

# Resource Summary Report

Generated by [dkNET](#) on Aug 12, 2026

## AMBER

RRID:SCR\_027131

Type: Tool

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### Proper Citation

AMBER (RRID:SCR\_027131)

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### 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:** 20260810T040938+0000

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### Ratings and Alerts

No rating or validation information has been found for AMBER.

No alerts have been found for AMBER.

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### 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 [dkNET](#) .

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.