Sevtap Savas

List of Publications by Year
in descending order

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68 papers	1,200 citations	430754 18 h-index	434063 31 g-index
69 all docs	69 docs citations	69 times ranked	2408 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies tumor anatomical site-specific risk variants for colorectal cancer survival. Scientific Reports, 2022, 12, 127.	1.6	6
2	GATA3 somatic mutations are associated with clinicopathological features and expression profile in TCGA breast cancer patients. Scientific Reports, 2021, 11, 1679.	1.6	15
3	A comprehensive analysis of SNPs and CNVs identifies novel markers associated with disease outcomes in colorectal cancer. Molecular Oncology, 2021, 15, 3329-3347.	2.1	9
4	The long-term survival characteristics of a cohort of colorectal cancer patients and baseline variables associated with survival outcomes with or without time-varying effects. BMC Medicine, 2019, 17, 150.	2.3	32
5	A genome-wide association study identifies single nucleotide polymorphisms associated with time-to-metastasis in colorectal cancer. BMC Cancer, 2019, 19, 133.	1.1	13
6	The SWI/SNF complex subunit genes: Their functions, variations, and links to risk and survival outcomes in human cancers. Critical Reviews in Oncology/Hematology, 2018, 123, 114-131.	2.0	70
7	Associations of single nucleotide polymorphisms with mucinous colorectal cancer: genome-wide common variant and gene-based rare variant analyses. Biomarker Research, 2018, 6, 17.	2.8	5
8	Association of rs2282679 A>C polymorphism in vitamin D binding protein gene with colorectal cancer risk and survival: effect modification by dietary vitamin D intake. BMC Cancer, 2018, 18, 155.	1.1	8
9	Two functional indel polymorphisms in the promoter region of the Brahma gene (BRM) and disease risk and progression-free survival in colorectal cancer. PLoS ONE, 2018, 13, e0198873.	1.1	6
10	XRCC3 Thr241Met and TYMS variable number tandem repeat polymorphisms are associated with time-to-metastasis in colorectal cancer. PLoS ONE, 2018, 13, e0192316.	1.1	6
11	Validation of micro<scp>RNA</scp> pathway polymorphisms in esophageal adenocarcinoma survival. Cancer Medicine, 2017, 6, 361-373.	1.3	11
12	Germline <scp>INDEL</scp>s and <scp>CNV</scp>s in a cohort of colorectal cancer patients: their characteristics, associations with relapseâ€free survival time, and potential timeâ€varying effects on the risk of relapse. Cancer Medicine, 2017, 6, 1220-1232.	1.3	14
13	Germline Mutations in the Kallikrein 6 Region and Predisposition for Aggressive Prostate Cancer. Journal of the National Cancer Institute, 2017, 109, .	3.0	13
14	PD65-01 GERMLINE MUTATIONS IN THE KALLIKREIN 6 REGION AND PREDISPOSITION FOR AGGRESSIVE PROSTATE CANCER. Journal of Urology, 2017, 197, .	0.2	0
15	Vitamin D receptor and calcium-sensing receptor polymorphisms and colorectal cancer survival in the Newfoundland population. British Journal of Cancer, 2017, 117, 898-906.	2.9	18
16	ABCC2 polymorphisms and survival in the Princess Margaret cohort study and the NCIC clinical trials group BR.24 trial of platinum-treated advanced stage non-small cell lung cancer patients. Cancer Epidemiology, 2016, 41, 50-56.	0.8	7
17	No associations of a set of SNPs in the Vascular Endothelial Growth Factor (VEGF) and Matrix Metalloproteinase (MMP) genes with survival of colorectal cancer patients. Cancer Medicine, 2016, 5, 2221-2231.	1.3	6
18	MP61-01 FUNCTIONAL ROLE OF THE KALLIKREIN 6 REGION OF THE KALLIKREIN LOCUS IN GENETIC PREDISPOSITION FOR AGGRESSIVE (GLEASON â‰¥8) PROSTATE CANCER: FINE-MAPPING AND METHYLATION STUDY IN A CANADIAN COHORT AND THE SWISS ARM OF THE EUROPEAN RANDOMIZED STUDY FOR PROSTATE CANCER SCREENING. Journal of Urology, 2015, 193, .	0.2	0

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19	A Survival Association Study of 102 Polymorphisms Previously Associated with Survival Outcomes in Colorectal Cancer. BioMed Research International, 2015, 2015, 1-9.	0.9	5
20	Biomarkers for Colon Cancer. Biomarkers in Cancer, 2015, 7s1, BIC.S39882.	3.6	5
21	Discovery and validation of vascular endothelial growth factor (VEGF) pathway polymorphisms in esophageal adenocarcinoma outcome. Carcinogenesis, 2015, 36, 956-962.	1.3	7
22	A genome wide association study on Newfoundland colorectal cancer patientsâ€™ survival outcomes. Biomarker Research, 2015, 3, 6.	2.8	17
23	Mitochondrial DNA polymorphisms, its copy number change and outcome in colorectal cancer. BMC Research Notes, 2015, 8, 272.	0.6	16
24	Inferring Gene Network from Candidate SNP Association Studies Using a Bayesian Graphical Model: Application to a Breast Cancer Case-Control Study from Ontario. Human Heredity, 2014, 78, 140-152.	0.4	3
25	Influence of pre-diagnostic cigarette smoking on colorectal cancer survival: overall and by tumour molecular phenotype. British Journal of Cancer, 2014, 110, 1359-1366.	2.9	42
26	Examining the Polymorphisms in the Hypoxia Pathway Genes in Relation to Outcome in Colorectal Cancer. PLoS ONE, 2014, 9, e113513.	1.1	7
27	Special considerations in prognostic research in cancer involving genetic polymorphisms. BMC Medicine, 2013, 11, 149.	2.3	8
28	Dietary patterns and colorectal cancer recurrence and survival: a cohort study. BMJ Open, 2013, 3, e002270.	0.8	57
29	MTHFR Glu429Ala and ERCC5 His46His Polymorphisms Are Associated with Prognosis in Colorectal Cancer Patients: Analysis of Two Independent Cohorts from Newfoundland. PLoS ONE, 2013, 8, e61469.	1.1	30
30	Abstract 2562: Polymorphisms in microRNA (miRNA) pathways and survival in esophageal cancer (EC) patients.. , 2013, , .		1
31	MicroRNA polymorphisms and esophageal cancer outcome.. Journal of Clinical Oncology, 2013, 31, 32-32.	0.8	1
32	Missense Variants of Uncertain Significance (VUS) Altering the Phosphorylation Patterns of BRCA1 and BRCA2. PLoS ONE, 2013, 8, e62468.	1.1	9
33	A curated database of genetic markers from the angiogenesis/VEGF pathway and their relation to clinical outcome in human cancers. Acta OncolÃ³gica, 2012, 51, 243-246.	0.8	7
34	Validation of Genetic Sequence Variants as Prognostic Factors in Early-Stage Head and Neck Squamous Cell Cancer Survival. Clinical Cancer Research, 2012, 18, 196-206.	3.2	39
35	Vascular Endothelial Growth Factor Pathway Polymorphisms as Prognostic and Pharmacogenetic Factors in Cancer: A Systematic Review and Meta-analysis. Clinical Cancer Research, 2012, 18, 4526-4537.	3.2	48
36	Serotonin Transporter Gene (SLC6A4) Variations Are Associated with Poor Survival in Colorectal Cancer Patients. PLoS ONE, 2012, 7, e38953.	1.1	26

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37	Genetic sequence variants and the development of secondary primary cancers in patients with head and neck cancers. Cancer, 2012, 118, 1554-1565.	2.0	15
38	Abstract 4505: Polymorphisms invascular endothelial growth factor(VEGF) and associated receptors as prognostic and predictive factors in advanced solid tumors. , 2012, , .		0
39	Single nucleotide polymorphisms (SNPs) of the platinum pharmacogenetic and VEGF pathways: Association with survival of platinum-treated stage IV non-small cell lung cancer (NSCLC) patients.. Journal of Clinical Oncology, 2012, 30, 7586-7586.	0.8	0
40	Bioinformatic analyses identifies novel protein-coding pharmacogenomic markers associated with paclitaxel sensitivity in NCI60 cancer cell lines. BMC Medical Genomics, 2011, 4, 18.	0.7	22
41	NCI60 Cancer Cell Line Panel Data and RNAi Analysis Help Identify EAF2 as a Modulator of Simvastatin and Lovastatin Response in HCT-116 Cells. PLoS ONE, 2011, 6, e18306.	1.1	15
42	dbCPCO: a database of genetic markers tested for their predictive and prognostic value in colorectal cancer. Human Mutation, 2010, 31, 901-907.	1.1	19
43	A Whole-Genome SNP Association Study of NCI60 Cell Line Panel Indicates a Role of Ca2+ Signaling in Selenium Resistance. PLoS ONE, 2010, 5, e12601.	1.1	17
44	Useful genetic variation databases for oncologists investigating the genetic basis of variable treatment response and survival in cancer. Acta OncolÃ³gica, 2010, 49, 1217-1226.	0.8	2
45	Abstract 1679: Identification of pharmacogenomic markers associated with paclitaxel and carboplatin response in cancer: The cross-talk between agents. , 2010, , .		0
46	Abstract 92: dbCPCO: The database of genetic predictive and prognostic factors in colorectal cancer. , 2010, , .		0
47	Studying Genetic Variations in Cancer Prognosis (and Risk): A Primer for Clinicians. Oncologist, 2009, 14, 657-666.	1.9	14
48	Genetic variations as cancer prognostic markers: review and update. Human Mutation, 2009, 30, 1369-1377.	1.1	32
49	A comprehensive catalogue of functional genetic variations in the EGFR pathway: Proteinâ€“protein interaction analysis reveals novel genes and polymorphisms important for cancer research. International Journal of Cancer, 2009, 125, 1257-1265.	2.3	13
50	Biological implications of SNPs in signal peptide domains of human proteins. Proteins: Structure, Function and Bioinformatics, 2008, 70, 394-403.	1.5	44
51	Discovery of genetic profiles impacting response to chemotherapy: application to gemcitabine. Human Mutation, 2008, 29, 461-467.	1.1	18
52	Functional nonsynonymous single nucleotide polymorphisms from the TGF-Î² protein interaction network. Physiological Genomics, 2007, 29, 109-117.	1.0	10
53	Human Non-synonymous Single Nucleotide Polymorphisms Can Influence Ubiquitin-mediated Protein Degradation. OMICS A Journal of Integrative Biology, 2007, 11, 200-208.	1.0	4
54	Polymorphisms cMyc-N11S and p27-V109G and breast cancer risk and prognosis. BMC Cancer, 2007, 7, 99.	1.1	21

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55	Genetic Variation and the Mitogen-Activated Protein Kinase (MAPK) Signaling Pathway. OMICS A Journal of Integrative Biology, 2006, 10, 66-81.	1.0	4
56	Human SNPs resulting in premature stop codons and protein truncation. Human Genomics, 2006, 2, 274.	1.4	36
57	Functional nsSNPs from carcinogenesis-related genes expressed in breast tissue: Potential breast cancer risk alleles and their distribution across human populations. Human Genomics, 2006, 2, 287.	1.4	17
58	Hereditary haemorrhagic telangiectasia: mutation detection, test sensitivity and novel mutations. Journal of Medical Genetics, 2006, 43, 722-728.	1.5	110
59	Phosphorylation states of cell cycle and DNA repair proteins can be altered by the nsSNPs. BMC Cancer, 2005, 5, 107.	1.1	23
60	The USH1C 216G?A splice-site mutation results in a 35-base-pair deletion. Human Genetics, 2005, 116, 225-227.	1.8	30
61	Candidate nsSNPs that can affect the functions and interactions of cell cycle proteins. Proteins: Structure, Function and Bioinformatics, 2004, 58, 697-705.	1.5	19
62	Genetic heterogeneity in Usher syndrome. American Journal of Medical Genetics Part A, 2004, 130A, 13-16.	2.4	51
63	Structure, diversity, and evolution of the 45-bp VNTR in intron 5 of the USH1C gene. Genomics, 2004, 83, 439-444.	1.3	1
64	Identifying functional genetic variants in DNA repair pathway using protein conservation analysis. Cancer Epidemiology Biomarkers and Prevention, 2004, 13, 801-7.	1.1	44
65	The USH1C 216Gâ†'A mutation and the 9-repeat VNTR(t,t) allele are in complete linkage disequilibrium in the Acadian population. Human Genetics, 2002, 110, 95-97.	1.8	17
66	Prenatal prediction of childhood-onset spinal muscular atrophy (SMA) in Turkish families. Prenatal Diagnosis, 2002, 22, 703-709.	1.1	11
67	Screening of Deletions in SMN, NAIP and BTF2p44 Genes in Turkish Spinal Muscular Atrophy Patients. Human Heredity, 2000, 50, 162-165.	0.4	9
68	Variable Distribution of TFF2 (Spasmolysin) Alleles in Europeans Does Not Indicate Predisposition to Gastric Cancer. Human Heredity, 1999, 49, 45-47.	0.4	5