Rolf Inge Skotheim

List of Publications by Year
in descending order

104	5,458	66343	88630
papers	citations	42 h-index	70 g-index

107	107	107	10315
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Systematic bioinformatic analysis of expression levels of 17,330 human genes across 9,783 samples from 175 types of healthy and pathological tissues. Genome Biology, 2008, 9, R139.	9.6	234
2	Multi-omics of 34 colorectal cancer cell lines - a resource for biomedical studies. Molecular Cancer, 2017, 16, 116.	19.2	232
3	TMPRSS2 Fusions with Oncogenic ETS Factors in Prostate Cancer Involve Unbalanced Genomic Rearrangements and Are Associated with HDAC1 and Epigenetic Reprogramming. Cancer Research, 2006, 66, 10242-10246.	0.9	209
4	PtdIns(3)P controls cytokinesis through KIF13A-mediated recruitment of FYVE-CENT to the midbody. Nature Cell Biology, 2010, 12, 362-371.	10.3	195
5	Differentiation of Human Embryonal Carcinomas In vitro and In vivo Reveals Expression Profiles Relevant to Normal Development. Cancer Research, 2005, 65, 5588-5598.	0.9	194
6	Oncogenicity of the Developmental Transcription Factor Sox9. Cancer Research, 2012, 72, 1301-1315.	0.9	180
7	ColoGuideEx: a robust gene classifier specific for stage II colorectal cancer prognosis. Gut, 2012, 61, 1560-1567.	12.1	179
8	Alternative splicing in cancer: Noise, functional, or systematic?. International Journal of Biochemistry and Cell Biology, 2007, 39, 1432-1449.	2.8	178
9	Three Epigenetic Biomarkers, GDF15, TMEFF2, and VIM, Accurately Predict Bladder Cancer from DNA-Based Analyses of Urine Samples. Clinical Cancer Research, 2010, 16, 5842-5851.	7.0	155
10	Meta-analysis identifies four new loci associated with testicular germ cell tumor. Nature Genetics, 2013, 45, 680-685.	21.4	154
11	New insights into testicular germ cell tumorigenesis from gene expression profiling. Cancer Research, 2002, 62, 2359-64.	0.9	134
12	BCL-XL Mediates the Strong Selective Advantage of a 20q11.21 Amplification Commonly Found in Human Embryonic Stem Cell Cultures. Stem Cell Reports, 2013, 1, 379-386.	4.8	132
13	Identification of an epigenetic biomarker panel with high sensitivity and specificity for colorectal cancer and adenomas. Molecular Cancer, 2011, 10, 85.	19.2	126
14	MiR-9, -31, and -182 Deregulation Promote Proliferation and Tumor Cell Survival in Colon Cancer. Neoplasia, 2012, 14, 868-IN21.	5.3	124
15	ColoGuidePro: A Prognostic 7-Gene Expression Signature for Stage III Colorectal Cancer Patients. Clinical Cancer Research, 2012, 18, 6001-6010.	7.0	109
16	Multifocal Primary Prostate Cancer Exhibits High Degree of Genomic Heterogeneity. European Urology, 2019, 75, 498-505.	1.9	108
17	Gene methylation profiles of normal mucosa, and benign and malignant colorectal tumors identify early onset markers. Molecular Cancer, 2008, 7, 94.	19.2	102
18	MicroRNAs as growth regulators, their function and biomarker status in colorectal cancer. Oncotarget, 2016, 7, 6476-6505.	1.8	93

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19	Genome profiles of familial/bilateral and sporadic testicular germ cell tumors. Genes Chromosomes and Cancer, 2002, 34, 168-174.	2.8	77
20	Whole-Transcriptome Sequencing Identifies Novel IRF2BP2-CDX1 Fusion Gene Brought about by Translocation t(1;5)(q42;q32) in Mesenchymal Chondrosarcoma. PLoS ONE, 2012, 7, e49705.	2.5	77
21	Molecular Characteristics of Malignant Ovarian Germ Cell Tumors and Comparison With Testicular Counterparts: Implications for Pathogenesis. Endocrine Reviews, 2013, 34, 339-376.	20.1	77
22	Distinct high resolution genome profiles of early onset and late onset colorectal cancer integrated with gene expression data identify candidate susceptibility loci. Molecular Cancer, 2010, 9, 100.	19.2	75
23	Topoisomerase-IÎ± Is Upregulated in Malignant Peripheral Nerve Sheath Tumors and Associated With Clinical Outcome. Journal of Clinical Oncology, 2003, 21, 4586-4591.	1.6	74
24	Evaluation of loss of heterozygosity/allelic imbalance scoring in tumor DNA. Cancer Genetics and Cytogenetics, 2001, 127, 64-70.	1.0	73
25	Transcriptome instability in colorectal cancer identified by exon microarray analyses: Associations with splicing factor expression levels and patient survival. Genome Medicine, 2011, 3, 32.	8.2	73
26	FLI1 is a novel ETS transcription factor involved in gene fusions in prostate cancer. Genes Chromosomes and Cancer, 2012, 51, 240-249.	2.8	73
27	Multilevel genomics of colorectal cancers with microsatellite instabilityâ€"clinical impact of JAK1 mutations and consensus molecular subtype 1. Genome Medicine, 2017, 9, 46.	8.2	71
28	The androgen receptor controls expression of the cancer-associated sTn antigen and cell adhesion through induction of ST6GalNAc1 in prostate cancer. Oncotarget, 2015, 6, 34358-34374.	1.8	68
29	Molecular Subtyping of Primary Prostate Cancer Reveals Specific and Shared Target Genes of Different ETS Rearrangements. Neoplasia, 2012, 14, 600-IN15.	5.3	63
30	The testicular germ cell tumour genome. Apmis, 2003, 111, 136-151.	2.0	61
31	Gene expression profiles of primary colorectal carcinomas, liver metastases, and carcinomatoses. Molecular Cancer, 2007, 6, 2.	19.2	61
32	The epigenome of testicular germ cell tumors. Apmis, 2007, 115, 1147-1160.	2.0	61
33	Unscrambling the genomic chaos of osteosarcoma reveals extensive transcript fusion, recurrent rearrangements and frequent novel TP53 aberrations. Oncotarget, 2016, 7, 5273-5288.	1.8	60
34	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. Human Molecular Genetics, 2013, 22, 2748-2753.	2.9	59
35	Phospholipase C Isozymes Are Deregulated in Colorectal Cancer â€“ Insights Gained from Gene Set Enrichment Analysis of the Transcriptome. PLoS ONE, 2011, 6, e24419.	2.5	58
36	The recently suggested intestinal cancer stem cell markerDCLK1is an epigenetic biomarker for colorectal cancer. Epigenetics, 2014, 9, 346-350.	2.7	55

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37	Genomic Changes in Chromosomes 10, 16, and X in Malignant Peripheral Nerve Sheath Tumors Identify a High-Risk Patient Group. Journal of Clinical Oncology, 2010, 28, 1573-1582.	1.6	54
38	Novel Genomic Aberrations in Testicular Germ Cell Tumors by Array-CGH, and Associated Gene Expression Changes. Analytical Cellular Pathology, 2006, 28, 315-326.	1.4	54
39	Hypermethylated MAL gene â€“ a silent marker of early colon tumorigenesis. Journal of Translational Medicine, 2008, 6, 13.	4.4	48
40	Profiling of the small RNA populations in human testicular germ cell tumors shows global loss of piRNAs. Molecular Cancer, 2015, 14, 153.	19.2	48
41	Improved gene expression signature of testicular carcinoma in situ. Journal of Developmental and Physical Disabilities, 2007, 30, 292-303.	3.6	47
42	Identification of p53 as a strong predictor of survival for patients with malignant peripheral nerve sheath tumors. Neuro-Oncology, 2009, 11, 514-528.	1.2	47
43	Candidate Genes for Testicular Cancer Evaluated by In Situ Protein Expression Analyses on Tissue Microarrays. Neoplasia, 2003, 5, 397-404.	5.3	46
44	PIKfyve, MTMR3 and their product PtdIns5P regulate cancer cell migration and invasion through activation of Rac1. Biochemical Journal, 2014, 461, 383-390.	3.7	42
45	Interfocal heterogeneity challenges the clinical usefulness of molecular classification of primary prostate cancer. Scientific Reports, 2019, 9, 13579.	3.3	38
46	Cysteine-Rich Secretory Protein-3 (CRISP3) Is Strongly Up-Regulated in Prostate Carcinomas with the TMPRSS2-ERG Fusion Gene. PLoS ONE, 2011, 6, e22317.	2.5	36
47	Novel 5â€² Fusion Partners of ETV1 and ETV4 in Prostate Cancer. Neoplasia, 2013, 15, 720-IN6.	5.3	36
48	Identification of Two Molecular Groups of Seminomas by Using Expression and Tissue Microarrays. Clinical Cancer Research, 2005, 11, 5722-5729.	7.0	34
49	Regulator of Chromosome Condensation 2 Identifies High-Risk Patients within Both Major Phenotypes of Colorectal Cancer. Clinical Cancer Research, 2015, 21, 3759-3770.	7.0	32
50	Protein expression of BIRC5, TK1, and TOP2A in malignant peripheral nerve sheath tumours â€“ A prognostic test after surgical resection. Molecular Oncology, 2015, 9, 1129-1139.	4.6	32
51	PBX3 is a putative biomarker of aggressive prostate cancer. International Journal of Cancer, 2016, 139, 1810-1820.	5.1	32
52	GREM1 is associated with metastasis and predicts poor prognosis in ER-negative breast cancer patients. Cell Communication and Signaling, 2019, 17, 140.	6.5	32
53	A Tumor-Associated Mutation of FYVE-CENT Prevents Its Interaction with Beclin 1 and Interferes with Cytokinesis. PLoS ONE, 2011, 6, e17086.	2.5	30
54	Common Fusion Transcripts Identified in Colorectal Cancer Cell Lines by High-Throughput RNA Sequencing. Translational Oncology, 2013, 6, 546-IN5.	3.7	29

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55	NKX3.1 Expression Is Lost in Testicular Germ Cell Tumors. American Journal of Pathology, 2003, 163, 2149-2154.	3.8	28
56	Familial/Bilateral and Sporadic Testicular Germ Cell Tumors Show Frequent Genetic Changes at Loci with Suggestive Linkage Evidence. Neoplasia, 2001, 3, 196-203.	5.3	27
57	Anticipating the Clinical Use of Prognostic Gene Expressionâ€"Based Tests for Colon Cancer Stage II and III: Is Godot Finally Arriving?. Clinical Cancer Research, 2013, 19, 6669-6677.	7.0	27
58	Identification of 22 susceptibility loci associated with testicular germ cell tumors. Nature Communications, 2021, 12, 4487.	12.8	27
59	High Frequency of Fusion Transcripts Involving TCF7L2 in Colorectal Cancer: Novel Fusion Partner and Splice Variants. PLoS ONE, 2014, 9, e91264.	2.5	26
60	CRABP1, C1QL1 and LCN2 are biomarkers of differentiated thyroid carcinoma, and predict extrathyroidal extension. BMC Cancer, 2018, 18, 68.	2.6	26
61	Alternative splicing expands the prognostic impact of KRAS in microsatellite stable primary colorectal cancer. International Journal of Cancer, 2019, 144, 841-847.	5.1	26
62	A universal assay for detection of oncogenic fusion transcripts by oligo microarray analysis. Molecular Cancer, 2009, 8, 5.	19.2	25
63	Identification of Novel Fusion Genes in Testicular Germ Cell Tumors. Cancer Research, 2016, 76, 108-116.	0.9	25
64	Specific and redundant activities ofETV1andETV4in prostate cancer aggressiveness revealed by co-overexpression cellular contexts. Oncotarget, 2015, 6, 5217-5236.	1.8	24
65	Reverse painting of microdissected chromosome 19 markers in ovarian carcinoma identifies a complex rearrangement map. Genes Chromosomes and Cancer, 2009, 48, 184-193.	2.8	23
66	chimeraviz: a tool for visualizing chimeric RNA. Bioinformatics, 2017, 33, 2954-2956.	4.1	23
67	Involvement of DPP9 in gene fusions in serous ovarian carcinoma. BMC Cancer, 2017, 17, 642.	2.6	22
68	Spindle proteins are differentially expressed in the various histological subtypes of testicular germ cell tumors. Journal of Carcinogenesis, 2010, 9, 1.	2.5	21
69	Potential Downstream Target Genes of Aberrant ETS Transcription Factors Are Differentially Affected in Ewingâ€™s Sarcoma and Prostate Carcinoma. PLoS ONE, 2012, 7, e49819.	2.5	21
70	Survey of 548 oncogenic fusion transcripts in thyroid tumors supports the importance of the already established thyroid fusions genes. Genes Chromosomes and Cancer, 2012, 51, 1154-1164.	2.8	20
71	The exonâ€level biomarker SLC39A14 has organâ€confined cancerâ€specificity in colorectal cancer. International Journal of Cancer, 2012, 131, 1479-1485.	5.1	20
72	Transcriptional and functional consequences of TP53 splice mutations in colorectal cancer. Oncogenesis, 2019, 8, 35.	4.9	19

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73	Arrayâ€CGH analysis of microdissected chromosome 19 markers in ovarian carcinoma identifies candidate target genes. Genes Chromosomes and Cancer, 2010, 49, 1046-1053.	2.8	18
74	A novel transcript, VNN1â€AB, as a biomarker for colorectal cancer. International Journal of Cancer, 2014, 135, 2077-2084.	5.1	18
75	Transforming Pluripotency: An Exon-Level Study of Malignancy-Specific Transcripts in Human Embryonal Carcinoma and Embryonic Stem Cells. Stem Cells and Development, 2013, 22, 1136-1146.	2.1	17
76	Exome Sequencing of Bilateral Testicular Germ Cell Tumors Suggests Independent Development Lineages. Neoplasia, 2015, 17, 167-174.	5.3	17
77	High expression of SCHLAP1 in primary prostate cancer is an independent predictor of biochemical recurrence, despite substantial heterogeneity. Neoplasia, 2021, 23, 634-641.	5.3	16
78	Fusion gene microarray reveals cancer typeâ€specificity among fusion genes. Genes Chromosomes and Cancer, 2011, 50, 348-357.	2.8	15
79	Transcriptome instability as a molecular pan-cancer characteristic of carcinomas. BMC Genomics, 2014, 15, 672.	2.8	15
80	Novel RNA variants in colorectal cancers. Oncotarget, 2015, 6, 36587-36602.	1.8	15
81	Microinvasive germ cell tumor of the testis. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2005, 447, 610-625.	2.8	14
82	Longâ€term firstâ€inâ€man Phase I/II study of an adjuvant dendritic cell vaccine in patients with highâ€risk prostate cancer after radical prostatectomy. Prostate, 2022, 82, 245-253.	2.3	13
83	Novel transcription-induced fusion RNAs in prostate cancer. Oncotarget, 2017, 8, 49133-49143.	1.8	11
84	TPD52, a candidate gene from genomic studies, is overexpressed in testicular germ cell tumours. Molecular and Cellular Endocrinology, 2009, 306, 75-80.	3.2	9
85	The loss of NKX3.1 expression in testicular--and prostate--cancers is not caused by promoter hypermethylation. Molecular Cancer, 2005, 4, 8.	19.2	8
86	Complex Polygenic Nature of Testicular Germ Cell Cancer Suggests Multifactorial Aetiology. European Urology, 2018, 73, 832-833.	1.9	8
87	NRF2 drives an oxidative stress response predictive of breast cancer. Free Radical Biology and Medicine, 2022, 184, 170-184.	2.9	8
88	Observed correlation between the expression levels of catalytic subunit, CÎ²2, of cyclic adenosine monophosphateâ€“dependent protein kinase and prostate cancer aggressiveness. Urologic Oncology: Seminars and Original Investigations, 2017, 35, 111.e1-111.e8.	1.6	6
89	Collision tumors revealed by prospectively assessing subtype-defining molecular alterations in 904 individual prostate cancer foci. JCI Insight, 2022, 7, .	5.0	6
90	Lack of parental origin specificity of altered alleles at 11p15 in testicular germ cell tumors. Cancer Genetics and Cytogenetics, 2003, 147, 1-8.	1.0	4

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91	Chromosome 19 rearrangements in ovarian carcinomas: Zinc finger genes are particularly targeted. Genes Chromosomes and Cancer, 2014, 53, 558-567.	2.8	4
92	TIN: An R Package for Transcriptome Instability Analysis. Cancer Informatics, 2015, 14, CIN.S31363.	1.9	4
93	The expressed mutational landscape of microsatellite stable colorectal cancers. Genome Medicine, 2021, 13, 142.	8.2	4
94	Frequent copy number gains of SLC2A3 and ETV1 in testicular embryonal carcinomas. Endocrine-Related Cancer, 2020, 27, 457-468.	3.1	4
95	Association Study between Polymorphisms in DNA Methylationâ€“Related Genes and Testicular Germ Cell Tumor Risk. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1769-1779.	2.5	4
96	Bilateral ovarian carcinomas differ in the expression of metastasis-related genes. Oncology Letters, 2017, 13, 184-190.	1.8	3
97	Assessment of Fusion Gene Status in Sarcomas Using a Custom Made Fusion Gene Microarray. PLoS ONE, 2013, 8, e70649.	2.5	3
98	Expressed prognostic biomarkers for primary prostate cancer independent of multifocality and transcriptome heterogeneity. Cancer Gene Therapy, 2022, 29, 1276-1284.	4.6	3
99	Inâ€‰situ expression of <scp>ERG</scp> protein in the context of tumor heterogeneity identifies prostate cancer patients with inferior prognosis. Molecular Oncology, 2022, 16, 2810-2822.	4.6	3
100	Frequent copy number gains of SLC2A3 and ETV1 in testicular embryonal carcinomas. Endocrine-Related Cancer, 2020, 27, 457-468.	3.1	2
101	Precursor lesions in testis and dysgenetic gonads. Human Pathology, 2006, 37, 773.	2.0	1
102	ScaRâ€”a tool for sensitive detection of known fusion transcripts: establishing prevalence of fusions in testicular germ cell tumors. NAR Genomics and Bioinformatics, 2020, 2, lqz025.	3.2	1
103	Re: Fibroblast Growth Factor Receptor 1 Drives the Metastatic Progression of Prostate Cancer. European Urology, 2022, 81, 431.	1.9	1
104	Array-Based Comparative Genomic Hybridization in Prostate Cancer: Research and Clinical Applications. , 2008, , 415-429.		0