 125: The End of the Beginning. Tumor Biology, 2001, 22, 345-347.	1.8	11
149	Identification of HLA-B27-restricted cytotoxic T lymphocyte epitope from carcinoembryonic antigen. International Journal of Cancer, 2002, 97, 58-63.	5.1	11
150	Bioinformatics Approaches to Profile the Tumor Microenvironment for Immunotherapeutic Discovery. Current Pharmaceutical Design, 2017, 23, 4716-4725.	1.9	11
151	Uptake of hysterectomy and bilateral salpingo-oophorectomy in carriers of pathogenic mismatch repair variants: a Prospective Lynch Syndrome Database report. European Journal of Cancer, 2021, 148, 124-133.	2.8	11
152	No Difference in Penetrance between Truncating and Missense/Aberrant Splicing Pathogenic Variants in MLH1 and MSH2: A Prospective Lynch Syndrome Database Study. Journal of Clinical Medicine, 2021, 10, 2856.	2.4	11
153	MITF depletion elevates expression levels of ERBB3 receptor and its cognate ligand NRG1-beta in melanoma. Oncotarget, 2016, 7, 55128-55140.	1.8	11
154	A TP53 mutation detected in cells established from an osteosarcoma, but not in the retinoblastoma of a patient with bilateral retinoblastoma and multiple primary osteosarcomas. Cancer Genetics and Cytogenetics, 1992, 64, 178-182.	1.0	10
155	No alterations in exon 21 of theRBI gene in sarcomas and carcinomas of the breast, colon, and lung. Genes Chromosomes and Cancer, 1992, 5, 97-103.	2.8	10
156	Large-scale inference of the point mutational spectrum in human segmental duplications. BMC Genomics, 2009, 10, 43.	2.8	10
157	Genome wide single cell analysis of chemotherapy resistant metastatic cells in a case of gastroesophageal adenocarcinoma. BMC Cancer, 2011, 11, 455.	2.6	10
158	Light-Controlled Modulation of Gene Expression Using Polyamidoamine Formulations. Nucleic Acid Therapeutics, 2013, 23, 160-165.	3.6	10
159	The genetic structure of Norway. European Journal of Human Genetics, 2021, 29, 1710-1718.	2.8	10
160	Norwegian e-Infrastructure for Life Sciences (NeLS). F1000Research, 2018, 7, 968.	1.6	10
161	Impact of DNA physical properties on local sequence bias of human mutation. Human Mutation, 2010, 31, 1316-1325.	2.5	9
162	The differential disease regulome. BMC Genomics, 2011, 12, 353.	2.8	9

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163	HPV Genotyping of Modified General Primer-Amplicons Is More Analytically Sensitive and Specific by Sequencing than by Hybridization. PLoS ONE, 2017, 12, e0169074.	2.5	9
164	Diagnostic Profiling of the Human Public IgM Repertoire With Scalable Mimotope Libraries. Frontiers in Immunology, 2019, 10, 2796.	4.8	9
165	Genetic Variation/Evolution and Differential Host Responses Resulting from In-Patient Adaptation ofMycobacterium avium. Infection and Immunity, 2019, 87, .	2.2	9
166	Analysis in the Prospective Lynch Syndrome Database identifies sarcoma as part of the Lynch syndrome tumor spectrum. International Journal of Cancer, 2021, 148, 512-513.	5.1	9
167	Introducing Dynamics into the Field of Biosemiotics. Biosemiotics, 2011, 4, 5-24.	1.4	8
168	Implementing precision cancer medicine in the public health services of Norway: the diagnostic infrastructure and a cost estimate. ESMO Open, 2017, 2, e000158.	4.5	8
169	Responsiveness to PD-1 Blockade in End-Stage Colon Cancer with Gene Locus 9p24.1 Copy-Number Gain. Cancer Immunology Research, 2019, 7, 701-706.	3.4	8
170	Breast cancer survival in Nordic BRCA2 mutation carriersâ€"unconventional association with oestrogen receptor status. British Journal of Cancer, 2020, 123, 1608-1615.	6.4	8
171	Molecularly matched therapy in the context of sensitivity, resistance, and safety; patient outcomes in end-stage cancer â€“ the MetAction study. Acta OncolÃ³gica, 2020, 59, 733-740.	1.8	8
172	CDKN2A (p16INK4A) somatic and germline mutations. Human Mutation, 1996, 7, 294-303.	2.5	8
173	The mathematics of tanning. BMC Systems Biology, 2009, 3, 60.	3.0	7
174	Transcriptomic Profiling of Tumor Aggressiveness in Sporadic Nonfunctioning Pancreatic Neuroendocrine Neoplasms. Pancreas, 2016, 45, 1196-1203.	1.1	7
175	Pre-diagnostic serum levels of EGFR and ErbB2 and genetic glioma risk variants: a nested case-control study. Tumor Biology, 2016, 37, 11065-11072.	1.8	7
176	Genetic variants of prospectively demonstrated phenocopies in BRCA1/2 kindreds. Hereditary Cancer in Clinical Practice, 2018, 16, 4.	1.5	7
177	Causes for Frequent Pathogenic BRCA1 Variants Include Low Penetrance in Fertile Ages, Recurrent De-Novo Mutations and Genetic Drift. Cancers, 2019, 11, 132.	3.7	7
178	Mutational dynamics and immune evasion in diffuse large B-cell lymphoma explored in a relapse-enriched patient series. Blood Advances, 2020, 4, 1859-1866.	5.2	7
179	Dysregulation of MITF Leads to Transformation in MC1R-Defective Melanocytes. Cancers, 2020, 12, 1719.	3.7	7
180	Recommendations for the FAIRification of genomic track metadata. F1000Research, 2021, 10, 268.	1.6	7

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181	Differential expression patterns of S100a2, S100a4 and S100a6 during progression of human malignant melanoma. International Journal of Cancer, 1997, 74, 464-469.	5.1	7
182	A national precision cancer medicine implementation initiative for Norway. Nature Medicine, 2022, 28, 885-887.	30.7	7
183	Improving public cancer care by implementing precision medicine in Norway: IMPRESS-Norway. Journal of Translational Medicine, 2022, 20, 225.	4.4	7
184	Chromosome 13 instability and esterase D expression in an osteosarcoma cell line. Cancer Genetics and Cytogenetics, 1987, 24, 327-334.	1.0	6
185	MUTYH Mutations Do Not Cause HNPCC or Late Onset Familial Colorectal Cancer. Hereditary Cancer in Clinical Practice, 2006, 4, 90.	1.5	6
186	Non-parametric estimation of reference intervals in small non-Gaussian sample sets. Accreditation and Quality Assurance, 2009, 14, 185-192.	0.8	6
187	A Novel Photosensitizer for Light-Controlled Gene Silencing. Nucleic Acid Therapeutics, 2011, 21, 359-367.	3.6	6
188	Evaluation of Biodegradable Peptide Carriers for Light-Directed Targeting. Nucleic Acid Therapeutics, 2013, 23, 131-139.	3.6	6
189	Automated amplicon design suitable for analysis of DNA variants by melting techniques. BMC Research Notes, 2015, 8, 667.	1.4	6
190	Gene expression profiling of Gram-negative bacteria-induced inflammation in human whole blood: The role of complement and CD14-mediated innate immune response. Genomics Data, 2015, 5, 176-183.	1.3	6
191	Genome build information is an essential part of genomic track files. Genome Biology, 2017, 18, 175.	8.8	6
192	Integrative genomic analysis of peritoneal malignant mesothelioma: understanding a case with extraordinary chemotherapy response. Journal of Physical Education and Sports Management, 2019, 5, a003566.	1.2	6
193	Chromosome 13 alterations in osteosarcoma cell lines derived from a patient with previous retinoblastoma. Cancer Genetics and Cytogenetics, 1991, 57, 31-40.	1.0	5
194	Detection of Mutations by Single-Strand Conformation Polymorphism (SSCP) Analysis and SSCP-Hybrid Methods. , 1997, Chapter 7, 7.4.1-7.4.23.		5
195	Optimization of Hammerhead Ribozymes for the Cleavage of S100A4 (CAPL) mRNA. Oligonucleotides, 2001, 11, 67-75.	4.3	5
196	The Detection of Hamster Connexins: A Comparison of Expression Profiles with Wild-Type Mouse and the Cancer-ProneMinMouse. Cell Communication and Adhesion, 2004, 11, 155-171.	1.0	5
197	Validation of oligoarrays for quantitative exploration of the transcriptome. BMC Genomics, 2008, 9, 258.	2.8	5
198	Potent Gene Silencing In Vitro at Physiological pH Using Chitosan Polymers. Nucleic Acid Therapeutics, 2012, 22, 96-102.	3.6	5

#	Article	IF	Citations
199	Towards a quantitative understanding of the MITF-PIAS3-STAT3 connection. BMC Systems Biology, 2012, 6, 11.	3.0	5
200	Differential Protein Network Analysis of the Immune Cell Lineage. BioMed Research International, 2014, 2014, 1-11.	1.9	5
201	Galaxy Portal: interacting with the galaxy platform through mobile devices. Bioinformatics, 2016, 32, 1743-1745.	4.1	5
202	The rainfall plot: its motivation, characteristics and pitfalls. BMC Bioinformatics, 2017, 18, 264.	2.6	5
203	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	1.6	5
204	A comprehensive framework for analysis of microRNA sequencing data in metastatic colorectal cancer. NAR Cancer, 2022, 4, zcab051.	3.1	5
205	Connectivity can be used to identify key genes in DNA microarray data: a study based on gene expression in nasal polyps before and after treatment with glucocorticoids. Acta Oto-Laryngologica, 2007, 127, 1074-1079.	0.9	4
206	Constant denaturant gel electrophoresis, a modification of denaturing gradient gel electrophoresis, in mutation detection. Mutation Research-Fundamental and Molecular Mechanisms of Mutagenesis, 1991, 263, 61.	1.1	3
207	Segmentation of DNA sequences into twostate regions and melting fork regions. Journal of Physics Condensed Matter, 2009, 21, 034109.	1.8	3
208	ClusTrack: Feature Extraction and Similarity Measures for Clustering of Genome-Wide Data Sets. PLoS ONE, 2015, 10, e0123261.	2.5	3
209	Monitoring B Cell Response to Immunoselected Phage-Displayed Peptides by Microarrays. Methods in Molecular Biology, 2009, 524, 273-285.	0.9	3
210	Detection of Mutations by Denaturing Gradient Gel Electrophoresis. Current Protocols in Human Genetics, 1998, 17, Unit 7.5.	3.5	2
211	Figsearch: using maximum entropy classifier to categorize biological figures. , 0, , .		2
212	Identifying pathogenic processes by integrating microarray data with prior knowledge. BMC Bioinformatics, 2014, 15, 115.	2.6	2
213	Ten modifiers of BRCA1 penetrance validated in a Norwegian series. Hereditary Cancer in Clinical Practice, 2015, 13, 14.	1.5	2
214	Reply to Towfic and othersâ€™ letter to the editor. Biostatistics, 2017, 18, 586-587.	1.5	2
215	Our genes, our selves: hereditary breast cancer and biological citizenship in Norway. Medicine, Health Care and Philosophy, 2018, 21, 239-242.	1.8	2
216	The Prospective Lynch Syndrome Database. , 2018, , 461-468.		2

#	Article	IF	Citations
217	PathTracer: High-sensitivity detection of differential pathway activity in tumours. Scientific Reports, 2019, 9, 16332.	3.3	2
218	A phase I/IIa clinical trial investigating the therapeutic cancer vaccine UV1 in combination with ipilimumab in patients with malignant melanoma: Four-year survival update.. Journal of Clinical Oncology, 2020, 38, 62-62.	1.6	2
219	Prototype precision oncology learning ecosystem: Norwegian precision cancer medicine implementation initiative.. Journal of Clinical Oncology, 2022, 40, e13634-e13634.	1.6	2
220	Double-sided silicon strip detectors: new applications within genomics and proteomics. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2004, 527, 68-72.	1.6	1
221	The Quandary of DNA-Based Treatment Assessment in De Novo Metastatic Prostate Cancer in the Era of Precision Oncology. Journal of Personalized Medicine, 2021, 11, 330.	2.5	1
222	Light-Directed Delivery of Nucleic Acids. Methods in Molecular Biology, 2011, 764, 107-121.	0.9	1
223	Abstract A101: The MetAction trial: long-lasting responses to molecularly matched therapy in end-stage cancer. , 2018, , .		1
224	Abstract 3432: microRNA expression reflects site specificity of metastatic colorectal cancer. , 2017, , .		1
225	Discovery of Recurrent Mutations Associated with Chemo-Immunotherapy Relapse in Diffuse Large B-Cell Lymphoma. Blood, 2015, 126, 110-110.	1.4	1
226	T-cell receptor tau delta +/CD3+4-8-T- cell acute lymphoblastic leukemias: a distinct subgroup of leukemias in children. A report of five cases. Blood, 1991, 77, 2023-2030.	1.4	1
227	Multilayer Modeling of Skin Color and Translucency. , 2016, , 27-48.		1
228	Denaturing gradient gel electrophoresis: A method for separation of DNA fragments differing by single base-pair substitution. Mutation Research - Environmental Mutagenesis and Related Subjects Including Methodology, 1988, 203, 204.	0.4	0
229	Analysis of inherited and acquired mutations using PCR and denaturing gradient gel electrophoresis (DGGE). Mutation Research - Environmental Mutagenesis and Related Subjects Including Methodology, 1991, 252, 175-176.	0.4	0
230	Light-Induced mRNA Transfection. Methods in Molecular Biology, 2013, 969, 89-100.	0.9	0
231	P17.94 * GLIOMA GWAS HITS - MARKERS FOR RISK OR FOR PROGNOSIS?. Neuro-Oncology, 2014, 16, ii109-ii110.	1.2	0
232	P1.02-028 Pathways Involved in Early Stage Lung Cancers. Journal of Thoracic Oncology, 2017, 12, S1934-S1935.	1.1	0
233	Filesystem Front-end for Seamless Job Management in Sensitive Data e-Infrastructures and Cloud Federation. , 2018, , .		0
234	P04.80 Diagnostic potential of the IgM igOme (IgM repertoire) biomarkers for brain tumors. Neuro-Oncology, 2018, 20, iii298-iii299.	1.2	0

#	Article	IF	Citations
235	Editorial: Genomic Colocalization and Enrichment Analyses. Frontiers in Genetics, 2020, 11, 617876.	2.3	0
236	Towards Knowledge Discovery from cDNA Microarray Gene Expression Data. Lecture Notes in Computer Science, 2000, , 470-475.	1.3	0
237	The Human Genomic Melting Map. PLoS Computational Biology, 2005, preprint, e93.	3.2	0
238	Abstract 5226:In vivoimaging and molecular characterization of site-specific growth of malignant melanoma: a study of melanoma metastasis in experimental animal models. , 2011, , .		0
239	CellLineMiner: a knowledge portal for human cell lines. Bioinformation, 2012, 8, 1119-1122.	0.5	0
240	Abstract C31: Characterization of malignant melanoma growth triggered by the brain microenvironment in experimental metastasis models. , 2013, , .		0
241	Mutations in NSCLC.. Journal of Clinical Oncology, 2014, 32, e18516-e18516.	1.6	0
242	Abstract 4876: Characterization of malignant melanoma growth triggered by the brain microenvironment in experimental metastasis models. , 2014, , .		0
243	Abstract 370: Modeling signaling networks in tumor immunology. , 2014, , .		0
244	Abstract 2850: Biomarkers for detection of exfoliated tumor cells in the peritoneal cavity in rectal cancer. , 2014, , .		0
245	Abstract 4197: Regulators of p21 transcription in melanoma. , 2014, , .		0
246	The MetAction project: Biomarker-directed molecularly matched therapy for end-stage cancer implemented in clinical practice.. Journal of Clinical Oncology, 2017, 35, e14033-e14033.	1.6	0
247	Abstract 5700: CircSarc: Disease monitoring by liquid biopsies in sarcomas. , 2017, , .		0
248	Abstract A08: Disease monitoring by liquid biopsies in sarcomas. , 2018, , .		0
249	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.	1.4	0
250	Physical 3D Modeling of Whole Genomes: Exploring Chromosomal Organization Properties and Principles. , 2019, , 331-360.		0
251	Deep Profiling of Genetic Aberrations and Clonal Evolution in Follicular Lymphoma. Blood, 2019, 134, 20-20.	1.4	0
252	Mutational Dynamics and Evolutionary Divergence in DLBCL: A Call for Relapse Sampling. Blood, 2019, 134, 1497-1497.	1.4	0

#	Article	IF	Citations
253	Abstract A31: Tracking the evolution of soft tissue sarcoma and GIST using liquid biopsies. , 2020, , .		0
254	382â€…The synthetic long peptide cancer vaccine UV1 in combination with ipilimumab induces a CD4+ Th1 anti-hTERT immune response and an inflammatory tumor microenvironment in patients with melanoma. , 2021, 9, A416-A416.		0