

# Package ‘phastCons100way.UCSC.hg19’

April 16, 2014

**Title** UCSC phastCons conservation scores

**Version** 1.1.0

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**License** Artistic-2.0

**Description** UCSC phastCons conservation scores from alignments of 100 vertebrate species

**Maintainer** Robert Castelo <robert.castelo@upf.edu>

**Depends** R (>= 3.0.0), VariantFiltering

**Imports** utils, IRanges, GenomicRanges, BSgenome

**biocViews** AnnotationData, Genetics, PhastConsDb, Homo\_sapiens

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phastCons100way.UCSC.hg19-package  
*Annotation package for phastCons scores from UCSC calculated from  
100 vertebrate species*

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## Description

This annotation package stores phastCons conservation scores from UCSC for the human genome (hg19), calculated from genome-wide alignments from 100 vertebrate species. The data is stored in the form of a RleList object and is loaded automatically in the as an object of class PhastConsDb. The name of the exposed object matches the name of the package and part of the filename that contained the data imported into the package. The class definition and methods to access MafDb objects are found in the [VariantFiltering](#) software package.

## Format

[phastCons100way.UCSC.hg19](#) PhastConsDb object containing phastCons conservation scores from UCSC for the human genome

**Author(s)**

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**Source**

UCSC Genome Browser (URL: <http://genome.ucsc.edu>) [November, 2013, accessed]

**See Also**

[PhastConsDb-class VariantFiltering](#)

**Examples**

```
library(GenomicRanges)
library(phastCons100way.UCSC.hg19)

ls("package:phastCons100way.UCSC.hg19")

phastCons100way.UCSC.hg19
scores(phastCons100way.UCSC.hg19,
       GRanges(seqnames="chr7", IRanges(start=117232380, width=5)))
```

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