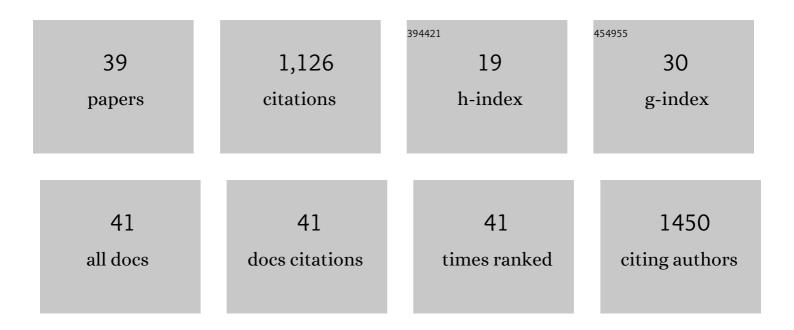
Tom Lesluyes

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Signatures of copy number alterations in human cancer. Nature, 2022, 606, 984-991.	27.8	154
2	A pan-cancer compendium of chromosomal instability. Nature, 2022, 606, 976-983.	27.8	111
3	RNA sequencing validation of the Complexity INdex inÂSARComas prognostic signature. European Journal of Cancer, 2016, 57, 104-111.	2.8	66
4	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
5	Alternative PDGFD rearrangements in dermatofibrosarcomas protuberans without PDGFB fusions. Modern Pathology, 2018, 31, 1683-1693.	5.5	56
6	An integrative analysis of the age-associated multi-omic landscape across cancers. Nature Communications, 2021, 12, 2345.	12.8	54
7	Genome-wide <i>in silico</i> prediction of gene expression. Bioinformatics, 2012, 28, 2789-2796.	4.1	50
8	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
9	Recurrent <i>TRIO</i> Fusion in Nontranslocation–Related Sarcomas. Clinical Cancer Research, 2017, 23, 857-867.	7.0	41
10	Specific immune landscapes and immune checkpoint expressions in histotypes and molecular subtypes of sarcoma. Oncolmmunology, 2020, 9, 1792036.	4.6	31
11	Expression and role of TYRO3 and AXL as potential therapeutical targets in leiomyosarcoma. British Journal of Cancer, 2017, 117, 1787-1797.	6.4	30
12	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
13	<i>GREB1â€CTNNB1</i> fusion transcript detected by RNAâ€sequencing in a uterine tumor resembling ovarian sex cord tumor (UTROSCT): A novel <i>CTNNB1</i> rearrangement. Genes Chromosomes and Cancer, 2019, 58, 155-163.	2.8	30
14	Genomic and transcriptomic comparison of post-radiation versus sporadic sarcomas. Modern Pathology, 2019, 32, 1786-1794.	5.5	25
15	The CINSARC signature as a prognostic marker for clinical outcome in multiple neoplasms. Scientific Reports, 2017, 7, 5480.	3.3	24
16	Vnn1 pantetheinase limits the Warburg effect and sarcoma growth by rescuing mitochondrial activity. Life Science Alliance, 2018, 1, e201800073.	2.8	24
17	Differential motif enrichment analysis of paired ChIP-seq experiments. BMC Genomics, 2014, 15, 752.	2.8	23
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	CINSARC signature as a prognostic marker for clinical outcome in sarcomas and beyond. Genes Chromosomes and Cancer, 2019, 58, 124-129.	2.8	23
20	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
21	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
22	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
23	Genome remodeling upon mesenchymal tumor cell fusion contributes to tumor progression and metastatic spread. Oncogene, 2020, 39, 4198-4211.	5.9	19
24	Heterogeneity in sarcoma cell lines reveals enhanced motility of tetraploid versus diploid cells. Oncotarget, 2017, 8, 16669-16689.	1.8	15
25	Recurrent DMD Deletions Highlight Specific Role of Dp71 Isoform in Soft-Tissue Sarcomas. Cancers, 2019, 11, 922.	3.7	13
26	The Nanocind Signature Is an Independent Prognosticator of Recurrence and Death in Uterine Leiomyosarcomas. Clinical Cancer Research, 2020, 26, 855-861.	7.0	13
27	Heterogeneous Mechanisms of Secondary Resistance and Clonal Selection in Sarcoma during Treatment with Nutlin. PLoS ONE, 2015, 10, e0137794.	2.5	12
28	LIX1 regulates YAP activity and controls gastrointestinal cancer cell plasticity. Journal of Cellular and Molecular Medicine, 2020, 24, 9244-9254.	3.6	11
29	ATRX Alteration Contributes to Tumor Growth and Immune Escape in Pleomorphic Sarcomas. Cancers, 2021, 13, 2151.	3.7	10
30	Cell–cell fusion of mesenchymal cells with distinct differentiations triggers genomic and transcriptomic remodelling toward tumour aggressiveness. Scientific Reports, 2020, 10, 21634.	3.3	9
31	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
32	A Global and Integrated Analysis of CINSARC-Associated Genetic Defects. Cancer Research, 2020, 80, 5282-5290.	0.9	8
33	Expression and prognostic significance of PDGF ligands and receptors across soft tissue sarcomas. ESMO Open, 2021, 6, 100037.	4.5	8
34	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
35	<scp>CINSARC</scp> in highâ€risk soft tissue sarcoma patients treated with neoadjuvant chemotherapy: Results from the <scp>ISGâ€6TS</scp> 1001 study. Cancer Medicine, 2023, 12, 1350-1357.	2.8	7
36	Tetraploidization of Immortalized Myoblasts Induced by Cell Fusion Drives Myogenic Sarcoma Development with DMD Deletion. Cancers, 2020, 12, 1281.	3.7	4

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37	RCBTB1 Deletion Is Associated with Metastatic Outcome and Contributes to Docetaxel Resistance in Nontranslocation-Related Pleomorphic Sarcomas. Cancers, 2019, 11, 81.	3.7	3
38	E3 ubiquitin ligase HECTD2 mediates melanoma progression and immune evasion. Oncogene, 2021, 40, 5567-5578.	5.9	3
39	Impact of preoperative treatment on the CINSARC prognostic signature: translational research results from aAphaseA1 trial of the German Interdisciplinary Sarcoma Group (GISG 03). Strahlentherapie Und Onkologie, 2020, 196, 280-285.	2.0	1