

# Find\_A\_Gene\_Project

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[Q7] Generate a sequence identity based heatmap of your aligned sequences using R.

```
library(bio3d)
```

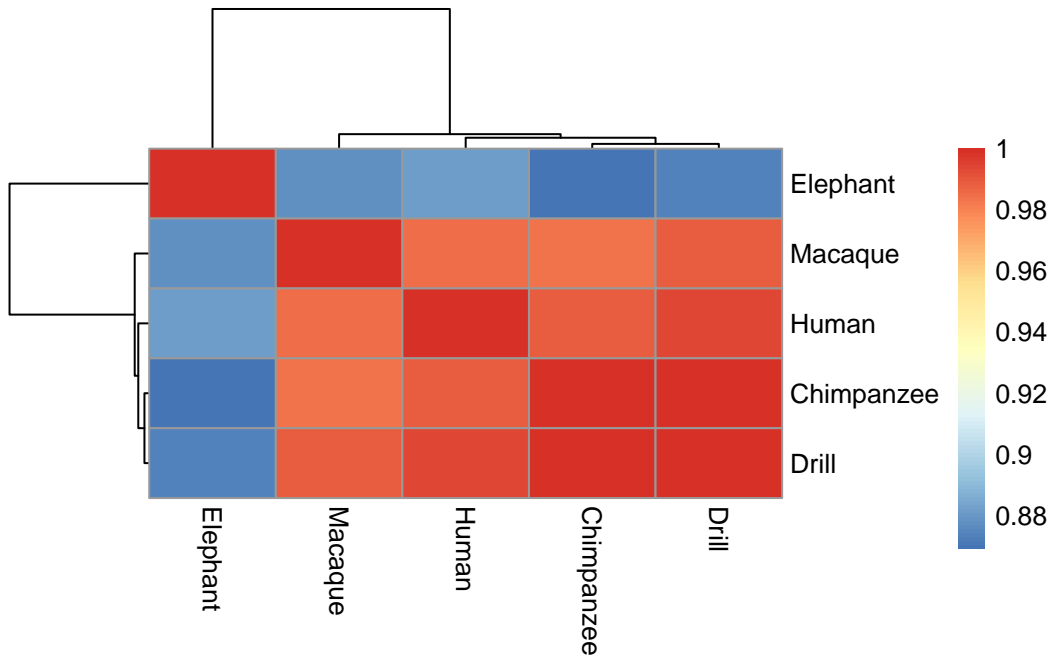
```
aligned <- read.fasta("muscle-I20250311-043109-0890-73887014-p1m.fa")
```

```
id_matrix <- seqidentity(aligned)
```

This map is created using the pheatmap package, creating a more detailed heatmap:

```
library(pheatmap)
```

```
pheatmap(id_matrix)
```



This map is created just using the heatmap function:

```
heatmap(id_matrix)
```

