

Extracting Selected as MSA

It is possible to extract a subalignment and save it as new multiple sequence alignment (MSA).

Select a subalignment and choose the *Export Save subalignment* item in the *Actions* main menu or in the context menu. The following dialog appears:

Save selection as subalignment

Columns from to

Selected sequences

- ☒ Phaneroptera_falcata
- ☒ Isophya_altaica_EF540820
- ☒ Bicolorana_bicolor_EF540830
- ☒ Roeseliana_roeseli
- ☒ Montana_montana
- ☒ Gampsocleis_sedakovii_EF540828
- ☒ Deracantha_deracantoides_EF540
- ☒ Tettigonia_viridissima
- ☒ Conocephalus_discolor
- ☒ Conocephalus_sp.

File name

File format to use

☒ Add to project

Specify the name and format of the new MSA file in the *File name* and *File format to use* fields. The currently selected region is extracted by default when you press the *Extract* button.

You can change the columns to be extracted using the *From* and *to* fields. And change the rows to be extracted by checking/unchecking required sequences in the *Selected sequences* list.

Use buttons:

- *Invert selection* — to invert the selection of the sequences.
- *Select all* — to select all sequences.
- *Clear selection* — to clear the selection of all sequences.

The *Add to project* check box specifies to add the MSA file created from the subalignment to the active project.