Our "must have" list with essential for replication checkpoints

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1. Give link to the common popset

Say we have 95 sequences in our research

2. Mark the settings, which were used in programmes

Skip this step, cause it is obvious

3. Accept trimming as a pre-analyse method

Say not a single word about it

4. Say after the alignment description that the sequences from the previous study were added

Immediately specify all the data we are working with

5. Describe which subsets the data is divided into

Dedicate one sentence to this and not to tell what tools were used

IN THIS CHECKLIST, BOLD TYPE INDICATES WHAT IS EXPECTED WHEN REPRODUCING AN ARTICLE, AND SMALLER TYPE INDICATES WHAT WE ENCOUNTERED WHEN STUDYING THESE ARTICLES.