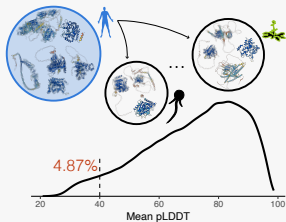


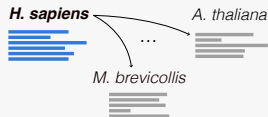
## A. Input

1 seed species (*H. sapiens*)  
+ 17 eukaryotic species

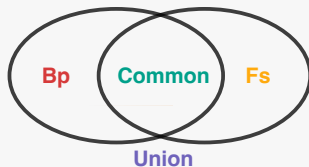
Excluding proteins with  
poor quality structures



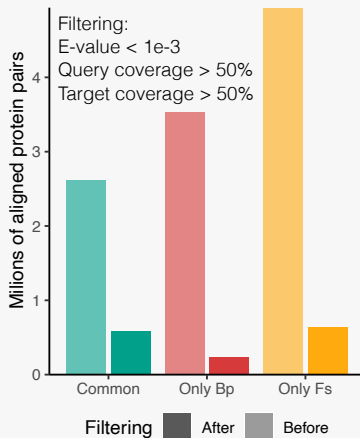
19,555 *H. sapiens* seeds vs  
325,576 proteins



## B. Homology search

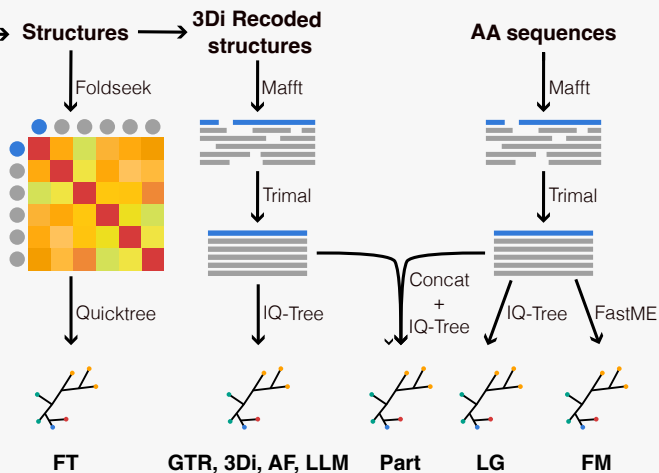


4 target sets  
1000 seeds\*



## C. Tree reconstruction method

For each seed:



- Compare distance to species tree (RF distance)
- Compute Quartet Frequencies (Astral-PRO)
- Count gene duplications and losses (Notung)