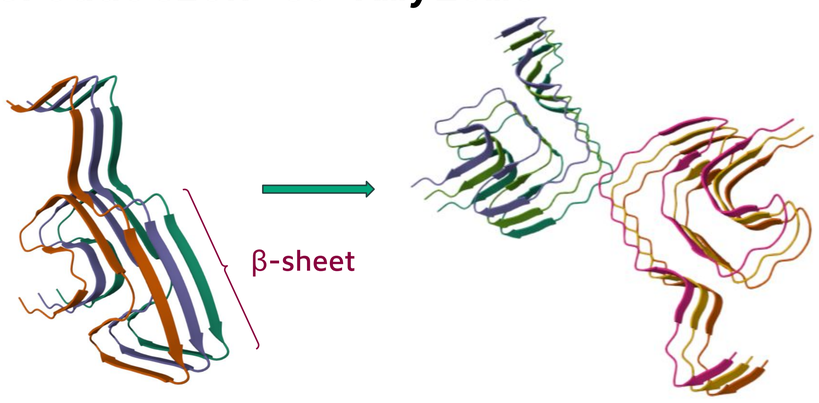
Bloom of Amylome | *LAB15*

Sabancı Üniversitesi

School of molecular and theoretical biology

Introduction to Amylome



Three peptide chains in a protofilament — Mature amyloid fibril

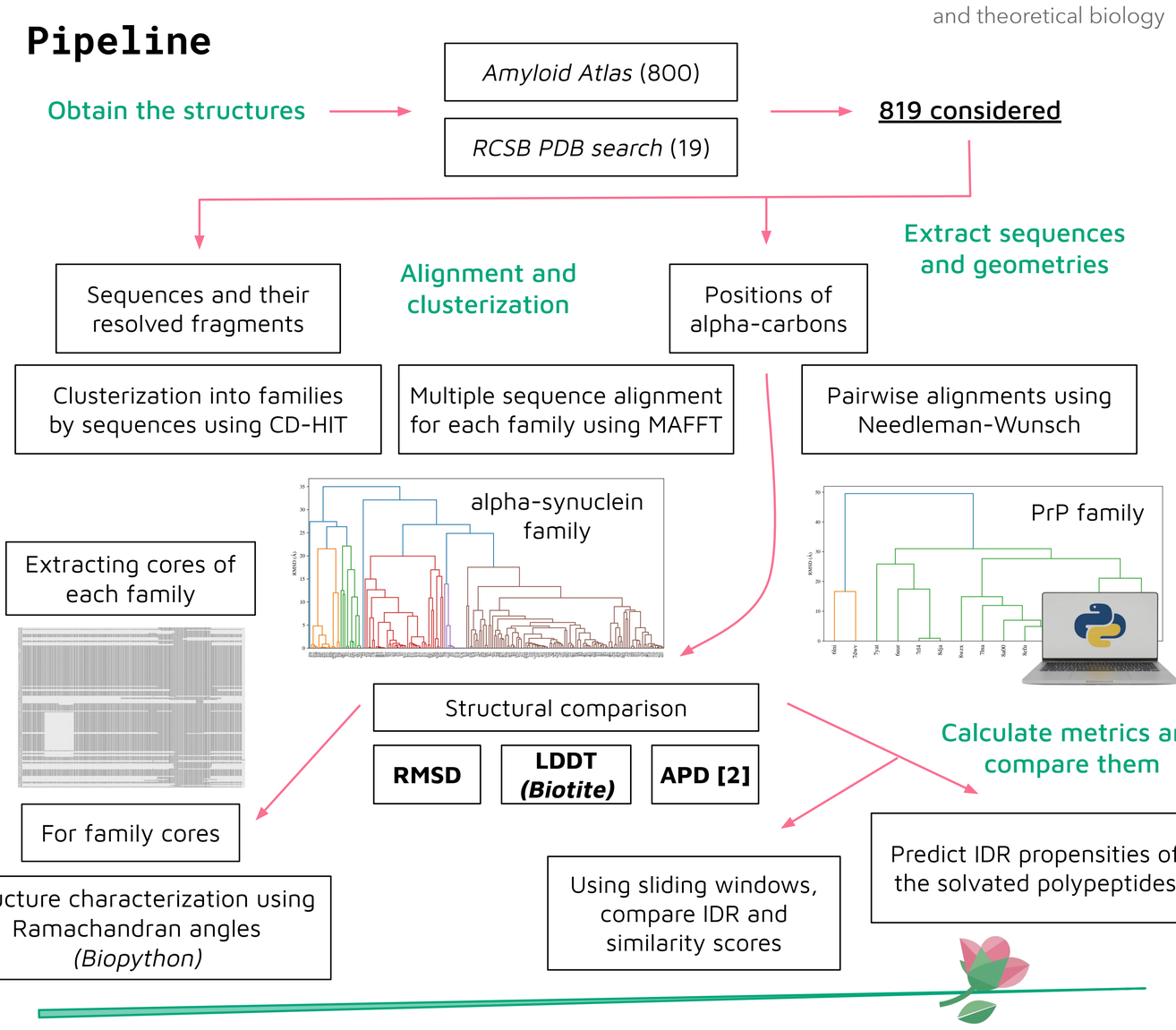
Amyloids: known & unknown

It is well known that proteins can form aggregates known as amyloids [1].
By 2026, ~1000 structures have been resolved, yet no comprehensive database exists: the most advanced resources are *Amyloid Atlas* (~800 structures) and *Amyloid Explorer* (~100 structures). Earlier research focused on selected proteins such as amyloid-β, α-synuclein, tau, PrP, and their energetics.

Amylome: diversity of amyloids

We explored *similarities* and *variances* of resolved structures within and between amyloid families across the entire known proteome.

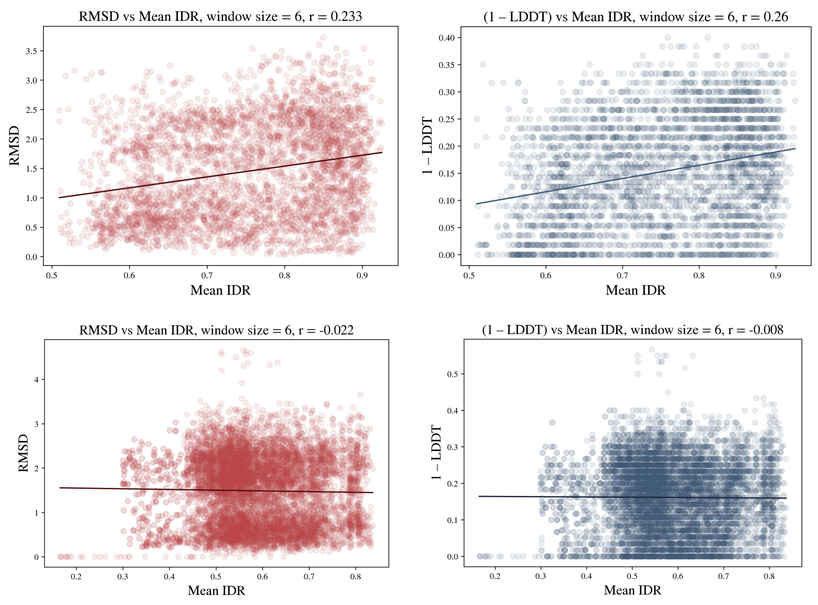
Pipeline



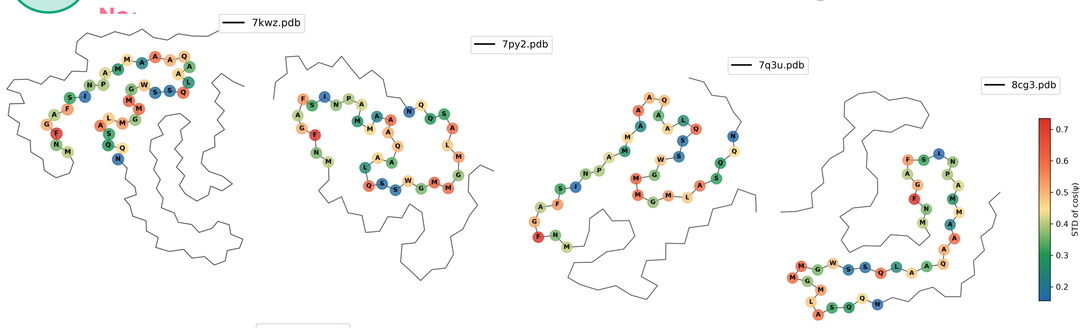
Results & Discussion

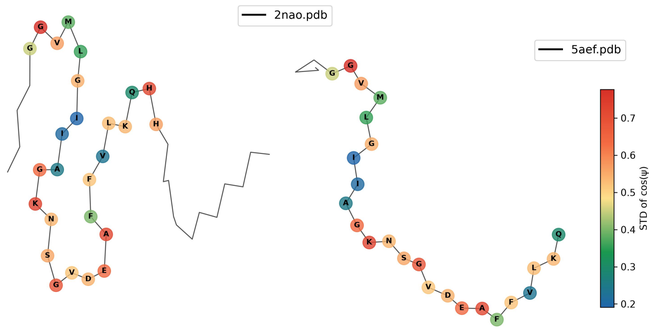
We calculated IDR propensity and structural variability of polymorphic regions (RMSD and LDDT). **No clear – or only weak – correlation emerged between these metrics.** Moreover, the correlation showed different signs across cases, suggesting that **amyloid cores may form preferentially kinetically** from disordered regions.

1

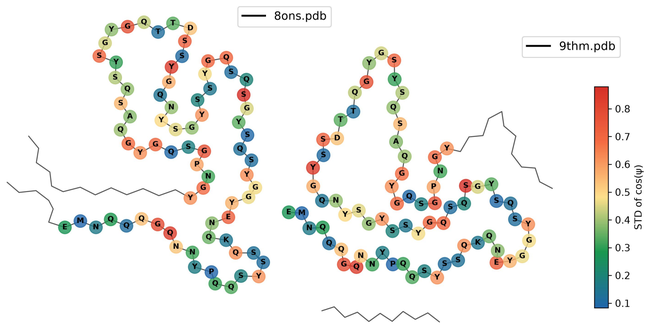


2 **Variable regions** were identified across all sufficiently large amyloidogenic families.
Is the variability confined to the termini, with cores remaining conserved?
No.



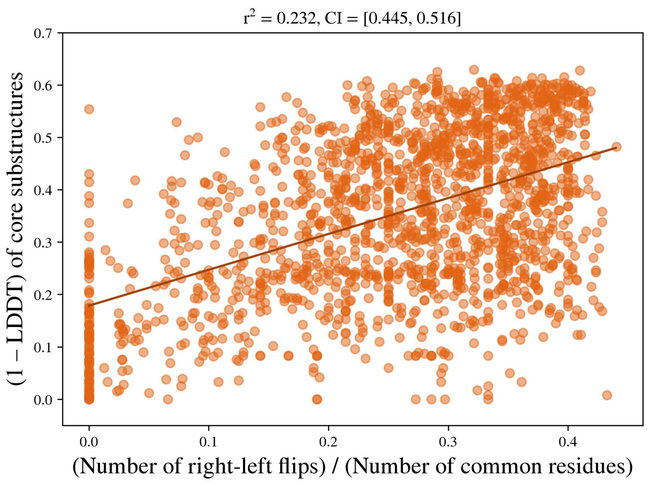


Depiction of variabilities of the core subsequence folding



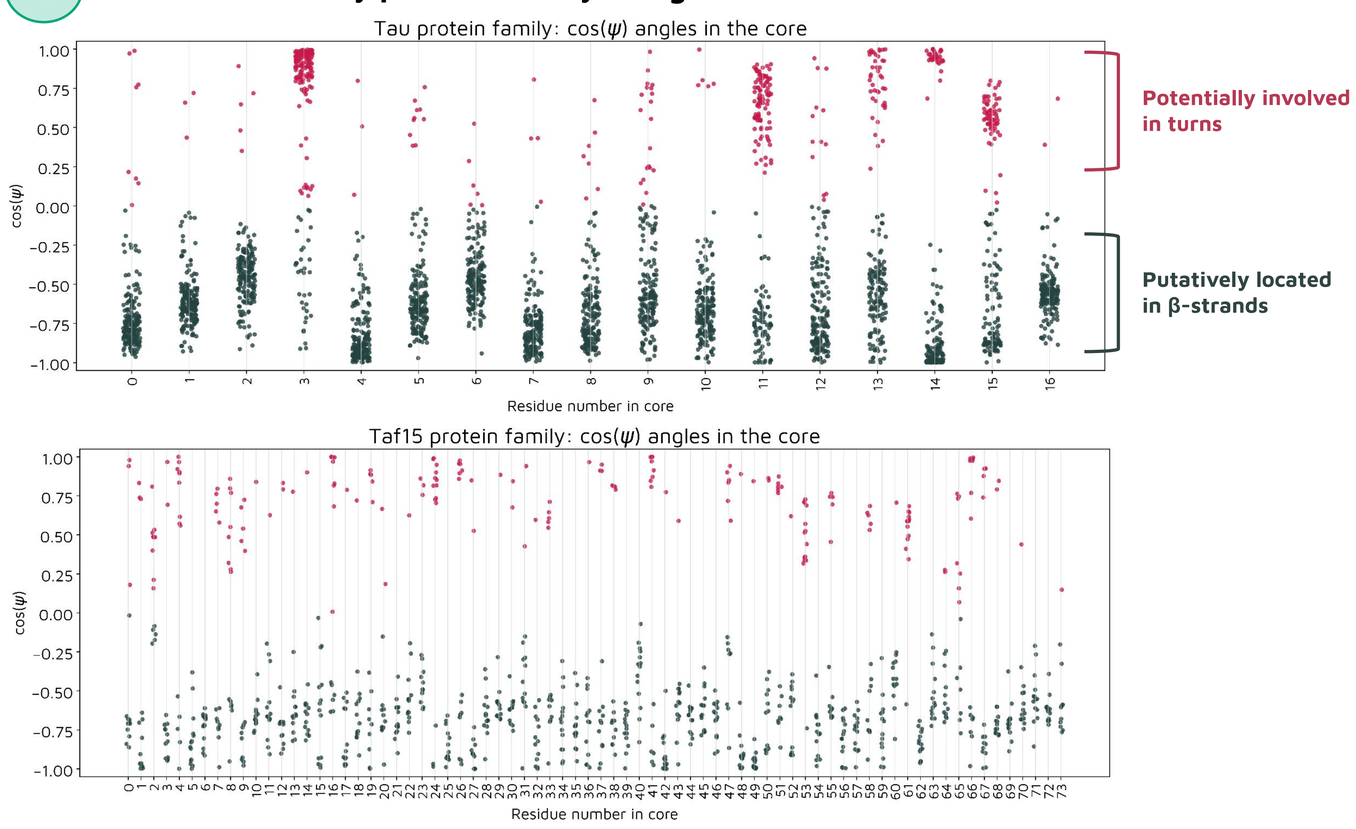
Variability is mainly concentrated in non-stranded regions

3

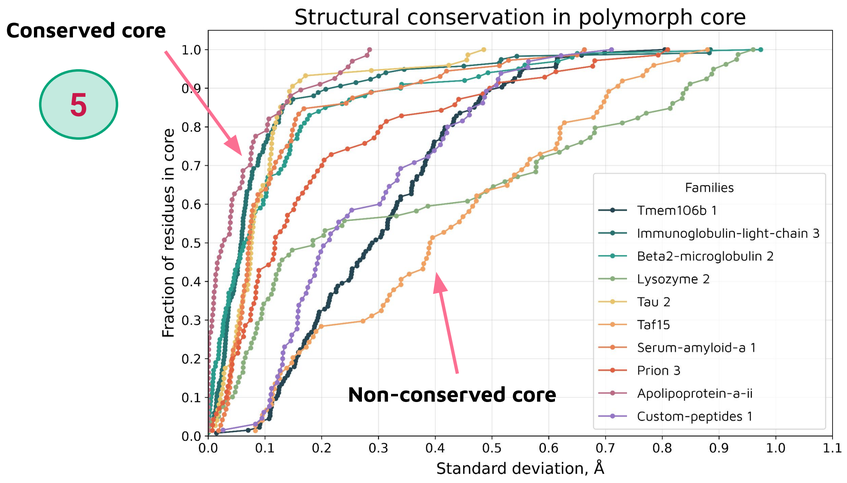


The fraction of flips among shared residues explains less than **25%** of the variance in LDDT

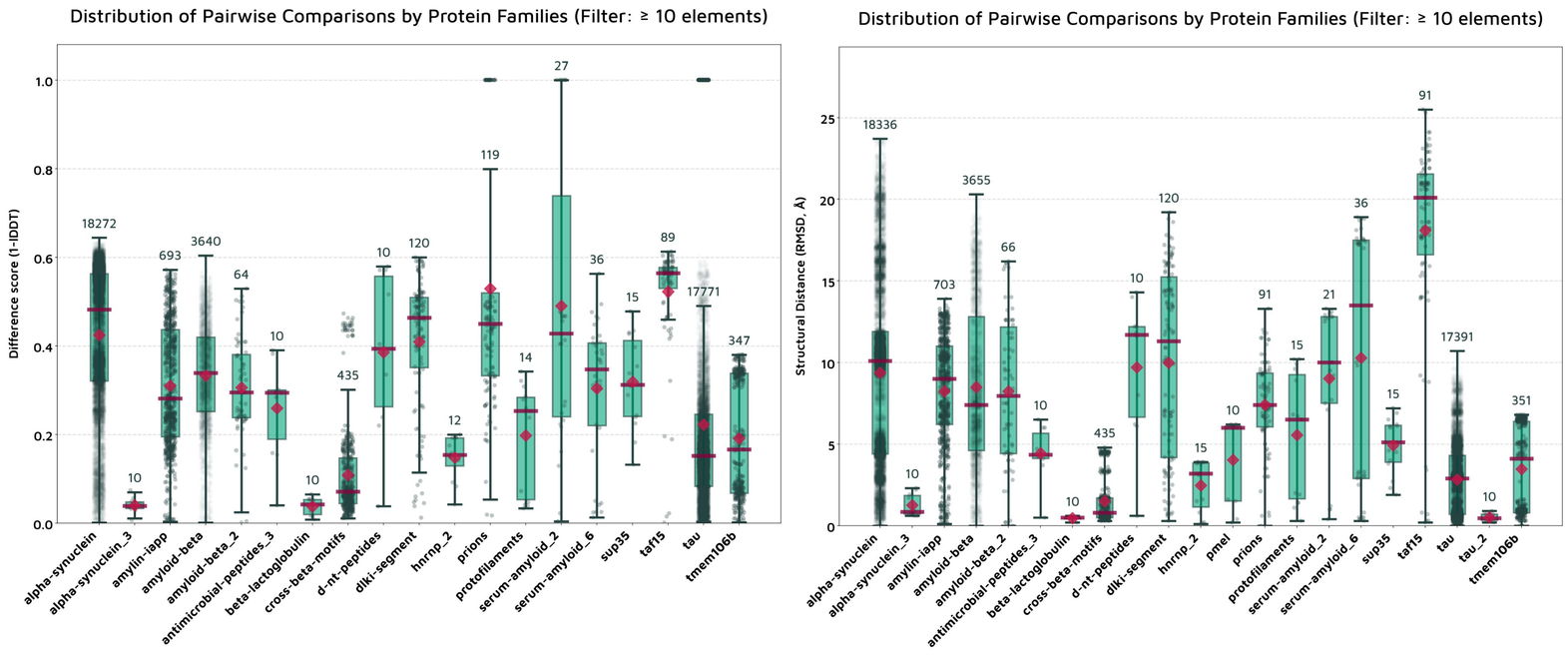
4 **Variability profiles of amyloidogenic families' cores**



5



6 **Pairwise comparisons of core structures**



A new approach was proposed to explore polymorphism in amyloid structural data using insane Python scripts.

Several genetic families have structural subfamilies

1. *Sawaya et al., 2021, Cell, 184:4857*
2. *Scheres et al., 2026, Structure, 34:1061*