Jan HojnÃ½

List of Publications by Year
in descending order

19	350	933447 10	839539 18
papers	citations	h-index	g-index

19	19	19	627
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Uterine cellular leiomyomas are characterized by common HMGA2 aberrations, followed by chromosome 1p deletion and MED12 mutation: morphological, molecular, and immunohistochemical study of 52 cases. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2022, 480, 281-291.	2.8	10
2	Comprehensive quantitative analysis of alternative splicing variants reveals the HNF1B mRNA splicing pattern in various tumour and non-tumour tissues. Scientific Reports, 2022, 12, 199.	3.3	2
3	Desmoplastic Small Round Cell Tumor of the Uterus: A Report of Molecularly Confirmed Case with EWSR1-WT1 Fusion. Diagnostics, 2022, 12, 1184.	2.6	2
4	A comprehensive analysis of the expression, epigenetic and genetic changes of HNF1B and ECI2 in 122Âcases of highâ€‘grade serous ovarian carcinoma. Oncology Letters, 2021, 21, 185.	1.8	4
5	Leiomyoma with Bizarre Nuclei: a Study of 108 Cases Focusing on Clinicopathological Features, Morphology, and Fumarate Hydratase Alterations. Pathology and Oncology Research, 2020, 26, 1527-1537.	1.9	22
6	Ovarian mesonephric-like adenocarcinoma arising in serous borderline tumor: a case report with complex morphological and molecular analysis. Diagnostic Pathology, 2020, 15, 91.	2.0	35
7	Analysis of expression, epigenetic, and genetic changes of HNF1B in 130 kidney tumours. Scientific Reports, 2020, 10, 17151.	3.3	5
8	HNF1B, EZH2 and ECI2 in prostate carcinoma. Molecular, immunohistochemical and clinico-pathological study. Scientific Reports, 2020, 10, 14365.	3.3	6
9	Microscopic extraovarian sex cord proliferation: report of a case with bilateral Fallopian tube involvement and a comprehensive molecular analysis. Polish Journal of Pathology, 2020, 71, 175-180.	0.3	2
10	Expression, Epigenetic, and Genetic Changes of HNF1B in Colorectal Lesions: an Analysis of 145 Cases. Pathology and Oncology Research, 2020, 26, 2337-2350.	1.9	7
11	Results of targeted next-generation sequencing in children with cystic kidney diseases often change the clinical diagnosis. PLoS ONE, 2020, 15, e0235071.	2.5	12
12	Identification of novel HNF1B mRNA splicing variants and their qualitative and semi-quantitative profile in selected healthy and tumour tissues. Scientific Reports, 2020, 10, 6958.	3.3	5
13	Synchronous endometrioid endometrial and ovarian carcinomas are biologically related: A clinicoâ€‘pathological and molecular (next generation sequencing) study of 22ï¿½cases. Oncology Letters, 2019, 17, 2207-2214.	1.8	12
14	Identification of deleterious germline CHEK2 mutations and their association with breast and ovarian cancer. International Journal of Cancer, 2019, 145, 1782-1797.	5.1	62
15	A comprehensive evaluation of pathogenic mutations in primary cutaneous melanomas, including the identification of novel loss-of-function variants. Scientific Reports, 2019, 9, 17050.	3.3	42
16	Germline mutation in the TP53 gene in uveal melanoma. Scientific Reports, 2018, 8, 7618.	3.3	13
17	Multiplex PCR and NGS-based identification of mRNA splicing variants: Analysis of BRCA1 splicing pattern as a model. Gene, 2017, 637, 41-49.	2.2	43
18	Association of Germline CHEK2 Gene Variants with Risk and Prognosis of Non-Hodgkin Lymphoma. PLoS ONE, 2015, 10, e0140819.	2.5	31

#	Article	IF	Citations
19	Expression of human BRCA1Î”17â€“19 alternative splicing variant with a truncated BRCT domain in MCF-7 cells results in impaired assembly of DNA repair complexes and aberrant DNA damage response. Cellular Signalling, 2013, 25, 1186-1193.	3.6	35