

Anita Sveen

List of Publications by Year in descending order

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47
papers

2,300
citations

448610

19
h-index

263392

45
g-index

48
all docs

48
docs citations

48
times ranked

4686
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiplex immunohistochemistry of metastatic colorectal cancer and ex vivo tumor avatars. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2022, 1877, 188682.	3.3	1
2	Expressed prognostic biomarkers for primary prostate cancer independent of multifocality and transcriptome heterogeneity. <i>Cancer Gene Therapy</i> , 2022, 29, 1276-1284.	2.2	3
3	Spatial analysis and CD25-expression identify regulatory T cells as predictors of a poor prognosis in colorectal cancer. <i>Modern Pathology</i> , 2022, 35, 1236-1246.	2.9	8
4	Genomic and prognostic heterogeneity among <i>RAS/BRAF</i> ^{V600E} / <i>TP53</i> co-mutated resectable colorectal liver metastases. <i>Molecular Oncology</i> , 2021, 15, 830-845.	2.1	11
5	Multiregional assessment of CIMP in primary colorectal cancers: Phenotype concordance but marker variability. <i>International Journal of Cancer</i> , 2021, 148, 1652-1657.	2.3	4
6	Treatment outcomes and prognostic factors after chemoradiotherapy for anal cancer. <i>Acta Oncologica</i> , 2021, 60, 921-930.	0.8	7
7	Metastatic heterogeneity of the consensus molecular subtypes of colorectal cancer. <i>Npj Genomic Medicine</i> , 2021, 6, 59.	1.7	29
8	De novo transcriptomic subtyping of colorectal cancer liver metastases in the context of tumor heterogeneity. <i>Genome Medicine</i> , 2021, 13, 143.	3.6	10
9	The expressed mutational landscape of microsatellite stable colorectal cancers. <i>Genome Medicine</i> , 2021, 13, 142.	3.6	4
10	Increased sensitivity to SMAC mimetic LCL161 identified by longitudinal ex vivo pharmacogenomics of recurrent, KRAS mutated rectal cancer liver metastases. <i>Journal of Translational Medicine</i> , 2021, 19, 384.	1.8	6
11	Biomarker-guided therapy for colorectal cancer: strength in complexity. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 11-32.	12.5	195
12	Technical differences between sequencing and microarray platforms impact transcriptomic subtyping of colorectal cancer. <i>Cancer Letters</i> , 2020, 469, 246-255.	3.2	12
13	Prediction of relapse-free survival according to adjuvant chemotherapy and regulator of chromosome condensation 2 (<i>RCC2</i>) expression in colorectal cancer. <i>ESMO Open</i> , 2020, 5, e001040.	2.0	6
14	Molecular correlates of sensitivity to PARP inhibition beyond homologous recombination deficiency in pre-clinical models of colorectal cancer point to wild-type TP53 activity. <i>EBioMedicine</i> , 2020, 59, 102923.	2.7	22
15	Mutational dynamics and immune evasion in diffuse large B-cell lymphoma explored in a relapse-enriched patient series. <i>Blood Advances</i> , 2020, 4, 1859-1866.	2.5	7
16	Improved prognostication of glioblastoma beyond molecular subtyping by transcriptional profiling of the tumor microenvironment. <i>Molecular Oncology</i> , 2020, 14, 1016-1027.	2.1	15
17	High Concordance and Negative Prognostic Impact of <i>RAS/BRAF/PIK3CA</i> Mutations in Multiple Resected Colorectal Liver Metastases. <i>Clinical Colorectal Cancer</i> , 2020, 19, e26-e47.	1.0	20
18	Patient-Derived Organoids from Multiple Colorectal Cancer Liver Metastases Reveal Moderate Intra-patient Pharmacotranscriptomic Heterogeneity. <i>Clinical Cancer Research</i> , 2020, 26, 4107-4119.	3.2	68

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19	Alternative splicing expands the prognostic impact of <i>KRAS</i> in microsatellite stable primary colorectal cancer. <i>International Journal of Cancer</i> , 2019, 144, 841-847.	2.3	26
20	Tumour-infiltrating CD8+ lymphocytes and colorectal cancer recurrence by tumour and nodal stage. <i>British Journal of Cancer</i> , 2019, 121, 474-482.	2.9	41
21	Gene expression profiles of CMS2-epithelial/canonical colorectal cancers are largely driven by DNA copy number gains. <i>Oncogene</i> , 2019, 38, 6109-6122.	2.6	20
22	Heterogeneous radiological response to neoadjuvant therapy is associated with poor prognosis after resection of colorectal liver metastases. <i>European Journal of Surgical Oncology</i> , 2019, 45, 2340-2346.	0.5	14
23	Combination therapies with HSP90 inhibitors against colorectal cancer. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2019, 1871, 240-247.	3.3	81
24	Transcriptional and functional consequences of TP53 splice mutations in colorectal cancer. <i>Oncogenesis</i> , 2019, 8, 35.	2.1	19
25	Exploratory analyses of consensus molecular subtype-dependent associations of TP53 mutations with immunomodulation and prognosis in colorectal cancer. <i>ESMO Open</i> , 2019, 4, e000523.	2.0	11
26	Long noncoding RNA <i>MIR31HG</i> is a <i>bona fide</i> prognostic marker with colorectal cancer cell-intrinsic properties. <i>International Journal of Cancer</i> , 2019, 144, 2843-2853.	2.3	33
27	Mutational Dynamics and Evolutionary Divergence in DLBCL: A Call for Relapse Sampling. <i>Blood</i> , 2019, 134, 1497-1497.	0.6	0
28	Colorectal Cancer Consensus Molecular Subtypes Translated to Preclinical Models Uncover Potentially Targetable Cancer Cell Dependencies. <i>Clinical Cancer Research</i> , 2018, 24, 794-806.	3.2	177
29	Inferior survival for patients with malignant peripheral nerve sheath tumors defined by aberrant TP53. <i>Modern Pathology</i> , 2018, 31, 1694-1707.	2.9	11
30	Prognostic, predictive, and pharmacogenomic assessments of <i>CDX2</i> refine stratification of colorectal cancer. <i>Molecular Oncology</i> , 2018, 12, 1639-1655.	2.1	40
31	CMScaller: an R package for consensus molecular subtyping of colorectal cancer pre-clinical models. <i>Scientific Reports</i> , 2017, 7, 16618.	1.6	229
32	Multilevel genomics of colorectal cancers with microsatellite instability—clinical impact of JAK1 mutations and consensus molecular subtype 1. <i>Genome Medicine</i> , 2017, 9, 46.	3.6	71
33	Observed correlation between the expression levels of catalytic subunit, $C\hat{2}$, of cyclic adenosine monophosphate-dependent protein kinase and prostate cancer aggressiveness. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2017, 35, 111.e1-111.e8.	0.8	6
34	Epigenetic disruption of miR-130a promotes prostate cancer by targeting SEC23B and DEPDC1. <i>Cancer Letters</i> , 2017, 385, 150-159.	3.2	70
35	Multi-omics of 34 colorectal cancer cell lines - a resource for biomedical studies. <i>Molecular Cancer</i> , 2017, 16, 116.	7.9	232
36	Somatic POLE proofreading domain mutation, immune response, and prognosis in colorectal cancer: a retrospective, pooled biomarker study. <i>The Lancet Gastroenterology and Hepatology</i> , 2016, 1, 207-216.	3.7	227

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37	Intra-patient Inter-metastatic Genetic Heterogeneity in Colorectal Cancer as a Key Determinant of Survival after Curative Liver Resection. PLoS Genetics, 2016, 12, e1006225.	1.5	64
38	Novel drug discovery by pharmacogenomic profiling of 36 colorectal cancer cell lines.. Journal of Clinical Oncology, 2016, 34, 604-604.	0.8	0
39	TIN: An R Package for Transcriptome Instability Analysis. Cancer Informatics, 2015, 14, CIN.S31363.	0.9	4
40	Novel RNA variants in colorectal cancers. Oncotarget, 2015, 6, 36587-36602.	0.8	15
41	Transcriptome instability as a molecular pan-cancer characteristic of carcinomas. BMC Genomics, 2014, 15, 672.	1.2	15
42	Anticipating the Clinical Use of Prognostic Gene Expression-Based Tests for Colon Cancer Stage II and III: Is Godot Finally Arriving?. Clinical Cancer Research, 2013, 19, 6669-6677.	3.2	27
43	ColoGuidePro: A Prognostic 7-Gene Expression Signature for Stage III Colorectal Cancer Patients. Clinical Cancer Research, 2012, 18, 6001-6010.	3.2	109
44	ColoGuideEx: a robust gene classifier specific for stage II colorectal cancer prognosis. Gut, 2012, 61, 1560-1567.	6.1	179
45	The exon-level biomarker <i>SLC39A14</i> has organ-confined cancer-specificity in colorectal cancer. International Journal of Cancer, 2012, 131, 1479-1485.	2.3	20
46	Transcriptome instability in colorectal cancer identified by exon microarray analyses: Associations with splicing factor expression levels and patient survival. Genome Medicine, 2011, 3, 32.	3.6	73
47	Phospholipase C Isozymes Are Deregulated in Colorectal Cancer - Insights Gained from Gene Set Enrichment Analysis of the Transcriptome. PLoS ONE, 2011, 6, e24419.	1.1	58