Resource Summary Report

Generated by NIF on Sep 2, 2026

APOLLOH

RRID:SCR_006648
Type: Tool

Proper Citation

APOLLOH (RRID:SCR_006648)

Resource Information

URL: http://compbio.bccrc.ca/software/apolloh/

Proper Citation: APOLLOH (RRID:SCR_006648)

Description: A hidden Markov model (HMM) for predicting somatic loss of heterozygosity and allelic imbalance in whole tumour genome sequencing data.

Abbreviations: APOLLOH

Resource Type: software resource

Resource Name: APOLLOH

Resource ID: SCR_006648

Alternate IDs: OMICS_00306

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260829T182241+0000

Ratings and Alerts

No rating or validation information has been found for APOLLOH.

No alerts have been found for APOLLOH.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Barnabas GD, et al. (2025) Proteomics and personalized PDX models identify treatment for a progressive malignancy within an actionable timeframe. EMBO molecular medicine, 17(4), 625.

Tsang ES, et al. (2023) Homologous recombination deficiency signatures in gastrointestinal and thoracic cancers correlate with platinum therapy duration. NPJ precision oncology, 7(1), 31.

Titmuss E, et al. (2023) Immune Activation following Irbesartan Treatment in a Colorectal Cancer Patient: A Case Study. International journal of molecular sciences, 24(6).

Reisle C, et al. (2022) A platform for oncogenomic reporting and interpretation. Nature communications, 13(1), 756.

Tessier-Cloutier B, et al. (2022) The impact of whole genome and transcriptome analysis (WGTA) on predictive biomarker discovery and diagnostic accuracy of advanced malignancies. The journal of pathology. Clinical research, 8(4), 395.

Lavoie JM, et al. (2022) Whole-genome and transcriptome analysis of advanced adrenocortical cancer highlights multiple alterations affecting epigenome and DNA repair pathways. Cold Spring Harbor molecular case studies, 8(3).

Majounie E, et al. (2020) Fluorouracil sensitivity in a head and neck squamous cell carcinoma with a somatic DPYD structural variant. Cold Spring Harbor molecular case studies, 6(1).

Thibodeau ML, et al. (2019) Base excision repair deficiency signatures implicate germline and somatic MUTYH aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. Cold Spring Harbor molecular case studies, 5(2).

Williamson LM, et al. (2019) Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. Cold Spring Harbor molecular case studies, 5(3).

Chun HE, et al. (2019) Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. Cell reports, 29(8), 2338.

Thibodeau ML, et al. (2018) Whole genome and whole transcriptome genomic profiling of a metastatic eccrine porocarcinoma. NPJ precision oncology, 2(1), 8.

Ko JJ, et al. (2018) Whole-genome and transcriptome profiling of a metastatic thyroid-like follicular renal cell carcinoma. Cold Spring Harbor molecular case studies, 4(6).

Boyd AL, et al. (2018) Identification of Chemotherapy-Induced Leukemic-Regenerating Cells Reveals a Transient Vulnerability of Human AML Recurrence. Cancer cell, 34(3), 483.

Wong HL, et al. (2018) Molecular characterization of metastatic pancreatic neuroendocrine tumors (PNETs) using whole-genome and transcriptome sequencing. Cold Spring Harbor molecular case studies, 4(1).

Grewal JK, et al. (2017) Detection and genomic characterization of a mammary-like adenocarcinoma. Cold Spring Harbor molecular case studies, 3(6).

Thibodeau ML, et al. (2017) Genomic profiling of pelvic genital type leiomyosarcoma in a woman with a germline CHEK2:c.1100delC mutation and a concomitant diagnosis of metastatic invasive ductal breast carcinoma. Cold Spring Harbor molecular case studies, 3(5).

Parker JD, et al. (2016) Molecular etiology of an indolent lymphoproliferative disorder determined by whole-genome sequencing. Cold Spring Harbor molecular case studies, 2(2), a000679.

Grinshtein N, et al. (2016) Small molecule epigenetic screen identifies novel EZH2 and HDAC inhibitors that target glioblastoma brain tumor-initiating cells. Oncotarget, 7(37), 59360.

Taylor KR, et al. (2014) Recurrent activating ACVR1 mutations in diffuse intrinsic pontine glioma. Nature genetics, 46(5), 457.

Ha G, et al. (2014) TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. Genome research, 24(11), 1881.