

## A common format for sequences is the **FASTA format**:

For each sequence there is a single line description (e.g. taxon name, clone identity) preceded by the symbol '>'. The second line (after a hard return) is comprised of the sequence - note that this should run contiguously with no hard returns.

Here is an example:

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>LEUCOPHRYS_OUTGROUP
GTTATGATCCTGAAGTTACAACCAATAGCGCAAAGAGCAAGAGTAGGAGATGTATGCGCCTGCAGTGAATAACTTAGGGT
ATATCTGACGTTGAGTAGCTCGGTTCTCGTGAGAAGCGCGATCAATAGATAACCATGTTCTCTGGCTTGGGAGTGCTTGAAG
GCTGTTGGTAGAGAATATTACCTAGGAGGTGGGCGAATTCAGTAGACTAGGGGAATGCAAAGGTGTACTGGGATATTCCTCG
>CAPENSIS_SCL504
GTTATGATCCTGAAGTTACAACCAATAGCGCAAAGAGCAAGGATAGGAGATGTATGGGCTCAAGGCCAATAACCGAGGGTA
TATATAACGTTGAGTAGCTCGGTTCTCGTGAGAAGCGCGATCAATAGATAACCATGTTCTCTGGCTTGGGAGTGCTTGAAGG
CTGTTGGAAGAGAATATTACCTAGGAGGTGGGCGAATTC AATAGACTAGGGGAATGCAAAGGTGTACTGGGATCTTCCTCGT
>CAPENSIS_SCL508
GTTATGATCCTGAAGTTACAACCAATAGCGCAAAGAGCAAGGATAGGAGATGTATGGGNGTCAAGGCCAATAACCGAGGGT
ATATATAACGTTGAGTAGCTCGGTTCTCGTGAGAAGCGCGATCAATAGATAACCATGTTCTCTGGCTTGGGAGTGCTTGAAG
GCTGTTGGAAGAGAATATTACCTAGGAGGTGGGCGAATTC AATAGACTAGGGGAATGCAAAGGTGTACTGGGATCTTCCTCG
>CAPENSIS_SCL107
GTTATGATCCTGAAGTTACAACCAATAGCGCAAAGAGCAAGGATAGGAGATGTATGGGCTCAAGGCCAATAACCGAGGGTA
TATATAACGTTGAGTAGCTCGGTTCTCGTGAGAAGCGCGATCAATAGATAACCATGTTCTCTGGCTTGGGAGTGCTTGAAGG
CTGTTGGAAGAGAATATTACCTAGGAGGTGGGCGAATTC AATAGACTAGGGGAATGCAAAGGTGTACTGGGATCTTCCTCGT
>CAPENSIS_SCL112
GTTATGTTCTGAAGTTACAACCAATAGCGCAAAGAGCAAGGAGTAGGAGATGTATGGGCTCAAGGCCAATAACCGAGGGT
ATATATAACGTTGAGTAGCTCGGTTCTCGTGAGAAGCGCGATCAATAGATAACCATGCTCTCTGGCTTGNGGAGTGCTTGAA
GGCTGTTGGAAGAGAATATTACCTAGGAGGTGGGCGAATTC AATAGACTAGGGGAATGCAAAGGTGTACTGGGATCTTCCTC
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