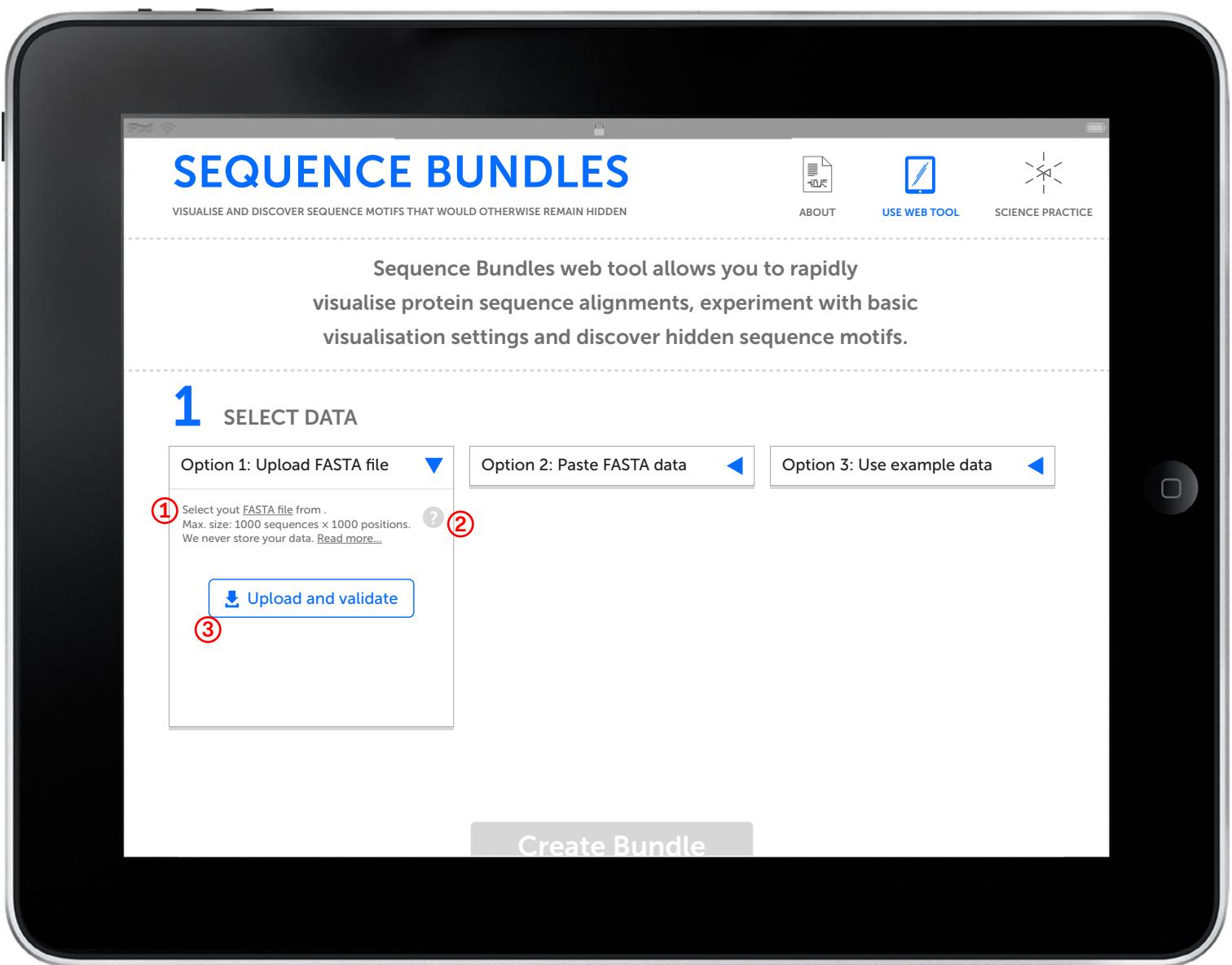


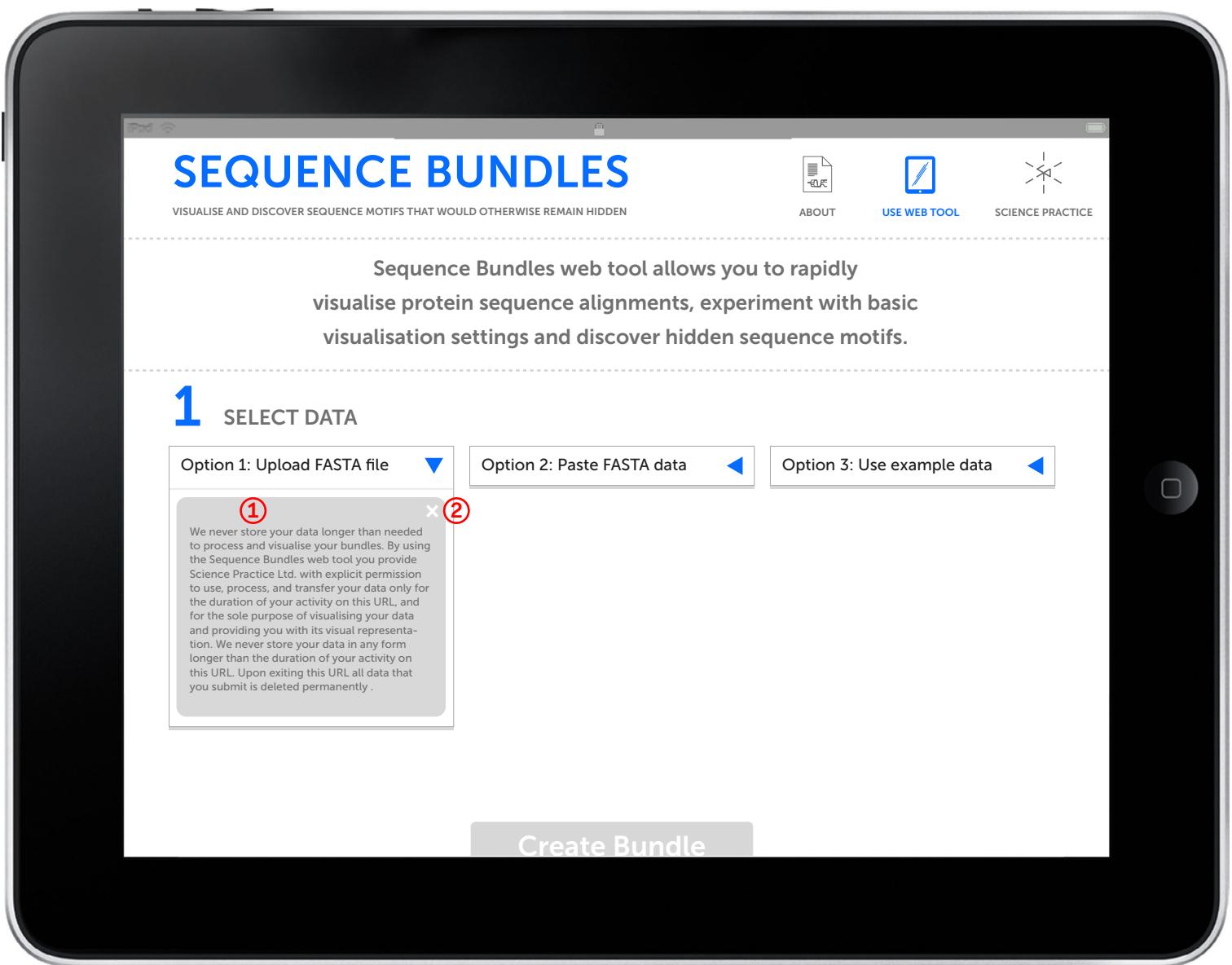
Changes:

1. We're using the Museo Sans 500, 700 and 900 font.
2. Add icons and links in nav bar. You will find the graphics in the Assets ZIP archive.
3. Bring back division of step one into three exclusive alternatives.
 - Option 1 is Uploading FASTA file from hard drive.
 - 4. Option 2 is pasting FASTA data into browser text box.
 - 5. Option 3 is the same as we have already implemented on Heroku.
 - 6. Bring back Step 3, where bundle can be downloaded.



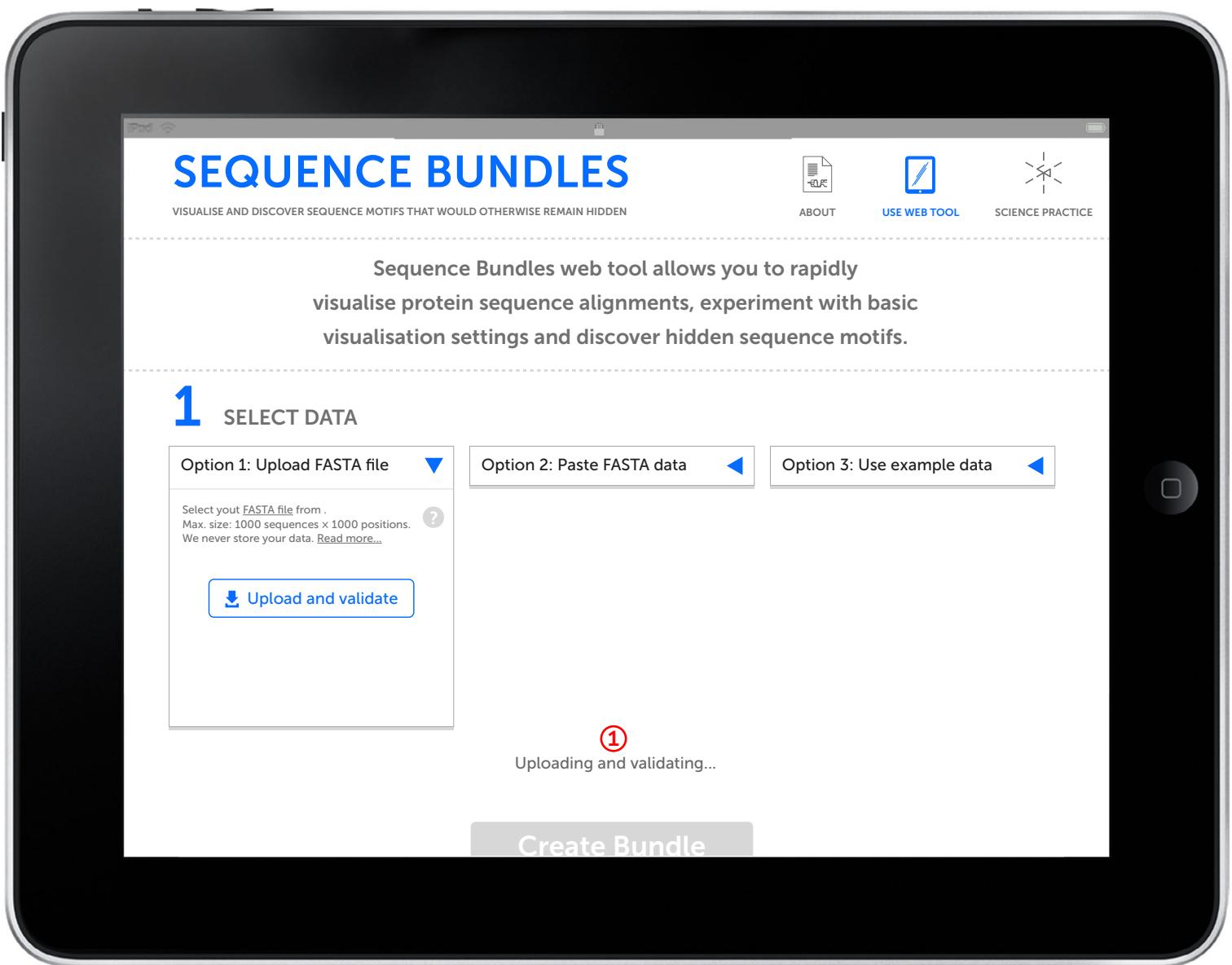
Changes:

1. When "Upload" box open, add a three-line text in the beginning.
"FASTA file" link goes to URL: http://en.wikipedia.org/wiki/FASTA_format
"Read more..." link opens data policy pop-up window (explained on page 3)
2. Question mark icon opens data policy pop-up window (explained on page 3)
3. "Upload and validate" button opens "Open file" window and allows to select file.
Icon for the button in Assets ZIP Archive



Changes:

1. Add grey pop-up box with more information about data policies.
2. The "x" button closes the pop-up window, just as clicking anywhere outside of the box.



Changes:

1. When file has been selected and is being uploaded and validated, contextual information should appear explaining why it takes a little time to wait.

Read more...' and a blue 'Upload and validate' button. A red circled '1' is placed next to this note. Below the input fields is a red error message: 'FASTA format not valid. Learn more about the FASTA format [here](#)'. At the bottom is a grey 'Create Bundle' button."/>

SEQUENCE BUNDLES

VISUALISE AND DISCOVER SEQUENCE MOTIFS THAT WOULD OTHERWISE REMAIN HIDDEN

Sequence Bundles web tool allows you to rapidly visualise protein sequence alignments, experiment with basic visualisation settings and discover hidden sequence motifs.

1 SELECT DATA

Option 1: Upload FASTA file ▾

Select your [FASTA file](#) from...
Max. size: 1000 sequences x 1000 positions.
We never store your data. [Read more...](#)

Upload and validate

Option 2: Paste FASTA data ←

Option 3: Use example data ←

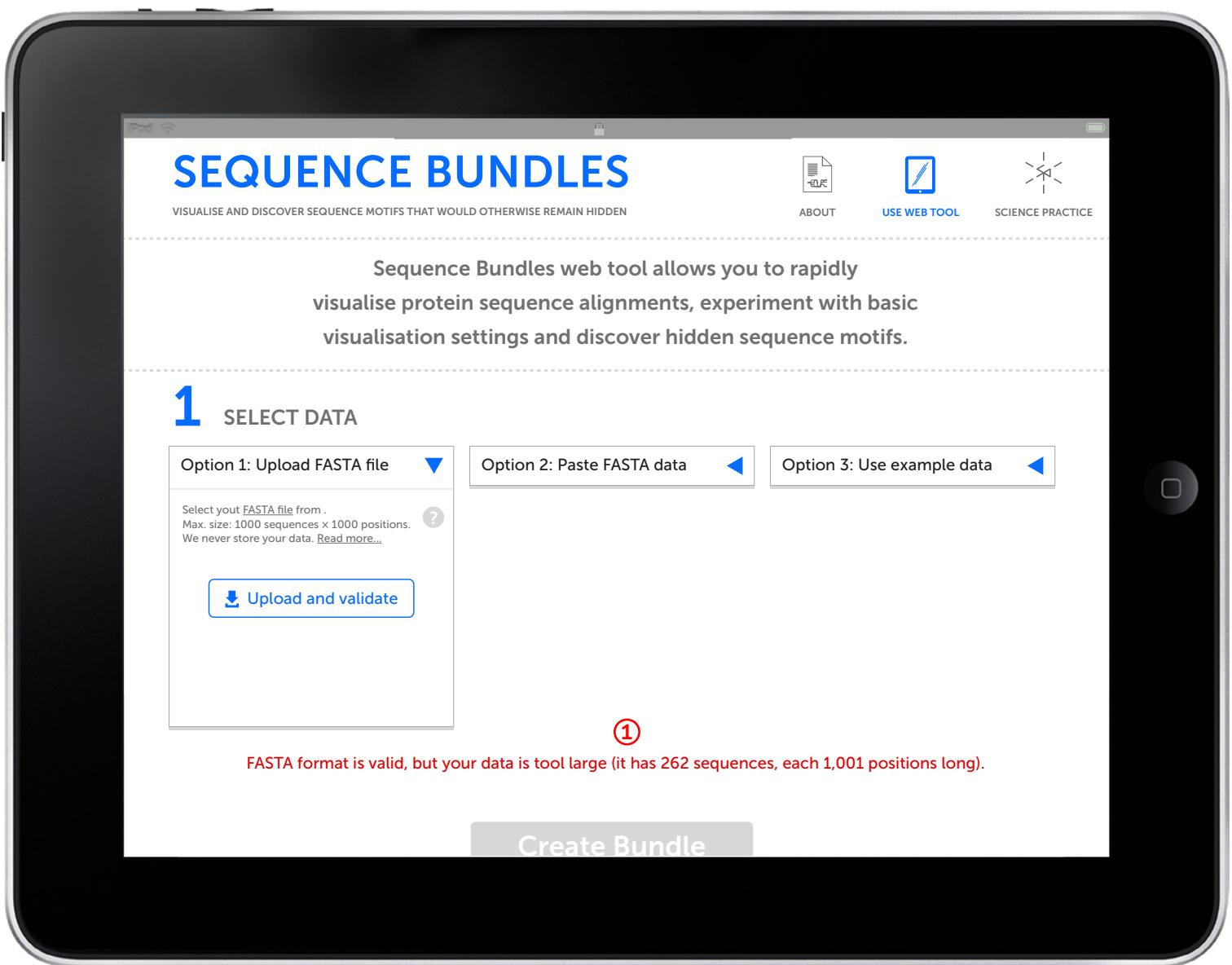
①

FASTA format not valid. Learn more about the FASTA format [here](#).

Create Bundle

Changes:

1. When FASTA format is invalid, show this feedback in red with an underlined link to URL:
http://en.wikipedia.org/wiki/FASTA_format



Changes:

1. When FASTA format is valid, but the alignment is too large (i.e. more than 1000 sequences or more than 1000 positions), this feedback information should appear in red with indication of the number of sequences and positions in the data that failed to validate.

SEQUENCE BUNDLES

VISUALISE AND DISCOVER SEQUENCE MOTIFS THAT WOULD OTHERWISE REMAIN HIDDEN

Sequence Bundles web tool allows you to rapidly visualise protein sequence alignments, experiment with basic visualisation settings and discover hidden sequence motifs.

1 SELECT DATA

Option 1: Upload FASTA file ▾

Select your [FASTA file](#) from .
Max. size: 1000 sequences x 1000 positions.
We never store your data. [Read more...](#)

Upload and validate

Option 2: Paste FASTA data ▶

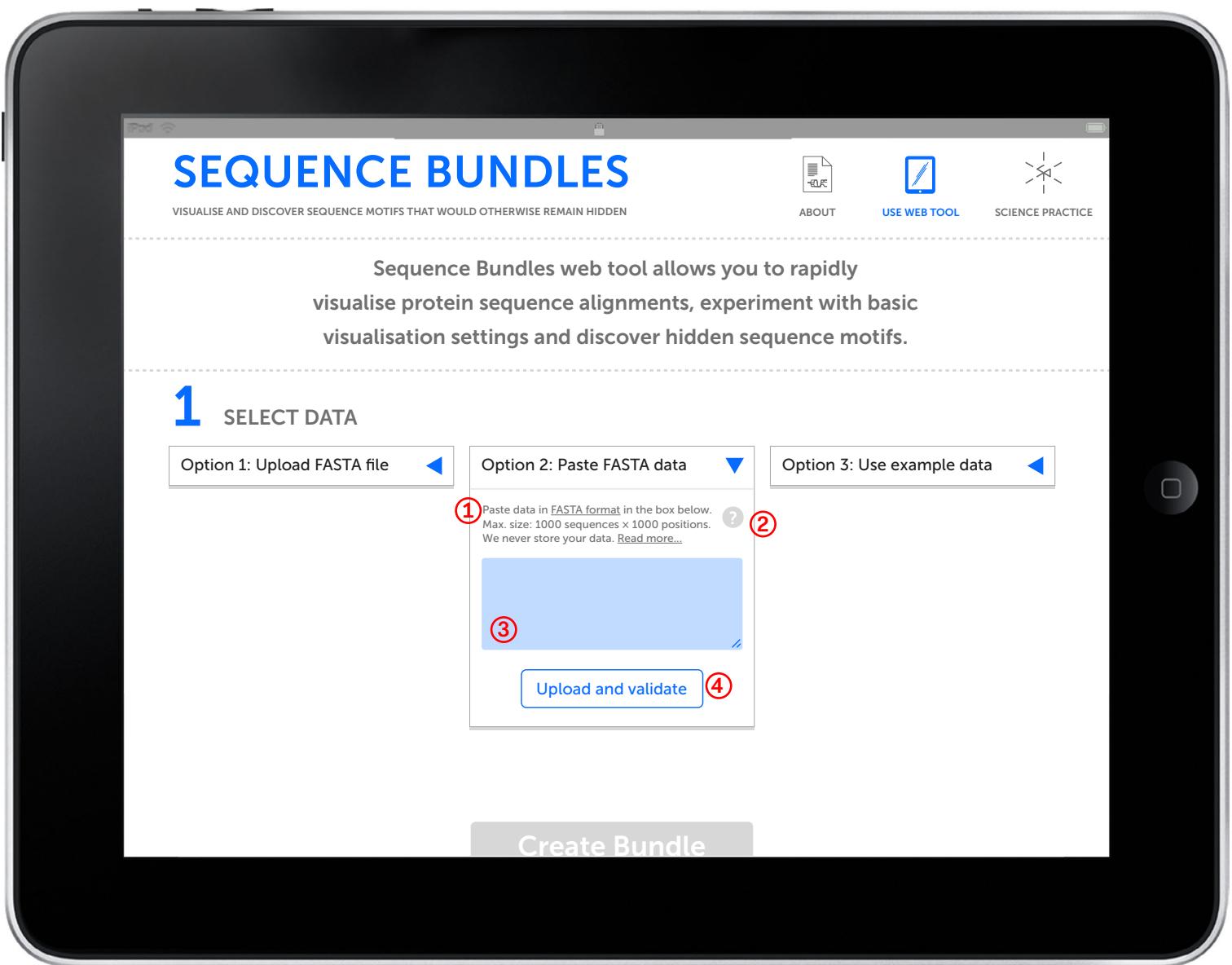
Option 3: Use example data ▶

① Your protein data contains 1000 sequences, each 36 positions long.

Create Bundle

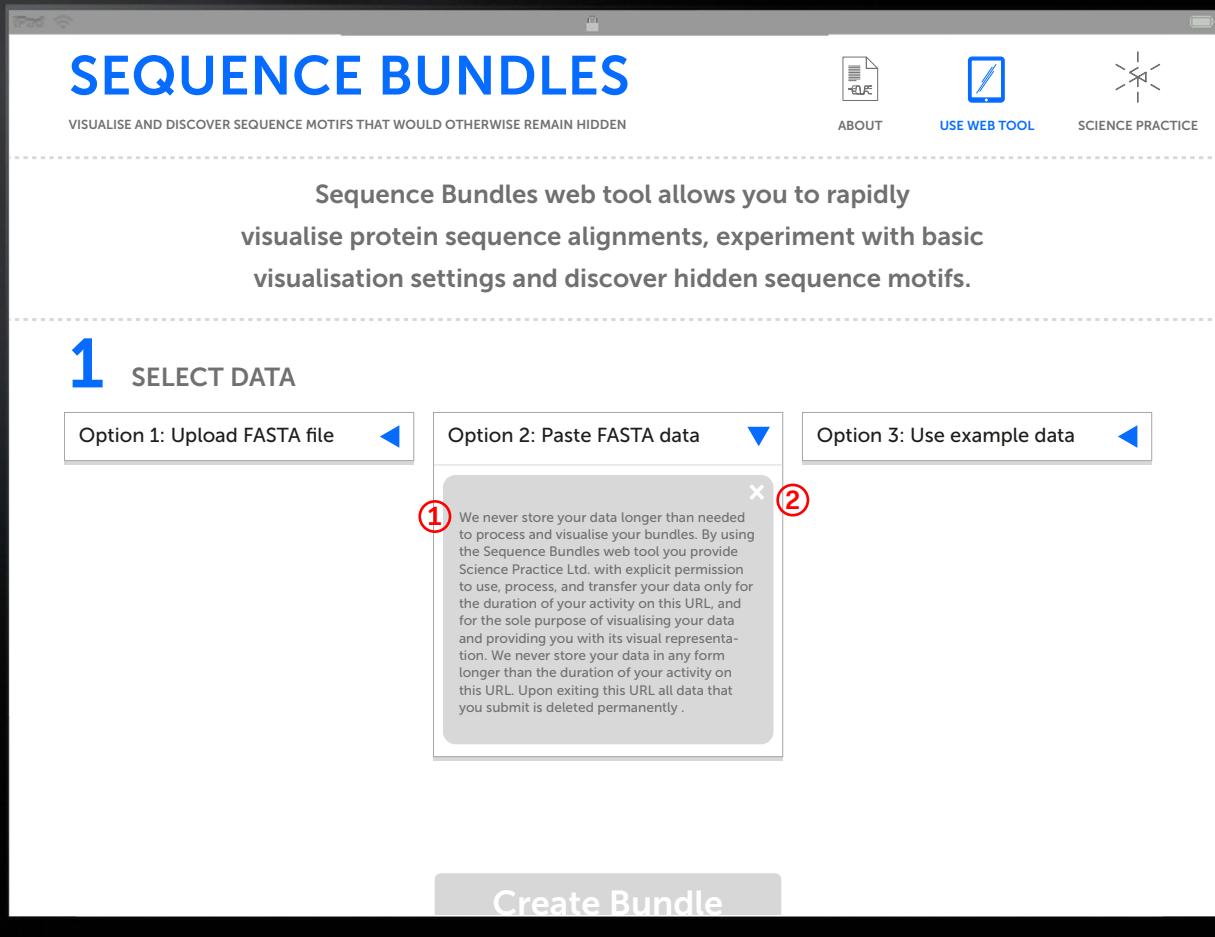
Changes:

1. When FASTA format is valid and correct size, display this feedback info in green and activate the "Create Button" below.



Changes:

1. When "Paste" box open, add a three-line text in the beginning.
"FASTA format" link goes to URL: http://en.wikipedia.org/wiki/FASTA_format
"Read more..." link opens data policy pop-up window (explained on page 9)
2. Question mark icon opens data policy pop-up window (explained on page 9)
3. "Upload and validate" button uploads pasted text and validates it.



Changes:

1. Same as on page 3
2. Same as on page 3

SEQUENCE BUNDLES

VISUALISE AND DISCOVER SEQUENCE MOTIFS THAT WOULD OTHERWISE REMAIN HIDDEN

Sequence Bundles web tool allows you to rapidly visualise protein sequence alignments, experiment with basic visualisation settings and discover hidden sequence motifs.

1 SELECT DATA

Option 1: Upload FASTA file

Option 2: Paste FASTA data

Option 3: Use example data

Paste data in **FASTA format** in the box below.
Max. size: 1000 sequences x 1000 positions.
We never store your data. [Read more...](#)

>fasta 1
RRICKTCGASYHLVFNPPAEEGKCDKGELYTRAD
>fasta 2
RPTCGGGCAGYHDDFKPKVEGTCDGCQEQQKRRAD
>fasta 3
RSTCGSCGEVYNDITKPIPQDGKCTKCGGEFKRRAD
>fasta 4
RPTCGGCAGEGYHDSPKQPQAMGTCDKCGGEFKRRAD

Upload and validate

(1) Uploading and validating...

Create Bundle

Changes:

1. Same as on page 4

SEQUENCE BUNDLES

VISUALISE AND DISCOVER SEQUENCE MOTIFS THAT WOULD OTHERWISE REMAIN HIDDEN

Sequence Bundles web tool allows you to rapidly visualise protein sequence alignments, experiment with basic visualisation settings and discover hidden sequence motifs.

1 SELECT DATA

Option 1: Upload FASTA file

Option 2: Paste FASTA data

Option 3: Use example data

Paste data in **FASTA format** in the box below.
Max. size: 1000 sequences x 1000 positions.
We never store your data. [Read more...](#)

② >fasta 1
RRICKTCGASYHLVFNPPAEEGKCDKGELYTRAD
>fasta 2
RVTGNGGAGYHDDFKPKVEGTCDGCQEQMRRAD
>fasta 3
RSTCGSCGEVYNDITKPIPQDGKCTKCGGEFKRAD
>fasta 4
RPTCGGCGEGYHDSPFQPAQMGTCDKCGGEFKRAD

Upload and validate

① FASTA format not valid. Learn more about the FASTA format [here](#).

Create Bundle

Changes:

1. Same as on page 5
2. If possible, pasted text stays in the box for reference

SEQUENCE BUNDLES

VISUALISE AND DISCOVER SEQUENCE MOTIFS THAT WOULD OTHERWISE REMAIN HIDDEN

Sequence Bundles web tool allows you to rapidly visualise protein sequence alignments, experiment with basic visualisation settings and discover hidden sequence motifs.

1 SELECT DATA

Option 1: Upload FASTA file

Option 2: Paste FASTA data

Option 3: Use example data

Paste data in **FASTA format** in the box below.
Max. size: 1000 sequences x 1000 positions.
We never store your data. [Read more...](#)

>fasta 1
RRICKTCGASYHLVFNPPAEEGKCDKGELYTRAD
>fasta 2
RVTGNGGAGYHDDFKPKVEGTCDGCQMKRRAD
>fasta 3
RSTCGSCGEVYNDITKPIPQDGKCTKCGGEFKRRAD
>fasta 4
RPTCGGCGEGYHDSFKQPQAMGTCDKCGGEFKRRAD

Upload and validate

①
FASTA format is valid, but your data is too large (it has 262 sequences, each 1,001 positions long.).

Create Bundle

Changes:

1. Same as on page 6
2. If possible, pasted text stays in the box for reference

SEQUENCE BUNDLES

VISUALISE AND DISCOVER SEQUENCE MOTIFS THAT WOULD OTHERWISE REMAIN HIDDEN

ABOUT USE WEB TOOL SCIENCE PRACTICE

Sequence Bundles web tool allows you to rapidly visualise protein sequence alignments, experiment with basic visualisation settings and discover hidden sequence motifs.

1 SELECT DATA

Option 1: Upload FASTA file

Option 2: Paste FASTA data

Option 3: Use example data

Paste data in **FASTA format** in the box below.
Max. size: 1000 sequences x 1000 positions.
We never store your data. [Read more...](#)

②

```
>fasta 1
RRICKTCGASYHLVFNPPAEEGKCDKGELYTRAD
>fasta 2
RVTGNGGAGYHDDFKPKVEGTCDGCQEQMRRAD
>fasta 3
RSTCGSCGEVYNDITKPIPQDGKCTKCGGEFKRAD
>fasta 4
RPTCGGCGEGYHDSFKQPQAMGTCDKCGGEFKRAD
```

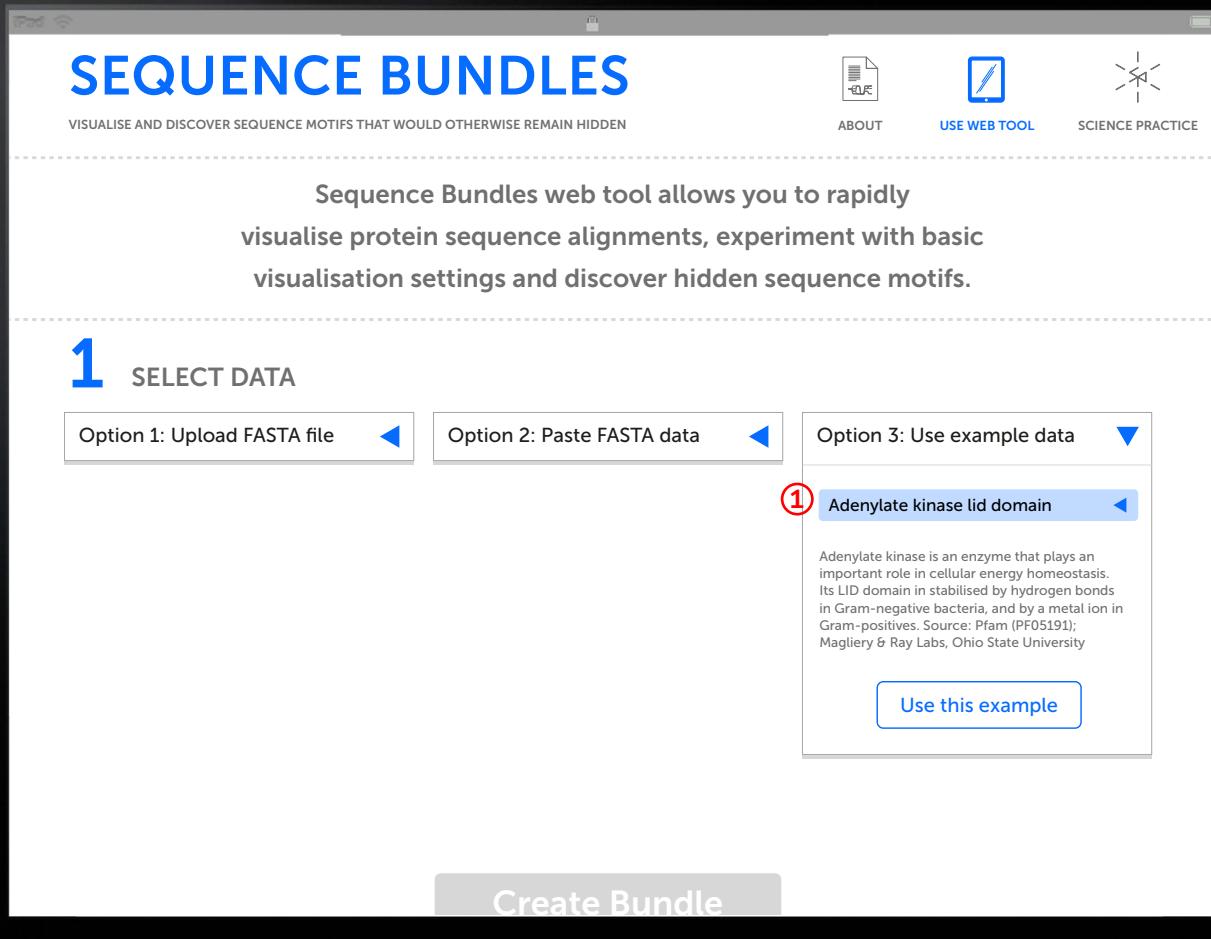
Upload and validate

① Your protein data contains 1000 sequences, each 36 positions long.

Create Bundle

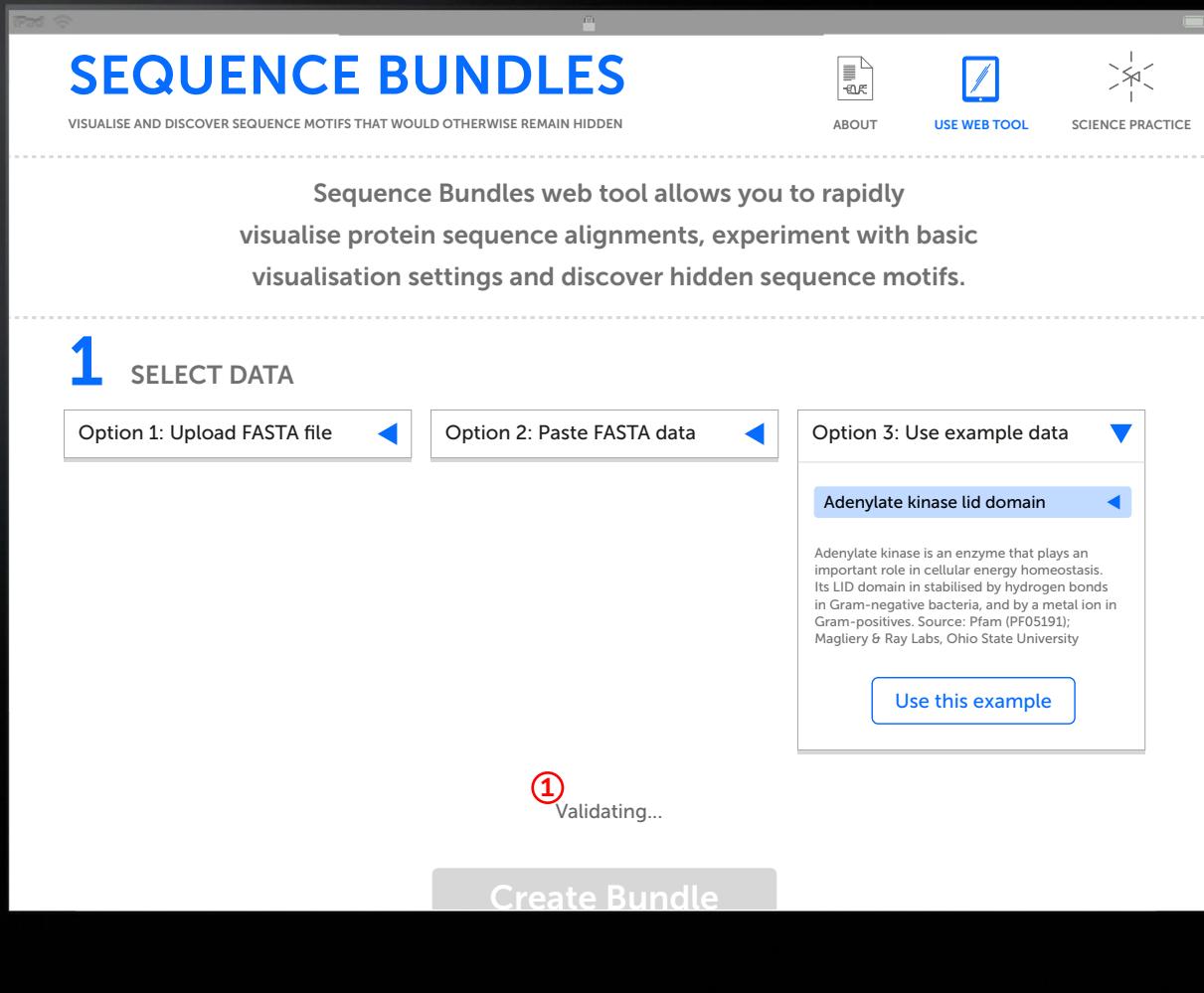
Changes:

1. Same as on page 7
2. If possible, pasted text stays in the box for reference



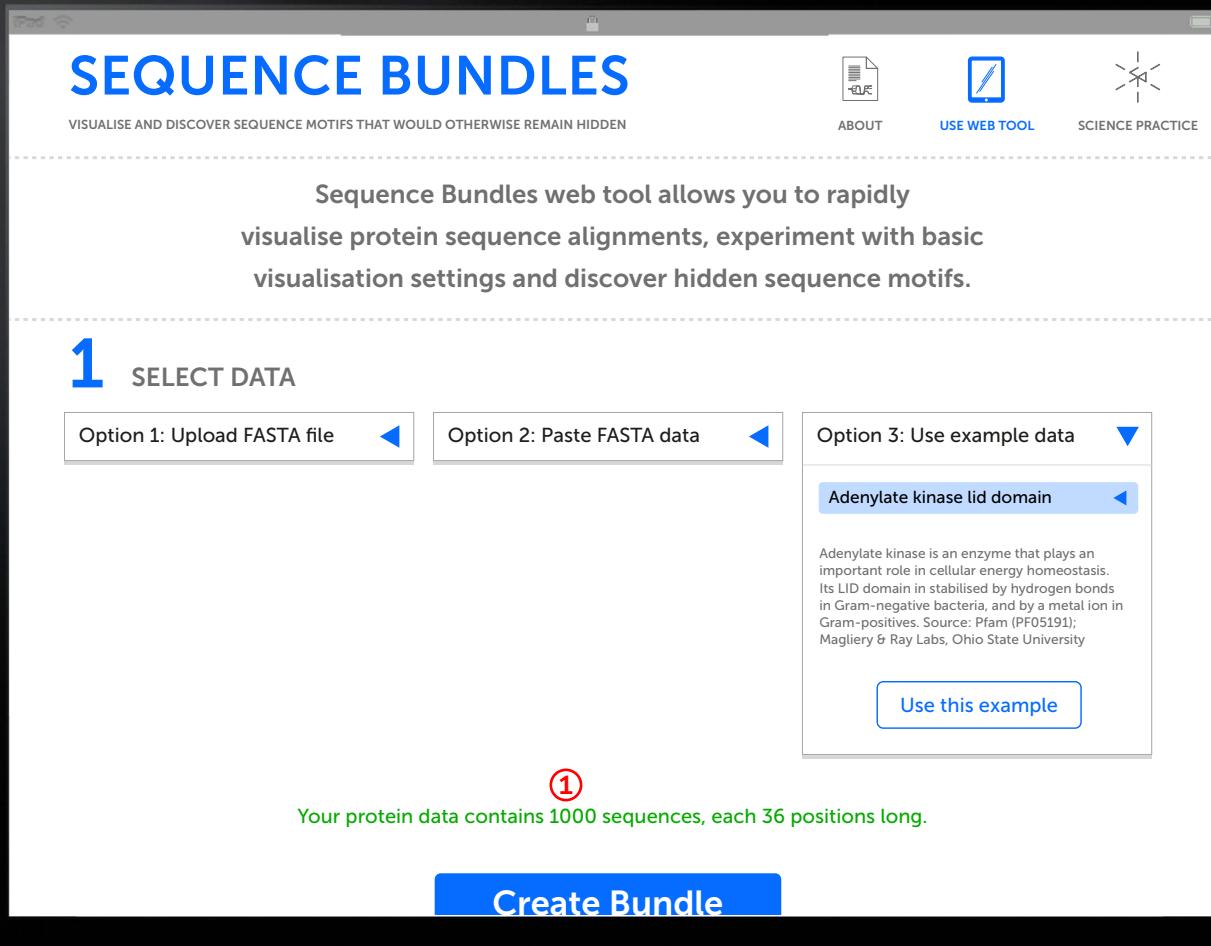
Changes:

1. When Option 3 selected ("Use Example data") retain the same functionality as already implemented in Heroku. The only thing changing if the width of the box and the number of lines in which little info text abou the selected example needs to fit.



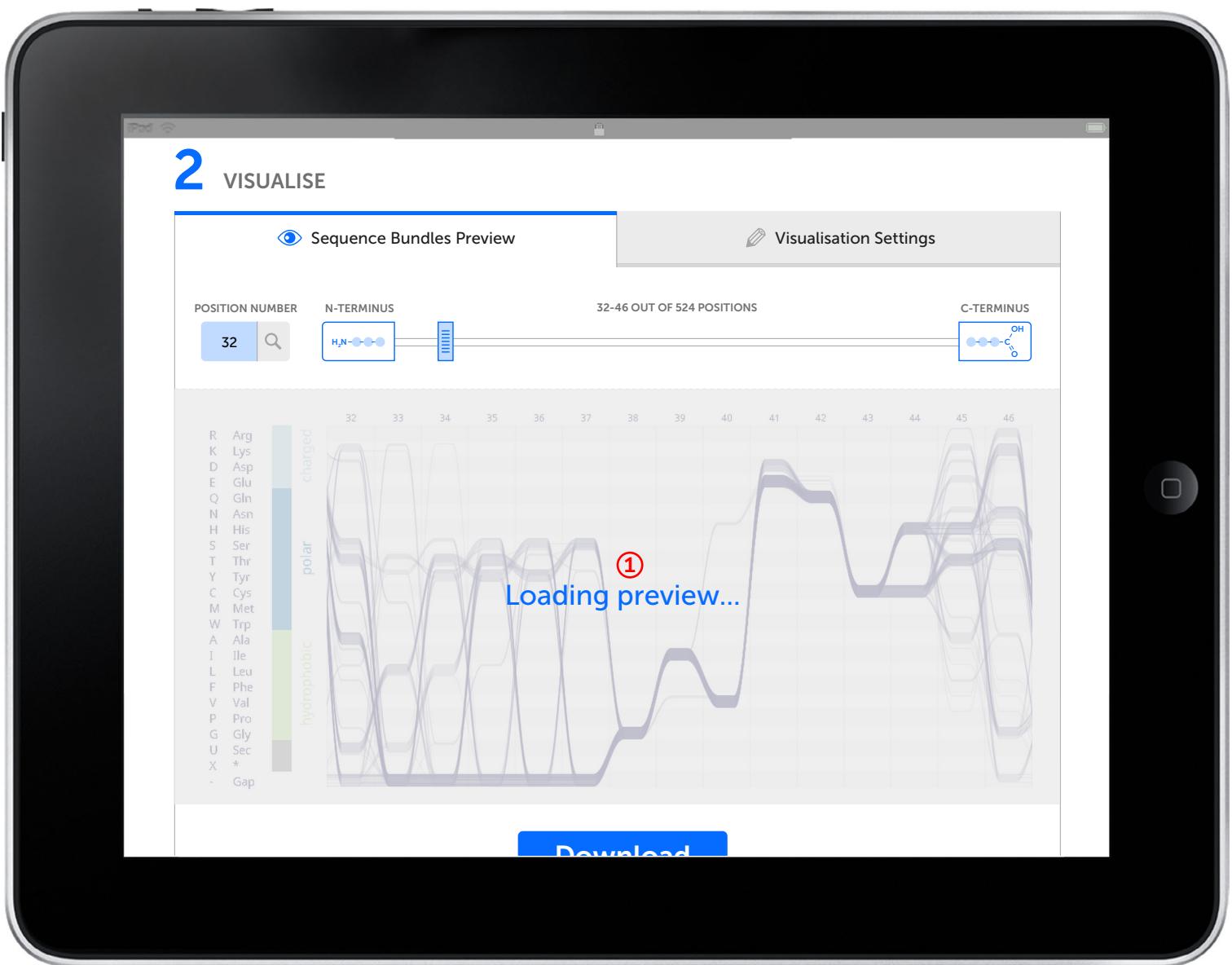
Changes:

1. Once the user presses “Use this example” button, “Validating...” text appears to indicate that the app is working. Same as on page 10.



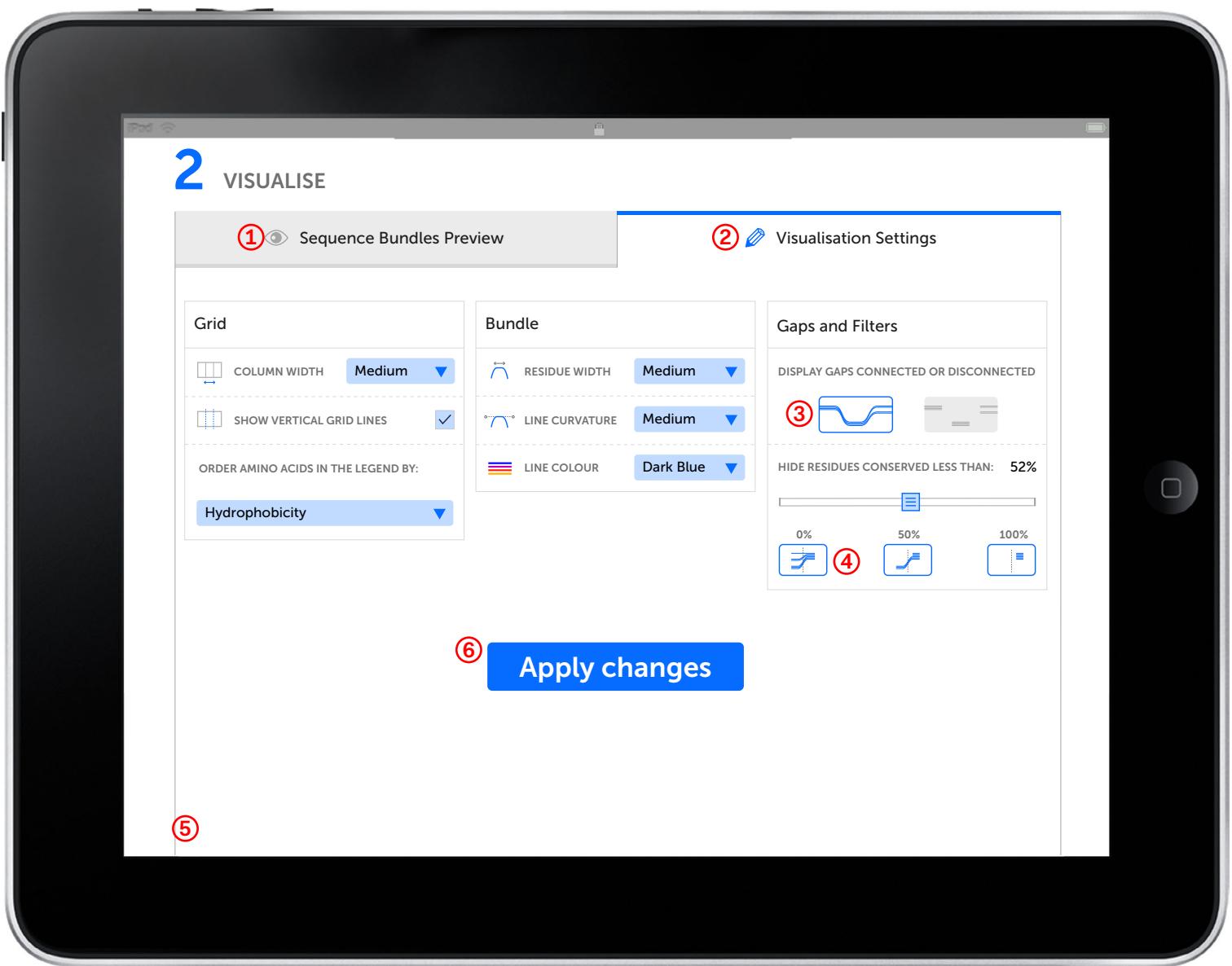
Changes:

1. Feedback information in green appears once the example data is loaded into app. "Create Bundle" button activates.



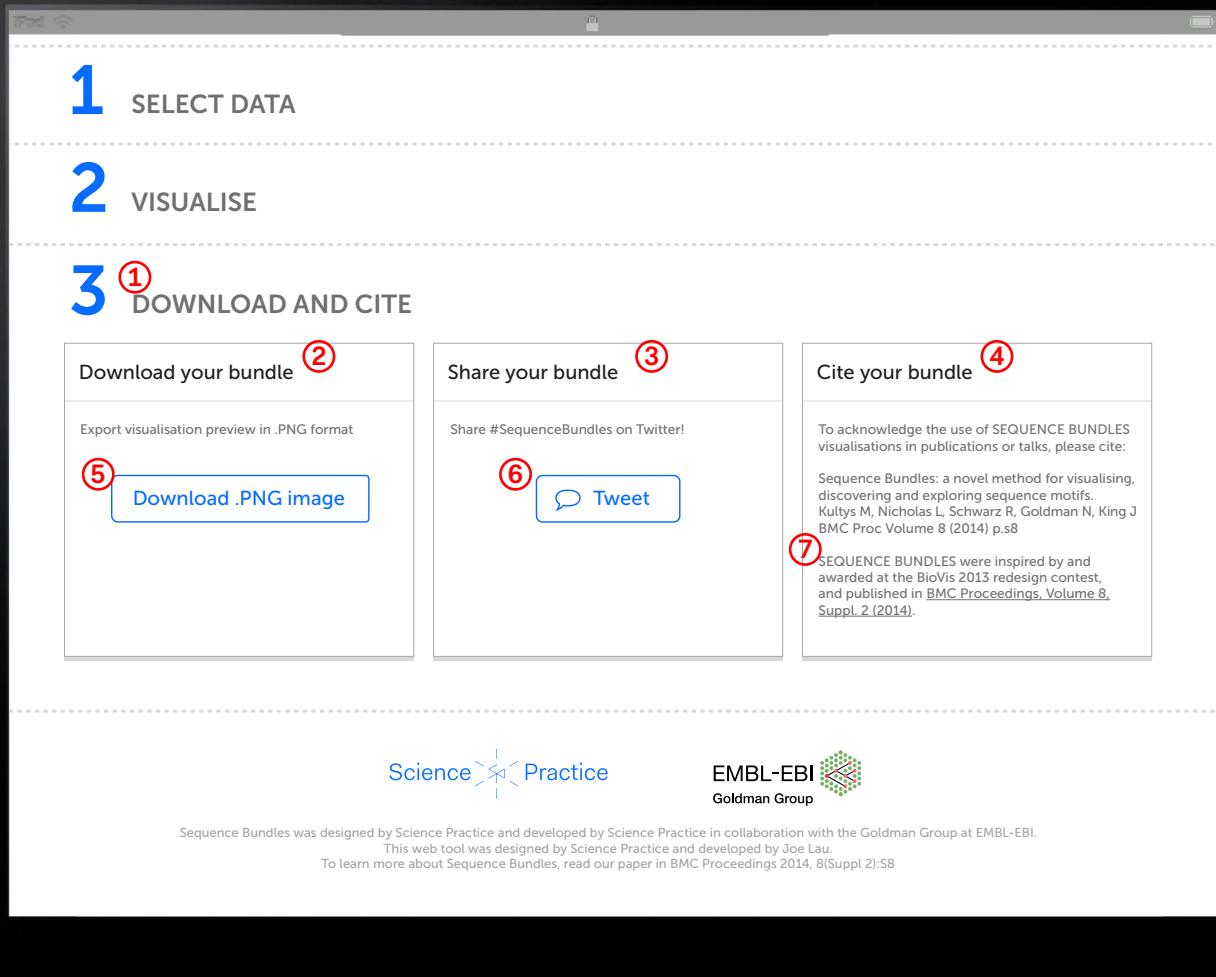
Changes:

1. When the preview is loading, simple static text feedback info appears on top of an 80% opaque div filled with grey background. In case this is the first preview generation, both the div and text appear the same but with no image below.



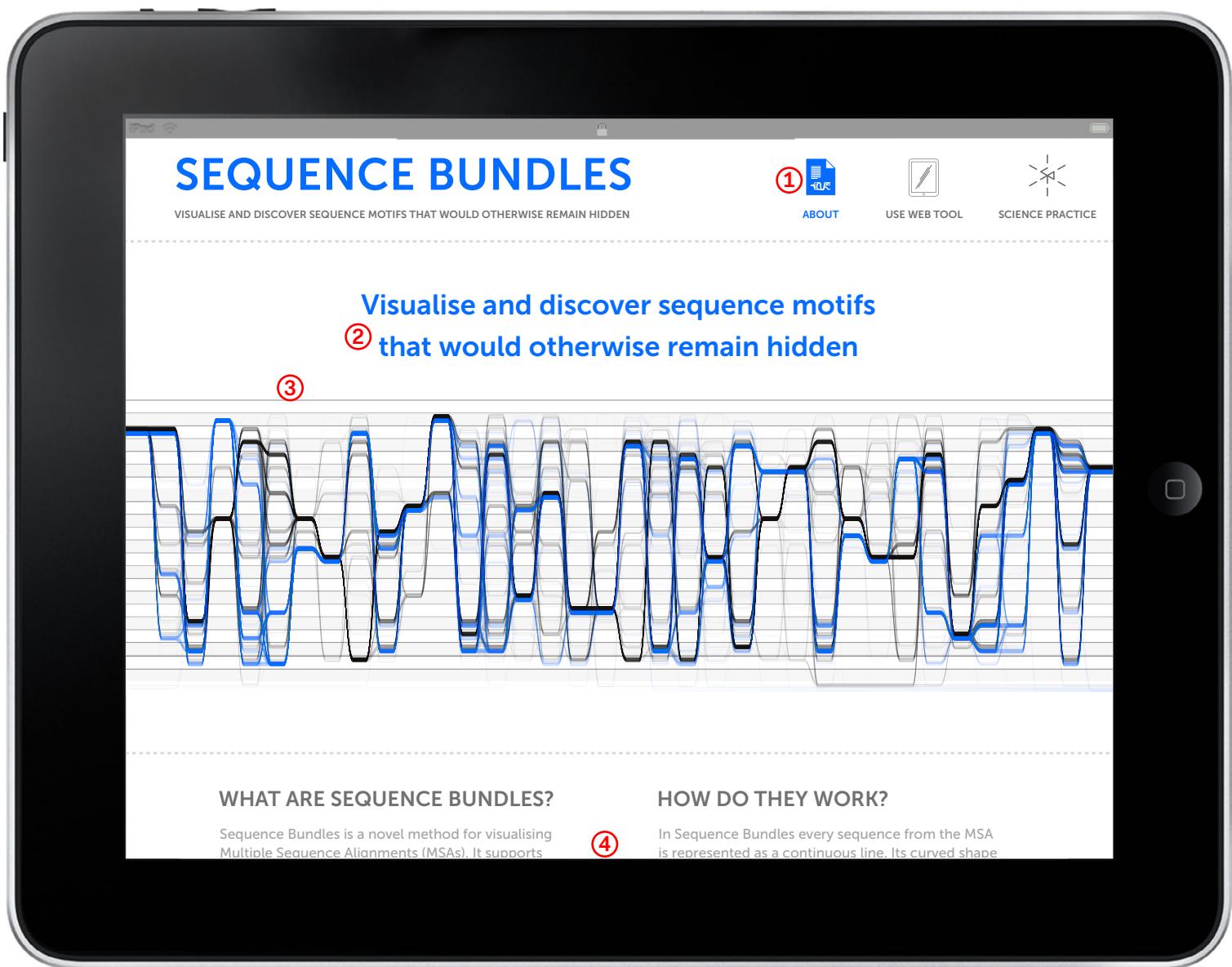
Changes:

1. As in previous spec, add icon to "Preview tab (when tab is inactive, icon should be grey)
Assets available in Archive ZIP
2. As in previous spec, add icon to "Settings" tab (when tab is active, icon should be blue)
Assets available in Archive ZIP
3. Change selection of gaps to two alternating buttons (Assets in ZIP Archive)
4. Add quick links to 0%, 50% and 100% of slider value together with icon buttons
(Assets available in Archive ZIP)
5. The box of the "Visualisations Settings" tab should always be the same height as the "Preview Sequence Bundles" tab
6. "Apply changes" button does not sit on bottom of tab box, but right below sections with visualisation properties



Changes:

1. Step 3 added and enabled (we get to it by clicking on "3" in the step numeral, or by clicking the "Download" button in the "Preview" tab in step 2).
2. As in step 1, division into three boxes, but these are non-collapsible — they stay open all time. There is "Download your bundle"
3. "Share your bundle"
4. and "Cite your bundle"
5. "Download .PNG image" allows user to download the preview image.
QUESTION A: how easy is it to set the download to full width of the bundle?
QUESTION B: how easy is it to set the download to higher resolution (e.g. 144 dpi)?
6. "Tweet" button automatically composes a tweet with this text:
"Try the #SequenceBundles web tool by @sciencepractice
<https://sequence-bundles.herokuapp.com/>"
7. In text underlined link goes to URL: <http://www.biomedcentral.com/1753-6561/8/S2/S8>



Changes:

1. This is the "About" page, so the active link in nav bar changes.
2. Add heading.
3. Add banner image (Asset in ZIP archive) — it should always stay 100% width of screen regardless until the screen goes beyond smartphone width — then it gets cropped.
4. More content below.

① WHAT ARE SEQUENCE BUNDLES?

Sequence Bundles is a novel method for visualising Multiple Sequence Alignments (MSAs). It supports interactive exploration of sequence data, sequence comparison and discovery of new sequence motifs that would otherwise remain hidden.

②

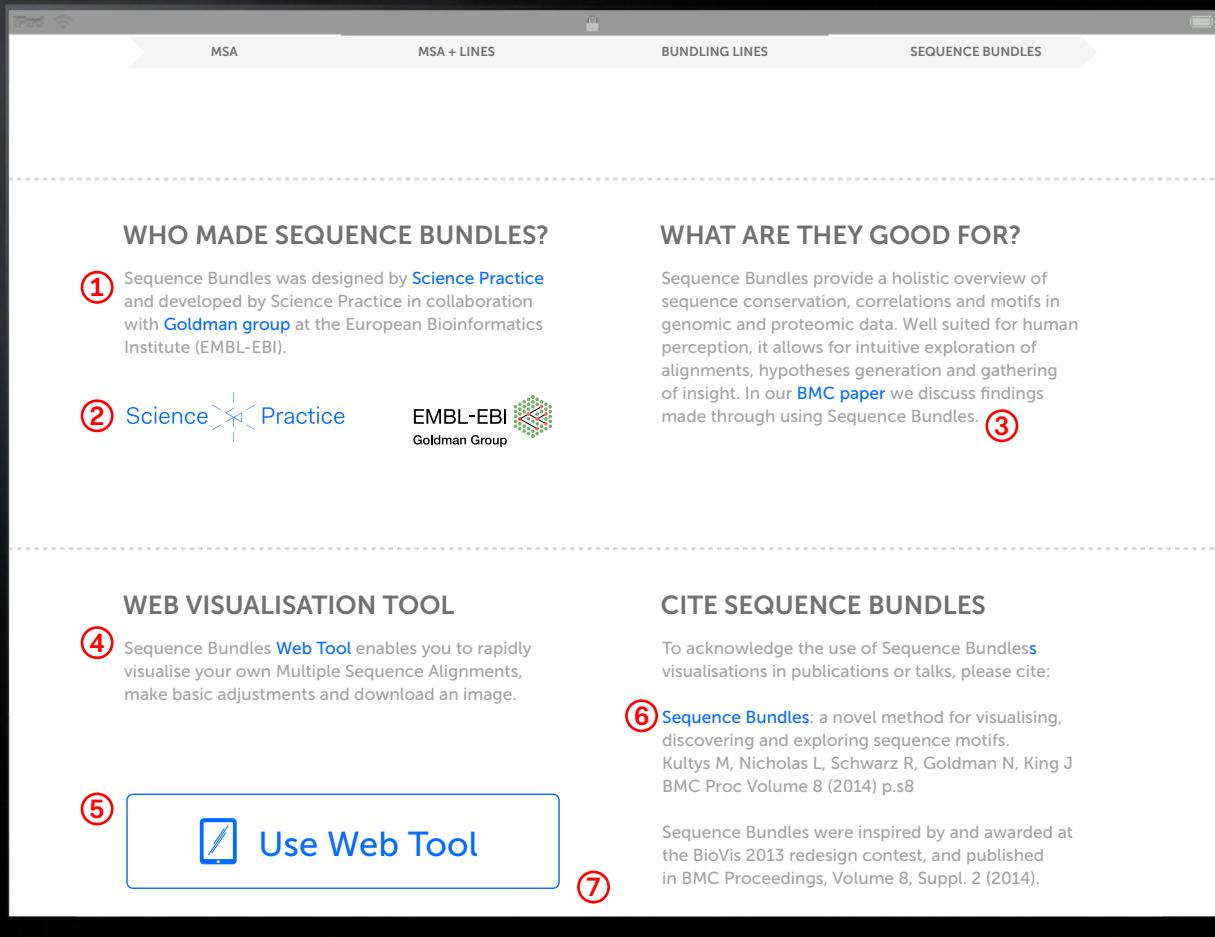
C A A T G T	C A A T G T
C C A T A A	C C A T A A
C G A T C A	C G A T C A
C G T T A C	C G T T A C
C T T T C A	C T T T C A
C T T T G T	C T T T G T

③

MSA MSA + LINES BUNDLING LINES SEQUENCE BUNDLES

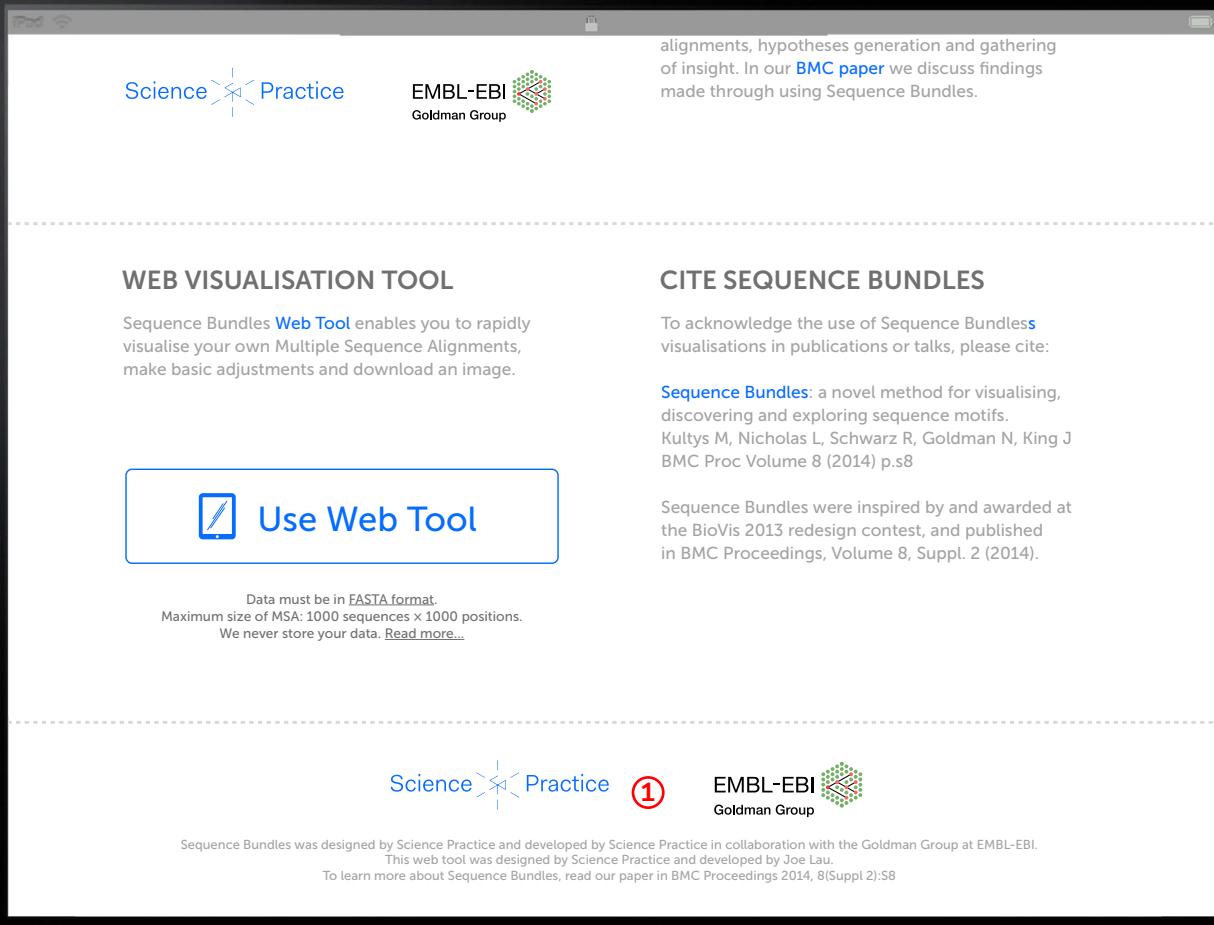
Changes:

1. Add paragraphs in two columns.
2. Add "Making of" image (Asset in ZIP Archive)
3. More content on scroll down.



Changes:

1. In "Who made" paragraph, "Science Practice" link goes to URL:
<http://science-practice.com/> and the "Goldman group" link goes to URL:
<http://www.ebi.ac.uk/research/goldman>
2. Add logos (Assets in ZIP Archive)
3. Link "BMC paper" links to URL: <http://www.biomedcentral.com/1753-6561/8/S2/S8>
4. Link "Web Tool" links to the web tool
5. Button "Use web tool" links to the web tool (Assets in ZIP Archive)
6. "Sequence Bundles" links to URL: <http://www.biomedcentral.com/1753-6561/8/S2/S8>
7. More content on scrolling down...



Changes:

1. Standard footer with logos (Assets in ZIP Archive).