

## How to read fasta sequences from a file using PHP?

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**Categories :** [Algorithms](#), [Bioinformatics Programming](#), [Fasta](#)

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Here is a simple function in PHP to read fasta sequences from a file.

Your multifasta input file is “input.fasta”.

```
function read_fastas($filename){          $fh = fopen($filename, 'r');
$i= 0 ;          $sequences = array();    while($line = fgets($fh)){
$i++;          if($i%2==1){          $sequence['header'] = $line;          }
    else{          $sequence['sequence'] = $line;          array_push($sequenc
es, $sequence);          }          }          return $sequences;          }
```

The rest of the script would go like this:

```
<?php $filename = "input.fasta";          //Define function function read_
fastas($filename){          $fh = fopen($filename, 'r');          if (filesize($
x) == 0) { //check if file is empty or not          echo "Input file is em
pty!";          }          else{          $i= 0 ;          $sequences = array();          while($l
ine = fgets($fh)){          $i++;          if($i%2==1){          $sequence['head
er'] = $line;          }          else{          $sequence['sequence'] = $line;
          array_push($sequences, $sequence);          }          }          return $sequ
ences;          }          }          //Call the function read_fastas(); //do something wi
th your fasta ?>
```

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