

# Package ‘AlphaMissense.v2023.hg38’

December 10, 2025

**Type** Package

**Title** AlphaMissense v2023 Pathogenicity Scores AnnotationHub Resource  
Metadata for hg38

**Version** 3.18.2

**Encoding** UTF-8

**Description** Store Google DeepMind AlphaMissense v2023 hg38 pathogenicity scores AnnotationHub Resource Metadata. Provide provenance and citation information for Google DeepMind AlphaMissense v2023 hg38 pathogenicity score AnnotationHub resources. Illustrate in a vignette how to access those resources.

**VignetteBuilder** knitr

**License** Artistic-2.0

**Depends** GenomicScores, AnnotationHub

**Suggests** knitr, rmarkdown, BiocStyle

**biocViews** AnnotationData, PackageType, AnnotationHub, Organism,  
Homo\_sapiens

**organism** Homo sapiens

**provider** Google DeepMind

**provider\_version** v2023

**git\_url** <https://git.bioconductor.org/packages/AlphaMissense.v2023.hg38>

**git\_branch** devel

**git\_last\_commit** 67a154f

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.23

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**Author** Robert Castelo [aut, cre]

**Maintainer** Robert Castelo <[robert.castelo@upf.edu](mailto:robert.castelo@upf.edu)>

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AlphaMissense.v2023.hg38

*AlphaMissense Pathogenicity Scores AnnotationHub Resource Metadata for Homo sapiens (hg38)*

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### Description

This annotation package stores AlphaMissense v2023 pathogenicity scores AnnotationHub resource metadata for Homo sapiens, genome version hg38.

### Note

This data package was made from resources at Google DeepMind based on version v2023.

### Author(s)

Robert Castelo <robert.castelo@upf.edu> [cre]

### See Also

[GenomicScores](#)

### Examples

```
library(GenomicScores)

gsco <- getGScores("AlphaMissense.v2023.hg38")
name(gsco)
type(gsco)
provider(gsco)
providerVersion(gsco)
organism(gsco)
referenceGenome(gsco)
seqlevelsStyle(gsco)
seqinfo(gsco)
head(seqnames(gsco))
head(seqlengths(gsco))
citation(gsco)
```

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