

```
from Bio.Seq import Seq
from Bio.Alphabet import Alphabet

def read_seq(file_path, start, end):
    with open(file_path, 'r') as f:
        return ChromosomeReader(f).read_seq(start, end)

class ChromosomeReader(object):

    def __init__(self, file_handler):
        self.file_handler = file_handler
        self.header_len = len(file_handler.readline())
        self.line_len = len(file_handler.readline()) - 1

    def read_seq(self, start, end):

        absolute_start = self.convert_to_absolute_coordinate(start)
        absolute_length = self.convert_to_absolute_coordinate(end) - absolute_start + 1

        self.file_handler.seek(absolute_start)
        str_seq = self.file_handler.read(absolute_length).replace('\n', '')
        return Seq(str_seq, Alphabet())

    def convert_to_absolute_coordinate(self, position):
        position_zero_index = position - 1
        return self.header_len + position_zero_index + (position_zero_index //
self.line_len)
```