Johan Staaf

List of Publications by Year in descending order

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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	Epigenomeâ€wide threeâ€way interaction study identifies a complex pattern between TRIM27, KIAA0226, and smoking associated with overall survival of earlyâ€stage NSCLC. Molecular Oncology, 2022, 16, 717-731.	4.6	4
2	Feasibility of EBUS-TBNA for histopathological and molecular diagnostics of NSCLCâ€"A retrospective single-center experience. PLoS ONE, 2022, 17, e0263342.	2.5	3
3	SRIQ clustering: A fusion of Random Forest, QT clustering, and KNN concepts. Computational and Structural Biotechnology Journal, 2022, 20, 1567-1579.	4.1	1
4	Abstract OT2-30-01: Nordictrip, a translational randomized phase-3study exploring the effect of the addition of capecitabine to carboplatinum-based chemotherapy in early â€œtriple negativeâ€•breast cancer, ClinicalTrials.gov Identifier: NCT04335669. Cancer Research, 2022, 82, OT2-30-01-OT2-30-01.	0.9	0
5	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
6	Molecular analyses of triple-negative breast cancer in the young and elderly. Breast Cancer Research, 2021, 23, 20.	5.0	23
7	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
8	Random Forest Modelling of High-Dimensional Mixed-Type Data for Breast Cancer Classification. Cancers, 2021, 13, 991.	3.7	21
9	Oncogenic translation directs spliceosome dynamics revealing an integral role for SF3A3 in breast cancer. Molecular Cell, 2021, 81, 1453-1468.e12.	9.7	31
10	Pan-cancer application of a lung-adenocarcinoma-derived gene-expression-based prognostic predictor. Briefings in Bioinformatics, 2021, 22, .	6.5	5
11	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
12	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
13	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
14	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
15	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
16	Analysis of human papillomaviruses and human polyomaviruses in lung cancer from Swedish never-smokers. Acta OncolÃ³gica, 2020, 59, 28-32.	1.8	4
17	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
18	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

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19	Methylation Patterns and Chromatin Accessibility in Neuroendocrine Lung Cancer. Cancers, 2020, 12, 2003.	3.7	5
20	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. Nature Communications, 2020, 11, 3747.	12.8	53
21	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
22	Comprehensive analysis of RNA binding motif protein 3 (RBM3) in nonâ€small cell lung cancer. Cancer Medicine, 2020, 9, 5609-5619.	2.8	10
23	Loss of <scp>NF2</scp> defines a genetic subgroup of <scp>nonâ€FOS</scp>â€rearranged osteoblastoma. Journal of Pathology: Clinical Research, 2020, 6, 231-237.	3.0	11
24	Analysis of DNA methylation patterns in the tumor immune microenvironment of metastatic melanoma. Molecular Oncology, 2020, 14, 933-950.	4.6	29
25	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
26	Epigenome-wide geneâ€“age interaction analysis reveals reversed effects of PRODH DNA methylation on survival between young and elderly early-stage NSCLC patients. Aging, 2020, 12, 10642-10662.	3.1	8
27	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
28	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
29	EGLN2 DNA methylation and expression interact with HIF1A to affect survival of early-stage NSCLC. Epigenetics, 2019, 14, 118-129.	2.7	28
30	The circular RNome of primary breast cancer. Genome Research, 2019, 29, 356-366.	5.5	85
31	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
32	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. Nature Communications, 2019, 10, 1749.	12.8	46
33	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
34	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
35	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. Nature Medicine, 2019, 25, 1526-1533.	30.7	218
36	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

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37	Trans-omics biomarker model improves prognostic prediction accuracy for early-stage lung adenocarcinoma. Aging, 2019, 11, 6312-6335.	3.1	13
38	A multiâ€omic study reveals BTG2 as a reliable prognostic marker for earlyâ€stage nonâ€small cell lung cancer. Molecular Oncology, 2018, 12, 913-924.	4.6	31
39	Epigenetic modifications in KDM lysine demethylases associate with survival of early-stage NSCLC. Clinical Epigenetics, 2018, 10, 41.	4.1	12
40	Mutational mechanisms of amplifications revealed by analysis of clustered rearrangements in breast cancers. Annals of Oncology, 2018, 29, 2223-2231.	1.2	26
41	DNA Methylation of LRRC3B: 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
42	Identification and validation of single-sample breast cancer radiosensitivity gene expression predictors. Breast Cancer Research, 2018, 20, 64.	5.0	40
43	Four evolutionary trajectories underlie genetic intratumoral variation in childhood cancer. Nature Genetics, 2018, 50, 944-950.	21.4	60
44	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
45	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
46	Targeted sequencing may facilitate differential diagnostics of pulmonary tumours: a case series. Diagnostic Pathology, 2017, 12, 31.	2.0	7
47	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	30.7	769
48	The scaffold protein p140Cap limits ERBB2-mediated breast cancer progression interfering with Rac GTPase-controlled circuitries. Nature Communications, 2017, 8, 14797.	12.8	26
49	<scp>NF</scp>1â€mutated melanoma tumors harbor distinct clinical and biological characteristics. Molecular Oncology, 2017, 11, 438-451.	4.6	112
50	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
51	CA 19-9 and CA 125 as potential predictors of disease recurrence in resectable lung adenocarcinoma. PLoS ONE, 2017, 12, e0186284.	2.5	26
52	Myc-induced glutaminolysis bypasses HIF-driven glycolysis in hypoxic small cell lung carcinoma cells. Oncotarget, 2017, 8, 48983-48995.	1.8	19
53	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
54	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	12.8	235

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55	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. Nature Communications, 2016, 7, 12910.	12.8	119
56	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
57	Consensus of Melanoma Gene Expression Subtypes Converges on Biological Entities. Journal of Investigative Dermatology, 2016, 136, 2502-2505.	0.7	23
58	Prognostic and Chemotherapy Predictive Value of Gene-Expression Phenotypes in Primary Lung Adenocarcinoma. Clinical Cancer Research, 2016, 22, 218-229.	7.0	29
59	Consensus of gene expression phenotypes and prognostic risk predictors in primary lung adenocarcinoma. Oncotarget, 2016, 7, 52957-52973.	1.8	11
60	DNA methylation subgroups in melanoma are associated with proliferative and immunological processes. BMC Medical Genomics, 2015, 8, 73.	1.5	29
61	Mutational and gene fusion analyses of primary large cell and large cell neuroendocrine lung cancer. Oncotarget, 2015, 6, 22028-22037.	1.8	61
62	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
63	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
64	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
65	Loss of CITED1, an MITF regulator, drives a phenotype switchin vitroand can predict clinical outcome in primary melanoma tumours. PeerJ, 2015, 3, e788.	2.0	20
66	Making Breast Cancer Molecular Subtypes Robust?. Journal of the National Cancer Institute, 2014, 107, dju386-dju386.	6.3	10
67	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
68	Genomic and Transcriptional Alterations in Lung Adenocarcinoma in Relation to Smoking History. Clinical Cancer Research, 2014, 20, 4912-4924.	7.0	24
69	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
70	Nonfamilial Breast Cancer Subtypes. Methods in Molecular Biology, 2013, 973, 279-295.	0.9	5
71	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
72	Landscape of somatic allelic imbalances and copy number alterations in human lung carcinoma. International Journal of Cancer, 2013, 132, 2020-2031.	5.1	32

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73	High expression of <scp>ZNF703</scp> independent of amplification indicates worse prognosis in patients with luminal B breast cancer. Cancer Medicine, 2013, 2, 437-446.	2.8	39
74	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
75	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
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	The Retinoblastoma Gene Undergoes Rearrangements in BRCA1-Deficient Basal-like Breast Cancer. Cancer Research, 2012, 72, 4028-4036.	0.9	41
78	Molecular Profiling Reveals Low- and High-Grade Forms of Primary Melanoma. Clinical Cancer Research, 2012, 18, 4026-4036.	7.0	96
79	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
80	Amplification and overexpression of the ABCC3 (MRP3) gene in primary breast cancer. Genes Chromosomes and Cancer, 2012, 51, 832-840.	2.8	23
81	Relation between smoking history and gene expression profiles in lung adenocarcinomas. BMC Medical Genomics, 2012, 5, 22.	1.5	41
82	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
83	Integrated Genomic and Gene Expression Profiling Identifies Two Major Genomic Circuits in Urothelial Carcinoma. PLoS ONE, 2012, 7, e38863.	2.5	167
84	Landscape of somatic allelic imbalances and copy number alterations in HER2-amplified breast cancer. Breast Cancer Research, 2011, 13, R129.	5.0	25
85	GOBO: Gene Expression-Based Outcome for Breast Cancer Online. PLoS ONE, 2011, 6, e17911.	2.5	361
86	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
87	Identification of New MicroRNAs in Paired Normal and Tumor Breast Tissue Suggests a Dual Role for the ERBB2/Her2 Gene. Cancer Research, 2011, 71, 78-86.	0.9	191
88	Genetic profiles of gastroesophageal cancer: combined analysis using expression array and tiling arrayâ€“comparative genomic hybridization. Cancer Genetics and Cytogenetics, 2010, 200, 120-126.	1.0	26
89	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
90	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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91	Molecular subtypes of breast cancer are associated with characteristic DNA methylation patterns. Breast Cancer Research, 2010, 12, R36.	5.0	251
92	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
93	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
94	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. Melanoma Research, 2010, 20, 381-391.	1.2	30
95	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. Melanoma Research, 2010, 20, 381-91.	1.2	22
96	Genomic Profiling of Chondrosarcoma: Chromosomal Patterns in Central and Peripheral Tumors. Clinical Cancer Research, 2009, 15, 2685-2694.	7.0	71
97	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
98	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
99	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
100	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
101	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
102	Heterogeneous genetic profiles in soft tissue myoepitheliomas. Modern Pathology, 2008, 21, 1311-1319.	5.5	44
103	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
104	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
105	Normalization of Illumina Infinium whole-genome SNP data improves copy number estimates and allelic intensity ratios. BMC Bioinformatics, 2008, 9, 409.	2.6	114
106	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
107	Array-CGH identifies cyclin D1 and UBCH10 amplicons in anaplastic thyroid carcinoma. Endocrine-Related Cancer, 2008, 15, 801-815.	3.1	53
108	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

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109	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
110	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
111	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
112	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
113	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
114	Normalization of array-CGH data: influence of copy number imbalances. BMC Genomics, 2007, 8, 382.	2.8	57
115	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
116	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
117	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
118	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
119	Distinct Genomic Profiles in Hereditary Breast Tumors Identified by Array-Based Comparative Genomic Hybridization. Cancer Research, 2005, 65, 7612-7621.	0.9	147
120	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
121	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