

Computational Approach to RNA-Protein Binding

Phoebe Dillon, Emily Oldani, Jake McGuire, Erich Chapman

Trans active
response DNA
Binding Protein
43 kDa (TDP-43)

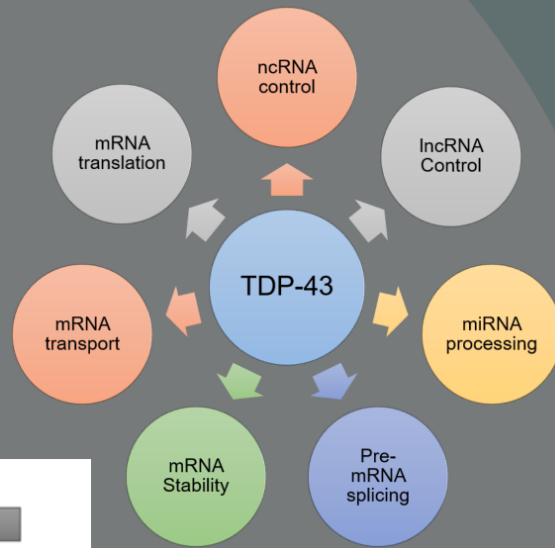
References

Chapman, E., Dillon, P. A., McGuire, J. K., et al. (2015). Computational Approach to RNA-Protein Binding. *Journal of Molecular Biology*, 517(1-2), 1-10. doi:10.1016/j.jmb.2015.05.010

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TDP-43

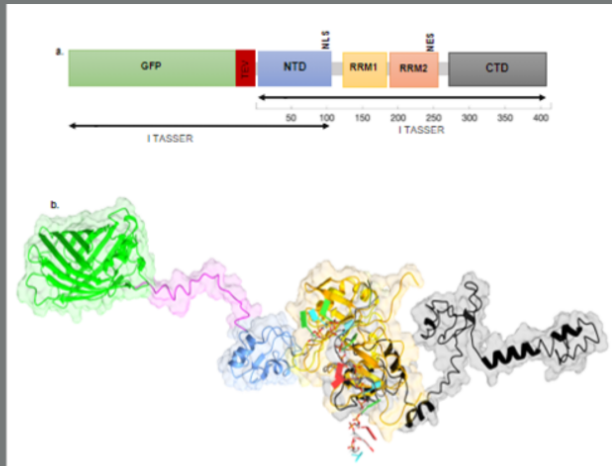


RNA Recognition Motifs (RRMs)

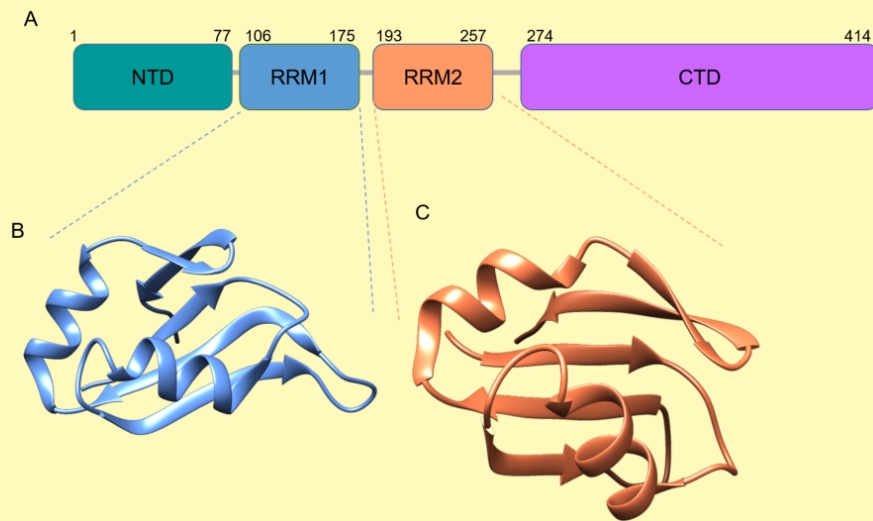
Important Amino Acids

Methods

Results

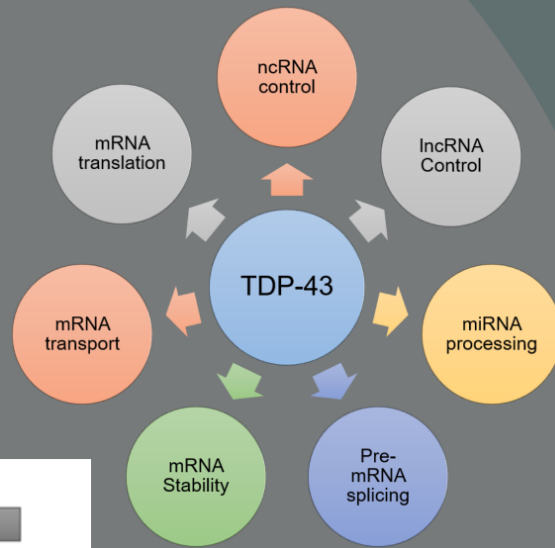


RRMS



- RRM1 (106-175)
- RRM2 (193-257)
 - RRM2 acts as a hinge to increase binding specificity

TDP-43

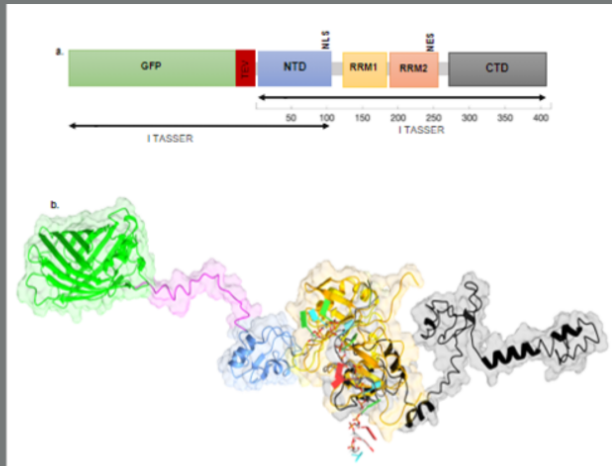


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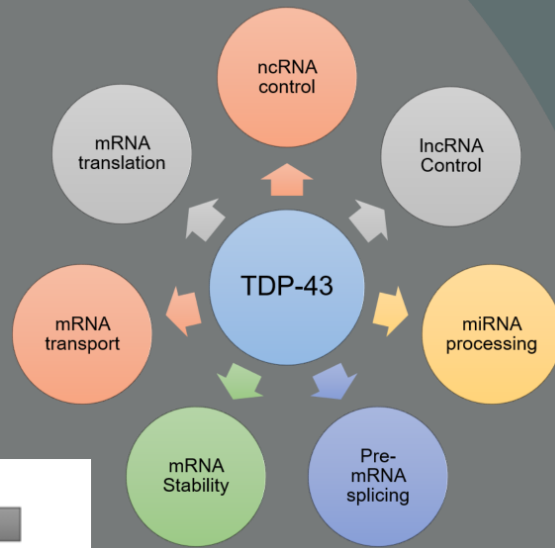
231, 147, 149, 229, 194

Phenylalanine (F)

- RRM1
 - F147, F149
- RRM2
 - F194, 229, 231

Serine 248

TDP-43

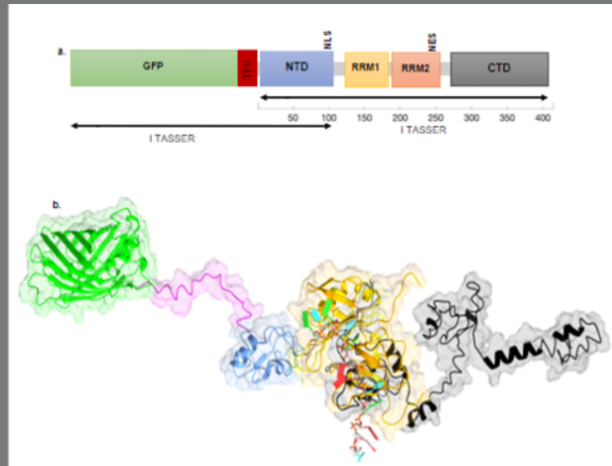


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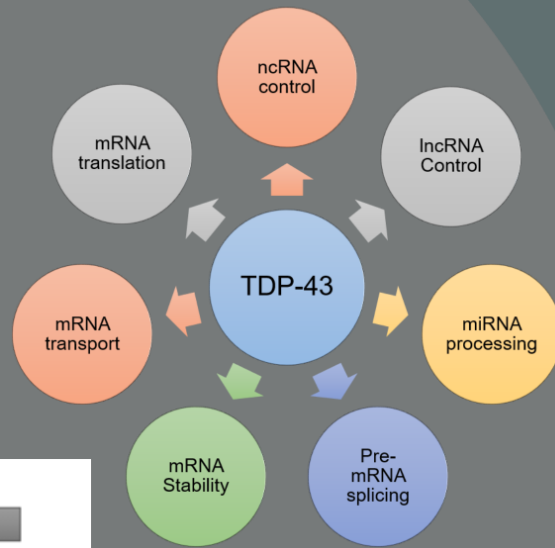


Modeling and Docking

- RNA 3-D Modeling
 - Find RNAs that are known to bind to the RRM
 - 3-D rendering of the RNAs
- Docking on the Protein
 - Isolate one conformation of the RRM NMR structure (4BS2)
 - Dock using HDOCK



TDP-43

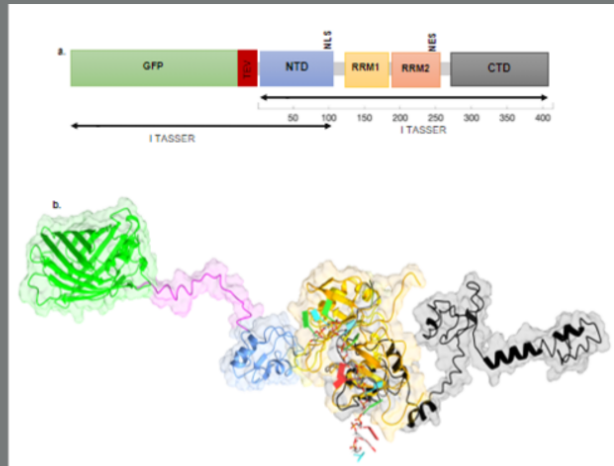


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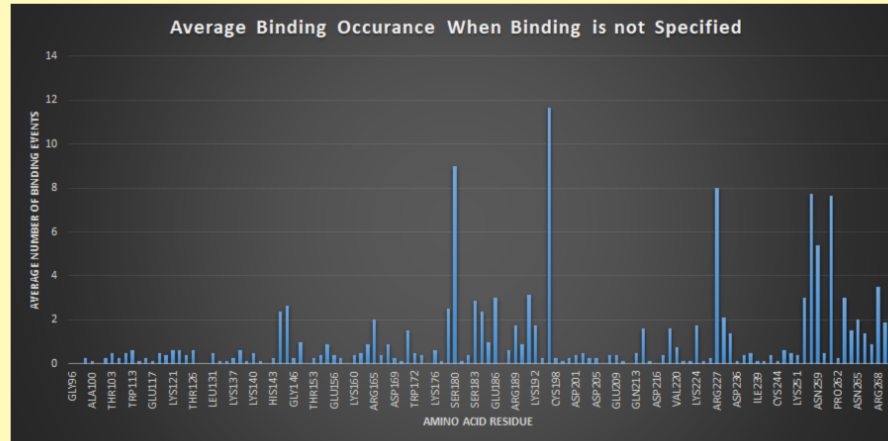
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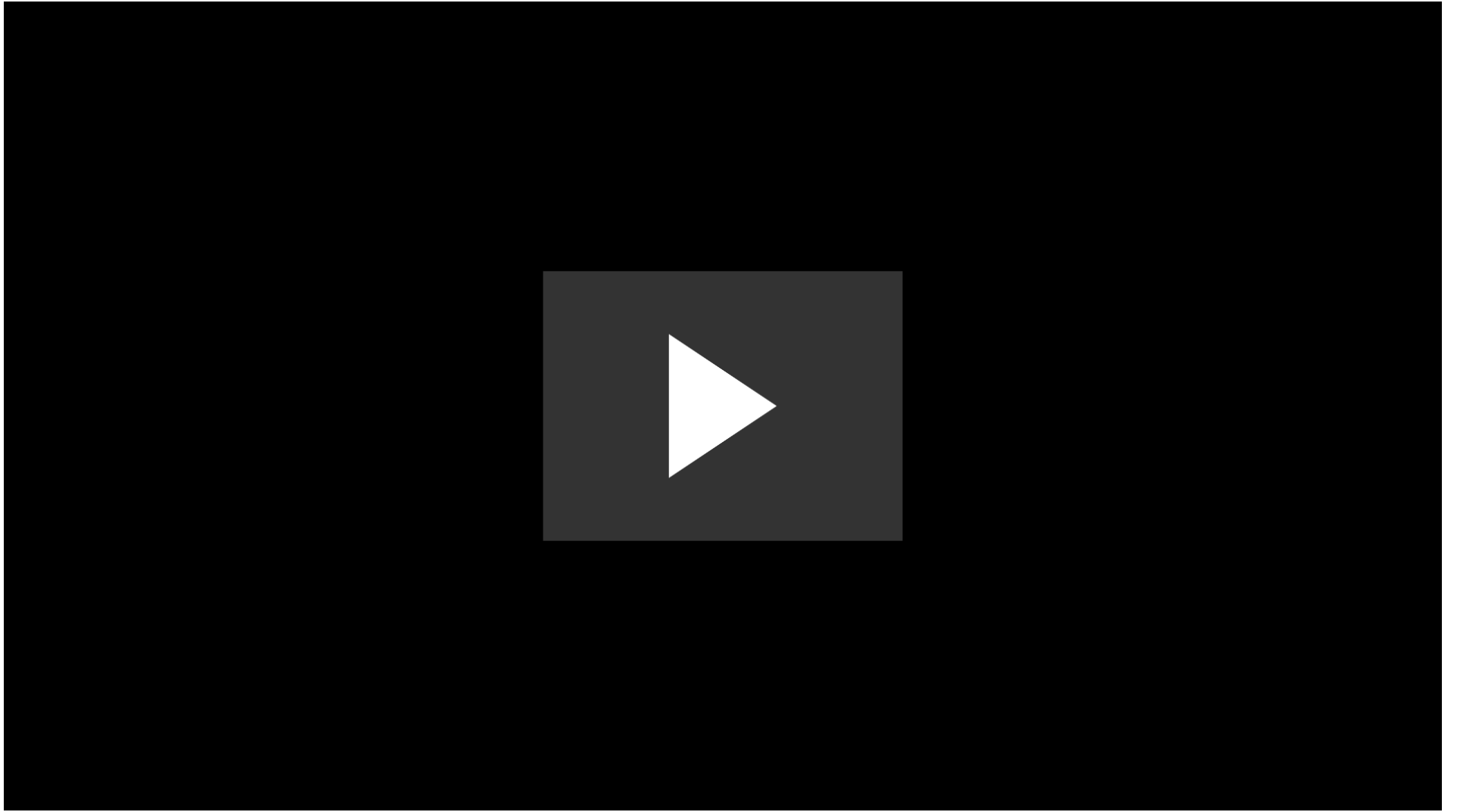


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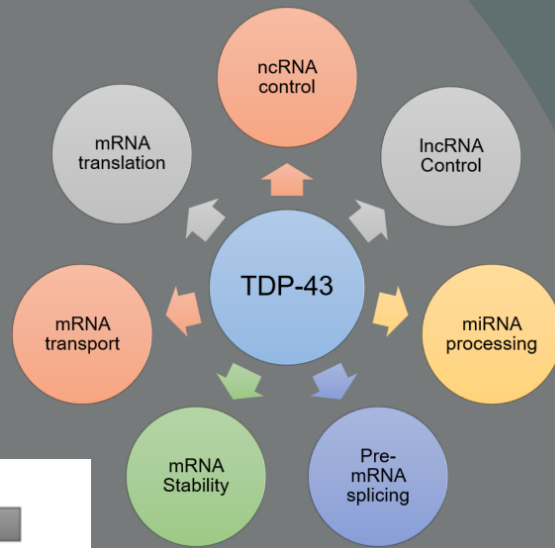


When the binding site was specified:





TDP-43

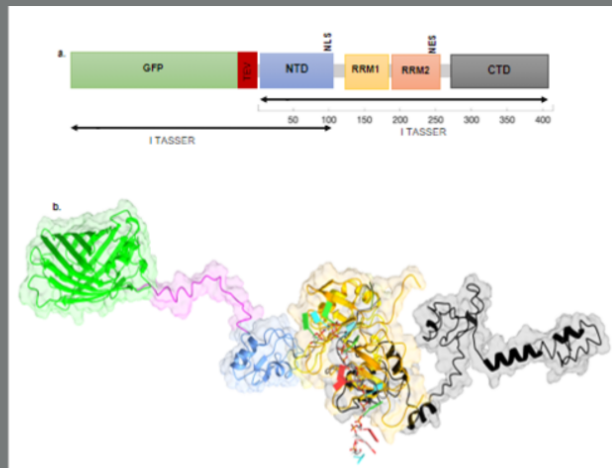


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