Tesa M Severson

List of Publications by Year
in descending order

31 papers	5,235 citations	331670 21 h-index	477307 29 g-index
32 all docs	32 docs citations	32 times ranked	9284 citing authors

#	Article	IF	Citations
1	Drug-Induced Epigenomic Plasticity Reprograms Circadian Rhythm Regulation to Drive Prostate Cancer toward Androgen Independence. Cancer Discovery, 2022, 12, 2074-2097.	9.4	22
2	Epigenetic and transcriptional analysis reveals a core transcriptional program conserved in clonal prostate cancer metastases. Molecular Oncology, 2021, 15, 1942-1955.	4.6	10
3	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	21.4	174
4	The MSPâ€RON axis stimulates cancer cell growth in models of triple negative breast cancer. Molecular Oncology, 2020, 14, 1868-1880.	4.6	15
5	EZH2 Is Overexpressed in BRCA1-like Breast Tumors and Predictive for Sensitivity to High-Dose Platinum-Based Chemotherapy. Clinical Cancer Research, 2019, 25, 4351-4362.	7.0	33
6	Lysine specific demethylase 1 inactivation enhances differentiation and promotes cytotoxic response when combined with all-trans retinoic acid in acute myeloid leukemia across subtypes. Haematologica, 2019, 104, 1156-1167.	3.5	50
7	Assessment of PD-L1 expression across breast cancer molecular subtypes, in relation to mutation rate, BRCA1-like status, tumor-infiltrating immune cells and survival. OncoImmunology, 2018, 7, e1509820.	4.6	80
8	ARID1A mutation sensitizes most ovarian clear cell carcinomas to BET inhibitors. Oncogene, 2018, 37, 4611-4625.	5.9	72
9	Fanconi anemia and homologous recombination gene variants are associated with functional DNA repair defects in vitro and poor outcome in patients with advanced head and neck squamous cell carcinoma. Oncotarget, 2018, 9, 18198-18213.	1.8	37
10	A review of estrogen receptor/androgen receptor genomics in male breast cancer. Endocrine-Related Cancer, 2017, 24, R27-R34.	3.1	23
11	DNA repair deficiency biomarkers and the 70-gene ultra-high risk signature as predictors of veliparib/carboplatin response in the I-SPY 2 breast cancer trial. Npj Breast Cancer, 2017, 3, 31.	5.2	64
12	The BRCA1ness signature is associated significantly with response to PARP inhibitor treatment versus control in the I-SPY 2 randomized neoadjuvant setting. Breast Cancer Research, 2017, 19, 99.	5.0	58
13	Integration of genomic, transcriptomic and proteomic data identifies two biologically distinct subtypes of invasive lobular breast cancer. Scientific Reports, 2016, 6, 18517.	3.3	143
14	Comparative Cistromics Reveals Genomic Cross-talk between FOXA1 and ERÎ± in Tamoxifen-Associated Endometrial Carcinomas. Cancer Research, 2016, 76, 3773-3784.	0.9	30
15	Neoadjuvant tamoxifen synchronizes ERÎ± binding and gene expression profiles related to outcome and proliferation. Oncotarget, 2016, 7, 33901-33918.	1.8	13
16	BRCA1â€like signature in triple negative breast cancer: Molecular and clinical characterization reveals subgroups with therapeutic potential. Molecular Oncology, 2015, 9, 1528-1538.	4.6	54
17	Robust BRCA1â€like classification of copy number profiles of samples repeated across different datasets and platforms. Molecular Oncology, 2015, 9, 1274-1286.	4.6	29
18	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	27.8	1,428

#	Article	IF	Citations
19	Hypomorphic Temperature-Sensitive Alleles of NSDHL Cause CK Syndrome. American Journal of Human Genetics, 2010, 87, 905-914.	6.2	64
20	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185.	21.4	1,504
21	Acquired TNFRSF14 Mutations in Follicular Lymphoma Are Associated with Worse Prognosis. Cancer Research, 2010, 70, 9166-9174.	0.9	160
22	Mutations In MLL2 and MEF2B Genes In Follicular Lymphoma and Diffuse Large B-Cell Lymphoma. Blood, 2010, 116, 473-473.	1.4	6
23	Identification of Genes Frequently Mutated In FL and DLBCL with Transcriptome, Genome and Exome Sequencing. Blood, 2010, 116, 804-804.	1.4	1
24	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. Nature, 2009, 461, 809-813.	27.8	984
25	Tyrosine 641 of the EZH2 Oncogene Is Frequently Mutated in Follicular and Diffuse Large B-Cell Lymphomas of Germinal Center Origin.. Blood, 2009, 114, 139-139.	1.4	3
26	Base-Pair Resolution of Somatic and Germline-Derived Genome Rearrangement Breakpoints in Follicular Lymphoma.. Blood, 2009, 114, 439-439.	1.4	0
27	TNFRSF14 Is Mutated in a Subset of Follicular Lymphoma and Correlated with Inferior Prognosis.. Blood, 2009, 114, 1919-1919.	1.4	1
28	FAS Mutations in Follicular Lymphoma Are Rare but Associated with Aggressive Clinical Behavior.. Blood, 2009, 114, 3967-3967.	1.4	0
29	A novel DNA sequence database for analyzing human demographic history. Genome Research, 2008, 18, 1354-1361.	5.5	74
30	Evidence for Archaic Asian Ancestry on the Human X Chromosome. Molecular Biology and Evolution, 2005, 22, 189-192.	8.9	81
31	Expression profile and genome location of cDNA clones from an infant human trabecular meshwork cell library. Investigative Ophthalmology and Visual Science, 2002, 43, 3698-704.	3.3	22