Welcome, Christoph!   *move to left*   Logout

Substitution   Insertion   Deletion   (Upload)   Database

NAME   *Sequence Identifier*

Please enter a name ~~for your DNA~~, *number, accession number or other ID for your sequence. This is for your reference only.*

UPLOAD

~~Please upload the DNA sequence in text format~~   *Currently accepted sequence file format : TXT, FASTA*

Browse...
~~Choose File~~ No file chosen

NOTES

Jot down any notes for yourself

buttons for formatting (italicize, bold, superscript)

make font in here smaller!

~~65535 characters left~~   → *provide popup if character # > 65k*

~~Submit!~~
Save

Make Favicon | M.A.T. |

Welcome, Christoph!   Logout

Substitution   Insertion   Deletion   Upload   Database

NG_012798.1

>gi|256985186|ref|NG_012798.1|...

provide calculations with a "Calculate" button

Choose Position: **500**   A   T   G   C

① Position: 500
Old codon: AGG
New codon: AAG
~~Nucleic acid level: c.500G>A~~ *splice junction distance, 3', 5'*
~~Protein level: p.580~~ *"*

~~Don't use~~

move lower

② **Mutation**

This should be a two-step approach:

① Calculate positional information

② Mutation

Welcome, Christoph!   Logout

Substitution   Insertion   Deletion   Upload   Database

NG_012798.1   ─ *Does this count as "sequence"?*
>gi|256985186|ref|NG_012798.1|...

Feature
Type   Start   End   Keep

| promoter | 1 | 5000 | ☑ |
| Exon | 5001 | | ☑ |

[Add Row] [Delete Row] [Clear]   [Submit] *Save*

allow field jumping via "Tab" key

provide "Exon, alternate"   ─→ if this
make "Exon" default

add column "~~Reason~~ (Note)" (with mouse-over:
"This field helps with exon numbering
or any other additional information"

call this page "Annotation"

[Sequence name]

How do I go back to this page to edit/add
to the annotations?