

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

HPeak

RRID:SCR_010859

Type: Tool

Proper Citation

HPeak (RRID:SCR_010859)

Resource Information

URL: <http://www.sph.umich.edu/csg/qin/HPeak/Readme.html>

Proper Citation: HPeak (RRID:SCR_010859)

Description: A Hidden Markov Model-based algorithm for the purpose of defining genome-wide ChIP-enriched peaks in the human genome using short sequence reads.

Abbreviations: HPeak

Synonyms: HPeak: An HMM-based algorithm for defining read-enriched regions from massive parallel sequencing data

Resource Type: software resource

Resource Name: HPeak

Resource ID: SCR_010859

Alternate IDs: OMICS_00444

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260725T191025+0000

Ratings and Alerts

No rating or validation information has been found for HPeak.

No alerts have been found for HPeak.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Collins JE, et al. (2015) High-throughput and quantitative genome-wide messenger RNA sequencing for molecular phenotyping. BMC genomics, 16(1), 578.