

Resource Summary Report

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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: 20260725T190624+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 [nidm-terms](#) .

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).

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

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).

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).

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).

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.

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.