# Eivind Hovig

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6751476/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 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 | MirGeneDB 2.1: toward a complete sampling of all major animal phyla. Nucleic Acids Research, 2022, 50, D204-D210. | 14.5 | 63 |
| 2 | A comprehensive framework for analysis of microRNA sequencing data in metastatic colorectal cancer. NAR Cancer, 2022, 4, zcab051. | 3.1 | 5 |
| 3 | A national precision cancer medicine implementation initiative for Norway. Nature Medicine, 2022, 28, 885-887. | 30.7 | 7 |
| 4 | Improving public cancer care by implementing precision medicine in Norway: IMPRESS-Norway. Journal of Translational Medicine, 2022, 20, 225. | 4.4 | 7 |
| 5 | Clonal evolution after treatment pressure in multiple myeloma: heterogenous genomic aberrations and transcriptomic convergence. Leukemia, 2022, 36, 1887-1897. | 7.2 | 23 |
| 6 | Prototype precision oncology learning ecosystem: Norwegian precision cancer medicine implementation initiative.. Journal of Clinical Oncology, 2022, 40, e13634-e13634. | 1.6 | 2 |
| 7 | 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 |
| 8 | 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 |
| 9 | 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 |
| 10 | Recommendations for the FAIRification of genomic track metadata. F1000Research, 2021, 10, 268. | 1.6 | 7 |
| 11 | 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 |
| 12 | 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 |
| 13 | The genetic structure of Norway. European Journal of Human Genetics, 2021, 29, 1710-1718. | 2.8 | 10 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | MirGeneDB 2.0: the metazoan microRNA complement. Nucleic Acids Research, 2020, 48, D132-D141. | 14.5 | 194 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | Accuracy and efficiency of germline variant calling pipelines for human genome data. Scientific Reports, 2020, 10, 20222. | 3.3 | 61 |
| 24 | 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 |
| 25 | 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 |
| 26 | Dysregulation of MITF Leads to Transformation in MC1R-Defective Melanocytes. Cancers, 2020, 12, 1719. | 3.7 | 7 |
| 27 | Tankyrase inhibition sensitizes melanoma to PD-1 immune checkpoint blockade in syngeneic mouse models. Communications Biology, 2020, 3, 196. | 4.4 | 27 |
| 28 | Editorial: Genomic Colocalization and Enrichment Analyses. Frontiers in Genetics, 2020, 11, 617876. | 2.3 | 0 |
| 29 | Loss of Snord116 impacts lateral hypothalamus, sleep, and food-related behaviors. JCI Insight, 2020, 5, . | 5.0 | 19 |
| 30 | 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 |
| 31 | The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229. | 1.6 | 5 |
| 32 | Abstract A31: Tracking the evolution of soft tissue sarcoma and GIST using liquid biopsies. , 2020, , . | | 0 |
| 33 | A snapshot of current genetic testing practice in Lynch syndrome: The results of a representative survey of 33 Latin American existing centres/registries. European Journal of Cancer, 2019, 119, 112-121. | 2.8 | 13 |
| 34 | 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 |
| 35 | Colocalization analyses of genomic elements: approaches, recommendations and challenges. Bioinformatics, 2019, 35, 1615-1624. | 4.1 | 53 |
| 36 | Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674. | 12.8 | 240 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | 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 |
| 38 | 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 |
| 39 | Roadmap for a precision-medicine initiative in the Nordic region. Nature Genetics, 2019, 51, 924-930. | 21.4 | 22 |
| 40 | 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 |
| 41 | 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 |
| 42 | Diagnostic Profiling of the Human Public IgM Repertoire With Scalable Mimotope Libraries. Frontiers in Immunology, 2019, 10, 2796. | 4.8 | 9 |
| 43 | PathTracer: High-sensitivity detection of differential pathway activity in tumours. Scientific Reports, 2019, 9, 16332. | 3.3 | 2 |
| 44 | Results of multigene panel testing in familial cancer cases without genetic cause demonstrated by single gene testing. Scientific Reports, 2019, 9, 18555. | 3.3 | 13 |
| 45 | Genetic Variation/Evolution and Differential Host Responses Resulting from In-Patient Adaptation ofMycobacterium avium. Infection and Immunity, 2019, 87, . | 2.2 | 9 |
| 46 | 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 |
| 47 | Physical 3D Modeling of Whole Genomes: Exploring Chromosomal Organization Properties and Principles. , 2019, , 331-360. | | 0 |
| 48 | Deep Profiling of Genetic Aberrations and Clonal Evolution in Follicular Lymphoma. Blood, 2019, 134, 20-20. | 1.4 | 0 |
| 49 | Mutational Dynamics and Evolutionary Divergence in DLBCL: A Call for Relapse Sampling. Blood, 2019, 134, 1497-1497. | 1.4 | 0 |
| 50 | Personal Cancer Genome Reporter: variant interpretation report for precision oncology. Bioinformatics, 2018, 34, 1778-1780. | 4.1 | 33 |
| 51 | Sample-Index Misassignment Impacts Tumour Exome Sequencing. Scientific Reports, 2018, 8, 5307. | 3.3 | 17 |
| 52 | Potentially pathogenic germline CHEK2 c.319+2T>A among multiple early-onset cancer families. Familial Cancer, 2018, 17, 141-153. | 1.9 | 12 |
| 53 | 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 |
| 54 | Our genes, our selves: hereditary breast cancer and biological citizenship in Norway. Medicine, Health Care and Philosophy, 2018, 21, 239-242. | 1.8 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 55 | Filesystem Front-end for Seamless Job Management in Sensitive Data e-Infrastructures and Cloud Federation. , 2018, , . | | 0 |
| 56 | P04.80 Diagnostic potential of the IgM igOme (IgM repertoire) biomarkers for brain tumors. Neuro-Oncology, 2018, 20, iii298-iii299. | 1.2 | 0 |
| 57 | Ancient genomes from Iceland reveal the making of a human population. Science, 2018, 360, 1028-1032. | 12.6 | 62 |
| 58 | Patterns of genomic evolution in advanced melanoma. Nature Communications, 2018, 9, 2665. | 12.8 | 62 |
| 59 | Identification of genetic variants for clinical management of familial colorectal tumors. BMC Medical Genetics, 2018, 19, 26. | 2.1 | 18 |
| 60 | Genetic variants of prospectively demonstrated phenocopies in BRCA1/2 kindreds. Hereditary Cancer in Clinical Practice, 2018, 16, 4. | 1.5 | 7 |
| 61 | The Prospective Lynch Syndrome Database. , 2018, , 461-468. | | 2 |
| 62 | Abstract A101: The MetAction trial: long-lasting responses to molecularly matched therapy in end-stage cancer. , 2018, , . | | 1 |
| 63 | Norwegian e-Infrastructure for Life Sciences (NeLS). F1000Research, 2018, 7, 968. | 1.6 | 10 |
| 64 | Abstract A08: Disease monitoring by liquid biopsies in sarcomas. , 2018, , . | | 0 |
| 65 | 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 |
| 66 | 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 |
| 67 | Use of liquid biopsies to monitor disease progression in a sarcoma patient: a case report. BMC Cancer, 2017, 17, 29. | 2.6 | 21 |
| 68 | GSuite HyperBrowser: integrative analysis of dataset collections across the genome and epigenome. GigaScience, 2017, 6, 1-12. | 6.4 | 22 |
| 69 | 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 |
| 70 | 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 |
| 71 | 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 |
| 72 | The rainfall plot: its motivation, characteristics and pitfalls. BMC Bioinformatics, 2017, 18, 264. | 2.6 | 5 |

| # | Article | IF | Citations |
|---|---|---|---|
| 73 | P1.02-028 Pathways Involved in Early Stage Lung Cancers. Journal of Thoracic Oncology, 2017, 12, S1934-S1935. | 1.1 | 0 |
| 74 | Bioinformatics Approaches to Profile the Tumor Microenvironment for Immunotherapeutic Discovery. Current Pharmaceutical Design, 2017, 23, 4716-4725. | 1.9 | 11 |
| 75 | Reply to Towfic and othersâ€™ letter to the editor. Biostatistics, 2017, 18, 586-587. | 1.5 | 2 |
| 76 | 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 |
| 77 | 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 |
| 78 | 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 |
| 79 | Genome build information is an essential part of genomic track files. Genome Biology, 2017, 18, 175. | 8.8 | 6 |
| 80 | Abstract 3432: microRNA expression reflects site specificity of metastatic colorectal cancer. , 2017, , . | | 1 |
| 81 | 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 |
| 82 | Abstract 5700: CircSarc: Disease monitoring by liquid biopsies in sarcomas. , 2017, , . | | 0 |
| 83 | TP53 Mutation Spectrum in Smokers and Never Smoking Lung Cancer Patients. Frontiers in Genetics, 2016, 07, 85. | 2.3 | 76 |
| 84 | Transcriptomic Profiling of Tumor Aggressiveness in Sporadic Nonfunctioning Pancreatic Neuroendocrine Neoplasms. Pancreas, 2016, 45, 1196-1203. | 1.1 | 7 |
| 85 | Subtypeâ€specific microâ€RNA expression signatures in breast cancer progression. International Journal of Cancer, 2016, 139, 1117-1128. | 5.1 | 53 |
| 86 | Profiling networks of distinct immune-cells in tumors. BMC Bioinformatics, 2016, 17, 263. | 2.6 | 26 |
| 87 | Hi-C-constrained physical models of human chromosomes recover functionally-related properties of genome organization. Scientific Reports, 2016, 6, 35985. | 3.3 | 72 |
| 88 | 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 |
| 89 | Galaxy Portal: interacting with the galaxy platform through mobile devices. Bioinformatics, 2016, 32, 1743-1745. | 4.1 | 5 |
| 90 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 91 | 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 |
| 92 | MITF depletion elevates expression levels of ERBB3 receptor and its cognate ligand NRG1-beta in melanoma. Oncotarget, 2016, 7, 55128-55140. | 1.8 | 11 |
| 93 | Multilayer Modeling of Skin Color and Translucency. , 2016, , 27-48. | | 1 |
| 94 | Ten modifiers of BRCA1 penetrance validated in a Norwegian series. Hereditary Cancer in Clinical Practice, 2015, 13, 14. | 1.5 | 2 |
| 95 | Automated amplicon design suitable for analysis of DNA variants by melting techniques. BMC Research Notes, 2015, 8, 667. | 1.4 | 6 |
| 96 | ClusTrack: Feature Extraction and Similarity Measures for Clustering of Genome-Wide Data Sets. PLoS ONE, 2015, 10, e0123261. | 2.5 | 3 |
| 97 | c-Myb Binding Sites in Haematopoietic Chromatin Landscapes. PLoS ONE, 2015, 10, e0133280. | 2.5 | 20 |
| 98 | A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001. | 12.8 | 266 |
| 99 | | | |

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|---|---|---|---|
| 109 | A statistical model of ChIA-PET data for accurate detection of chromatin 3D interactions. Nucleic Acids Research, 2014, 42, e143-e143. | 14.5 | 50 |
| 110 | HiBrowse: multi-purpose statistical analysis of genome-wide chromatin 3D organization. Bioinformatics, 2014, 30, 1620-1622. | 4.1 | 37 |
| 111 | From proteomes to complexomes in the era of systems biology. Proteomics, 2014, 14, 24-41. | 2.2 | 35 |
| 112 | Performance comparison of four exome capture systems for deep sequencing. BMC Genomics, 2014, 15, 449. | 2.8 | 152 |
| 113 | Identifying pathogenic processes by integrating microarray data with prior knowledge. BMC Bioinformatics, 2014, 15, 115. | 2.6 | 2 |
| 114 | Melanoma brain colonization involves the emergence of a brain-adaptive phenotype. Oncoscience, 2014, 1, 82-94. | 2.2 | 39 |
| 115 | Mutations in NSCLC.. Journal of Clinical Oncology, 2014, 32, e18516-e18516. | 1.6 | 0 |
| 116 | Abstract 4876: Characterization of malignant melanoma growth triggered by the brain microenvironment in experimental metastasis models. , 2014, , . | | 0 |
| 117 | Abstract 370: Modeling signaling networks in tumor immunology. , 2014, , . | | 0 |
| 118 | Abstract 2850: Biomarkers for detection of exfoliated tumor cells in the peritoneal cavity in rectal cancer. , 2014, , . | | 0 |
| 119 | Abstract 4197: Regulators of p21 transcription in melanoma. , 2014, , . | | 0 |
| 120 | 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 |
| 121 | Light-Controlled Modulation of Gene Expression Using Polyamidoamine Formulations. Nucleic Acid Therapeutics, 2013, 23, 160-165. | 3.6 | 10 |
| 122 | Light-Induced mRNA Transfection. Methods in Molecular Biology, 2013, 969, 89-100. | 0.9 | 0 |
| 123 | Substantial Loss of Conserved and Gain of Novel MicroRNA Families in Flatworms. Molecular Biology and Evolution, 2013, 30, 2619-2628. | 8.9 | 84 |
| 124 | The Genomic HyperBrowser: an analysis web server for genome-scale data. Nucleic Acids Research, 2013, 41, W133-W141. | 14.5 | 32 |
| 125 | Ten Simple Rules for Reproducible Computational Research. PLoS Computational Biology, 2013, 9, e1003285. | 3.2 | 509 |
| 126 | Predicting Physical Interactions between Protein Complexes. Molecular and Cellular Proteomics, 2013, 12, 1723-1734. | 3.8 | 21 |

| # | Article | IF | Citations |
|---|---|---|---|
| 127 | Handling realistic assumptions in hypothesis testing of 3D co-localization of genomic elements. Nucleic Acids Research, 2013, 41, 5164-5174. | 14.5 | 22 |
| 128 | Evaluation of Biodegradable Peptide Carriers for Light-Directed Targeting. Nucleic Acid Therapeutics, 2013, 23, 131-139. | 3.6 | 6 |
| 129 | Enhancing nucleic acid delivery by photochemical internalization. Therapeutic Delivery, 2013, 4, 1125-1140. | 2.2 | 17 |
| 130 | Deep Sequencing the MicroRNA Transcriptome in Colorectal Cancer. PLoS ONE, 2013, 8, e66165. | 2.5 | 132 |
| 131 | Abstract C31: Characterization of malignant melanoma growth triggered by the brain microenvironment in experimental metastasis models. , 2013, , . | | 0 |
| 132 | Potent Gene Silencing In Vitro at Physiological pH Using Chitosan Polymers. Nucleic Acid Therapeutics, 2012, 22, 96-102. | 3.6 | 5 |
| 133 | Towards a quantitative understanding of the MITF-PIAS3-STAT3 connection. BMC Systems Biology, 2012, 6, 11. | 3.0 | 5 |
| 134 | Performance Comparison of Multiple Microarray Platforms for Gene Expression Profiling. Methods in Molecular Biology, 2012, 802, 141-155. | 0.9 | 13 |
| 135 | Increased expression of IRF4 and ETS1 in CD4<sup>+</sup> cells from patients with intermittent allergic rhinitis. Allergy: European Journal of Allergy and Clinical Immunology, 2012, 67, 33-40. | 5.7 | 25 |
| 136 | A Primer on the Current State of Microarray Technologies. Methods in Molecular Biology, 2012, 802, 3-17. | 0.9 | 12 |
| 137 | Understanding the Melanocyte Distribution in Human Epidermis: An Agent-Based Computational Model Approach. PLoS ONE, 2012, 7, e40377. | 2.5 | 26 |
| 138 | Integrative Analysis Reveals Relationships of Genetic and Epigenetic Alterations in Osteosarcoma. PLoS ONE, 2012, 7, e48262. | 2.5 | 87 |
| 139 | CellLineMiner: a knowledge portal for human cell lines. Bioinformation, 2012, 8, 1119-1122. | 0.5 | 0 |
| 140 | A Novel Photosensitizer for Light-Controlled Gene Silencing. Nucleic Acid Therapeutics, 2011, 21, 359-367. | 3.6 | 6 |
| 141 | Identifying elemental genomic track types and representing them uniformly. BMC Bioinformatics, 2011, 12, 494. | 2.6 | 20 |
| 142 | Genome wide single cell analysis of chemotherapy resistant metastatic cells in a case of gastroesophageal adenocarcinoma. BMC Cancer, 2011, 11, 455. | 2.6 | 10 |
| 143 | Introducing Dynamics into the Field of Biosemiotics. Biosemiotics, 2011, 4, 5-24. | 1.4 | 8 |
| 144 | Immunological network signatures of cancer progression and survival. BMC Medical Genomics, 2011, 4, 28. | 1.5 | 17 |

| # | Article | IF | Citations |
|---|---|---|---|
| 145 | The differential disease regulome. BMC Genomics, 2011, 12, 353. | 2.8 | 9 |
| 146 | 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 |
| 147 | Light-Directed Delivery of Nucleic Acids. Methods in Molecular Biology, 2011, 764, 107-121. | 0.9 | 1 |
| 148 | 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 |
| 149 | Impact of DNA physical properties on local sequence bias of human mutation. Human Mutation, 2010, 31, 1316-1325. | 2.5 | 9 |
| 150 | Light-Induced Gene Expression Using Messenger RNA Molecules. Oligonucleotides, 2010, 20, 1-6. | 2.7 | 16 |
| 151 | Cyclodextrin-Containing Polymer Delivery System for Light-Directed siRNA Gene Silencing. Oligonucleotides, 2010, 20, 175-182. | 2.7 | 25 |
| 152 | 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 |
| 153 | The Genomic HyperBrowser: inferential genomics at the sequence level. Genome Biology, 2010, 11, R121. | 9.6 | 78 |
| 154 | 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 |
| 155 | Segmentation of DNA sequences into twostate regions and melting fork regions. Journal of Physics Condensed Matter, 2009, 21, 034109. | 1.8 | 3 |
| 156 | Large-scale inference of the point mutational spectrum in human segmental duplications. BMC Genomics, 2009, 10, 43. | 2.8 | 10 |
| 157 | The mathematics of tanning. BMC Systems Biology, 2009, 3, 60. | 3.0 | 7 |
| 158 | Non-parametric estimation of reference intervals in small non-Gaussian sample sets. Accreditation and Quality Assurance, 2009, 14, 185-192. | 0.8 | 6 |
| 159 | Upregulation of stem cell genes in multidrug resistant K562 leukemia cells. Leukemia Research, 2009, 33, 1379-1385. | 0.8 | 23 |
| 160 | Monitoring B Cell Response to Immunoselected Phage-Displayed Peptides by Microarrays. Methods in Molecular Biology, 2009, 524, 273-285. | 0.9 | 3 |
| 161 | Methods for quantitation of gene expression. Frontiers in Bioscience - Landmark, 2009, Volume, 552. | 3.0 | 19 |
| 162 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 163 | Validation of oligoarrays for quantitative exploration of the transcriptome. BMC Genomics, 2008, 9, 258. | 2.8 | 5 |
| 164 | Evaluation of Various Polyethylenimine Formulations for Light-Controlled Gene Silencing using Small Interfering RNA Molecules. Oligonucleotides, 2008, 18, 123-132. | 2.7 | 29 |
| 165 | GeneCount: genome-wide calculation of absolute tumor DNA copy numbers from array comparative genomic hybridization data. Genome Biology, 2008, 9, R86. | 9.6 | 14 |
| 166 | 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 |
| 167 | Protein Arrays: A Versatile Toolbox for Target Identification and Monitoring of Patient Immune Responses. , 2007, 360, 335-348. | | 18 |
| 168 | Photochemically Induced Gene Silencing Using Small Interfering RNA Molecules in Combination with Lipid Carriers. Oligonucleotides, 2007, 17, 166-173. | 2.7 | 31 |
| 169 | The Human Genomic Melting Map. PLoS Computational Biology, 2007, 3, e93. | 3.2 | 44 |
| 170 | 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 |
| 171 | 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 |
| 172 | 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 |
| 173 | Comparison of hybridization-based and sequencing-based gene expression technologies on biological replicates. BMC Genomics, 2007, 8, 153. | 2.8 | 61 |
| 174 | Mapping of oxidative stress responses of human tumor cells following photodynamic therapy using hexaminolevulinate. BMC Genomics, 2007, 8, 273. | 2.8 | 21 |
| 175 | Photochemically Induced Gene Silencing Using PNA-Peptide Conjugates. Oligonucleotides, 2006, 16, 145-157. | 2.7 | 25 |
| 176 | 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 |
| 177 | MUTYH Mutations Do Not Cause HNPCC or Late Onset Familial Colorectal Cancer. Hereditary Cancer in Clinical Practice, 2006, 4, 90. | 1.5 | 6 |
| 178 | A sequence-oriented comparison of gene expression measurements across different hybridization-based technologies. Nature Biotechnology, 2006, 24, 832-840. | 17.5 | 144 |
| 179 | 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 |
| 180 | Limitations of mRNA amplification from small-size cell samples. BMC Genomics, 2005, 6, 147. | 2.8 | 35 |

| # | Article | IF | Citations |
|---|---|---|---|
| 181 | Response of malignant B lymphocytes to ionizing radiation: Gene expression and genotype. International Journal of Cancer, 2005, 115, 935-942. | 5.1 | 21 |
| 182 | Stitchprofiles.uio.no: analysis of partly melted DNA conformations using stitch profiles. Nucleic Acids Research, 2005, 33, W573-W576. | 14.5 | 19 |
| 183 | Gene-expression profiling in breast cancer. Lancet, The, 2005, 365, 634-635. | 13.7 | 34 |
| 184 | Parallel nanoliter detection of cancer markers using polymer microchips. Lab on A Chip, 2005, 5, 416-420. | 6.0 | 91 |
| 185 | Gene-expression profiling in breast cancer. Lancet, The, 2005, 365, 634-635. | 13.7 | 22 |
| 186 | The Human Genomic Melting Map. PLoS Computational Biology, 2005, preprint, e93. | 3.2 | 0 |
| 187 | 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 |
| 188 | Profound influence of microarray scanner characteristics on gene expression ratios: analysis and procedure for correction. BMC Genomics, 2004, 5, 10. | 2.8 | 63 |
| 189 | Analysis of the humoral immune response to immunoselected phage-displayed peptides by a microarray-based method. Proteomics, 2004, 4, 2572-2582. | 2.2 | 36 |
| 190 | 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 |
| 191 | FigSearch: a figure legend indexing and classification system. Bioinformatics, 2004, 20, 2880-2882. | 4.1 | 25 |
| 192 | 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 |
| 193 | Determination of Hereditary Mutations in the BRCA1 Gene Using Archived Serum Samples and Capillary Electrophoresis. Analytical Chemistry, 2004, 76, 4406-4409. | 6.5 | 13 |
| 194 | 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 |
| 195 | Real-Time Nucleic Acid Sequence-Based Amplification in Nanoliter Volumes. Analytical Chemistry, 2004, 76, 9-14. | 6.5 | 122 |
| 196 | S100A4 regulates membrane induced activation of matrix metalloproteinase-2 in osteosarcoma cells. Clinical and Experimental Metastasis, 2003, 20, 701-711. | 3.3 | 55 |
| 197 | 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 |
| 198 | Effects of mRNA amplification on gene expression ratios in cDNA experiments estimated by analysis of variance. BMC Genomics, 2003, 4, 11. | 2.8 | 66 |

| # | Article | IF | Citations |
|---|---|---|---|
| 199 | Speed-up of DNA melting algorithm with complete nearest neighbor properties. Biopolymers, 2003, 70, 364-376. | 2.4 | 22 |
| 200 | MGraph: graphical models for microarray data analysis. Bioinformatics, 2003, 19, 2210-2211. | 4.1 | 29 |
| 201 | Interferon-Î³ suppresses S100A4 transcription independently of apoptosis or cell cycle arrest. British Journal of Cancer, 2003, 88, 1995-2001. | 6.4 | 20 |
| 202 | MArray: analysing single, replicated or reversed microarray experiments. Bioinformatics, 2002, 18, 1139-1140. | 4.1 | 30 |
| 203 | Analysis of repeatability in spotted cDNA microarrays. Nucleic Acids Research, 2002, 30, 3235-3244. | 14.5 | 49 |
| 204 | The semantic web and biology. Drug Discovery Today, 2002, 7, 992. | 6.4 | 12 |
| 205 | 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 |
| 206 | Identification of HLA-B27-restricted cytotoxic T lymphocyte epitope from carcinoembryonic antigen. International Journal of Cancer, 2002, 97, 58-63. | 5.1 | 11 |
| 207 | Associations between gene expressions in breast cancer and patient survival. Human Genetics, 2002, 111, 411-420. | 3.8 | 78 |
| 208 | CA 125: The End of the Beginning. Tumor Biology, 2001, 22, 345-347. | 1.8 | 11 |
| 209 | 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 |
| 210 | Genetic epidemiology of BRCA1 mutations in Norway. European Journal of Cancer, 2001, 37, 2428-2434. | 2.8 | 47 |
| 211 | Optimization of Hammerhead Ribozymes for the Cleavage of S100A4 (CAPL) mRNA. Oligonucleotides, 2001, 11, 67-75. | 4.3 | 5 |
| 212 | A literature network of human genes for high-throughput analysis of gene expression. Nature Genetics, 2001, 28, 21-28. | 21.4 | 655 |
| 213 | Title is missing!. Nature Genetics, 2001, 28, 21-28. | 21.4 | 482 |
| 214 | Towards Knowledge Discovery from cDNA Microarray Gene Expression Data. Lecture Notes in Computer Science, 2000, , 470-475. | 1.3 | 0 |
| 215 | 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 |
| 216 | Disentangling the perturbational effects of amino acid substitutions in the DNA-binding domain of p53. Human Genetics, 1999, 104, 15-22. | 3.8 | 16 |

| # | Article | IF | Citations |
|---|---|---|---|
| 217 | 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 |
| 218 | 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 |
| 219 | 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 |
| 220 | 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 |
| 221 | Detection of Mutations by Denaturing Gradient Gel Electrophoresis. Current Protocols in Human Genetics, 1998, 17, Unit 7.5. | 3.5 | 2 |
| 222 | 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 |
| 223 | 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 |
| 224 | Detection of Mutations by Single-Strand Conformation Polymorphism (SSCP) Analysis and SSCP-Hybrid Methods. , 1997, Chapter 7, 7.4.1-7.4.23. | | 5 |
| 225 | 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 |
| 226 | 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 |
| 227 | Differential expression patterns ofS100a2, S100a4 andS100a6 during progression of human malignant melanoma. , 1997, 74, 464-469. | | 155 |
| 228 | 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 |
| 229 | 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 |
| 230 | CDKN2A (p16INK4A) somatic and germline mutations. Human Mutation, 1996, 7, 294-303. | 2.5 | 83 |
| 231 | 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 |
| 232 | CDKN2A (p16INK4A) somatic and germline mutations. Human Mutation, 1996, 7, 294-303. | 2.5 | 8 |
| 233 | 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 |
| 234 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 235 | 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 |
| 236 | 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 |
| 237 | Database of p53 gene somatic mutations in human tumors and cell lines. Nucleic Acids Research, 1994, 22, 3551-5. | 14.5 | 646 |
| 238 | Genome Scanning of Human Breast Carcinomas Using Micro- and Minisatellite Core Probes. Genomics, 1993, 17, 66-75. | 2.9 | 19 |
| 239 | Detection of DNA variation in cancer. Pharmacogenetics and Genomics, 1992, 2, 317-328. | 5.7 | 13 |
| 240 | 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 |
| 241 | 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 |
| 242 | 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 |
| 243 | Screening for germ line TP53 mutations in breast cancer patients. Cancer Research, 1992, 52, 3234-6. | 0.9 | 139 |
| 244 | 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 |
| 245 | 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 |
| 246 | 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 |
| 247 | 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 |
| 248 | 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 |
| 249 | 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 |
| 250 | 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 |
| 251 | 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 |
| 252 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 253 | Chromosome 13 instability and esterase D expression in an osteosarcoma cell line. Cancer Genetics and Cytogenetics, 1987, 24, 327-334. | 1.0 | 6 |
| 254 | Figsearch: using maximum entropy classifier to categorize biological figures. , 0, , . | | 2 |