

**Hands-on exercises** to the lecture „Modern Methods in Drug Discovery“ WS19/20

1. The common degu (*Octodon degus*) develops diabetes quickly upon sugar containing nutrients. Therefore it has been suggest as potential model organism for the study of diabetes and corresponding drugs that i.e. influence insulin.

Retrieve the amino acid sequences (FASTA format) of insulin of the following species from UniProt ([www.uniprot.org](http://www.uniprot.org)) and perform a multiple alignment with Clustal Omega ([www.ebi.ac.uk/Tools/msa/clustalo](http://www.ebi.ac.uk/Tools/msa/clustalo)). Have a look at the clustering. Use the sequence alignment to argue if the degu would be a suitable model organism or not.

human (homo sapiens) INS\_HUMAN  
pig (sus scrofa) INS\_PIG  
degu (Octodon degus) INS\_OCTDE  
chinese hamster (Cricetulus longicaudatus) INS\_CRILO  
chinchilla (chinchilla chinchilla)  
rabbit (oryctolagus cuniculus)  
North American opossum (Didelphis voirginiana) INS\_DIDVI  
mouse (mus musculus) INS1\_MOUSE  
rat (rattus norvegicus) INS1\_RAT  
chimpanzee (pan troglodytes)  
Lowland gorilla (gorilla gorilla gorilla)  
guinea pig (cavia porcellus)  
dog (canis familiaris)  
bovine (bos taurus)  
sheep (ovis aries)

Have a look at the phylogenetic tree (tab above the multiple sequence alignment output).

Which species are closest related to human?

Argue upon the sequence alignment if the degu would be a suitable model organism or not, based on the multiple sequence alignment?