

How to read fasta sequences as hash using perl?

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Categories : [Algorithms](#), [Bioinformatics Programming](#), [Perl](#)

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This is a simple Perl script to read a multifasta file as a hash.

Suppose, your multifasta file is “input.fasta”, which you want to read as the hash.

```
#!/usr/bin/perl use warnings; use strict; my $infile = "input.fasta"; my %sequences; open( FH, '<', $infile ) or die $!; while( my $line = <FH> ){ chomp $line; if ( $line =~ /^(>.*)$/ ) ){ my $id = $1; } elseif ( $line !~ /^\\s*$/ ) ){ $sequences{$id} .= $line; } } close (FH); exit;
```

If you want to write a subroutine for reading a fasta file, then you can do like this:

```
#!/usr/bin/perl use warnings; use strict 'vars'; my $infile = "input.fasta"; my %seqs = %{ read_fasta_as_hash($infile) };#call the subroutine #your code goes here sub read_fasta_as_hash{ my $inputfile = shift; my $id = ''; my %sequences; open( INFILE, '<', $inputfile ) or die $!; while( my $line = <INFILE> ){ chomp $line; if ( $line =~ /^(>.*)$/ )){ my $id = $1; } elseif ( $line !~ /^\\s*$/ ) { $sequences{$id} .= $line; } } close (INFILE); return %sequences; } exit;
```

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