

```
function [seq, len, GCcont, Weight, properties, name, Path] = parseFASTA(Path, Name)
% Opens a FASTA text file and parses sequence and file name
%
% See also

% Open the file, get name/path, trim to get locus tag ('name'), concatenate
switch nargin
case 2
    filename = strcat(Path, Name, '.txt');
otherwise
    % clc, clear all, close all
    [Name, Path] = uigetfile('.txt');
    % If want to strip extension
    name = Name(1:strfind(Name, '.')-1);
    filename = strcat(Path, Name);
end

% retrieve sequence, ignore header
[~, seq] = fastaread(filename);

% Collect biological Information
len = length(seq);
properties = oligoprop(seq);

GCcont = properties.GC;
Weight = properties.MolWeight;

end
```