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## Defining functions
```

```
# Example function
```

```
sub read_seq {  
    $file=shift(@_);  
    open(IN,"<$file") or die "I cannot read the file\n";  
    my $description=<IN>;  
    my $sequence="";  
    while(my $line=<IN>) {  
        chomp($line);  
        $sequence.=$line;  
    }  
    close(IN);  
    return $sequence;  
}
```

```
my $seq=read_seq("sequence.fasta");  
print $seq."\n";
```

```
# See examples:
```

```
# find_pattern.pl
```

```
# BioPerl: http://www.bioperl.org/wiki/HOWTO:Beginners
```

```
# calculate_ratio.pl
```