A Guide to Writing Helpful Bug Reports
By Carla Mann, 09/21/2017

In your bug report email, please include an email header with:
1. The site you are using
2. The words "Bug Report"

Example of a helpful email header:

MEDJED Bug Report: Site crashes when submitting lowercase sequence

Example of a not-helpful email header:

the website crashed

In the body of the email, please include:
1. (Optional, but highly suggested) A polite or humorous salutation
2. The **time you were using the site**, and **your time zone**
3. **Information necessary to reproduce** the issue you found; examples include, but are not limited to:
   a. Sequence(s) inputs
   b. Radio buttons you selected
   c. Checkboxes you selected
   d. Dropdown menu choices
   e. Button(s) you pressed
   f. Any red error messages displayed on screen, after you put in your inputs
4. **What you were doing when the error/crash occurred** (e.g., pasting a sequence input, choosing a radio button, hitting submit, etc)
5. **What happened** (e.g., did the website crash? Are you receiving a red error message you can't resolve? Are you not getting results?)
6. (Optional) A screenshot of what happened (e.g., error message, weird output, etc.)

Example of a Helpful Bug Report:

Hi MENTHU Support,

I was using MENTHU at 10:24am (US Central Time) when I got some weird output results.

Here are the inputs I used:
1) All PAM sequences selected
2) This sequence: AAAAAAAAAAAAAAAACCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
3) Threshold score of 60

After I hit submit, instead of getting predictions I got this empty table:

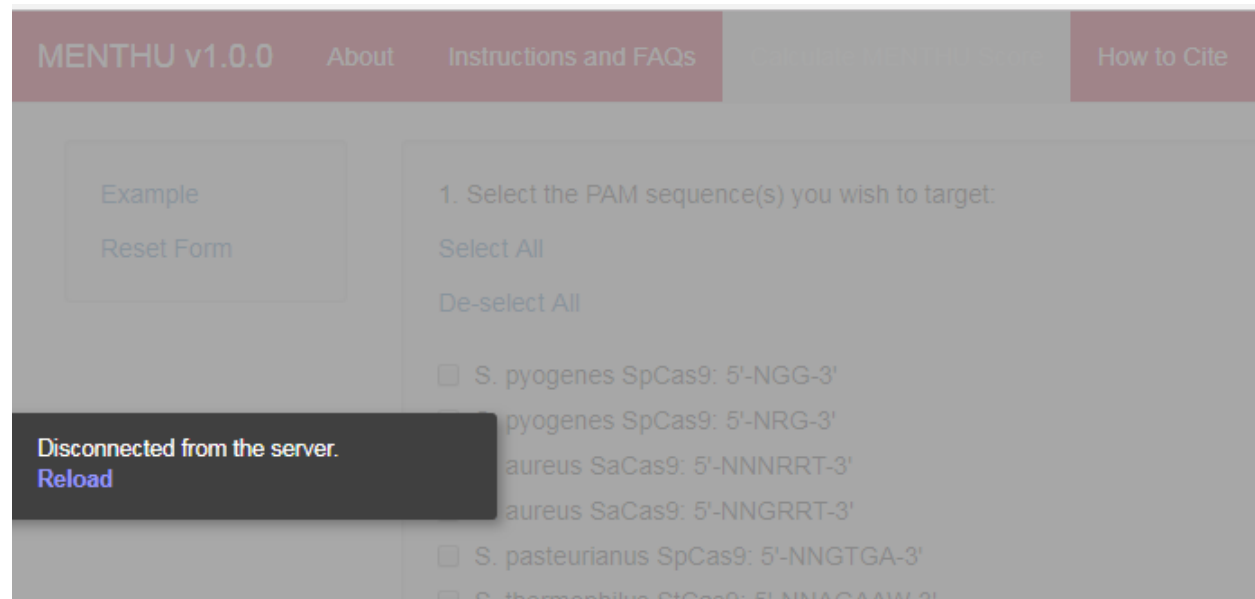| Submit					
targetSeq	menthuScore	toolType	strand	exon	location

I'm not sure why I'm not getting results. Can you help?

Thanks,
Jane Smith

For reference, a website crash looks like this:

MENTHU v1.0.0   About   Instructions and FAQs   Calculate MENTHU Score   How to Cite

Example

Reset Form

1. Select the PAM sequence(s) you wish to target:

Select All

De-select All

☐ S. pyogenes SpCas9: 5'-NGG-3'
☐ S. pyogenes SpCas9: 5'-NRG-3'
☐ S. aureus SaCas9: 5'-NNNRRT-3'
☐ S. aureus SaCas9: 5'-NNGRRT-3'
☐ S. pasteurianus SpCas9: 5'-NNGTGA-3'
☐ S. thermophilus StCas9: 5'-NNAGAAW-3'

Disconnected from the server.
Reload

Red error messages look like this:

Please paste your sequence in PLAIN TEXT format. (No FASTA headers.)

Error: Input DNA sequence contains non-standard nucleotides. Allowed nucleotides are A, C, G, and T.

ACACTGATCGATCGATCGAGCATGCTAGCTGAC?ACATGCTAGTCGACTAG

Error messages appear in red. **These are FEATURES, not bugs – these messages appear in order to let you know that there is an issue with one or more of your inputs that prevents you from getting results.** Error messages will tell you what the problem with the input is, and give you an idea of how to fix the error(s). GTagHD, MEDJED, and MENTHU will not process inputs via the submit button if there are any red error messages present.