Johan Staaf

List of Publications by Year
in descending order

121 papers	8,985 citations	71102 41 h-index	46799 89 g-index
134 all docs	134 docs citations	134 times ranked	16240 citing authors

#	Article	IF	Citations
1	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
2	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	30.7	769
3	GOBO: Gene Expression-Based Outcome for Breast Cancer Online. PLoS ONE, 2011, 6, e17911.	2.5	361
4	Recurrent gross mutations of the PTEN tumor suppressor gene in breast cancers with deficient DSB repair. Nature Genetics, 2008, 40, 102-107.	21.4	316
5	Molecular subtypes of breast cancer are associated with characteristic DNA methylation patterns. Breast Cancer Research, 2010, 12, R36.	5.0	251
6	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	12.8	235
7	MiRNA expression in urothelial carcinomas: Important roles of miRâ€10a, miRâ€222, miRâ€125b, miRâ€7 and miRâ€452 for tumor stage and metastasis, and frequent homozygous losses of miRâ€31. International Journal of Cancer, 2009, 124, 2236-2242.	5.1	222
8	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. Nature Medicine, 2019, 25, 1526-1533.	30.7	218
9	Identification of New MicroRNAs in Paired Normal and Tumor Breast Tissue Suggests a Dual Role for the <i>ERBB2/Her2</i> Gene. Cancer Research, 2011, 71, 78-86.	0.9	191
10	Highâ€resolution genomic profiles of breast cancer cell lines assessed by tiling BAC array comparative genomic hybridization. Genes Chromosomes and Cancer, 2007, 46, 543-558.	2.8	176
11	Genomic subtypes of breast cancer identified by array-comparative genomic hybridization display distinct molecular and clinical characteristics. Breast Cancer Research, 2010, 12, R42.	5.0	167
12	Integrated Genomic and Gene Expression Profiling Identifies Two Major Genomic Circuits in Urothelial Carcinoma. PLoS ONE, 2012, 7, e38863.	2.5	167
13	Molecular stratification of metastatic melanoma using gene expression profiling : Prediction of survival outcome and benefit from molecular targeted therapy. Oncotarget, 2015, 6, 12297-12309.	1.8	148
14	Distinct Genomic Profiles in Hereditary Breast Tumors Identified by Array-Based Comparative Genomic Hybridization. Cancer Research, 2005, 65, 7612-7621.	0.9	147
15	Identification of Subtypes in Human Epidermal Growth Factor Receptor 2â€"Positive Breast Cancer Reveals a Gene Signature Prognostic of Outcome. Journal of Clinical Oncology, 2010, 28, 1813-1820.	1.6	145
16	Two genetic pathways, t(1;10) and amplification of 3p11â€"12, in myxoinflammatory fibroblastic sarcoma, haemosiderotic fibrolipomatous tumour, and morphologically similar lesions. Journal of Pathology, 2009, 217, 716-727.	4.5	137
17	Segmentation-based detection of allelic imbalance and loss-of-heterozygosity in cancer cells using whole genome SNP arrays. Genome Biology, 2008, 9, R136.	9.6	127
18	High-resolution genomic and expression analyses of copy number alterations in HER2-amplified breast cancer. Breast Cancer Research, 2010, 12, R25.	5.0	123

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19	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. Nature Communications, 2016, 7, 12910.	12.8	119
20	Normalization of Illumina Infinium whole-genome SNP data improves copy number estimates and allelic intensity ratios. BMC Bioinformatics, 2008, 9, 409.	2.6	114
21	<i><scp>NF</scp>1</i>â€mutated melanoma tumors harbor distinct clinical and biological characteristics. Molecular Oncology, 2017, 11, 438-451.	4.6	112
22	Screening for copyâ€number alterations and loss of heterozygosity in chronic lymphocytic leukemiaâ€"A comparative study of four differently designed, high resolution microarray platforms. Genes Chromosomes and Cancer, 2008, 47, 697-711.	2.8	111
23	Recurrent 10q22-q23 Deletions: A Genomic Disorder on 10q Associated with Cognitive and Behavioral Abnormalities. American Journal of Human Genetics, 2007, 80, 938-947.	6.2	101
24	Molecular Profiling Reveals Low- and High-Grade Forms of Primary Melanoma. Clinical Cancer Research, 2012, 18, 4026-4036.	7.0	96
25	Genome-wide DNA Methylation Analysis of Lung Carcinoma Reveals One Neuroendocrine and Four Adenocarcinoma Epitypes Associated with Patient Outcome. Clinical Cancer Research, 2014, 20, 6127-6140.	7.0	91
26	The circular RNome of primary breast cancer. Genome Research, 2019, 29, 356-366.	5.5	85
27	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. Nature Genetics, 2017, 49, 341-348.	21.4	75
28	Genomic Profiling of Chondrosarcoma: Chromosomal Patterns in Central and Peripheral Tumors. Clinical Cancer Research, 2009, 15, 2685-2694.	7.0	71
29	High-resolution genomic profiling of male breast cancer reveals differences hidden behind the similarities with female breast cancer. Breast Cancer Research and Treatment, 2011, 129, 747-760.	2.5	70
30	An integrated genomics analysis of epigenetic subtypes in human breast tumors links DNA methylation patterns to chromatin states in normal mammary cells. Breast Cancer Research, 2016, 18, 27.	5.0	67
31	Mapping of a Novel Ocular and Cutaneous Malignant Melanoma Susceptibility Locus to Chromosome 9q21.32. Journal of the National Cancer Institute, 2005, 97, 1377-1382.	6.3	63
32	Mutational and gene fusion analyses of primary large cell and large cell neuroendocrine lung cancer. Oncotarget, 2015, 6, 22028-22037.	1.8	61
33	Four evolutionary trajectories underlie genetic intratumoral variation in childhood cancer. Nature Genetics, 2018, 50, 944-950.	21.4	60
34	Normalization of array-CGH data: influence of copy number imbalances. BMC Genomics, 2007, 8, 382.	2.8	57
35	Array-CGH identifies cyclin D1 and UBCH10 amplicons in anaplastic thyroid carcinoma. Endocrine-Related Cancer, 2008, 15, 801-815.	3.1	53
36	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. Nature Communications, 2020, 11, 3747.	12.8	53

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37	Characterisation of dic(9;20)(p11â€"13;q11) in childhood Bâ€cell precursor acute lymphoblastic leukaemia by tiling resolution arrayâ€based comparative genomic hybridisation reveals clustered breakpoints at 9p13.2 and 20q11.2. British Journal of Haematology, 2006, 135, 492-499.	2.5	51
38	The gene expression landscape of breast cancer is shaped by tumor protein p53 status and epithelial-mesenchymal transition. Breast Cancer Research, 2012, 14, R113.	5.0	49
39	Genome-Wide DNA Methylation Analysis in Melanoma Reveals the Importance of CpG Methylation in MITF Regulation. Journal of Investigative Dermatology, 2015, 135, 1820-1828.	0.7	46
40	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. Nature Communications, 2019, 10, 1749.	12.8	46
41	Clinical framework for next generation sequencing based analysis of treatment predictive mutations and multiplexed gene fusion detection in non-small cell lung cancer. Oncotarget, 2017, 8, 34796-34810.	1.8	45
42	Heterogeneous genetic profiles in soft tissue myoepitheliomas. Modern Pathology, 2008, 21, 1311-1319.	5.5	44
43	Characterisation of amplification patterns and target genes at chromosome 11q13 in CCND1-amplified sporadic and familial breast tumours. Breast Cancer Research and Treatment, 2012, 133, 583-594.	2.5	44
44	Gene Expression Profiling of Large Cell Lung Cancer Links Transcriptional Phenotypes to the New Histological WHO 2015 Classification. Journal of Thoracic Oncology, 2017, 12, 1257-1267.	1.1	43
45	Detection and precise mapping of germline rearrangements inBRCA1, BRCA2, MSH2, andMLH1using zoom-in array comparative genomic hybridization (aCGH). Human Mutation, 2008, 29, 555-564.	2.5	42
46	Comprehensive mutational analysis of a cohort of Swedish Cornelia de Lange syndrome patients. European Journal of Human Genetics, 2007, 15, 143-149.	2.8	41
47	The Retinoblastoma Gene Undergoes Rearrangements in <i>BRCA1</i>-Deficient Basal-like Breast Cancer. Cancer Research, 2012, 72, 4028-4036.	0.9	41
48	Relation between smoking history and gene expression profiles in lung adenocarcinomas. BMC Medical Genomics, 2012, 5, 22.	1.5	41
49	Identification and validation of single-sample breast cancer radiosensitivity gene expression predictors. Breast Cancer Research, 2018, 20, 64.	5.0	40
50	High expression of <scp><i>ZNF703</i></scp> independent of amplification indicates worse prognosis in patients with luminal B breast cancer. Cancer Medicine, 2013, 2, 437-446.	2.8	39
51	Cross comparison and prognostic assessment of breast cancer multigene signatures in a large population-based contemporary clinical series. Scientific Reports, 2019, 9, 12184.	3.3	39
52	Diagnostic Value of Insulinoma-Associated Protein 1 (INSM1) and Comparison With Established Neuroendocrine Markers in Pulmonary Cancers. Archives of Pathology and Laboratory Medicine, 2020, 144, 1075-1085.	2.5	38
53	Prediction of Lymph Node Metastasis in Breast Cancer by Gene Expression and Clinicopathological Models: Development and Validation within a Population-Based Cohort. Clinical Cancer Research, 2019, 25, 6368-6381.	7.0	37
54	Proteogenomics of non-small cell lung cancer reveals molecular subtypes associated with specific therapeutic targets and immune-evasion mechanisms. Nature Cancer, 2021, 2, 1224-1242.	13.2	37

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55	Landscape of somatic allelic imbalances and copy number alterations in human lung carcinoma. International Journal of Cancer, 2013, 132, 2020-2031.	5.1	32
56	A multi-omic study reveals *BTG2* as a reliable prognostic marker for early-stage non-small cell lung cancer. Molecular Oncology, 2018, 12, 913-924.	4.6	31
57	Oncogenic translation directs spliceosome dynamics revealing an integral role for SF3A3 in breast cancer. Molecular Cell, 2021, 81, 1453-1468.e12.	9.7	31
58	Detection of submicroscopic constitutional chromosome aberrations in clinical diagnostics: a validation of the practical performance of different array platforms. European Journal of Human Genetics, 2008, 16, 786-792.	2.8	30
59	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. Melanoma Research, 2010, 20, 381-391.	1.2	30
60	DNA methylation subgroups in melanoma are associated with proliferative and immunological processes. BMC Medical Genomics, 2015, 8, 73.	1.5	29
61	Prognostic and Chemotherapy Predictive Value of Gene-Expression Phenotypes in Primary Lung Adenocarcinoma. Clinical Cancer Research, 2016, 22, 218-229.	7.0	29
62	Analysis of DNA methylation patterns in the tumor immune microenvironment of metastatic melanoma. Molecular Oncology, 2020, 14, 933-950.	4.6	29
63	*EGLN2* DNA methylation and expression interact with *HIF1A* to affect survival of early-stage NSCLC. Epigenetics, 2019, 14, 118-129.	2.7	28
64	Genetic profiles of gastroesophageal cancer: combined analysis using expression array and tiling array—comparative genomic hybridization. Cancer Genetics and Cytogenetics, 2010, 200, 120-126.	1.0	26
65	The scaffold protein p140Cap limits ERBB2-mediated breast cancer progression interfering with Rac GTPase-controlled circuitries. Nature Communications, 2017, 8, 14797.	12.8	26
66	Mutational mechanisms of amplifications revealed by analysis of clustered rearrangements in breast cancers. Annals of Oncology, 2018, 29, 2223-2231.	1.2	26
67	Independent Validation of Early-Stage Non-Small Cell Lung Cancer Prognostic Scores Incorporating Epigenetic and Transcriptional Biomarkers With Gene-Gene Interactions and Main Effects. Chest, 2020, 158, 808-819.	0.8	26
68	An Open-Source, Automated Tumor-Infiltrating Lymphocyte Algorithm for Prognosis in Triple-Negative Breast Cancer. Clinical Cancer Research, 2021, 27, 5557-5565.	7.0	26
69	CA 19-9 and CA 125 as potential predictors of disease recurrence in resectable lung adenocarcinoma. PLoS ONE, 2017, 12, e0186284.	2.5	26
70	Landscape of somatic allelic imbalances and copy number alterations in HER2-amplified breast cancer. Breast Cancer Research, 2011, 13, R129.	5.0	25
71	Genomic and Transcriptional Alterations in Lung Adenocarcinoma in Relation to Smoking History. Clinical Cancer Research, 2014, 20, 4912-4924.	7.0	24
72	Array-CGH reveals hidden gene dose changes in children with acute lymphoblastic leukaemia and a normal or failed karyotype by G-banding. British Journal of Haematology, 2008, 140, 572-577.	2.5	23

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73	Amplification and overexpression of the *ABCC3* (MRP3) gene in primary breast cancer. Genes Chromosomes and Cancer, 2012, 51, 832-840.	2.8	23
74	Consensus of Melanoma Gene Expression Subtypes Converges on Biological Entities. Journal of Investigative Dermatology, 2016, 136, 2502-2505.	0.7	23
75	Molecular analyses of triple-negative breast cancer in the young and elderly. Breast Cancer Research, 2021, 23, 20.	5.0	23
76	Genomic and Transcriptional Alterations in Lung Adenocarcinoma in Relation to EGFR and KRAS Mutation Status. PLoS ONE, 2013, 8, e78614.	2.5	23
77	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. Melanoma Research, 2010, 20, 381-91.	1.2	22
78	Identification of Transcriptional Subgroups in *EGFR*-Mutated and *EGFR*/*KRAS* Wild-Type Lung Adenocarcinoma Reveals Gene Signatures Associated with Patient Outcome. Clinical Cancer Research, 2013, 19, 5116-5126.	7.0	21
79	Random Forest Modelling of High-Dimensional Mixed-Type Data for Breast Cancer Classification. Cancers, 2021, 13, 991.	3.7	21
80	Loss of CITED1, an MITF regulator, drives a phenotype switch *in vitro* and can predict clinical outcome in primary melanoma tumours. PeerJ, 2015, 3, e788.	2.0	20
81	Cytogenetic characterization and gene expression profiling of the trastuzumab-resistant breast cancer cell line JIMT-1. Cancer Genetics and Cytogenetics, 2007, 172, 95-106.	1.0	19
82	*SIPA1L3* methylation modifies the benefit of smoking cessation on lung adenocarcinoma survival: an epigenomicâ€"smoking interaction analysis. Molecular Oncology, 2019, 13, 1235-1248.	4.6	19
83	Distinct mechanisms of resistance to fulvestrant treatment dictate level of ER independence and selective response to CDK inhibitors in metastatic breast cancer. Breast Cancer Research, 2021, 23, 26.	5.0	19
84	Myc-induced glutaminolysis bypasses HIF-driven glycolysis in hypoxic small cell lung carcinoma cells. Oncotarget, 2017, 8, 48983-48995.	1.8	19
85	Pre-operative plasma cell-free circulating tumor DNA and serum protein tumor markers as predictors of lung adenocarcinoma recurrence. Acta OncolÃ³gica, 2019, 58, 1079-1086.	1.8	18
86	Detection and delineation of an unusual 17p11.2 deletion by array-CGH and refinement of the Smithâ€"Magenis syndrome minimum deletion to ~650Âkb. European Journal of Medical Genetics, 2005, 48, 290-300.	1.3	17
87	Duplication 16q12.1â€"q22.1 characterized by array CGH in a girl with spina bifida. European Journal of Medical Genetics, 2007, 50, 237-241.	1.3	17
88	Histological specificity of alterations and expression of *KIT* and *KITLG* in nonâ€"small cell lung carcinoma. Genes Chromosomes and Cancer, 2013, 52, 1088-1096.	2.8	17
89	A combined gene expression tool for parallel histological prediction and gene fusion detection in non-small cell lung cancer. Scientific Reports, 2019, 9, 5207.	3.3	17
90	Performance of gene expressionâ€"based single sample predictors for assessment of clinicopathological subgroups and molecular subtypes in cancers: a case comparison study in non-small cell lung cancer. Briefings in Bioinformatics, 2020, 21, 729-740.	6.5	17

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91	Different cell cycle kinetic effects of N 1,N 11-diethylnorspermine-induced polyamine depletion in four human breast cancer cell lines. Anti-Cancer Drugs, 2008, 19, 359-368.	1.4	14
92	Genome methylation patterns in male breast cancer â€" Identification of an epitype with hypermethylation of polycomb target genes. Molecular Oncology, 2015, 9, 1565-1579.	4.6	14
93	Epigeneticâ€"smoking interaction reveals histologically heterogeneous effects of TRIM27 DNA methylation on overall survival among earlyâ€stage NSCLC patients. Molecular Oncology, 2020, 14, 2759-2774.	4.6	13
94	Trans-omics biomarker model improves prognostic prediction accuracy for early-stage lung adenocarcinoma. Aging, 2019, 11, 6312-6335.	3.1	13
95	Epigenetic modifications in KDM lysine demethylases associate with survival of early-stage NSCLC. Clinical Epigenetics, 2018, 10, 41.	4.1	12
96	Loss of <scp><i>NF2</i></scp> defines a genetic subgroup of <scp>nonâ€<i>FOS</i></scp>â€rearranged osteoblastoma. Journal of Pathology: Clinical Research, 2020, 6, 231-237.	3.0	11
97	Consensus of gene expression phenotypes and prognostic risk predictors in primary lung adenocarcinoma. Oncotarget, 2016, 7, 52957-52973.	1.8	11
98	Making Breast Cancer Molecular Subtypes Robust?. Journal of the National Cancer Institute, 2014, 107, dju386-dju386.	6.3	10
99	DNA Methylation of <i>LRRC3B</i>: A Biomarker for Survival of Early-Stage Nonâ€Small Cell Lung Cancer Patients. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1527-1535.	2.5	10
100	Comprehensive analysis of RNA binding motif protein 3 (RBM3) in nonâ€small cell lung cancer. Cancer Medicine, 2020, 9, 5609-5619.	2.8	10
101	A gene expressionâ€based single sample predictor of lung adenocarcinoma molecular subtype and prognosis. International Journal of Cancer, 2021, 148, 238-251.	5.1	10
102	Complement inhibitor CSMD1 modulates epidermal growth factor receptor oncogenic signaling and sensitizes breast cancer cells to chemotherapy. Journal of Experimental and Clinical Cancer Research, 2021, 40, 258.	8.6	10
103	Detailed Analysis of Focal Chromosome Arm 1q and 6p Amplifications in Urothelial Carcinoma Reveals Complex Genomic Events on 1q, and SOX4 as a Possible Auxiliary Target on 6p. PLoS ONE, 2013, 8, e67222.	2.5	10
104	Molecular mechanisms underlying N 1, N 11-diethylnorspermine-induced apoptosis in a human breast cancer cell line. Anti-Cancer Drugs, 2008, 19, 871-883.	1.4	9
105	Primary Melanoma Tumors from CDKN2A Mutation Carriers Do Not Belong to a Distinct Molecular Subclass. Journal of Investigative Dermatology, 2014, 134, 3000-3003.	0.7	8
106	Epigenome-wide geneâ€age interaction analysis reveals reversed effects of <i>PRODH</i> DNA methylation on survival between young and elderly early-stage NSCLC patients. Aging, 2020, 12, 10642-10662.	3.1	8
107	Targeted sequencing may facilitate differential diagnostics of pulmonary tumours: a case series. Diagnostic Pathology, 2017, 12, 31.	2.0	7
108	Tumor genome wide DNA alterations assessed by array CGH in patients with poor and excellent survival following operation for colorectal cancer. Cancer Informatics, 2007, 3, 341-55.	1.9	7

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109	Nonfamilial Breast Cancer Subtypes. Methods in Molecular Biology, 2013, 973, 279-295.	0.9	5
110	Methylation Patterns and Chromatin Accessibility in Neuroendocrine Lung Cancer. Cancers, 2020, 12, 2003.	3.7	5
111	Pan-cancer application of a lung-adenocarcinoma-derived gene-expression-based prognostic predictor. Briefings in Bioinformatics, 2021, 22, .	6.5	5
112	Analysis of human papillomaviruses and human polyomaviruses in lung cancer from Swedish never-smokers. Acta Oncológica, 2020, 59, 28-32.	1.8	4
113	Clinical Utility of Targeted Sequencing in Lung Cancer: Experience From an Autonomous Swedish Health Care Center. JTO Clinical and Research Reports, 2020, 1, 100013.	1.1	4
114	Screening for Copy Number Alterations and Loss of Heterozygosity in Chronic Lymphocytic Leukemia - A Comparative Study of Four Differently Designed, High Resolution Microarray Platforms.. Blood, 2007, 110, 2084-2084.	1.4	4
115	Epigenome-wide three-way interaction study identifies a complex pattern between *TRIM27*, *KIAA0226*, and smoking associated with overall survival of early-stage NSCLC. Molecular Oncology, 2022, 16, 717-731.	4.6	4
116	Zoom-In Array Comparative Genomic Hybridization (aCGH) to Detect Germline Rearrangements in Cancer Susceptibility Genes. Methods in Molecular Biology, 2010, 653, 221-235.	0.9	3
117	Feasibility of EBUS-TBNA for histopathological and molecular diagnostics of NSCLC—A retrospective single-center experience. PLoS ONE, 2022, 17, e0263342.	2.5	3
118	Clinical Application of Fusion Gene Detection Using Next-Generation Sequencing and the NanoString Technology. Methods in Molecular Biology, 2019, 1908, 139-152.	0.9	1
119	SRIQ clustering: A fusion of Random Forest, QT clustering, and KNN concepts. Computational and Structural Biotechnology Journal, 2022, 20, 1567-1579.	4.1	1
120	Detection of Non-Small Lung Cell Carcinoma-Associated Genetic Alterations Using a NanoString Gene Expression Platform Approach. Methods in Molecular Biology, 2021, 2279, 91-107.	0.9	0
121	Abstract OT2-30-01: Nordictrip, a translational randomized phase-3 study exploring the effect of the addition of capecitabine to carboplatinum-based chemotherapy in early "triple negative" breast cancer, ClinicalTrials.gov Identifier: NCT04335669. Cancer Research, 2022, 82, OT2-30-01-OT2-30-01.	0.9	0