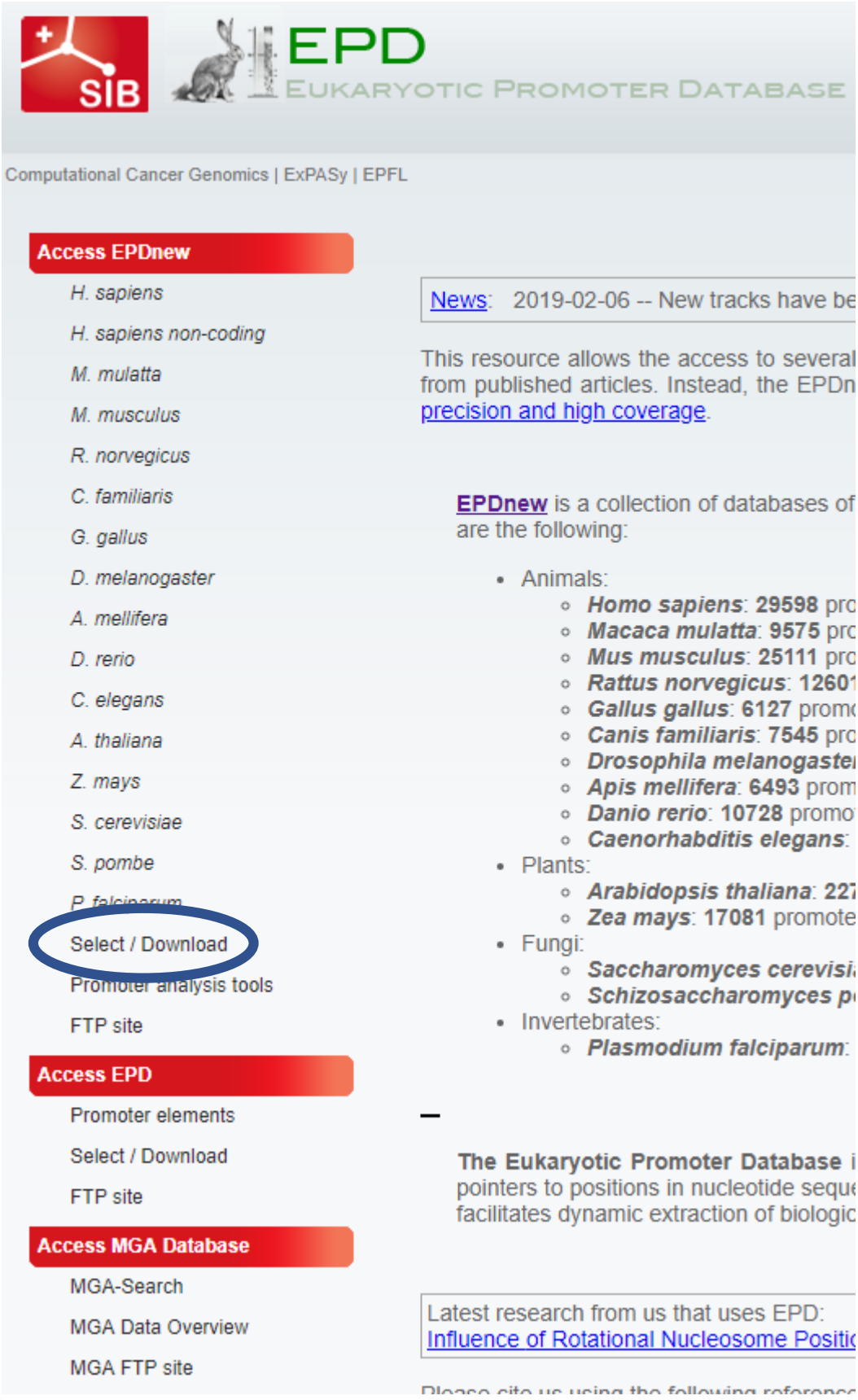
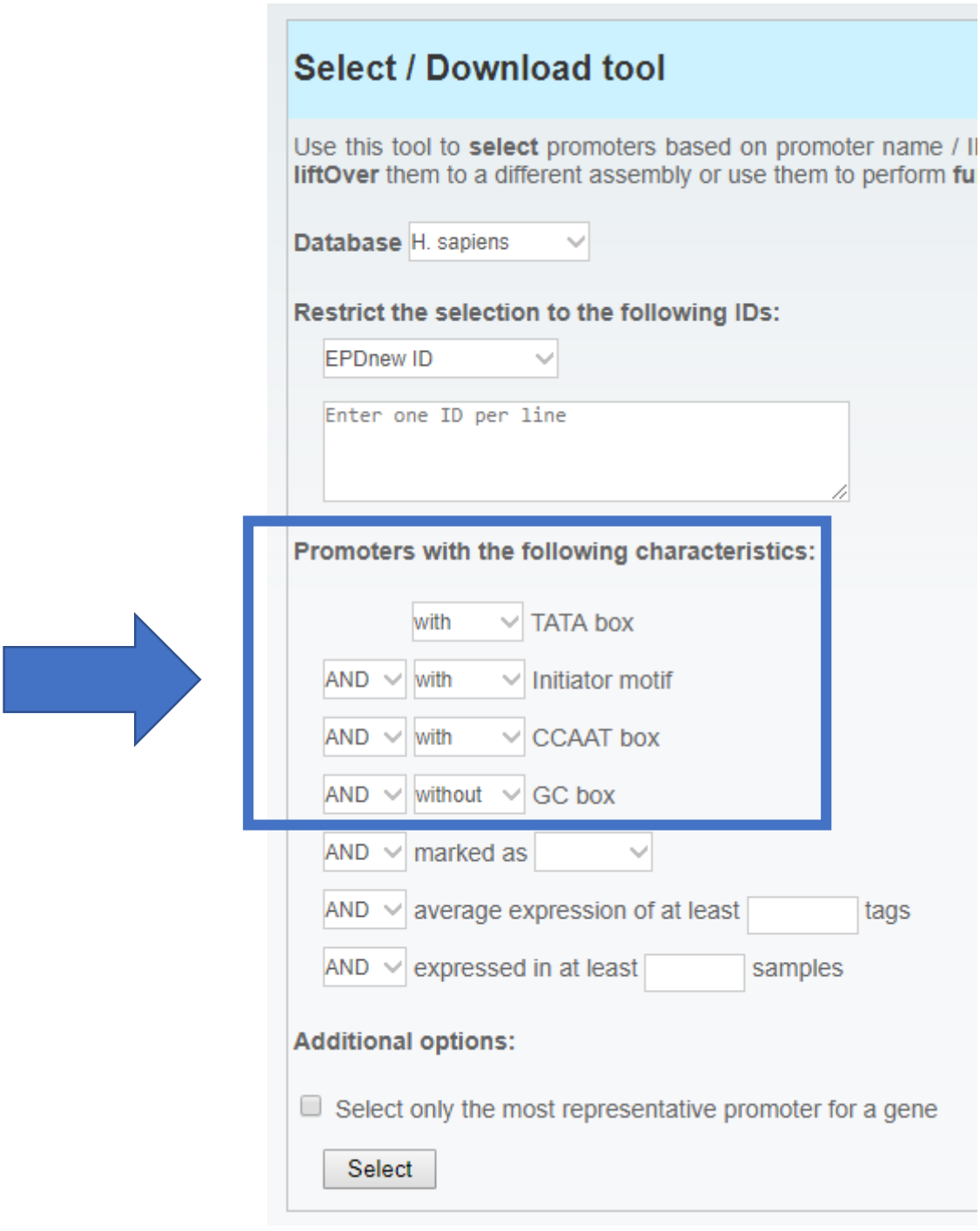
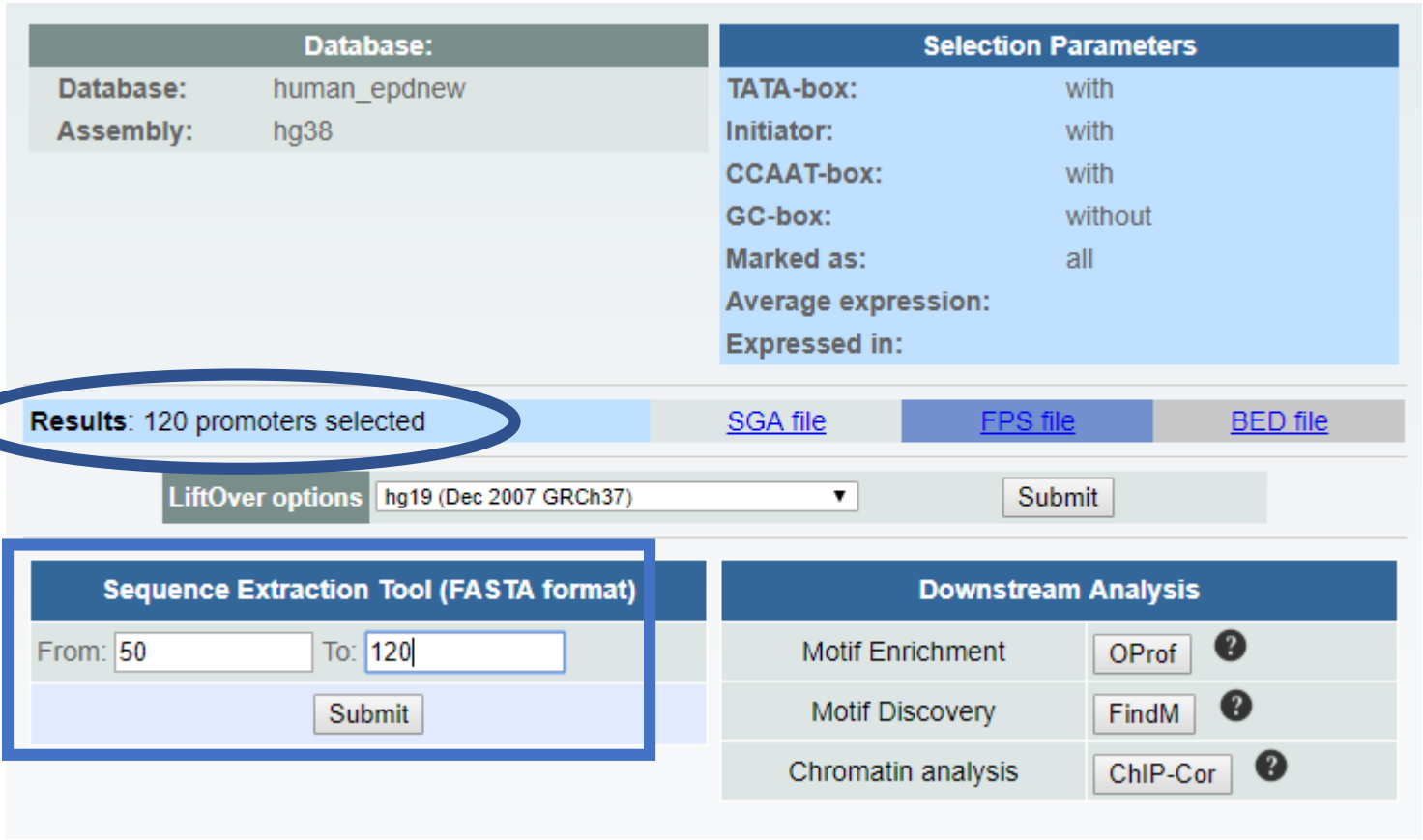
Navigate to https://epd.epfl.ch//index.php
Then click on Select / Download



Choose any combination of the four highlighted boxes and click ‘select’



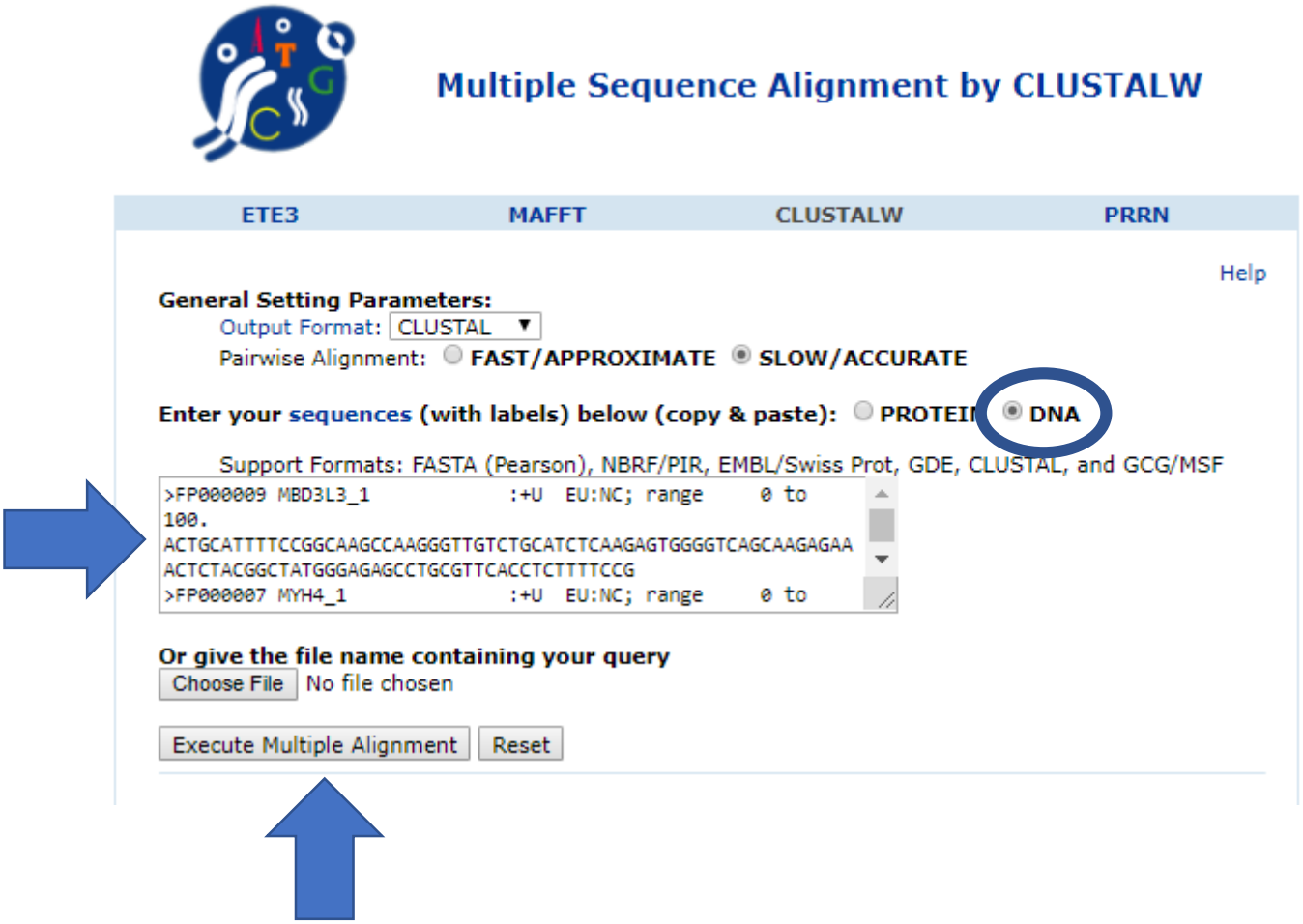
Note how many promoters are selected (circled)
Choose the start and end base to extract then hit ‘submit’ to get the fasta



Now we need to align the sequences we got. Copy the entire fasta output and go to https://www.genome.jp/tools-bin/clustalw

Paste the output in the text box and select the DNA check box, then hit ‘Execute Multiple Alignment’.

```
>FP000093 TUBB3_1              :+U  EU:NC; range  -499 to   100.
GGGCCAGCCTTTACCTACCTCCCCCACCCAAAACCGGCAAAAGCTCAGAGCACCTTGTCT
GCCAAAAGACAGGGAGCTGGGATGGTGCGGGTTGGTCTCTAAACCGGCGTGGGGAAAAAA
GACCCTCCGTACAAAGCCGCAGGGTGGGGCTGTCGCAAGGGCGGAACCGAGAGGGTAGCT
GGGGGCGGGGTTCCCAGGGCCAAGAGGGGCCATTGTCCTCCCTGGAGCCCGGCGCCCCCA
CAGCCAGCTCCTCTGGGAGACAGCCCCTCCTTTCGAATGCGCGGGGCCCTCAGACCGCGC
CCGGCCCAGCGCTGGGGGATCCTTGGCTGCGGGAGGGGCGCCGCATTGCGCGCGGCGGGC
GGGGACGCGCGGTGCGGAGCCTGCGGGCCGGGCGGGGCTCTGCGGCGGCGCCTCCCGATT
GGCCACCCGCGGTGACATCAGCCGATGCGAAGGGCGGGGCCGCGGCTATAAGAGCGCGCG
GCCGCGGTCCCCGACCCTCAGCAGCCAGCCCGGCCCGCCCGCGCCCGTCCGCAGCCGCCC
GCCAGACGCGCCCAGTATGAGGGAGATCGTGCACATCCAGGCCGGCCAGTGCGGCAACCA
>FP000052 STC1_1              :+U  EU:NC; range  -499 to   100.
ATGTACACACAGAGAAGATAGGGAGTTATTGCATTTGTAGCCTACAAAACAGAACCGAGA
ATGTGCTGTTAAAATTAGAGTAAAACTGCTGTAAGCAGGTTAAGTTCTCATCTAAAGAGA
TCACATTTCCCCACCATACCCCTGCTATCCATTTCCCCCAAGTGGCTCATTAGAAAAAAA
GATGGCTAGATTTCAAAAAGCAACTTGGAGAGATTTCTATAGGATTTTTCTTTAGTTCAA
TCAATACAGAGTTATCTCTTACTTCCACGAAAATAGCTTTTTCACACATCTCTGCACACA
CAGTCACACACACATATAAAACATTGGCAGCAGGTACTTTTAATTTGCTGGAAAATATTT
CTAAGAAGTCAAAAAGCTCCAGCTGAATTGCATGCCCTCTTATTGGCTCACCAGACCAGT
TGAGGGACCTGATTGGTCCTTGATCCTGAGGACCGATAAGAACGGCTATAAAATCCCTGG
GTGCAGCTCTTGGGCCCCCAGTTTGCAAAAGCCAGAGGTGCAAGAAGCAGCGACTGCAGC
AGCAGCAGCAGCAGCGGCGGTGGCAGCAGCAGCAGCAGCGGCGGCAGCAGCAGCAGCAGC
```



Finally, we'll take our multiple sequence alignment and create a sequence Logo using WebLogo. Copy the multiple sequence alignment (like the example Below), then go to https://weblogo.berkeley.edu/logo.cgi

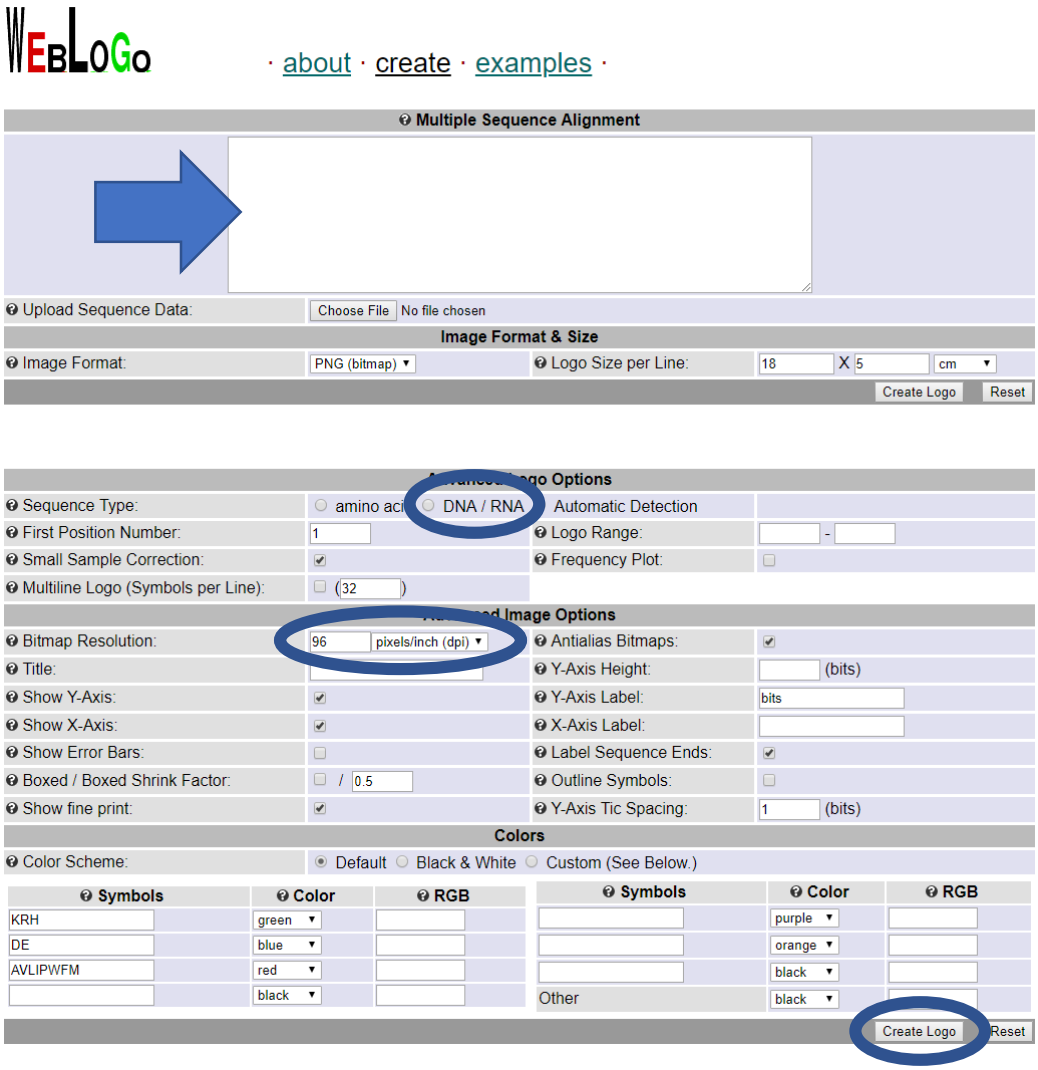
Paste the multiple sequence alignment into the box at the top, then select DNA/RNA, increase the bitmap resolution and hit create logo

```
clustalw.aln

CLUSTAL 2.1 multiple sequence alignment


FP000009        ------------------ACTGCATTTTCC----GGCAAGCCAAGGGTTGTCTGCATCTC
FP000008        ------------------ACTGCATTTTCC----GGCAAGCCAAGGGTTGTCTGCATCTC
FP000005        ------------------ACTCTGCCTTTG----GACGTGAGAGAGAGCGCACCTTTCAC
FP000003        ------------------ACTCTGCCTTTG----GACGTGAGAGAGAGCGCACCTTTCAC
FP000001        --------------ATCTGCTCTGACTCCCCAGGGACGTGTCTGTGCTCCTGCGTGTGAC
FP000006        AGCACAGTTGAGTCTCCAGCCTTGACTCTTC--TCAAGAGCCTGTGACTTTCCTC----C
FP000002        --------------ATCATCTTGGTCATCAACACAACTTGCTTCTCTCCAGACTTGGGCT
FP000004        --------------AGCCTCTCCCAGCCCCAGCAAGCGACCTGTCAGGCGGCCGTGGACT
FP000007        ------------------------ATCCTTCCTCAAAATTCTTGAAGGTATGTATATGTG
FP000010        ------------------AGCAGACAGAGAGAGGAGGTTGTCTGGGACAGACTGCTCCT


FP000009        AAGAGTGGG-GTCAGCAAGAGAAACTCTACGGCTATGGGAGAGC-CTGCGTTCACCTCTT
FP000008        AAGAGTGGG-GTCAGCAAGAGAAACTCTACGGCTATGGGAGAGC-CTGCGTTCACCTCTT
FP000005        TTGAGCT----TCAACATGGGAAAG-----GGAAATGAAGACCC-CGATCTCCACTGCTC
FP000003        TTGAGCT----TCAACATGGGAAAG-----GGAAATGAAGACTC-CGATCTCCACTGCTC
FP000001        CAGGGTGAGTGGCAACCTGGGATACCAGAGGGGTATGAGCAAGG-CAGAGGG-ATGG---
FP000006        CTGGACAAA-GGCATCATGAGTTGTC--AGATCTCTTGCAAATC-TCGAGG---------
FP000002        TAAGGTA----CTGCGTTTACATACAGCAAAATTGCTATCATTT-TACATTATCTAATCT
FP000004        CAGACTC----CGGAGATGAAGCCCCTGCTCCTGGCCGTCAGCC-TTGGCCTCATTGCTG
FP000007        GAAGAACAC--TTACTTTTACATTCCTGATGATGATGATTTTTCATTTAAGGGATGTCTA
FP000010        GACAGAAGGTGCCAGGCTGGGG-GTGGCAGGCCTGGGGGGGGTCCTGGCCTGGGATGGAG
```



And there’s a representative output! There are many parameters you can modify, for example if you have a very long sequence logo but you see something interesting, you can zoom in on that area by changing the Logo Range
parameter. You can also modify the multiple alignment parameters to get slightly
different alignment outputs. Play around and see how different combinations of promoters, alignment parameters and logo output parameters change your final image.