

Specify Input Parameters

Aligned FASTA file

/tmp/theFile.fasta

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Sequence data type

☒ Nucleotides ☐ Amino Acids

Anchor motif

AGATTA

Anchor position

1750

Loci

1762,1764,1809-1812,1858,1862,1888,1896

Output grouping

2,4,1,1,1

Include ▼

sequence ID pattern

Tutorial