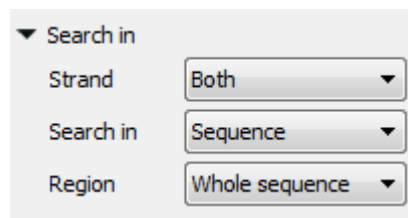


# Search in



▼ Search in

Strand Both ▼

Search in Sequence ▼

Region Whole sequence ▼

In this group you can specify where to search for a pattern: in what region and in which strand (for nucleotide sequences). Also for nucleotide sequences it is possible to search for a pattern on the sequence translations.

*Strand* — for nucleotide sequences only. Specifies on which strand to search for a pattern: *Direct*, *Reverse-complementary* or *Both* strands.

*Search in* — for nucleotide sequences you can select the *Translation* value for this option. In this case the input pattern will be searched in the amino acid translations.

*Region* — specifies the sequence range where to search for a pattern. You can search in the whole sequence, specify a custom region or search in the selected region.