

# Package: AHMassBank (via r-universe)

July 13, 2024

**Type** Package

**Title** MassBank Annotation Resources for AnnotationHub

**Version** 1.5.0

**Encoding** UTF-8

**Depends** R (>= 4.2)

**Imports** AnnotationHubData (>= 1.5.24)

**Suggests** BiocStyle, knitr, AnnotationHub (>= 2.7.13), rmarkdown, methods, CompoundDb (>= 1.1.4)

**Description** Supplies AnnotationHub with MassBank metabolite/compound annotations bundled in CompDb SQLite databases. CompDb SQLite databases contain general compound annotation as well as fragment spectra representing fragmentation patterns of compounds' ions. MassBank data is retrieved from <https://massbank.eu/MassBank> and processed using helper functions from the CompoundDb Bioconductor package into redistributable SQLite databases.

**VignetteBuilder** knitr

**License** Artistic-2.0

**LazyLoad** yes

**BugReports** <https://github.com/jorainer/AHMassBank/issues>

**URL** <https://github.com/jorainer/AHMassBank>

**biocViews** MassSpectrometry, AnnotationHubSoftware

**Roxygen** list(markdown=TRUE)

**RoxygenNote** 7.2.3

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/AHMassBank>

**RemoteRef** HEAD

**RemoteSha** ba4122730edb6cb4d6ade17393ccc64b41e68efd

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