

# Package ‘rRDPData’

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**Title** Database for the Default RDP Classifier

**Description** Database used by the default RDP Classifier

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**biocViews** SequencingData, MicrobiomeData

**Depends** rRDP

**SystemRequirements** Java

**License** GPL-2

**git\_url** <https://git.bioconductor.org/packages/rRDPData>

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16SrRNA	<i>RDP Classifier Model for RDP 16S rRNA Trainingset No 9</i>
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### Description

Model data for the RDP classifier trained with the RDP 16S rRNA Trainingset No 9. This is the default model data used by RDP.

### Details

`rdp()` creates a default classifier using this data set.

The model data is stored in `system.file("16srrna", package="rRDPData")` and consists of several files in proprietary format used by the RDP software. Since RDP is a naive Bayes classifier the data mainly contain conditional word (8-mer) probabilities.

## References

RDP Classifier <http://sourceforge.net/projects/rdp-classifier/>

## Examples

```
### Use the RDP with the default classifier model data
seq <- readRNAStringSet(system.file("examples/RNA_example.fasta",
package="rRDP"))

## shorten names
names(seq) <- sapply(strsplit(names(seq), " "), "[", 1)
seq

## use RDP for classification
pred <- predict(rdp(), seq)
pred

attr(pred, "confidence")
```

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\*Topic **model**

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