Netta MÃ¤kinen

List of Publications by Year
in descending order

22 papers	1,994 citations	471509 17 h-index	713466 21 g-index
22 all docs	22 docs citations	22 times ranked	2155 citing authors

#	Article	IF	Citations
1	Comparison of 2SC, AKR1B10, and FH Antibodies as Potential Biomarkers for FH-deficient Uterine Leiomyomas. American Journal of Surgical Pathology, 2022, 46, 537-546.	3.7	8
2	Genomic Evolution in a Patient With Lung Adenocarcinoma With a Germline EGFR T790M Mutation. JTO Clinical and Research Reports, 2021, 2, 100146.	1.1	0
3	Deficient H2A.Z deposition is associated with genesis of uterine leiomyoma. Nature, 2021, 596, 398-403.	27.8	53
4	Parity associates with chromosomal damage in uterine leiomyomas. Nature Communications, 2021, 12, 5448.	12.8	2
5	Patterns of chromosome 18 loss of heterozygosity in multifocal ileal neuroendocrine tumors. Genes Chromosomes and Cancer, 2020, 59, 535-539.	2.8	16
6	Exome-wide somatic mutation characterization of small bowel adenocarcinoma. PLoS Genetics, 2018, 14, e1007200.	3.5	62
7	Somatic MED12 Nonsense Mutation Escapes mRNA Decay and Reveals a Motif Required for Nuclear Entry. Human Mutation, 2017, 38, 269-274.	2.5	20
8	Global metabolomic profiling of uterine leiomyomas. British Journal of Cancer, 2017, 117, 1855-1864.	6.4	29
9	Characterization of MED12, HMGA2, and FH alterations reveals molecular variability in uterine smooth muscle tumors. Molecular Cancer, 2017, 16, 101.	19.2	74
10	Exome Sequencing of Uterine Leiomyosarcomas Identifies Frequent Mutations in TP53, ATRX, and MED12. PLoS Genetics, 2016, 12, e1005850.	3.5	94
11	Somatic MED12 mutations in prostate cancer and uterine leiomyomas promote tumorigenesis through distinct mechanisms. Prostate, 2016, 76, 22-31.	2.3	33
12	MED12 mutations and FH inactivation are mutually exclusive in uterine leiomyomas. British Journal of Cancer, 2016, 114, 1405-1411.	6.4	43
13	Integrated data analysis reveals uterine leiomyoma subtypes with distinct driver pathways and biomarkers. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1315-1320.	7.1	166
14	Clonally related uterine leiomyomas are common and display branched tumor evolution. Human Molecular Genetics, 2015, 24, 4407-4416.	2.9	19
15	Exomic landscape of MED12 mutationâ€negative and â€positive uterine leiomyomas. International Journal of Cancer, 2014, 134, 1008-1012.	5.1	36
16	Genomics of uterine leiomyomas:Âinsights from high-throughput sequencing. Fertility and Sterility, 2014, 102, 621-629.	1.0	164
17	MED12 mutation frequency in unselected sporadic uterine leiomyomas. Fertility and Sterility, 2014, 102, 1137-1142.	1.0	62
18	Uterine Leiomyoma-Linked MED12 Mutations Disrupt Mediator-Associated CDK Activity. Cell Reports, 2014, 7, 654-660.	6.4	125

#	Article	IF	Citations
19	Characterization of Uterine Leiomyomas by Whole-Genome Sequencing. New England Journal of Medicine, 2013, 369, 43-53.	27.0	280
20	MED12 exon 2 mutations in histopathological uterine leiomyoma variants. European Journal of Human Genetics, 2013, 21, 1300-1303.	2.8	66
21	MED12 , the Mediator Complex Subunit 12 Gene, Is Mutated at High Frequency in Uterine Leiomyomas. Science, 2011, 334, 252-255.	12.6	547
22	MED12 exon 2 mutations are common in uterine leiomyomas from South African patients. Oncotarget, 2011, 2, 966-969.	1.8	95