

# Resource Summary Report

Generated by SPARC SAWG on Sep 12, 2026

## BPPH

RRID:SCR\_009136

Type: Tool

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### Proper Citation

BPPH (RRID:SCR\_009136)

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### Resource Information

**URL:** <http://www.csif.ucdavis.edu/~gusfield/bpph.html>

**Proper Citation:** BPPH (RRID:SCR\_009136)

**Description:** Software application for inferring haplotypes from genotypes to determine if there are resulting haplotypes that fit a tree model (i.e. a perfect phylogeny, a coalescent). In population genetic terms, BPPH determines whether a set of SNP genotypes can be explained by haplotype pairs that could have evolved on a coalescent under the no-recombination, infinite sites model. (entry from Genetic Analysis Software)

**Abbreviations:** BPPH

**Synonyms:** Berkeley method for Perfect Phylogeny Haplotyping

**Resource Type:** software application, software resource

**Keywords:** gene, genetic, genomic

**Resource Name:** BPPH

**Resource ID:** SCR\_009136

**Alternate IDs:** nlx\_154251

**Record Creation Time:** 20220129T080251+0000

**Record Last Update:** 20260912T200240+0000

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### Ratings and Alerts

No rating or validation information has been found for BPPH.

No alerts have been found for BPPH.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.