Requirements Gathering

Author	John Gomez Carvajal
Intended Audience	Anyone involved in the creation, modification or replacement of graphical components belonging to EBI groups.
Use	The document contains a form that should be completed. The form within the document is intended to gather all the graphical components requirements for representing biological information on the web.
Keywords	biojs, requirements, questionaire

Reference	Date	Last Reviewed	Description	Version
BIOJS_082011_01	09/08/2011	09/08/2011	Initial draft	1.0

1. Sequence

High level details

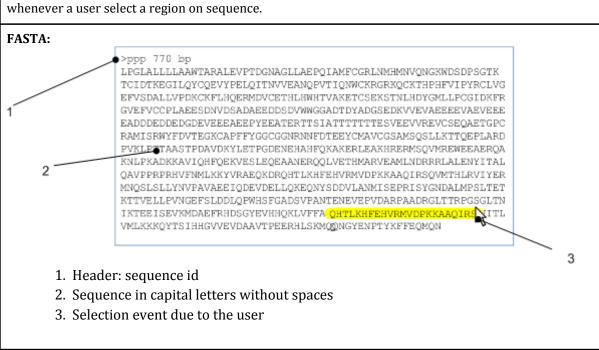|		
1	Component name?	Sequence
2	What kind of multimedia should it show?	Text
3	What pattern must be used? *(i.e. text, tree, table, canvas, accordion …)*	Text area
4	Size?	Default: 200 x 300 Min: 0 x 0 Max: 800 x 600 Resizable: Yes

Style issues

Colors			
	Name	*Default*	*Description*
	defaultFontColor	Black	
	defaultBackgroundColor	White	
	selectionFontColor	Black	
	selectionBackgroundColor	Yellow	
	highlightFontColor	Red	
	highlightBackgroundColor	White	

Fonts?			
	Name	*Default*	
	defaultFont	Courrier New	

Icons?	None

How to draw it?

Please draw a detailed sketch for the component (note that it would be a drawing on paper). Feel free to describe the relevant information.

There are different formats that can be used to display a sequence: FASTA, CODATA, RAW and PRIDE. All of them must raise an *onSelectionChanged* or *onSelectionChange* (detailed in Events section) whenever a user select a region on sequence.
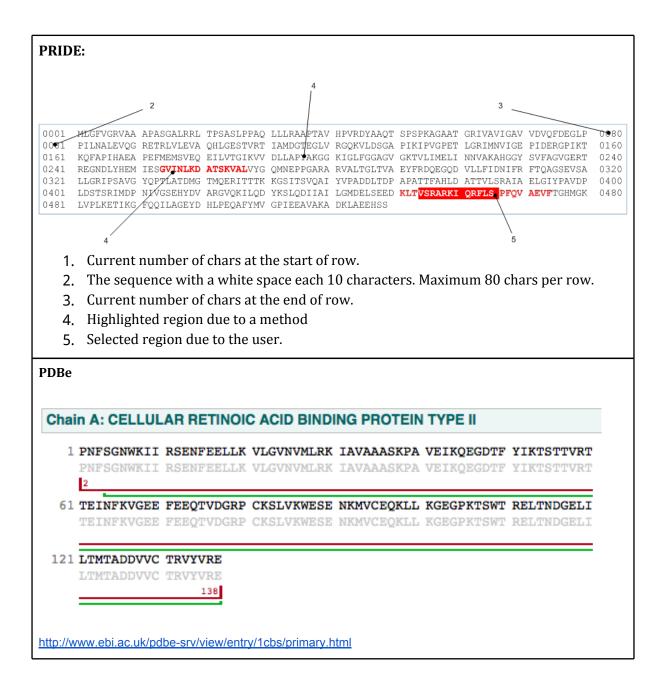
FASTA:

1. Header: sequence id
2. Sequence in capital letters without spaces
3. Selection event due to the user

CODATA:

```
ENTRY            ppp
SEQUENCE
              5        10        15        20        25        30
     1 M L P G L A L L L L A A W T A R A L E V P T D G N A G L L A
    31 E P Q I A M F C G R L N M H M N V Q N G K W D S D P S G T M
    61 T C I D T K E G I L Q Y C Q E V Y P E L Q I T N V V E A N Q
    91 P V T I Q N W C K R G R K Q C K T H P H F V I P Y R C L V G
   121 E F V S D A L L V P D K C K F L H Q E R M D V C E T H L H W
   151 H T V A K E T C S E K S T N L H D Y G M L L P C G I D K F R
   181 G V E F V C C P L A E E S D N V D S A D A E E D D S D V W W
   211 G G A D T D Y A D G S E D K V V E V A E E E E V A E V E E E
   241 E A D D D E D D E D G D E V E E E A E E P Y E E A T E R T T
   271 S I A T T T T W Y F D V T E G K C A P F F Y G G C T G P C
   301 R A M I S R W Y F D V T E G K C A P F F Y G G C G N R N N
   331 F D T E E Y C M A V C G S A M S Q S L L K T T Q E P L A R D
   361 P V K L P T T A A S T P D A V D K Y L E T P G D E N E H A H
   391 F Q K A K E R L E A K H R E R M S Q V M R E W E E A E R Q A
   421 K N L P K A D K K A V I Q H F Q E K V E S L E Q E A A N E R
   451 Q Q L V E T H M A R V E A M L N D R R R L A L E N Y I T A L
   481 Q A V P P R P R H V F N M L K K Y V R A E Q K D R Q H T L K
   511 H F E H V R M V D P K K A A Q I R S Q V M T H L R V I Y E R
   541 M N Q S L S L L Y N V P A V A E E I Q D E V D E L L Q K E Q
   571 N Y S D D V L A N M I S E P R I S Y G N D A L M P S L T E T
   601 K T T V E L L P V N G E F S L D D L Q P W H S F G A D S V P
   631 A N T E N E V E P V D A R P A A D R G L T T R P G S G L T N
   661 I K T E E I S E V K M D A E F R H D S G Y E V H H Q K L V F
   691 F A E D V G S N K G A I I G L M V G G V V I A T V I V I T L
   721 V M L K K K Q Y T S I H H G V V E V D A A V T P E E R H L S
   751 K M Q Q N G Y E N P T Y K F F E Q M Q N
///
```

1. Header: sequence id
2. Horizontal enumeration. It must appear on the top of sequence, counting each 5 chars.
3. Vertical enumeration. It must appear at the beginning of each row, indicating the number of characters before of the current row plus one.
4. Sequence in capital letters, separated by a space. Maximum of 30 characters per row
5. Selection event due to the user

RAW:

```
mlpglallllaawtaralevptdgnagllaepqiamfcgrlnmhmnvqngkwdsdpsgtktcidtkegilqycqevypel
qitnvveanqpvtiqnwckrgrkqckthphfvipyrclvgefvsdallvpdkckflhqermdvcethlhwhtvaketcse
kstnlhdygmllpcgidkfrgvefvccplaeesdnvdsadaeeddsdvwwggadtdyadgsedkvvevaeeeevaeveee
eadddeddedgdeveeeaeepyeeaterttsiattttttesveevvrevcseqaetgpcramisrwyfdvtegkcapff
yggcggnrnnfdteeycmavcgsamsqsllkttqeplardpvklpt vdpkkaaqirsqvmthlrviyermnqskerlea
khrermsqvmreweeaerqaknlpkadkkaviqhfqekvesleqeanerqqlvethmarveamlndrrrlalenyital
qavpprprhvfnmlkkyvraeqkdrqhtlkhfehvrmvdpkkaaqirsqvmthlrviyermnqslsllynvpavaeeiqd
evdelqkeqnysddvlanmiseprisygndalmpsltetkttvellpvngefslddlqpwhsfgadsvpanteneveypv
darpaadrglttrpgsgltniktteeisevkmdaefrhdsgyevhhqklvffaedvgsnkgaiiglmvggvviatvivitl
vmlkkkqytsihhgvvevdaavtpeerhlskmqqngyenptykffeqmqn
```

1. Sequence in lower case letters
2. onSelectionChanged event

PRIDE:

```
0001  MLGFVGRVAA APASGALRRL TPSASLPPAQ LLLRAAPTAV HPVRDYAAQT SPSPKAGAAT GRIVAVIGAV VDVQFDEGLP 0080
0081  PILNALEVQG RETRLVLEVA QHLGESTVRT IAMDGTEGLV RGQKVLDSGA PIKIPVGPET LGRIMNVIGE PIDERGPIKT 0160
0161  KQFAPIHAEA PEFMEMSVEQ EILVTGIKVV DLLAPYAKGG KIGLFGGAGV GKTVLIMELI NNVAKAHGGY SVFAGVGERT 0240
0241  REGNDLYHEM IESGVINLKD ATSKVALVYG QMNEPPGARA RVALTGLTVA EYFRDQEGQD VLLFIDNIFR FTQAGSEVSA 0320
0321  LLGRIPSAVG YQPTLATDMG TMQERITTTK KGSITSVQAI YVPADDLTDP APATTFAHLD ATTVLSRAIA ELGIYPAVDP 0400
0401  LDSTSRIMDP NIVGSEHYDV ARGVQKILQD YKSLQDIIAI LGMDELSEED KLTVSRARKI QRFLSQPFQV AEVFTGHMGK 0480
0481  LVPLKETIKG FQQILAGEYD HLPEQAFYMV GPIEEAVAKA DKLAEEHSS
```

1. Current number of chars at the start of row.
2. The sequence with a white space each 10 characters. Maximum 80 chars per row.
3. Current number of chars at the end of row.
4. Highlighted region due to a method
5. Selected region due to the user.

PDBe

Chain A: CELLULAR RETINOIC ACID BINDING PROTEIN TYPE II

```
  1 PNFSGNWKII RSENFEELLK VLGVNVMLRK IAVAAASKPA VEIKQEGDTF YIKTSTTVRT
    PNFSGNWKII RSENFEELLK VLGVNVMLRK IAVAAASKPA VEIKQEGDTF YIKTSTTVRT
    2

 61 TEINFKVGEE FEEQTVDGRP CKSLVKWESE NKMVCEQKLL KGEGPKTSWT RELTNDGELI
    TEINFKVGEE FEEQTVDGRP CKSLVKWESE NKMVCEQKLL KGEGPKTSWT RELTNDGELI


121 LTMTADDVVC TRVYVRE
    LTMTADDVVC TRVYVRE
                138
```

http://www.ebi.ac.uk/pdbe-srv/view/entry/1cbs/primary.html

Input data

Name	Mandatory	Type	Description
sequence	yes	string	raw text
target	yes	string	identifier of the <div> where the component must be displayed.

Events

Please specify which events must be listened and which ones must be triggered by the component , and what must be the response/action must realise. Answer the following questions for each event:

What is the type of the event?

Which key was pressed during the event?
Which mouse button was pressed during the event?
What was the mouse position during the event?
What is the response of the component? step-by-step

Name	Key/Mouse button(s)	Position	Response
onSelectionChanged	Left + Drag	Within the text sequence	This event must be raised whenever the user clicks, drags and releases the mouse within the sequence. 1. Reset both the background and the font colors of the entire sequence. 2. Change the selected text using *fontSeletedColor and backgroundSelectedColor* for the font and the background, respectly. 3. Determine both positions the initial and the final of the selected text. 4. Raise an event to registered listeners containing the positions: <table><tr><td>*name*</td><td>*type*</td><td>*description*</td></tr><tr><td>start</td><td>int</td><td>starting position</td></tr><tr><td>end</td><td>int</td><td>final position</td></tr></table>

Methods

Name	Arguments	Action

highlight					Change both the background and the font colors between initial and final positions.
	Name	*M*	*Type*	*Description*	
	start	yes	int	Initial position in the sequence	
	end	yes	int	Final position in the sequence	
	fontColor	no	string	HTML color code for the font of the selected text. By default is the value of *fontHighlightedColor*. *example: #FF0000*	
	backgroundColor	no	string	HTML color code for the background of the selected text. By default is the value of *backgroundHighlightedColor* *example: #FF0000*	

unHighlight					Reset both the background and the font colors between initial and final positions.
	Name	**M**	**Type**	**Description**	
	start	yes	int	Initial position in text	
	end	yes	int	Final position in text	

unHighlightAll	None	Reset both the background and font colors for entire sequence.

select					Raise the event onSelectionChanged.
	Name	**M**	**Type**	**Description**	
	start	yes	int	Initial position in text	
	end	yes	int	Final position in text	

unSelect	None	Reset the current selection

Glosary

Sequence: Is a string of letters representing a real or hypothetical nucleic acid molecule or strand.

FASTA: text-based format for representing either nucleotide sequences or peptide sequences, in which nucleotides or amino acids are represented using single-letter codes. The format also allows for sequence names and comments to precede the sequences.

CODATA