

CREATING FUNCTION LOGOS, ID LOGOS, KLD LOGOS AND BUBBLE PLOT TABLE WITH TSFM

1. The input is ready in folder 74sites.
2. For generating the logos of site74 we only need this folder which has 9 subfolders one for each class of TriTryp genomes, and Homo. Each of these folders include the fasta files for 21 classes of tRNA.
3. Keep the file **tRNA_L_skel_Leish_sites74_struct.txt** and the script **generateLogos.sh** inside folder 74sites.
4. In script generateLogos.sh, change the variable **tsfmpath** to the tsfm.py on your laptop as the example. The last version of tsfm is provided in folder tsfm, you can provide the path to tsfm.py from this folder.
5. Finally:


```
cd workflow/74sites
chmod +x generateLogos.sh
./generateLogos.sh
```

 This should create ID logos, KLD logos along with the table at the same time.
Then it will move each group into a directory
6. Later, I used the **bubbleV2.R** to generate the bubble plots one pdf file per functional class. This version of all.bubble.R script will take three path to skel file, tables, and output file and reads all the tables from folder 74sites, aligns them to sprinzl using the tRNA_L_skel_Leish.sites74.txt file and creates the bubble plots. All the outputs will be in directory /74sites/Logos.