W Patrick Devine

List of Publications by Year
in descending order

15	488	1163117 8	1199594 12
papers	citations	h-index	g-index

17	17	17	901
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Early patterning and specification of cardiac progenitors in gastrulating mesoderm. ELife, 2014, 3, .	6.0	202
2	Modeling Human TBX5 Haploinsufficiency Predicts Regulatory Networks for Congenital Heart Disease. Developmental Cell, 2021, 56, 292-309.e9.	7.0	63
3	NTRK fusion cervical sarcoma: a report of three cases, emphasising morphological and immunohistochemical distinction from other uterine sarcomas, including adenosarcoma. Histopathology, 2020, 77, 100-111.	2.9	61
4	Identification of high-risk human papillomavirus and Rb/E2F pathway genomic alterations in mutually exclusive subsets of colorectal neuroendocrine carcinoma. Modern Pathology, 2019, 32, 290-305.	5.5	45
5	Next-Generation Sequencing of Retinoblastoma Identifies Pathogenic Alterations beyond RB1 Inactivation That Correlate with Aggressive Histopathologic Features. Ophthalmology, 2020, 127, 804-813.	5.2	39
6	Practical roles for molecular diagnostic testing in ovarian adult granulosa cell tumour, Sertoliâ€“Leydig cell tumour, microcystic stromal tumour and their mimics. Histopathology, 2020, 76, 11-24.	2.9	25
7	New cases that expand the genotypic and phenotypic spectrum of Congenital NAD Deficiency Disorder. Human Mutation, 2021, 42, 862-876.	2.5	16
8	Exome sequencing vs targeted gene panels for the evaluation of nonimmune hydrops fetalis. American Journal of Obstetrics and Gynecology, 2022, 226, 128.e1-128.e11.	1.3	14
9	A novel reporter allele for monitoringDll4expression within the embryonic and adult mouse. Biology Open, 2018, 7, .	1.2	10
10	Tumor and Constitutional Sequencing for Neurofibromatosis Type 1. JCO Precision Oncology, 2022, 6, e2100540.	3.0	4
11	Expanding the phenotype of males with OFD1 pathogenic variants-a case report and literature review. European Journal of Medical Genetics, 2022, , 104496.	1.3	2
12	Hydra: A mixture modeling framework for subtyping pediatric cancer cohorts using multimodal gene expression signatures. PLoS Computational Biology, 2020, 16, e1007753.	3.2	1
13	Title is missing!. , 2020, 16, e1007753.		0
14	Title is missing!. , 2020, 16, e1007753.		0
15	Title is missing!. , 2020, 16, e1007753.		0