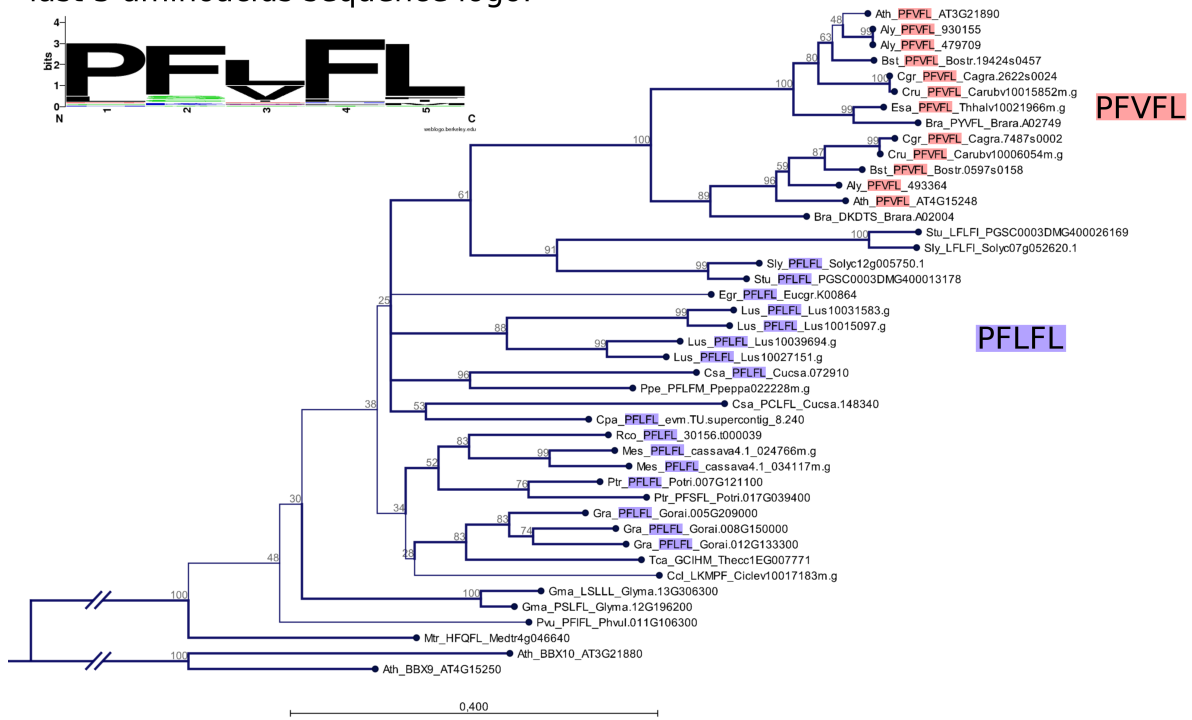


last 5 aminoacids sequence logo:



Suppl. Fig. S16. Phylogenetic tree. ClustalW-alignment of miP1a/b-type protein sequences. The tree was created using the Neighbor-joining method with 1000 bootstrap replications. Branches equal or bigger 0.25 are shown, branches >0.5 are shown in bold.