seqiolite Documentation
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Very simplistic fasta and fastq file reading with minimal dependencies. For a much more thourough sequence reading package check out Biopython's SeqIO module

Contents:

Fasta

Fasta sequence file reading

1.1 FastaFile

Reads fasta formatted files and returns FastaRecords

```
>>> from seqiolite import fasta
>>> records = fasta.FastaFile('/path/to/my.fasta')
>>> for rec in records:
...     print rec.id
...     print rec.seq
```

1.2 FastaRecord

A FastaRecord represents a single fasta record.

It contains the identifier, sequence and description if there was a description

Here you can see an example of how to create a fasta record

```
>>> from seqiolite import fasta
>>> example = fasta.FastaRecord('>identifier description', 'ATGC')
>>> print example.id
identifier
>>> print example.description
description
>>> print example.seq
ATGC
```

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