SÃ¸ren Vang

List of Publications by Year
in descending order

55 papers	5,420 citations	117453 34 h-index	182168 51 g-index
57 all docs	57 docs citations	57 times ranked	10260 citing authors

#	Article	IF	Citations
1	Circulating tumor <scp>DNA</scp> for prognosis assessment and postoperative management after curativeâ€intent resection of colorectal liver metastases. International Journal of Cancer, 2022, 150, 1537-1548.	2.3	22
2	A Capsid Virus-Like Particle-Based SARS-CoV-2 Vaccine Induces High Levels of Antibodies and Protects Rhesus Macaques. Frontiers in Immunology, 2022, 13, 857440.	2.2	15
3	The alpha/B.1.1.7 SARS-CoV-2 variant exhibits significantly higher affinity for ACE-2 and requires lower inoculation doses to cause disease in K18-hACE2 mice. ELife, 2021, 10, .	2.8	24
4	Transcriptome-wide profiles of circular RNA and RNA-binding protein interactions reveal effects on circular RNA biogenesis and cancer pathway expression. Genome Medicine, 2020, 12, 112.	3.6	106
5	Deleterious misâ€splicing of STK11 caused by a novel singleâ€nucleotide substitution in the 3â€² polypyrimidine tract of intron five. Molecular Genetics & Genomic Medicine, 2020, 8, e1381.	0.6	3
6	Epigenetic and transcriptomic consequences of excess Xâ€chromosome material in 47,<scp>XXX</scp> syndromeâ€"A comparison with Turner syndrome and 46,<scp>XX</scp> females. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2020, 184, 279-293.	0.7	21
7	Phenotypic and genotypic features of a large kindred with a germline AIP variant. Clinical Endocrinology, 2020, 93, 146-153.	1.2	3
8	Transcriptomic and proteomic intra-tumor heterogeneity of colorectal cancer varies depending on tumor location within the colorectum. PLoS ONE, 2020, 15, e0241148.	1.1	13
9	Title is missing!. , 2020, 15, e0241148.		0
10	Title is missing!. , 2020, 15, e0241148.		0
11	Title is missing!. , 2020, 15, e0241148.		0
12	Title is missing!. , 2020, 15, e0241148.		0
13	Correlation between early dynamics in circulating tumour DNA and outcome from FOLFIRI treatment in metastatic colorectal cancer. Scientific Reports, 2019, 9, 11542.	1.6	25
14	Analysis of Plasma Cell-Free DNA by Ultradeep Sequencing in Patients With Stages I to III Colorectal Cancer. JAMA Oncology, 2019, 5, 1124.	3.4	538
15	Early Detection of Metastatic Relapse and Monitoring of Therapeutic Efficacy by Ultra-Deep Sequencing of Plasma Cell-Free DNA in Patients With Urothelial Bladder Carcinoma. Journal of Clinical Oncology, 2019, 37, 1547-1557.	0.8	298
16	Optimized targeted sequencing of cell-free plasma DNA from bladder cancer patients. Scientific Reports, 2018, 8, 1917.	1.6	50
17	Characterization of genetic intratumor heterogeneity in colorectal cancer and matching patientâ€derived spheroid cultures. Molecular Oncology, 2018, 12, 132-147.	2.1	49
18	Exploring the transcriptome of hormone-naive multifocal prostate cancer and matched lymph node metastases. British Journal of Cancer, 2018, 119, 1527-1537.	2.9	10

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19	DNA hypermethylation and differential gene expression associated with Klinefelter syndrome. Scientific Reports, 2018, 8, 13740.	1.6	75
20	Molecular-Subtype-Specific Biomarkers Improve Prediction of Prognosis in Colorectal Cancer. Cell Reports, 2017, 19, 1268-1280.	2.9	79
21	Clinical Implications of Monitoring Circulating Tumor DNA in Patients with Colorectal Cancer. Clinical Cancer Research, 2017, 23, 5437-5445.	3.2	232
22	Enrichment of Genetic Variants in the Glucocorticoid Receptor Signalling Pathway in Autoimmune Hepatitis with Failure of Standard Treatment. Basic and Clinical Pharmacology and Toxicology, 2017, 121, 189-194.	1.2	5
23	Comprehensive multiregional analysis of molecular heterogeneity in bladder cancer. Scientific Reports, 2017, 7, 11702.	1.6	110
24	Circular RNA expression is abundant and correlated to aggressiveness in early-stage bladder cancer. Npj Genomic Medicine, 2017, 2, 36.	1.7	105
25	A Rare Case of Embryonal Carcinoma in a Patient with Turner Syndrome without Y Chromosomal Material but Mutations in <i>KIT</i>, <i>AKT1</i>, and <i>ZNF358</i> Demonstrated Using Exome Sequencing. Sexual Development, 2017, 11, 262-268.	1.1	8
26	SNHG16 is regulated by the Wnt pathway in colorectal cancer and affects genes involved in lipid metabolism. Molecular Oncology, 2016, 10, 1266-1282.	2.1	151
27	SNHG5 promotes colorectal cancer cell survival by counteracting STAU1-mediated mRNA destabilization. Nature Communications, 2016, 7, 13875.	5.8	170
28	Paired Exome Analysis Reveals Clonal Evolution and Potential Therapeutic Targets in Urothelial Carcinoma. Cancer Research, 2016, 76, 5894-5906.	0.4	87
29	Spatial and temporal clonal evolution during development of metastatic urothelial carcinoma. Molecular Oncology, 2016, 10, 1450-1460.	2.1	44
30	Widespread DNA hypomethylation and differential gene expression in Turner syndrome. Scientific Reports, 2016, 6, 34220.	1.6	106
31	Comprehensive Transcriptional Analysis of Early-Stage Urothelial Carcinoma. Cancer Cell, 2016, 30, 27-42.	7.7	486
32	Analysis of circulating tumour DNA to monitor disease burden following colorectal cancer surgery. Gut, 2016, 65, 625-634.	6.1	381
33	Genomic Alterations in Liquid Biopsies from Patients with Bladder Cancer. European Urology, 2016, 70, 75-82.	0.9	174
34	Largeâ€scale evaluation of SLC18A2 in prostate cancer reveals diagnostic and prognostic biomarker potential at three molecular levels. Molecular Oncology, 2016, 10, 825-837.	2.1	20
35	Next-Generation Sequencing of RNA and DNA Isolated from Paired Fresh-Frozen and Formalin-Fixed Paraffin-Embedded Samples of Human Cancer and Normal Tissue. PLoS ONE, 2014, 9, e98187.	1.1	284
36	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. Genome Research, 2014, 24, 454-466.	2.4	161

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37	Identification of expressed and conserved human noncoding RNAs. Rna, 2014, 20, 236-251.	1.6	47
38	Mutational Context and Diverse Clonal Development in Early and Late Bladder Cancer. Cell Reports, 2014, 7, 1649-1663.	2.9	128
39	Proteomics Reveals that Redox Regulation Is Disrupted in Patients with Ethylmalonic Encephalopathy. Journal of Proteome Research, 2011, 10, 2389-2396.	1.8	35
40	Quantitative Proteomics Reveals Cellular Targets of Celastrol. PLoS ONE, 2011, 6, e26634.	1.1	48
41	Toxic response caused by a misfolding variant of the mitochondrial protein short-chain acyl-CoA dehydrogenase. Journal of Inherited Metabolic Disease, 2011, 34, 465-475.	1.7	10
42	Tumor-specific usage of alternative transcription start sites in colorectal cancer identified by genome-wide exon array analysis. BMC Genomics, 2011, 12, 505.	1.2	57
43	Antioxidant dysfunction: potential risk for neurotoxicity in ethylmalonic aciduria. Journal of Inherited Metabolic Disease, 2010, 33, 211-222.	1.7	37
44	Measuring Consequences of Protein Misfolding and Cellular Stress Using OMICS Techniques. Methods in Molecular Biology, 2010, 648, 119-135.	0.4	2
45	Correlation Between Ka/Ks and Ks is Related to Substitution Model and Evolutionary Lineage. Journal of Molecular Evolution, 2009, 68, 414-423.	0.8	71
46	Mitochondrial proteomics on human fibroblasts for identification of metabolic imbalance and cellular stress. Proteome Science, 2009, 7, 20.	0.7	37
47	The ACADS gene variation spectrum in 114 patients with short-chain acyl-CoA dehydrogenase (SCAD) deficiency is dominated by missense variations leading to protein misfolding at the cellular level. Human Genetics, 2008, 124, 43-56.	1.8	101
48	Gene conversion in the rice genome. BMC Genomics, 2008, 9, 93.	1.2	42
49	FGF: A web tool for Fishing Gene Family in a whole genome database. Nucleic Acids Research, 2007, 35, W121-W125.	6.5	6
50	Snap: an integrated SNP annotation platform. Nucleic Acids Research, 2007, 35, D707-D710.	6.5	36
51	TreeFam: 2008 Update. Nucleic Acids Research, 2007, 36, D735-D740.	6.5	294
52	High Rate of Chimeric Gene Origination by Retroposition in Plant Genomes. Plant Cell, 2006, 18, 1791-1802.	3.1	207
53	Protein Misfolding and Human Disease. Annual Review of Genomics and Human Genetics, 2006, 7, 103-124.	2.5	258
54	Actin mutations in hypertrophic and dilated cardiomyopathy cause inefficient protein folding and perturbed filament formation. FEBS Journal, 2005, 272, 2037-2049.	2.2	71

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55	Mutational analysis of the active site of human insulin-regulated aminopeptidase. FEBS Journal, 2001, 268, 98-104.	0.2	77