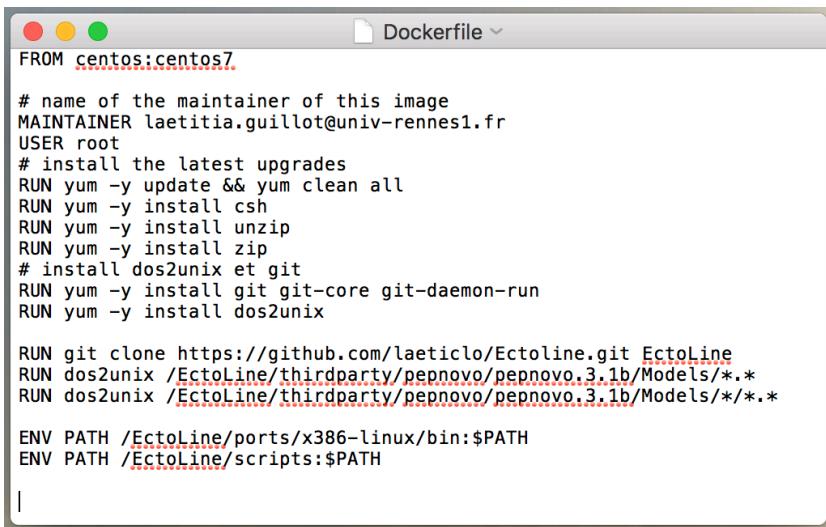


A.



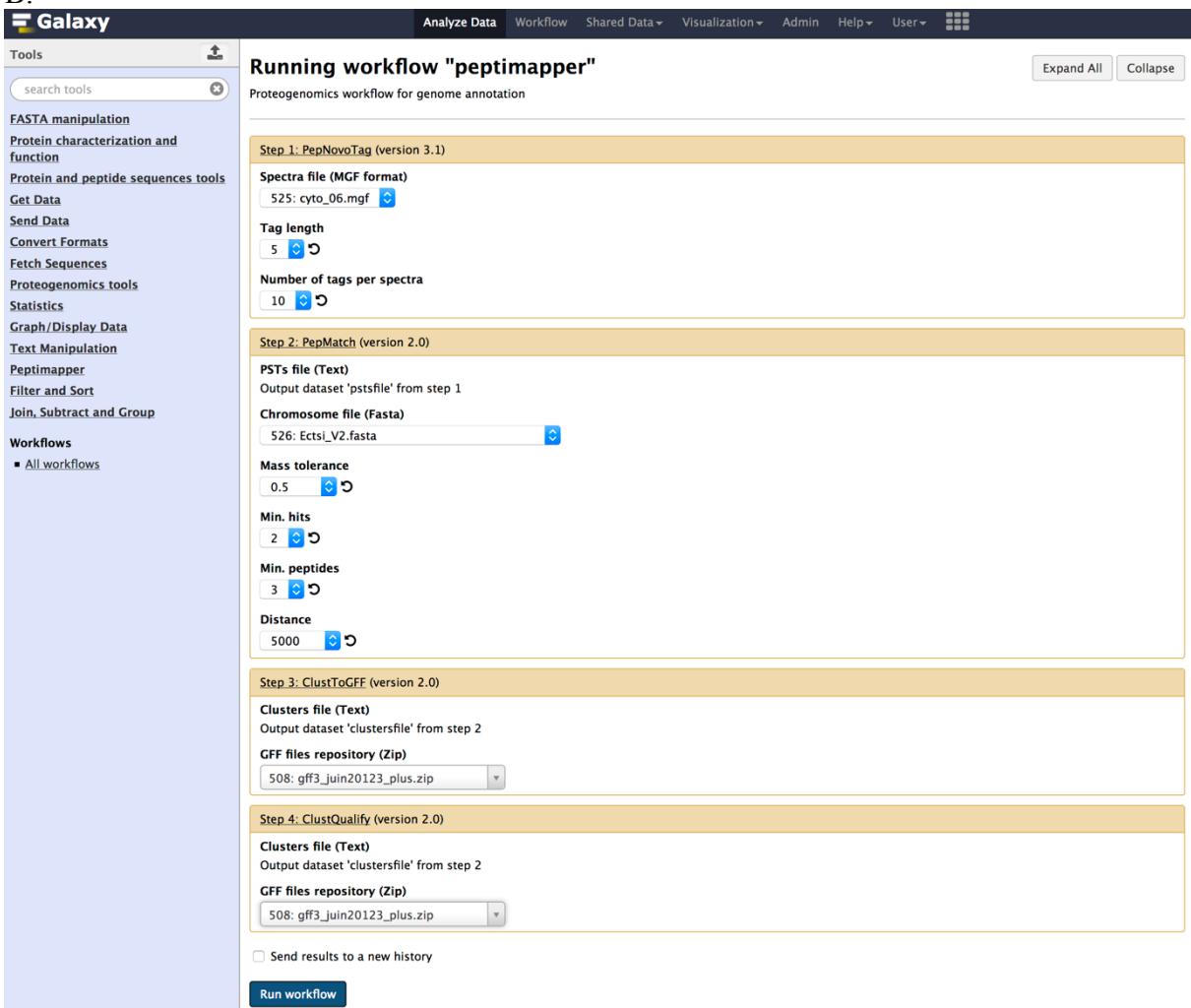
```
FROM centos:centos7

# name of the maintainer of this image
MAINTAINER laetitia.guillot@univ-rennes1.fr
USER root
# install the latest upgrades
RUN yum -y update && yum clean all
RUN yum -y install csh
RUN yum -y install unzip
RUN yum -y install zip
# install dos2unix et git
RUN yum -y install git git-core git-daemon-run
RUN yum -y install dos2unix

RUN git clone https://github.com/laeticlo/Ectoline.git EctoLine
RUN dos2unix /EctoLine/thirdparty/pepnovo/pepnovo.3.1b/Models/*.*
RUN dos2unix /EctoLine/thirdparty/pepnovo/pepnovo.3.1b/Models/*/*.*

ENV PATH /EctoLine/ports/x86-linux/bin:$PATH
ENV PATH /EctoLine/scripts:$PATH
```

B.



The screenshot shows the Galaxy web interface with a workflow titled "peptimapper". The workflow is designed for genome annotation and consists of four steps:

- Step 1: PepNovoTag (version 3.1)**
 - Spectra file (MGF format): 525: cyto_06.mgf
 - Tag length: 5
 - Number of tags per spectra: 10
- Step 2: PepMatch (version 2.0)**
 - PSTs file (Text): Output dataset 'pstsfle' from step 1
 - Chromosome file (Fasta): 526: Ectsi_V2.fasta
 - Mass tolerance: 0.5
 - Min. hits: 2
 - Min. peptides: 3
 - Distance: 5000
- Step 3: ClustToGFF (version 2.0)**
 - Clusters file (Text): Output dataset 'clustersfle' from step 2
 - GFF files repository (Zip): 508: gff3_juin20123_plus.zip
- Step 4: ClustQualify (version 2.0)**
 - Clusters file (Text): Output dataset 'clustersfle' from step 2
 - GFF files repository (Zip): 508: gff3_juin20123_plus.zip

At the bottom of the workflow interface, there is a checkbox labeled "Send results to a new history" and a blue "Run workflow" button.

