

## 論文の内容の要旨

論文題目 : The Conservation and Classification of Intrinsically Disordered Regions in Proteins  
(タンパク質の天然変性領域の保存と分類)

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Intrinsically disordered proteins are considered as established concepts due to the importance of their function in protein network. While maintaining their function, intrinsically disordered regions in proteins are known to evolve rapidly while maintaining their function. However, given their poor sequence conservation, it is still not clear how these disordered regions can maintain their function.

In this study, we focused on the sequence conservation of a large number of predicted and experimentally determined intrinsically disordered regions in the human proteome across 7 other eukaryotes. We inspected the type content conservation of disordered regions by determining the fraction of positive, negative, polar, hydrophobic and special (Pro, Gly) residues maintained across the orthologous regions. A significant number of disordered regions with low sequence conservation showed not only high amino acid content similarity between orthologs, but higher type content similarity. Based on amino acid similarity, type similarity and type content similarity, we divided the IDRs into groups.

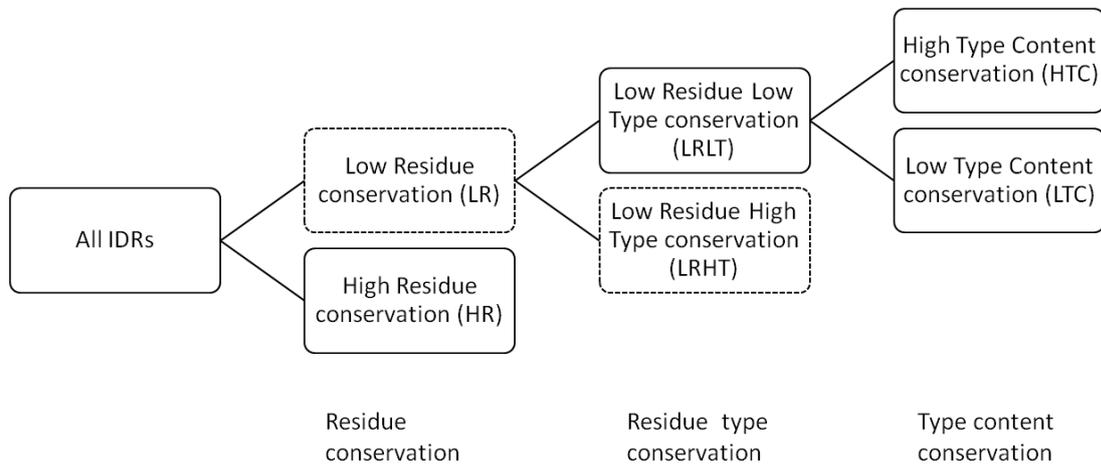
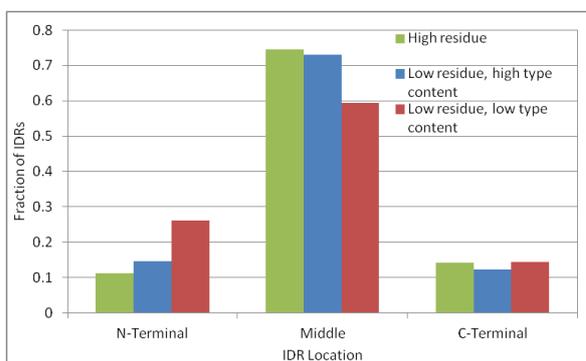
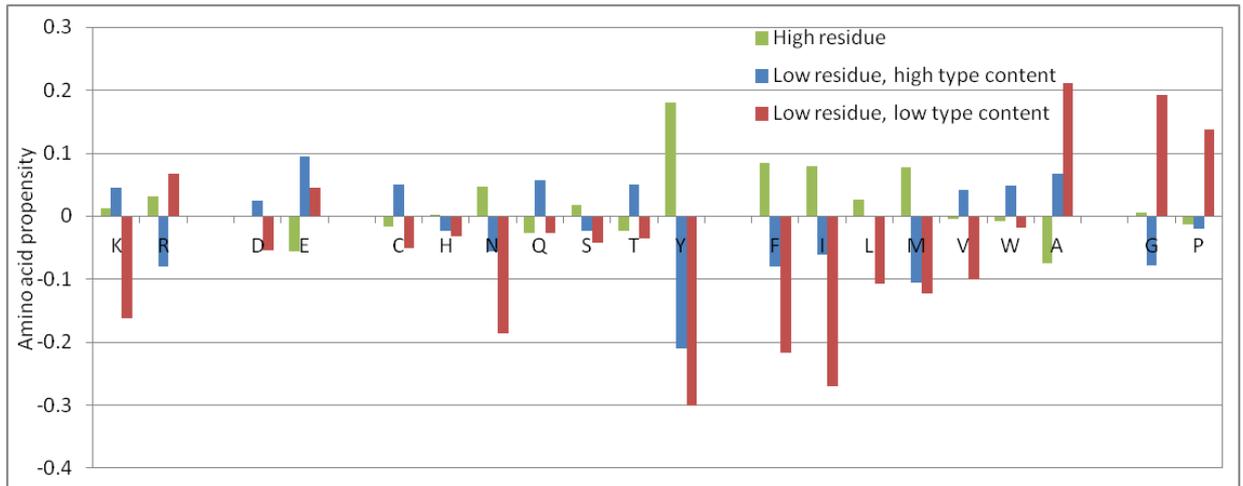


Figure 1. Flowchart groups of IDRs based on their residue, residue type and type content conservation. Groups marked in solid lines were specifically studied in this work.

Clustering disordered regions based on the enrichment of each residue type resulted in functionally distinct groups for all regions, as well as those with high residue or high type conservation. Disordered regions enriched in certain types of residues also showed location preference within the proteins.



A.



B.

Figure 3 A) Location preferences, and B) Amino acid propensity of IDRs with high residue conservation (green), low residue conservation with high type content similarity (blue) and low residue conservation with low type content similarity (red).

From our calculation, we propose that maintaining the overall type content is one of the ways through which intrinsically disordered regions maintain their flexibility and function, despite high rates of evolution showed by the low residue similarity. We demonstrate the feasibility of a classification scheme for intrinsically disordered regions based on their conservation, type content and location within the protein.