**<Pre-step information>**

*This considers {mouse and rat} as the [examined organisms].*

1. We initially perform the {sequence alignment} [stage]. Generate [sequence alignment] for {GluN1}, {GluN2}, and {GluN3}. {MAAFT Server}[[1]](#footnote-1) is used as the alignment [software]. Apply the {default} [settings]. This assumes that [version] {7} is used.
2. Next, perform {alignment refinement} [stage]. {GLProbs} [software] is used for this purpose. Apply {2} [consistency transformation passes]. Subsequently, apply {100} [iterative refinement passes].
3. A {manual sequence alignment} [stage] is later needed. For this alignment, use [base template] from the {result of previous step}. The first [template structure] uses {GluN2DLBD}. GluN3DLBD has [PDB ID] {3OEK}. The second [template structure] uses {GluN3BLBD}. GluN3BLBD has [PDB ID] {2RCA}. Use {BioLuminate package} [software] for this alignment. This procedure is necessary to account for insertions and deletions present in the template structures.

1. Katoh, K., Rozewicki, J. & Yamada, K. D. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform, https://doi.org/10.1093/bib/bbx108 [↑](#footnote-ref-1)