

There are 9 regions from the wheat genome (triticum aestivum ) to annotate.

The annotation project is to be submitted by groups of 2 or 3:

think about the potential difficulties of annotating wheat before you start predicting genes (hexaploid genome, homeologous genes, 80% of transposable elements)

you must completely annotate the given sequence:

- genes: complete coordinates of intron-exon structure and UTR, , validation by the presence of transcribed sequences and/or homologous genes. [mRNA, RNAseq](#)
- proteins : potential protein functions, motifs and domaines [analyze blast results, also go back to publications to analyze the biological functions \(not just biochemical ones\)](#)
- transposable elements: [coordinates](#) and [family](#) of the transposable element. [only these 2, not the complete seq](#)

The report must be written in laboratory notebook format. It must be made in such a way that I can repeat the analysis you have carried out with all parameters for each tool [write each step of the project, define the technical part of the tools \(with all the parameters\) define each tool u use for annotation, why this and not that can add some screenshots, make tables... no limitation](#)

Send me a table with the names in each groups and the sequence to be annotated.

deadline : end of december, submission on ecampus

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