

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

AMBER

RRID:SCR_027131

Type: Tool

Proper Citation

AMBER (RRID:SCR_027131)

Resource Information

URL: <https://github.com/hartwigmedical/hmftools/tree/master/amber>

Proper Citation: AMBER (RRID:SCR_027131)

Description: Software tool to generate tumor BAF file for use in PURPLE from provided VCF of likely heterozygous SNP sites.

Resource Type: software application, software resource

Keywords: generate tumor BAF file, VCF, heterozygous SNP sites,

Availability: Free, Available for download, Freely available,

Resource Name: AMBER

Resource ID: SCR_027131

License: GNU GPL v2

Record Creation Time: 20250703T065557+0000

Record Last Update: 20260904T001132+0000

Ratings and Alerts

No rating or validation information has been found for AMBER.

No alerts have been found for AMBER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Micoli G, et al. (2025) Decoding the Genomic and Functional Landscape of Emerging Subtypes in Ovarian Cancer. Cancer discovery, 15(11), 2262.

Ariotta V, et al. (2023) H&E image analysis pipeline for quantifying morphological features. Journal of pathology informatics, 14, 100339.