Tom Lesluyes

List of Publications by Year
in descending order

39 papers	1,126 citations	394421 19 h-index	454955 30 g-index
41 all docs	41 docs citations	41 times ranked	1450 citing authors

#	Article	IF	Citations
1	<scp>CINSARC</scp> in highâ€risk soft tissue sarcoma patients treated with neoadjuvant chemotherapy: Results from the <scp>ISGâ€STS</scp> 1001 study. Cancer Medicine, 2023, 12, 1350-1357.	2.8	7
2	Signatures of copy number alterations in human cancer. Nature, 2022, 606, 984-991.	27.8	154
3	A pan-cancer compendium of chromosomal instability. Nature, 2022, 606, 976-983.	27.8	111
4	Expression and prognostic significance of PDGF ligands and receptors across soft tissue sarcomas. ESMO Open, 2021, 6, 100037.	4.5	8
5	ATRX Alteration Contributes to Tumor Growth and Immune Escape in Pleomorphic Sarcomas. Cancers, 2021, 13, 2151.	3.7	10
6	An integrative analysis of the age-associated multi-omic landscape across cancers. Nature Communications, 2021, 12, 2345.	12.8	54
7	E3 ubiquitin ligase HECTD2 mediates melanoma progression and immune evasion. Oncogene, 2021, 40, 5567-5578.	5.9	3
8	The Nanocind Signature Is an Independent Prognosticator of Recurrence and Death in Uterine Leiomyosarcomas. Clinical Cancer Research, 2020, 26, 855-861.	7.0	13
9	Impact of preoperative treatment on the CINSARC prognostic signature: translational research results from aÂphaseÂ1 trial of the German Interdisciplinary Sarcoma Group (GISG 03). Strahlentherapie Und Onkologie, 2020, 196, 280-285.	2.0	1
10	A Global and Integrated Analysis of CINSARC-Associated Genetic Defects. Cancer Research, 2020, 80, 5282-5290.	0.9	8
11	Value of peri-operative chemotherapy in patients with CINSARC high-risk localized grade 1 or 2 soft tissue sarcoma: study protocol of the target selection phase III CHIC-STS trial. BMC Cancer, 2020, 20, 716.	2.6	7
12	Specific immune landscapes and immune checkpoint expressions in histotypes and molecular subtypes of sarcoma. OncoImmunology, 2020, 9, 1792036.	4.6	31
13	Cellâ€"cell fusion of mesenchymal cells with distinct differentiations triggers genomic and transcriptomic remodelling toward tumour aggressiveness. Scientific Reports, 2020, 10, 21634.	3.3	9
14	LIX1 regulates YAP activity and controls gastrointestinal cancer cell plasticity. Journal of Cellular and Molecular Medicine, 2020, 24, 9244-9254.	3.6	11
15	Genome remodeling upon mesenchymal tumor cell fusion contributes to tumor progression and metastatic spread. Oncogene, 2020, 39, 4198-4211.	5.9	19
16	Tetraploidization of Immortalized Myoblasts Induced by Cell Fusion Drives Myogenic Sarcoma Development with DMD Deletion. Cancers, 2020, 12, 1281.	3.7	4
17	Genomic and transcriptomic comparison of post-radiation versus sporadic sarcomas. Modern Pathology, 2019, 32, 1786-1794.	5.5	25
18	Fusion-mediated chromosomal instability promotes aneuploidy patterns that resemble human tumors. Oncogene, 2019, 38, 6083-6094.	5.9	23

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19	Recurrent DMD Deletions Highlight Specific Role of Dp71 Isoform in Soft-Tissue Sarcomas. Cancers, 2019, 11, 922.	3.7	13
20	Clinicopathologic and Molecular Features of a Series of 41 Biphenotypic Sinonasal Sarcomas Expanding Their Molecular Spectrum. American Journal of Surgical Pathology, 2019, 43, 747-754.	3.7	65
21	CINSARC signature as a prognostic marker for clinical outcome in sarcomas and beyond. Genes Chromosomes and Cancer, 2019, 58, 124-129.	2.8	23
22	RCBTB1 Deletion Is Associated with Metastatic Outcome and Contributes to Docetaxel Resistance in Nontranslocation-Related Pleomorphic Sarcomas. Cancers, 2019, 11, 81.	3.7	3
23	*GREB1–CTNNB1* fusion transcript detected by RNA–sequencing in a uterine tumor resembling ovarian sex cord tumor (UTROSCT): A novel *CTNNB1* rearrangement. Genes Chromosomes and Cancer, 2019, 58, 155-163.	2.8	30
24	Chemotherapy in localized soft tissue sarcoma: will we soon have to treat grade 1 tumors? Update on CINSARC performances. Annals of Oncology, 2019, 30, 153-155.	1.2	8
25	Genome profiling is an efficient tool to avoid the STUMP classification of uterine smooth muscle lesions: a comprehensive array-genomic hybridization analysis of 77 tumors. Modern Pathology, 2018, 31, 816-828.	5.5	46
26	The Role of the Anti-Aging Protein Klotho in IGF-1 Signaling and Reticular Calcium Leak: Impact on the Chemosensitivity of Dedifferentiated Liposarcomas. Cancers, 2018, 10, 439.	3.7	19
27	Alternative PDGFD rearrangements in dermatofibrosarcomas protuberans without PDGFB fusions. Modern Pathology, 2018, 31, 1683-1693.	5.5	56
28	Gastrointestinal stromal tumor enhancers support a transcription factor network predictive of clinical outcome. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5746-E5755.	7.1	20
29	Validation of the Complexity INdex in SARComas prognostic signature on formalin-fixed, paraffin-embedded, soft-tissue sarcomas. Annals of Oncology, 2018, 29, 1828-1835.	1.2	30
30	Regulation of RNA polymerase III transcription during transformation of human IMR90 fibroblasts with defined genetic elements. Cell Cycle, 2018, 17, 605-615.	2.6	21
31	Vnn1 pantetheinase limits the Warburg effect and sarcoma growth by rescuing mitochondrial activity. Life Science Alliance, 2018, 1, e201800073.	2.8	24
32	The CINSARC signature as a prognostic marker for clinical outcome in multiple neoplasms. Scientific Reports, 2017, 7, 5480.	3.3	24
33	Recurrent *TRIO* Fusion in Nontranslocation–Related Sarcomas. Clinical Cancer Research, 2017, 23, 857-867.	7.0	41
34	Expression and role of TYRO3 and AXL as potential therapeutical targets in leiomyosarcoma. British Journal of Cancer, 2017, 117, 1787-1797.	6.4	30
35	Heterogeneity in sarcoma cell lines reveals enhanced motility of tetraploid versus diploid cells. Oncotarget, 2017, 8, 16669-16689.	1.8	15
36	RNA sequencing validation of the Complexity INdex in SARComas prognostic signature. European Journal of Cancer, 2016, 57, 104-111.	2.8	66

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37	Heterogeneous Mechanisms of Secondary Resistance and Clonal Selection in Sarcoma during Treatment with Nutlin. PLoS ONE, 2015, 10, e0137794.	2.5	12
38	Differential motif enrichment analysis of paired ChIP-seq experiments. BMC Genomics, 2014, 15, 752.	2.8	23
39	Genome-wide *in silico* prediction of gene expression. Bioinformatics, 2012, 28, 2789-2796.	4.1	50