Andreas Laner

List of Publications by Year
in descending order

12	407	1163117 8	1199594 12
papers	citations	h-index	g-index

12	12	12	971
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Solving the genetic aetiology of hereditary gastrointestinal tumour syndromesâ€“ a collaborative multicentre endeavour within the project Solve-RD. European Journal of Medical Genetics, 2022, 65, 104475.	1.3	2
2	Long-term chemoprevention in patients with adenomatous polyposis coli: an observational study. Familial Cancer, 2022, 21, 463-472.	1.9	4
3	Splicing analyses for variants in MMR genes: best practice recommendations from the European Mismatch Repair Working Group. European Journal of Human Genetics, 2022, 30, 1051-1059.	2.8	7
4	A mosaic PIK3CA variant in a young adult with diffuse gastric cancer: case report. European Journal of Human Genetics, 2021, 29, 1354-1358.	2.8	9
5	Solving patients with rare diseases through programmatic reanalysis of genome-phenome data. European Journal of Human Genetics, 2021, 29, 1337-1347.	2.8	34
6	Targeted deep-intronic sequencing in a cohort of unexplained cases of suspected Lynch syndrome. European Journal of Human Genetics, 2020, 28, 597-608.	2.8	10
7	Prevalence of CNV-neutral structural genomic rearrangements in MLH1, MSH2, and PMS2 not detectable in routine NGS diagnostics. Familial Cancer, 2020, 19, 161-167.	1.9	11
8	Analysis of 3297 individuals suggests that the pathogenic germline 5â€²-UTR variant BRCA1 c.-107Aâ€‰>â€‰T is not common in south-east Germany. Familial Cancer, 2020, 19, 211-213.	1.9	6
9	Full-length transcript amplification and sequencing as universal method to test mRNA integrity and biallelic expression in mismatch repair genes. European Journal of Human Genetics, 2019, 27, 1808-1820.	2.8	16
10	Comprehensive analysis of the MLH1 promoter region in 480 patients with colorectal cancer and 1150 controls reveals new variants including one with a heritable constitutional MLH1 epimutation. Journal of Medical Genetics, 2018, 55, 240-248.	3.2	23
11	Exome Sequencing Identifies Biallelic MSH3 Germline Mutations as a Recessive Subtype of Colorectal Adenomatous Polyposis. American Journal of Human Genetics, 2016, 99, 337-351.	6.2	198
12	Biallelic MUTYH mutations can mimic Lynch syndrome. European Journal of Human Genetics, 2014, 22, 1334-1337.	2.8	87