

# Søren Vang

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Analysis of Plasma Cell-Free DNA by Ultradeep Sequencing in Patients With Stages I to III Colorectal Cancer. <i>JAMA Oncology</i> , 2019, 5, 1124.	3.4	538
2	Comprehensive Transcriptional Analysis of Early-Stage Urothelial Carcinoma. <i>Cancer Cell</i> , 2016, 30, 27-42.	7.7	486
3	Analysis of circulating tumour DNA to monitor disease burden following colorectal cancer surgery. <i>Gut</i> , 2016, 65, 625-634.	6.1	381
4	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. <i>Journal of Clinical Oncology</i> , 2019, 37, 1547-1557.	0.8	298
5	TreeFam: 2008 Update. <i>Nucleic Acids Research</i> , 2007, 36, D735-D740.	6.5	294
6	Next-Generation Sequencing of RNA and DNA Isolated from Paired Fresh-Frozen and Formalin-Fixed Paraffin-Embedded Samples of Human Cancer and Normal Tissue. <i>PLoS ONE</i> , 2014, 9, e98187.	1.1	284
7	Protein Misfolding and Human Disease. <i>Annual Review of Genomics and Human Genetics</i> , 2006, 7, 103-124.	2.5	258
8	Clinical Implications of Monitoring Circulating Tumor DNA in Patients with Colorectal Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 5437-5445.	3.2	232
9	High Rate of Chimeric Gene Origination by Retroposition in Plant Genomes. <i>Plant Cell</i> , 2006, 18, 1791-1802.	3.1	207
10	Genomic Alterations in Liquid Biopsies from Patients with Bladder Cancer. <i>European Urology</i> , 2016, 70, 75-82.	0.9	174
11	SNHG5 promotes colorectal cancer cell survival by counteracting STAU1-mediated mRNA destabilization. <i>Nature Communications</i> , 2016, 7, 13875.	5.8	170
12	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. <i>Genome Research</i> , 2014, 24, 454-466.	2.4	161
13	SNHG16 is regulated by the Wnt pathway in colorectal cancer and affects genes involved in lipid metabolism. <i>Molecular Oncology</i> , 2016, 10, 1266-1282.	2.1	151
14	Mutational Context and Diverse Clonal Development in Early and Late Bladder Cancer. <i>Cell Reports</i> , 2014, 7, 1649-1663.	2.9	128
15	Comprehensive multiregional analysis of molecular heterogeneity in bladder cancer. <i>Scientific Reports</i> , 2017, 7, 11702.	1.6	110
16	Widespread DNA hypomethylation and differential gene expression in Turner syndrome. <i>Scientific Reports</i> , 2016, 6, 34220.	1.6	106
17	Transcriptome-wide profiles of circular RNA and RNA-binding protein interactions reveal effects on circular RNA biogenesis and cancer pathway expression. <i>Genome Medicine</i> , 2020, 12, 112.	3.6	106
18	Circular RNA expression is abundant and correlated to aggressiveness in early-stage bladder cancer. <i>Npj Genomic Medicine</i> , 2017, 2, 36.	1.7	105

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19	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. <i>Human Genetics</i> , 2008, 124, 43-56.	1.8	101
20	Paired Exome Analysis Reveals Clonal Evolution and Potential Therapeutic Targets in Urothelial Carcinoma. <i>Cancer Research</i> , 2016, 76, 5894-5906.	0.4	87
21	Molecular-Subtype-Specific Biomarkers Improve Prediction of Prognosis in Colorectal Cancer. <i>Cell Reports</i> , 2017, 19, 1268-1280.	2.9	79
22	Mutational analysis of the active site of human insulin-regulated aminopeptidase. <i>FEBS Journal</i> , 2001, 268, 98-104.	0.2	77
23	DNA hypermethylation and differential gene expression associated with Klinefelter syndrome. <i>Scientific Reports</i> , 2018, 8, 13740.	1.6	75
24	Actin mutations in hypertrophic and dilated cardiomyopathy cause inefficient protein folding and perturbed filament formation. <i>FEBS Journal</i> , 2005, 272, 2037-2049.	2.2	71
25	Correlation Between Ka/Ks and Ks is Related to Substitution Model and Evolutionary Lineage. <i>Journal of Molecular Evolution</i> , 2009, 68, 414-423.	0.8	71
26	Tumor-specific usage of alternative transcription start sites in colorectal cancer identified by genome-wide exon array analysis. <i>BMC Genomics</i> , 2011, 12, 505.	1.2	57
27	Optimized targeted sequencing of cell-free plasma DNA from bladder cancer patients. <i>Scientific Reports</i> , 2018, 8, 1917.	1.6	50
28	Characterization of genetic intratumor heterogeneity in colorectal cancer and matching patient-derived spheroid cultures. <i>Molecular Oncology</i> , 2018, 12, 132-147.	2.1	49
29	Quantitative Proteomics Reveals Cellular Targets of Celastrol. <i>PLoS ONE</i> , 2011, 6, e26634.	1.1	48
30	Identification of expressed and conserved human noncoding RNAs. <i>Rna</i> , 2014, 20, 236-251.	1.6	47
31	Spatial and temporal clonal evolution during development of metastatic urothelial carcinoma. <i>Molecular Oncology</i> , 2016, 10, 1450-1460.	2.1	44
32	Gene conversion in the rice genome. <i>BMC Genomics</i> , 2008, 9, 93.	1.2	42
33	Mitochondrial proteomics on human fibroblasts for identification of metabolic imbalance and cellular stress. <i>Proteome Science</i> , 2009, 7, 20.	0.7	37
34	Antioxidant dysfunction: potential risk for neurotoxicity in ethylmalonic aciduria. <i>Journal of Inherited Metabolic Disease</i> , 2010, 33, 211-222.	1.7	37
35	Snap: an integrated SNP annotation platform. <i>Nucleic Acids Research</i> , 2007, 35, D707-D710.	6.5	36
36	Proteomics Reveals that Redox Regulation Is Disrupted in Patients with Ethylmalonic Encephalopathy. <i>Journal of Proteome Research</i> , 2011, 10, 2389-2396.	1.8	35

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37	Correlation between early dynamics in circulating tumour DNA and outcome from FOLFIRI treatment in metastatic colorectal cancer. <i>Scientific Reports</i> , 2019, 9, 11542.	1.6	25
38	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. <i>ELife</i> , 2021, 10, .	2.8	24
39	Circulating tumor <sc>DNA</sc> for prognosis assessment and postoperative management after curativeâ€”intent resection of colorectal liver metastases. <i>International Journal of Cancer</i> , 2022, 150, 1537-1548.	2.3	22
40	Epigenetic and transcriptomic consequences of excess Xâ€”chromosome material in 47,<sc>XXX</sc> syndromeâ€”A comparison with Turner syndrome and 46,<sc>XX</sc> females. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2020, 184, 279-293.	0.7	21
41	Largeâ€”scale evaluation of SLC18A2 in prostate cancer reveals diagnostic and prognostic biomarker potential at three molecular levels. <i>Molecular Oncology</i> , 2016, 10, 825-837.	2.1	20
42	A Capsid Virus-Like Particle-Based SARS-CoV-2 Vaccine Induces High Levels of Antibodies and Protects Rhesus Macaques. <i>Frontiers in Immunology</i> , 2022, 13, 857440.	2.2	15
43	Transcriptomic and proteomic intra-tumor heterogeneity of colorectal cancer varies depending on tumor location within the colorectum. <i>PLoS ONE</i> , 2020, 15, e0241148.	1.1	13
44	Toxic response caused by a misfolding variant of the mitochondrial protein short-chain acyl-CoA dehydrogenase. <i>Journal of Inherited Metabolic Disease</i> , 2011, 34, 465-475.	1.7	10
45	Exploring the transcriptome of hormone-naïve multifocal prostate cancer and matched lymph node metastases. <i>British Journal of Cancer</i> , 2018, 119, 1527-1537.	2.9	10
46	A Rare Case of Embryonal Carcinoma in a Patient with Turner Syndrome without Y Chromosomal Material but Mutations in <b><i>KIT</i></b>, <b><i>AKT1</i></b>, and <b><i>ZNF358</i></b> Demonstrated Using Exome Sequencing. <i>Sexual Development</i> , 2017, 11, 262-268.	1.1	8
47	FGF: A web tool for Fishing Gene Family in a whole genome database. <i>Nucleic Acids Research</i> , 2007, 35, W121-W125.	6.5	6
48	Enrichment of Genetic Variants in the Glucocorticoid Receptor Signalling Pathway in Autoimmune Hepatitis with Failure of Standard Treatment. <i>Basic and Clinical Pharmacology and Toxicology</i> , 2017, 121, 189-194.	1.2	5
49	Deleterious misâ€”splicing of <i>STK11</i> caused by a novel singleâ€”nucleotide substitution in the 3â€” polypyrimidine tract of intron five. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1381.	0.6	3
50	Phenotypic and genotypic features of a large kindred with a germline AIP variant. <i>Clinical Endocrinology</i> , 2020, 93, 146-153.	1.2	3
51	Measuring Consequences of Protein Misfolding and Cellular Stress Using OMICS Techniques. <i>Methods in Molecular Biology</i> , 2010, 648, 119-135.	0.4	2
52	Title is missing!. , 2020, 15, e0241148.		0
53	Title is missing!. , 2020, 15, e0241148.		0
54	Title is missing!. , 2020, 15, e0241148.		0

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55	Title is missing!. , 2020, 15, e0241148.		0