

Report the length of both M1 and M2 models (1 point).

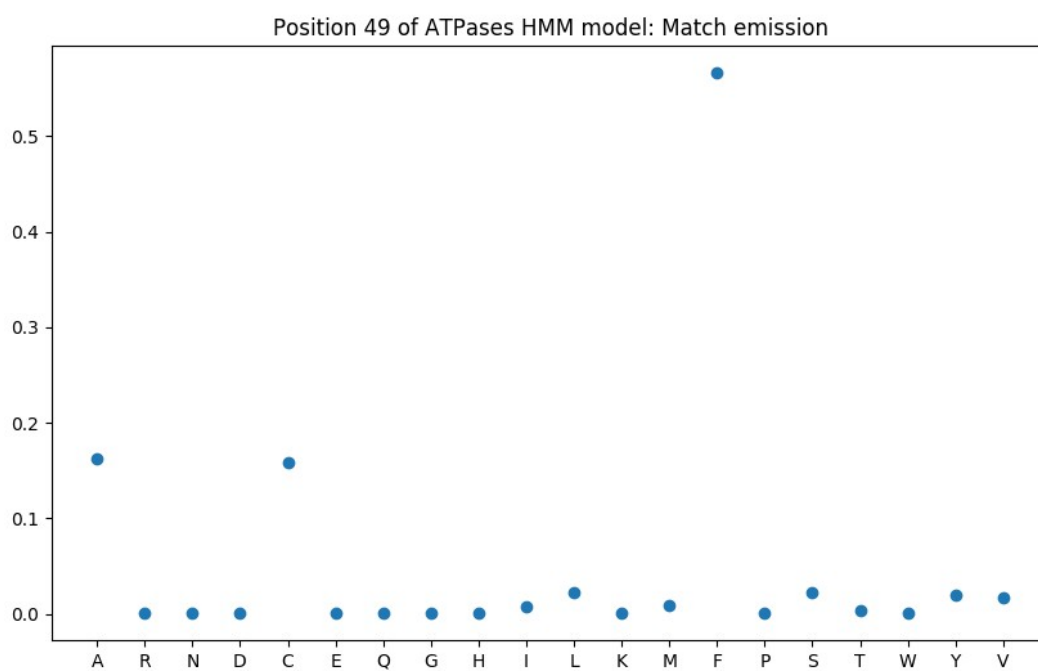
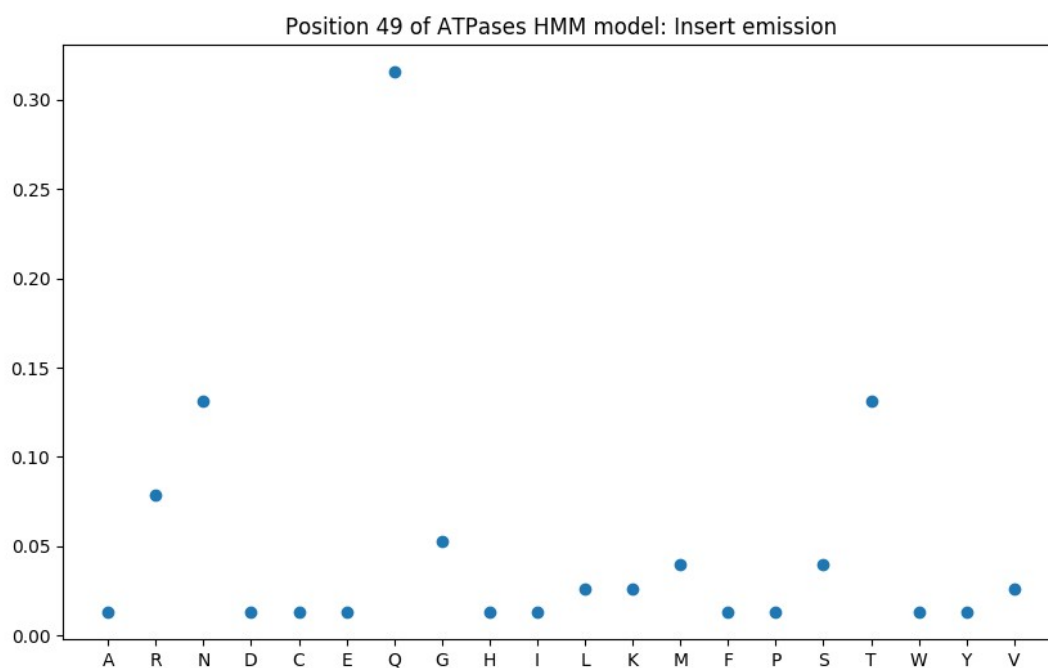
```
ATPase model len: 81  
GTP model len: 115
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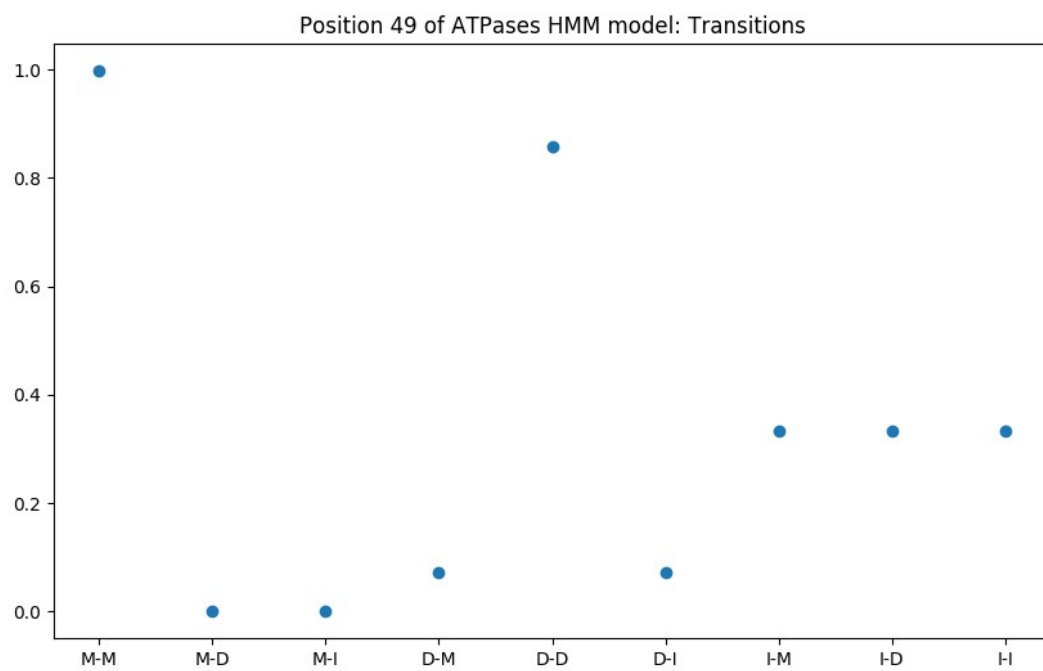
Report the dimensions of your T, mE and iE for both models (1 point)

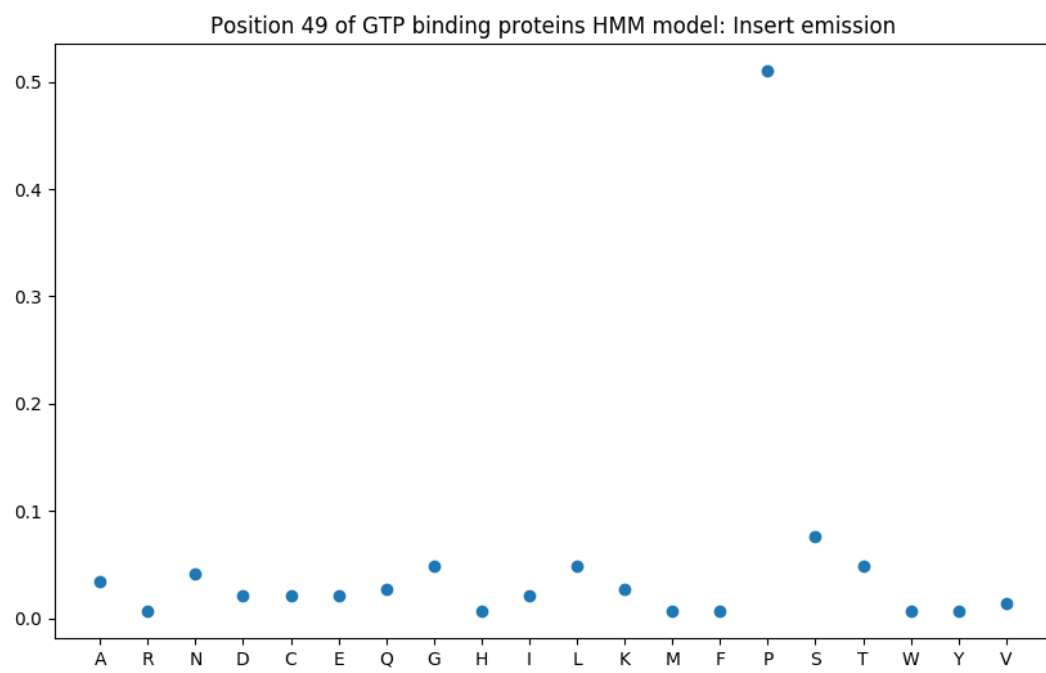
```
ATPase T, mE, iE shapes: (9, 82), (20, 82), (20, 82)  
GTP T, mE, iE shapes: (9, 116), (20, 116), (20, 116)
```

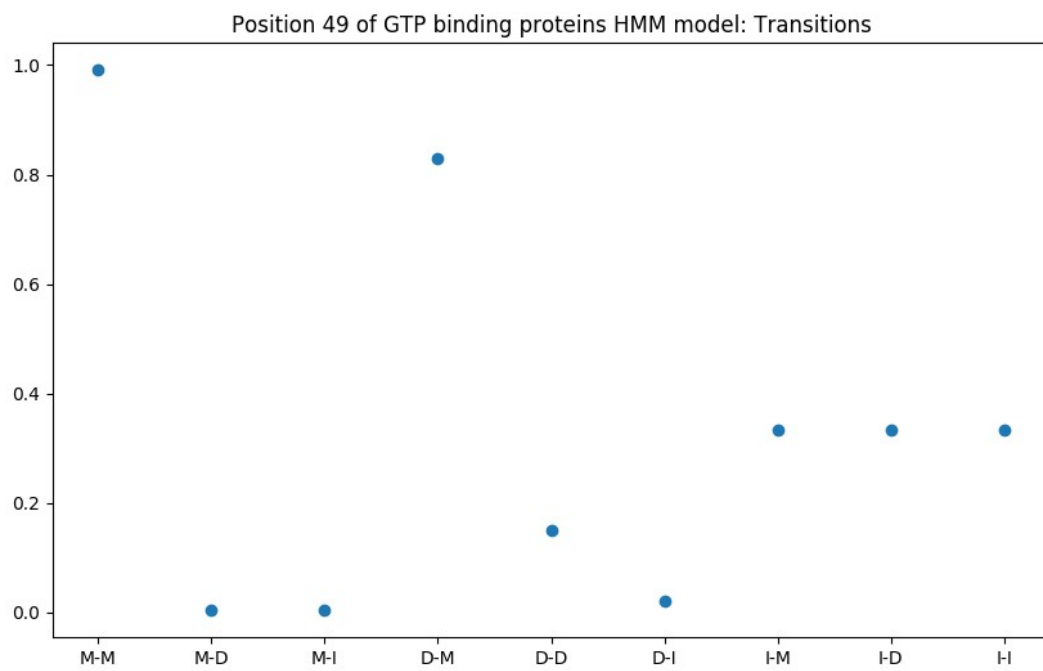
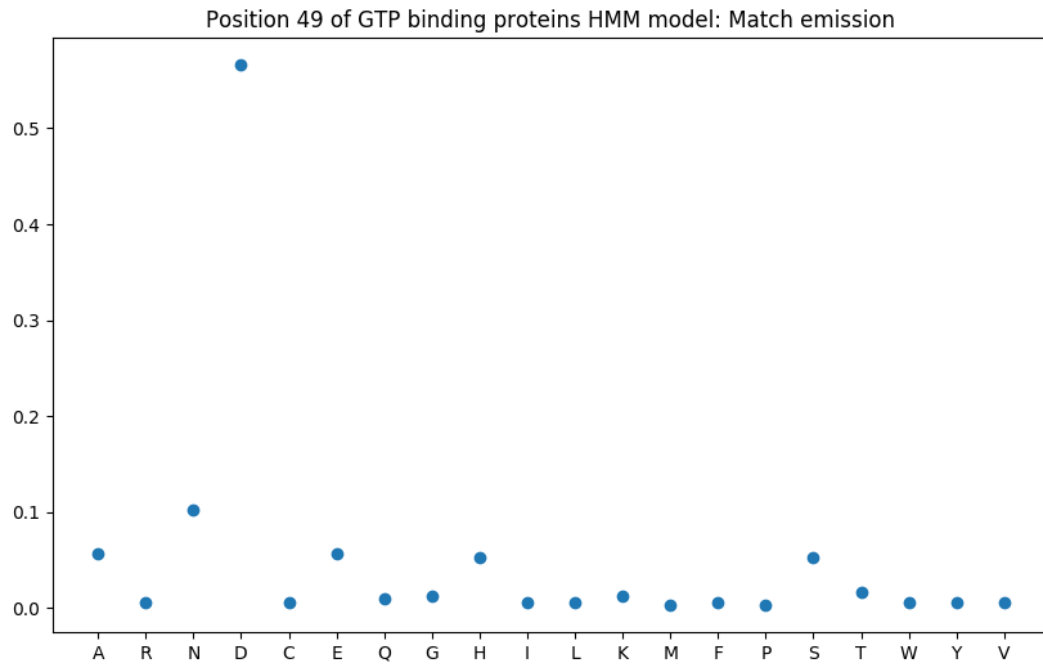
For position 50 in each model, plot the transition and emission frequencies. (3 points)

I printed position. I am not sure because 49 is more interesting so I attached also this one. There is difference in lists in python: starts from zero, it corresponds to your example. If you wanted position number 50 in R notation it is described as position 49.

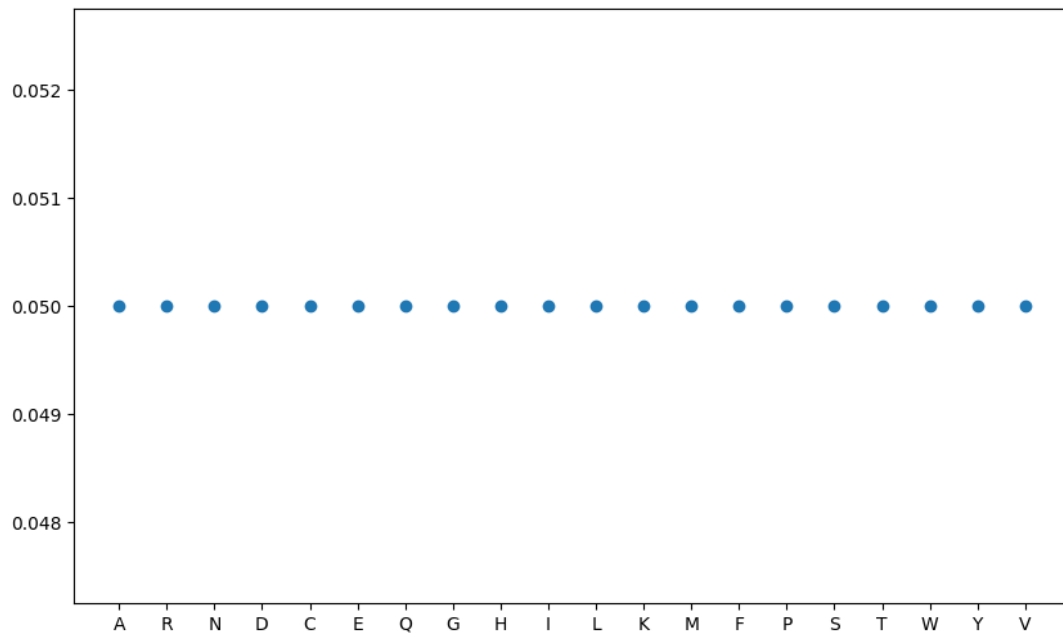




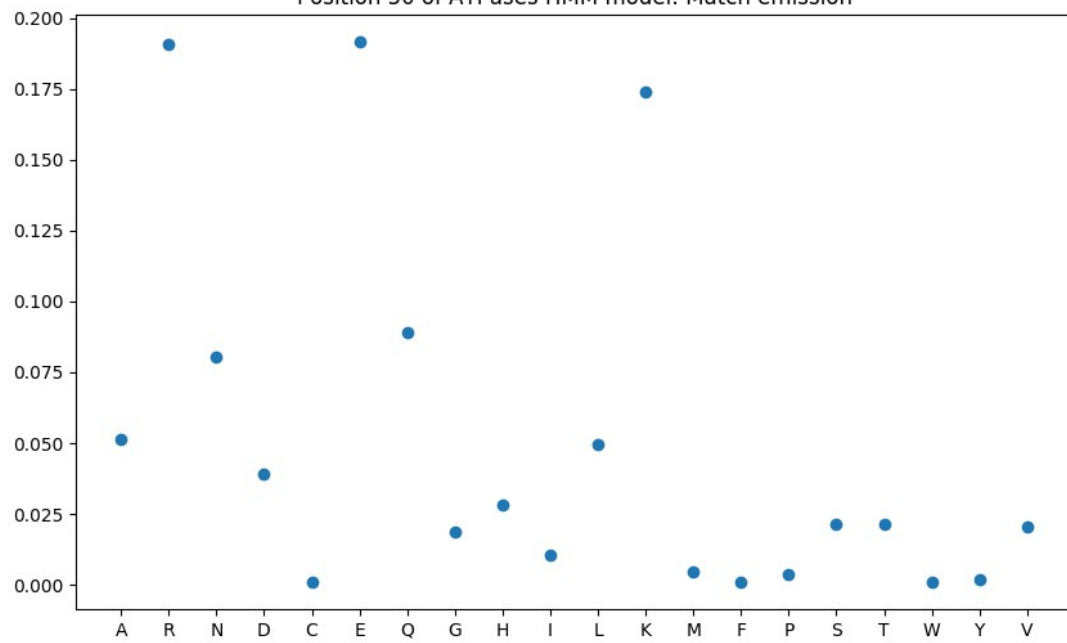


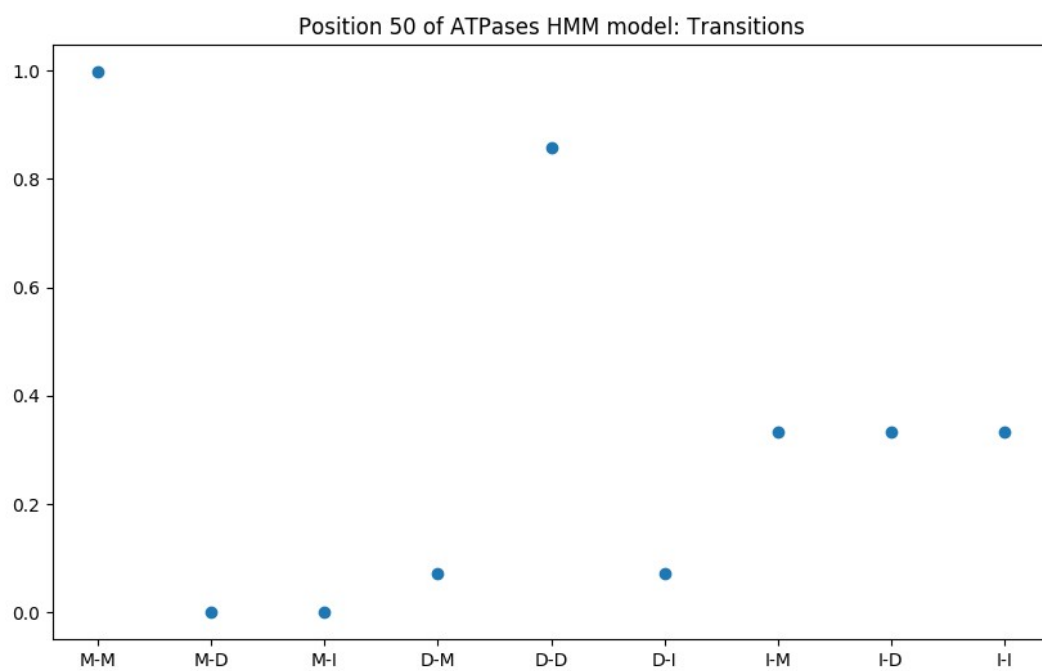


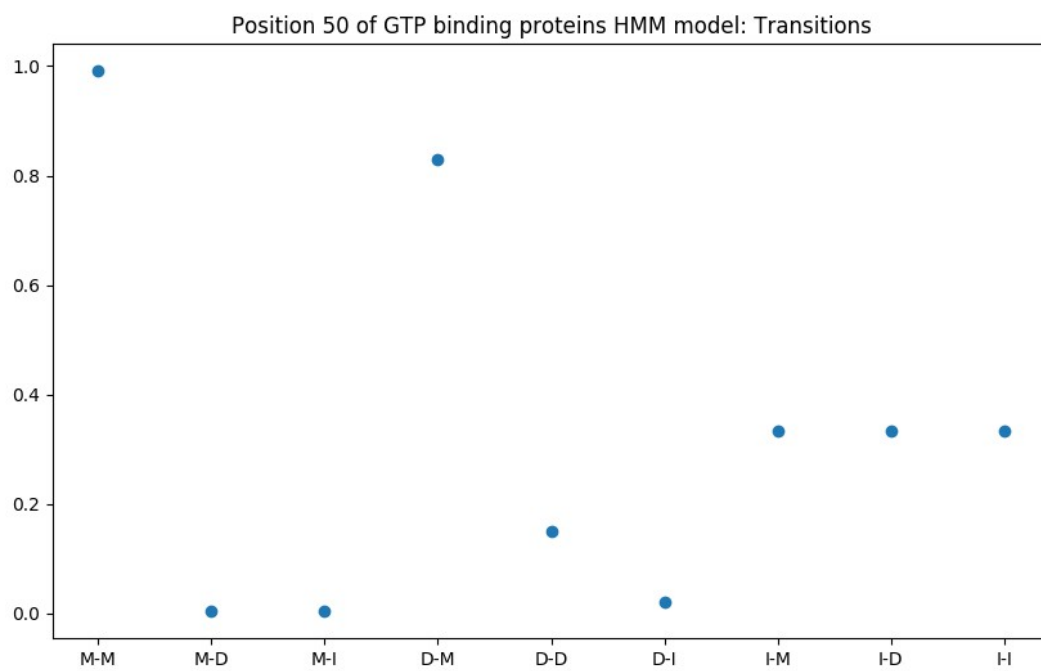
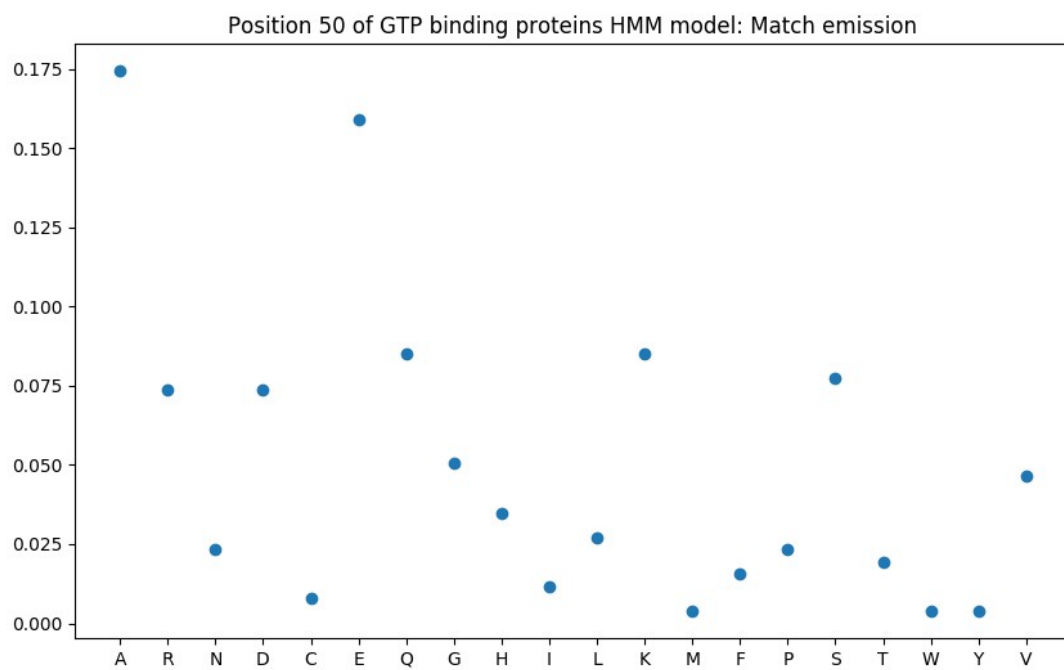
Position 50 of ATPases HMM model: Insert emission



Position 50 of ATPases HMM model: Match emission

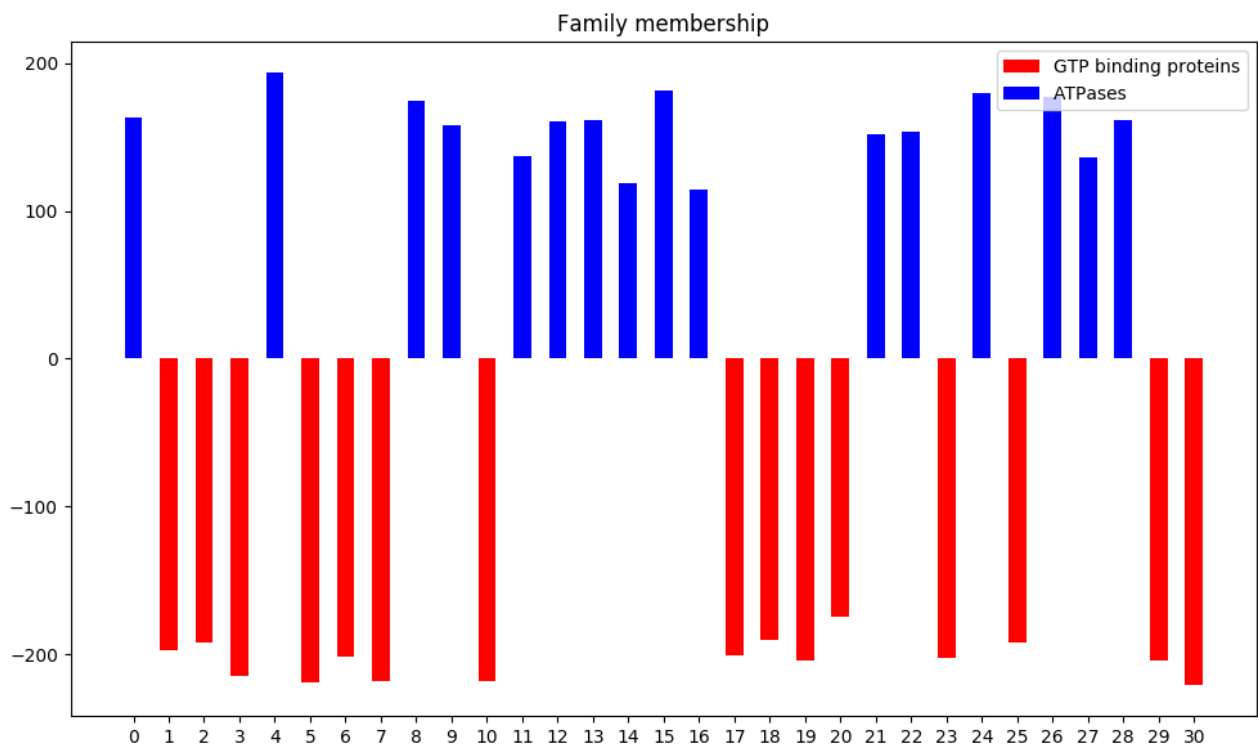








Plot the values  $q(x_i)$  and include this in your report. Which proteins in the list belong to which family? Can you clearly decide for each protein? (5 points)



I can really clearly decide to which class given proteins belong.