

Supplementary Materials

Autophagy-related intrinsically disordered proteins in intra-nuclear compartments

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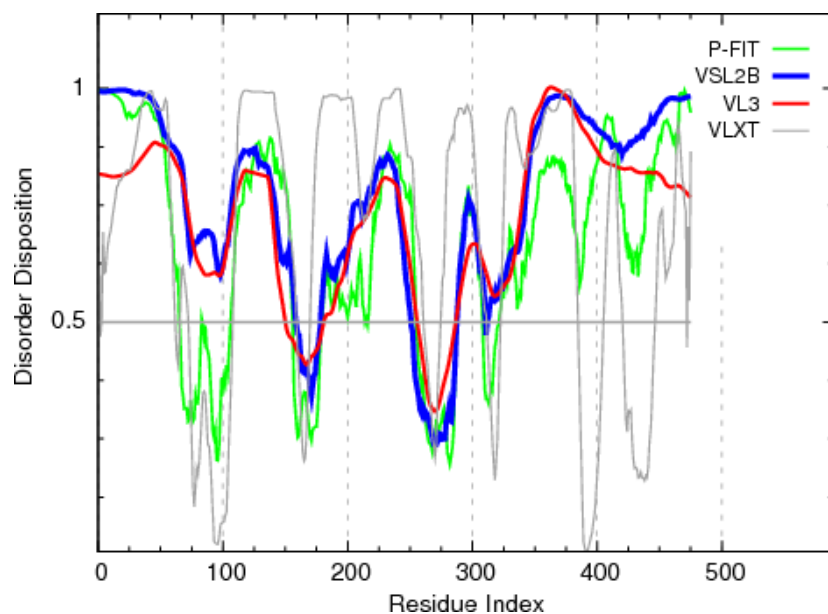
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In all supplementary figures:

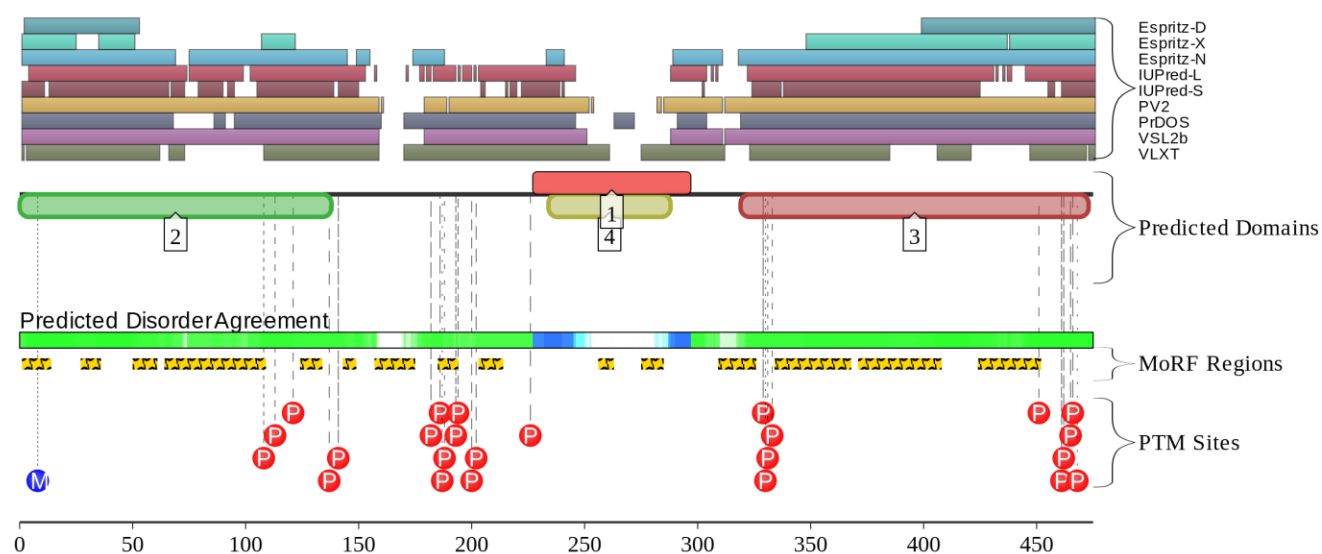
Top panel. Evaluation of the per-residue disorder propensity by the members of the PONDR family of disorder predictors. A disorder threshold is indicated as a thin line (at score of 0.5) to show a boundary between disorder (>0.5) and order (<0.5).

Middle panel (if present). Evaluation of the functional intrinsic disorder propensity by the D²P² database (<http://d2p2.pro/>). In the corresponding plot, top nine colored bars represent location of disordered regions predicted by different disorder predictors (Espritz-D, Espritz-N, Espritz-X, IUPred-L, IUPred-S, PV2, PrDOS, PONDR[®] VSL2b, and PONDR[®] VLXT, see keys for the corresponding color codes). Green-and-white bar in the middle of the plot shows the predicted disorder agreement between these nine predictors, with green parts corresponding to disordered regions by consensus. Yellow bar shows the location of the predicted disorder-based binding site (MoRF region), whereas variously colored circles at the bottom of the plots show locations of post-translational modification sites.

Bottom panel. Analysis of the interactivity of the bloom syndrome protein homolog (UniProt ID: O88700) by STRING computational platform. STRING produces the network of predicted associations for a particular protein and its interactome. The network nodes are proteins, whereas the edges represent the predicted or known functional associations. There are seven types of evidence used in predicting the associations which are indicated in the resulting network by the differently colored lines, where a red line indicates the presence of fusion evidence; a green line - neighborhood evidence; a blue line – co-occurrence evidence; a purple line - experimental evidence; a yellow line – text mining evidence; a light blue line - database evidence; a black line – co-expression evidence.



ENSMUSP00000108913, ENSMUSP00000084151



Key:

- Predicted SCOP Structure
- ⋯ Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- ⚡ Predicted MoRFs
- Ⓟ Curated PTM Site

Disorder:

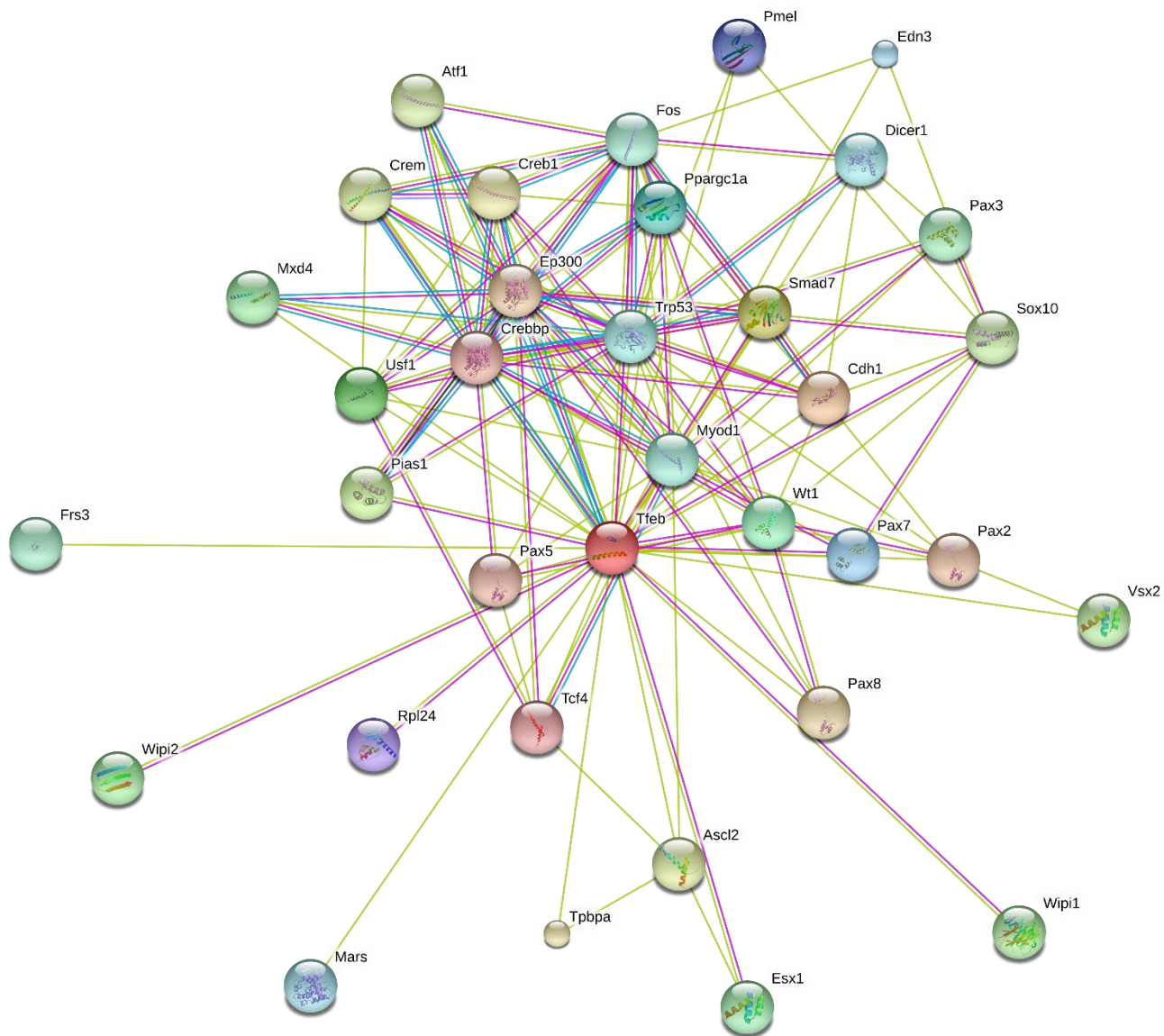
- Espritz-D
- Espritz-X
- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

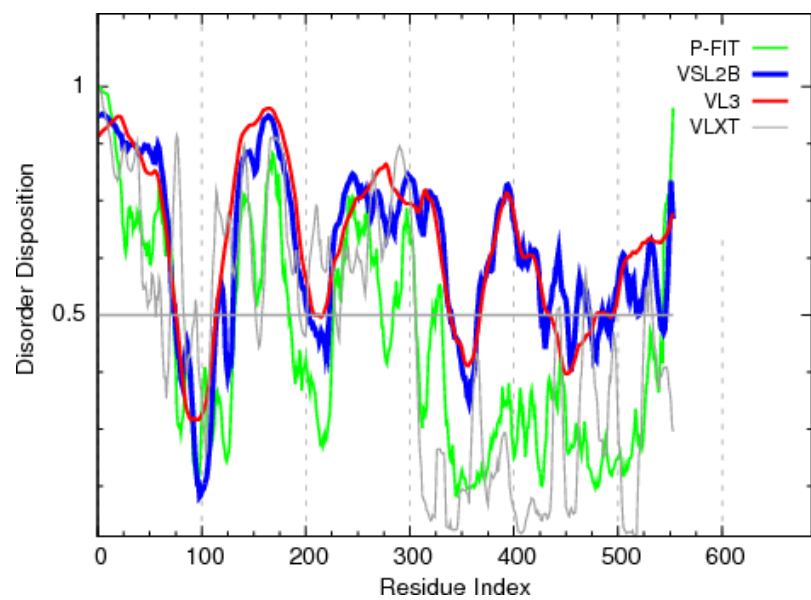
- [1] HLH, helix-loop-helix DNA-binding domain

Pfams:

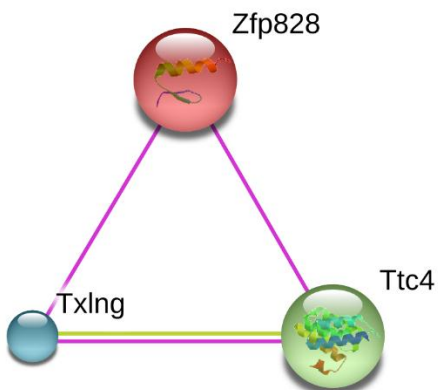
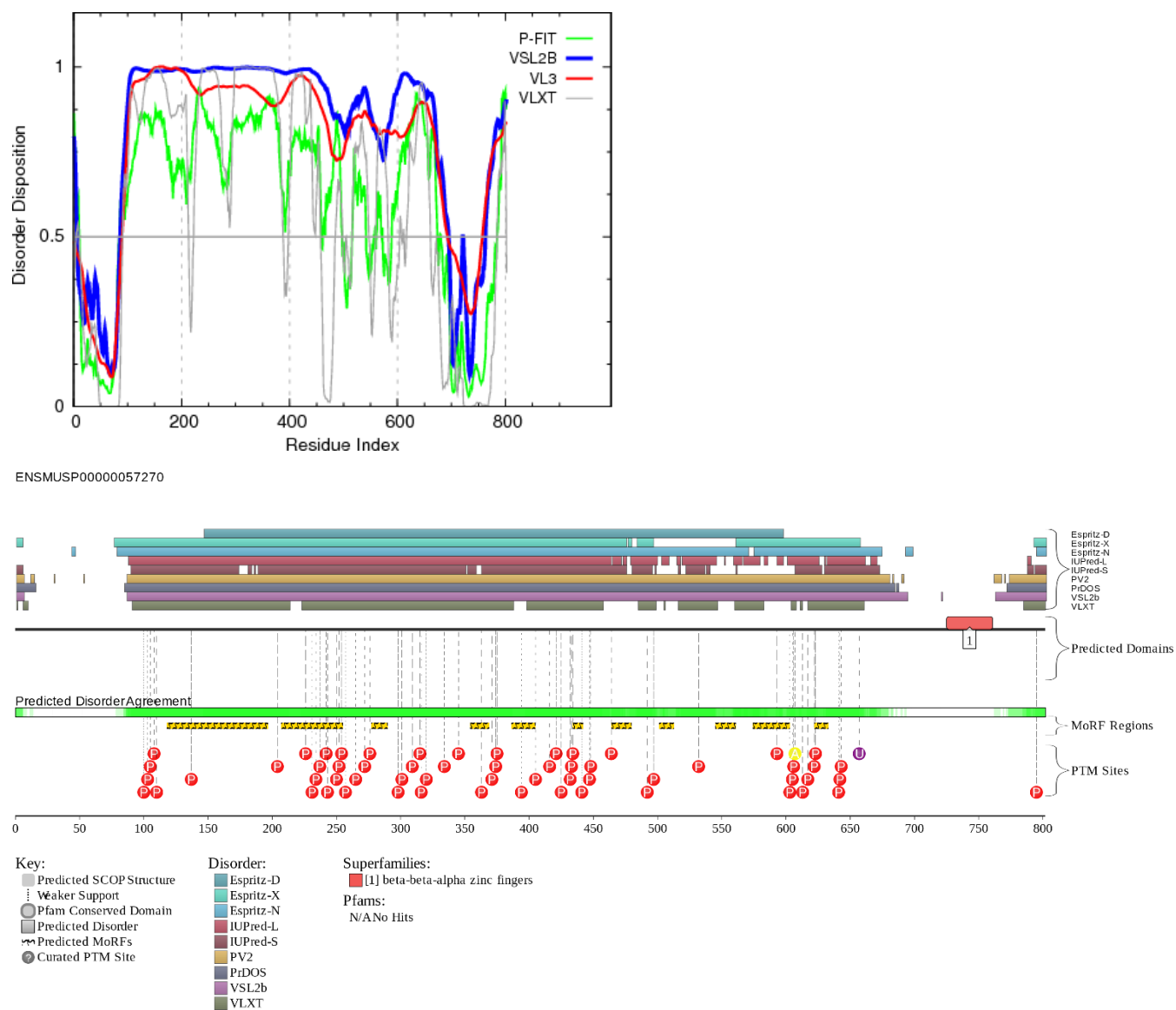
- [2] PB007402 (Pfam-B)
- [3] PF11851.3 (Family)
- [4] Helix-loop-helix DNA-binding domain



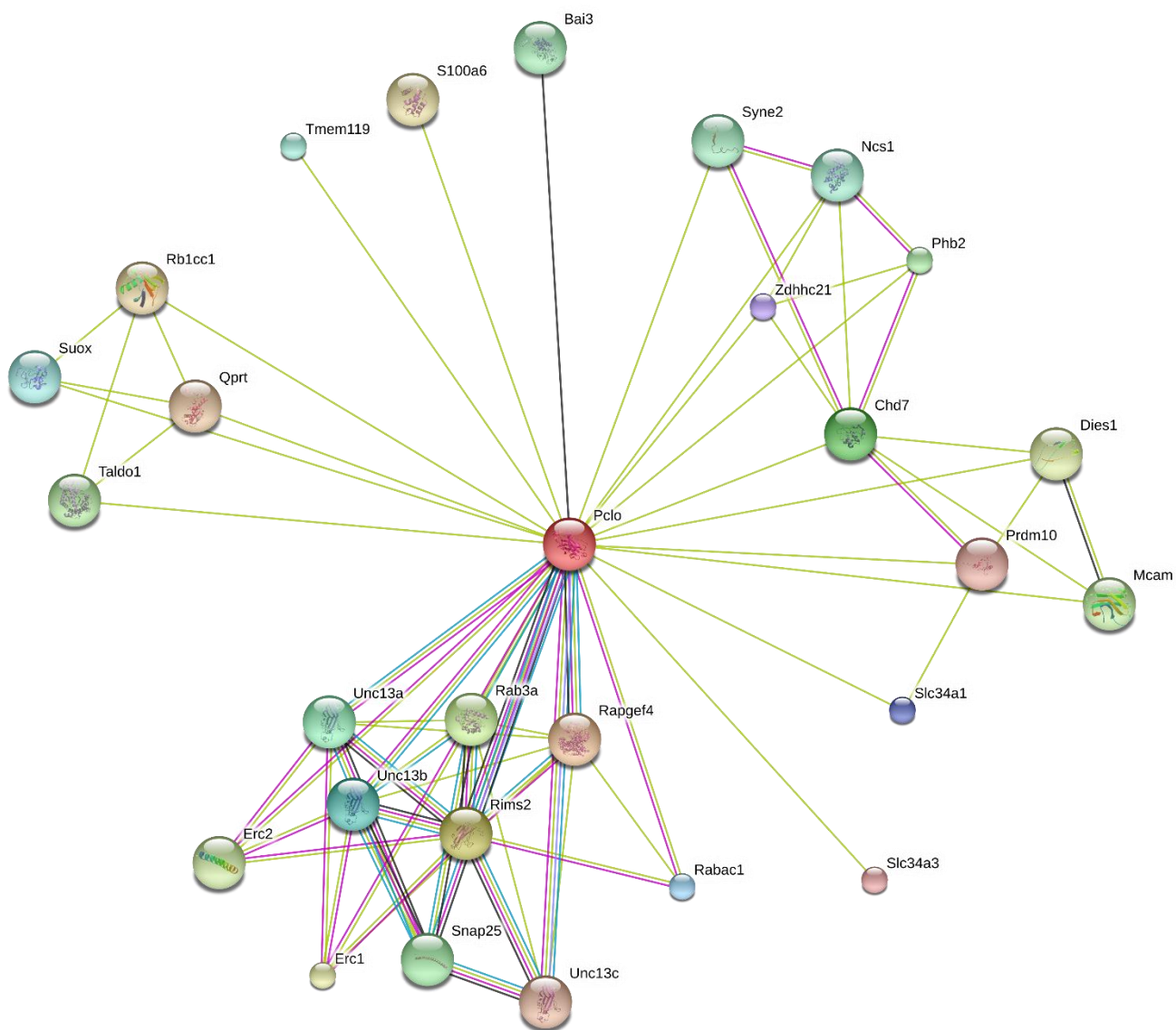
Supplementary Figure S1. Abundance and functionality of intrinsic disorder in TFEB (Q9R210).



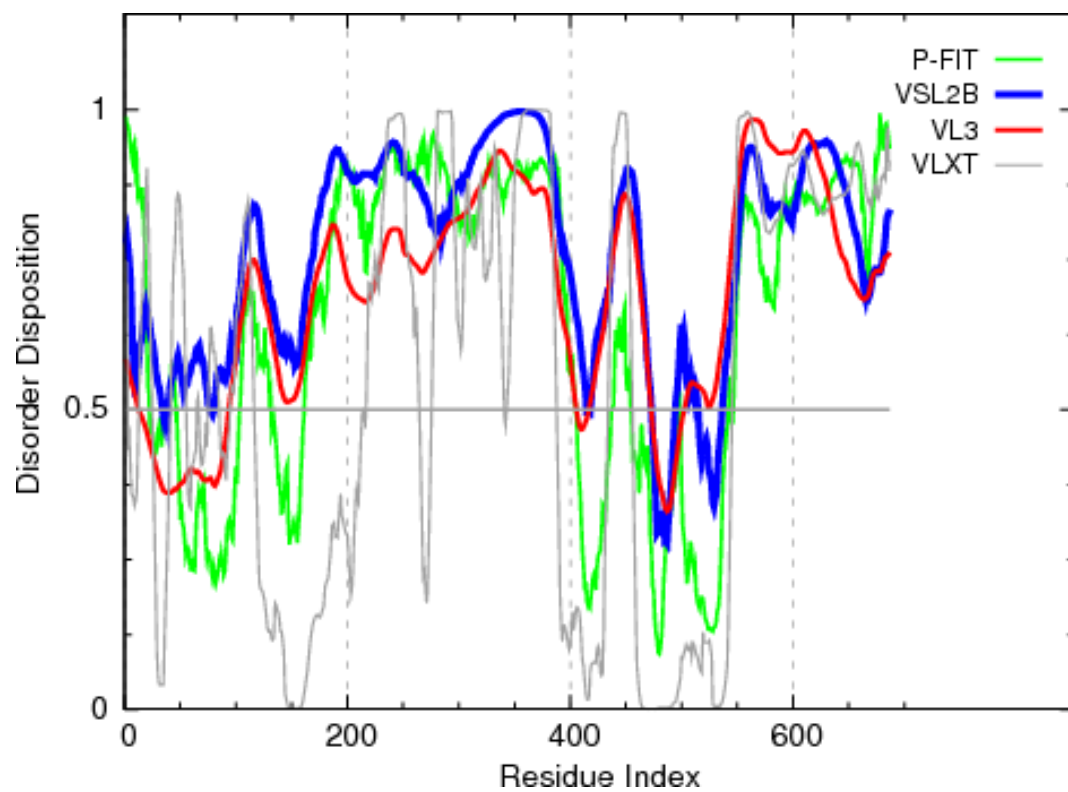
Supplementary Figure S2. Abundance and functionality of intrinsic disorder in ZKSCAN3 (Q91VW9).



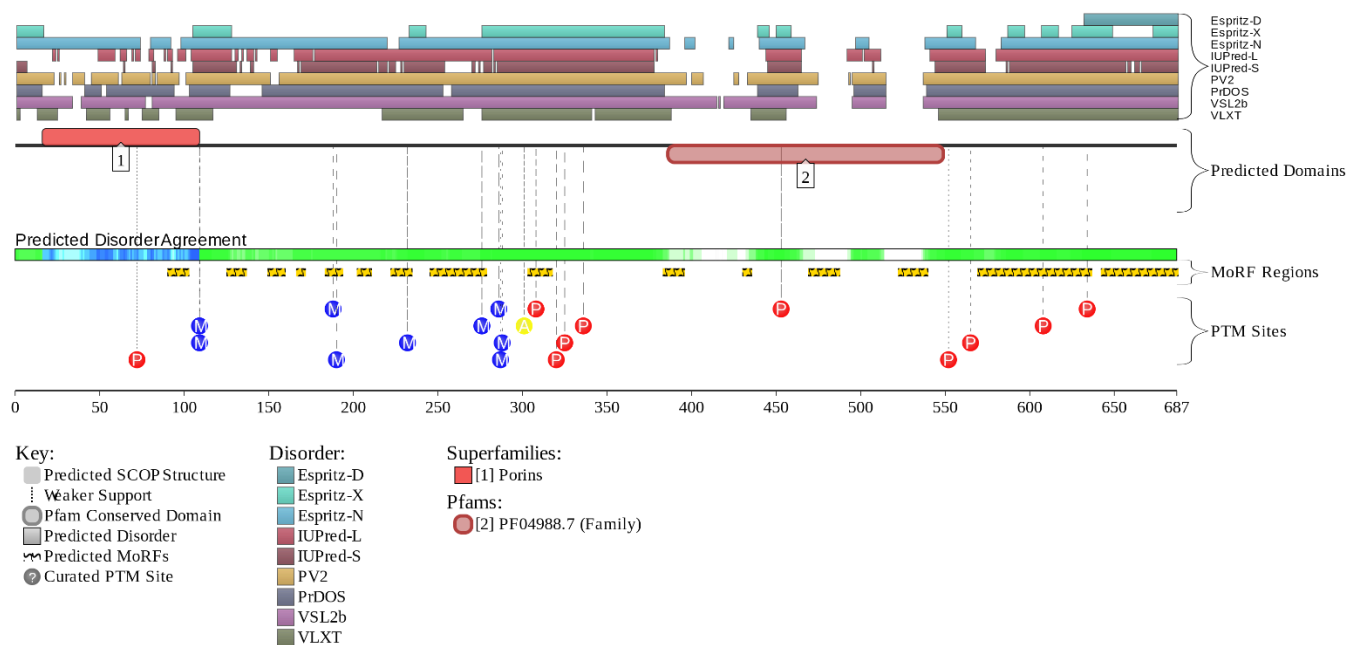
Supplementary Figure S3. Abundance and functionality of intrinsic disorder in Champ1 (Q8K327).

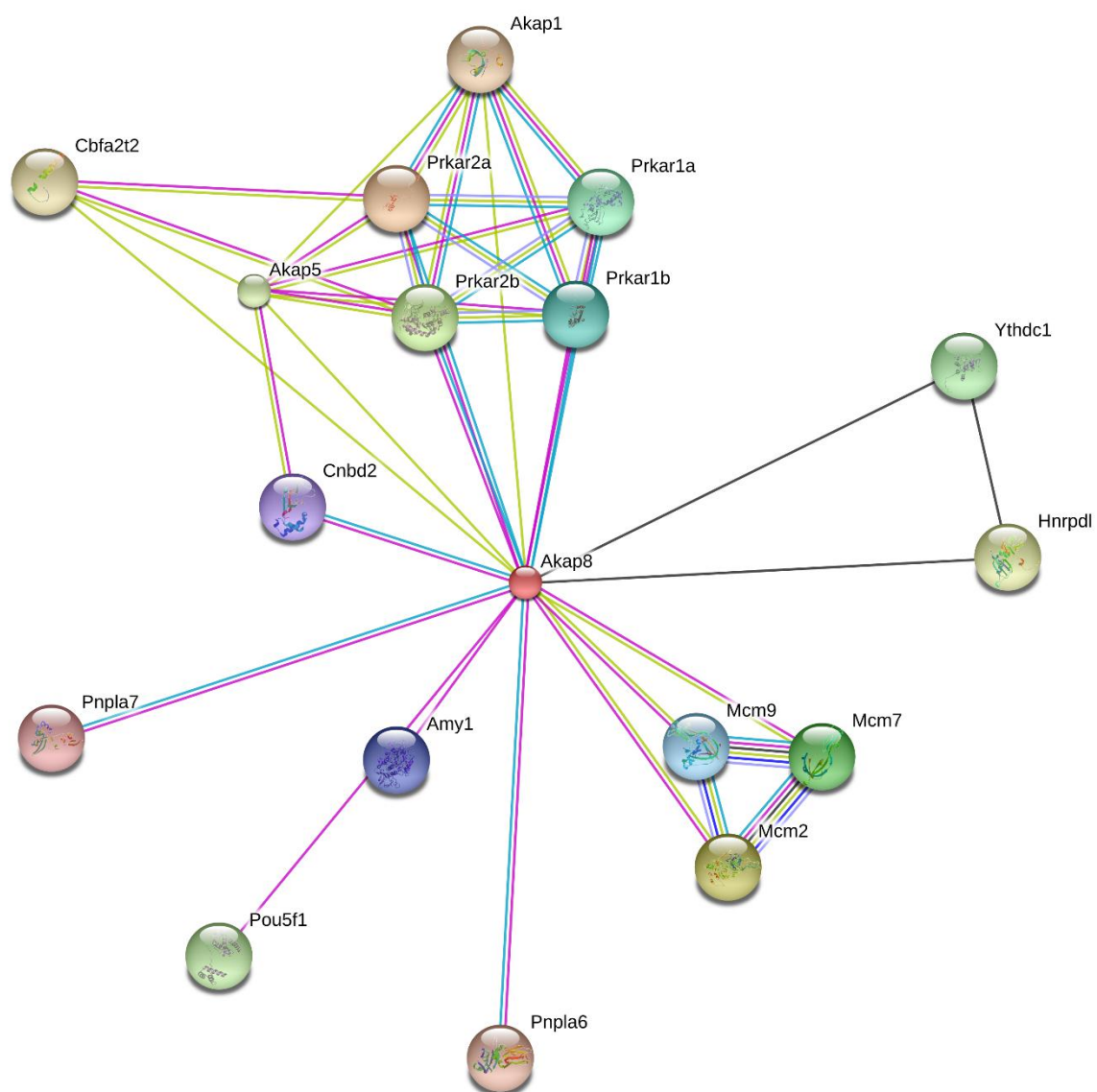


Supplementary Figure S4. Abundance and functionality of intrinsic disorder in Piccolo (Q9QYX7).

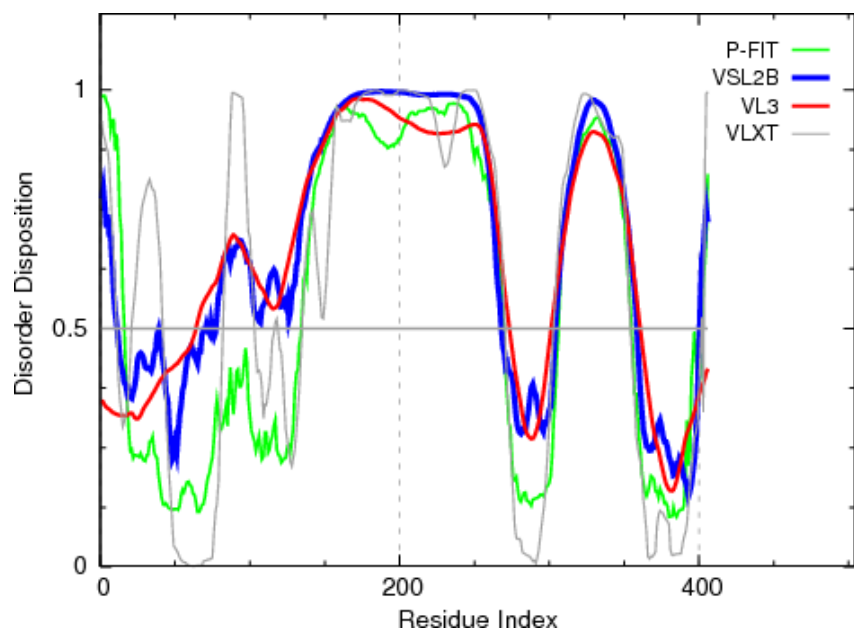


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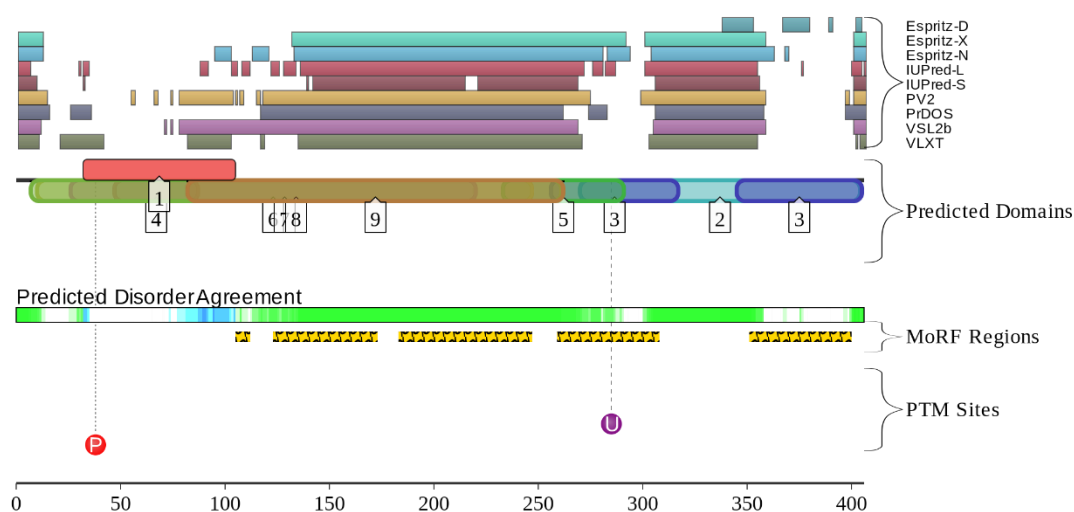




Supplementary Figure S5. Abundance and functionality of intrinsic disorder in Akap8 (Q9DBR0).



ENSMUSP00000025183



Key:

- Predicted SCOP Structure
- ⋯ Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- ⋈ Predicted MoRFs
- Curated PTM Site

Disorder:

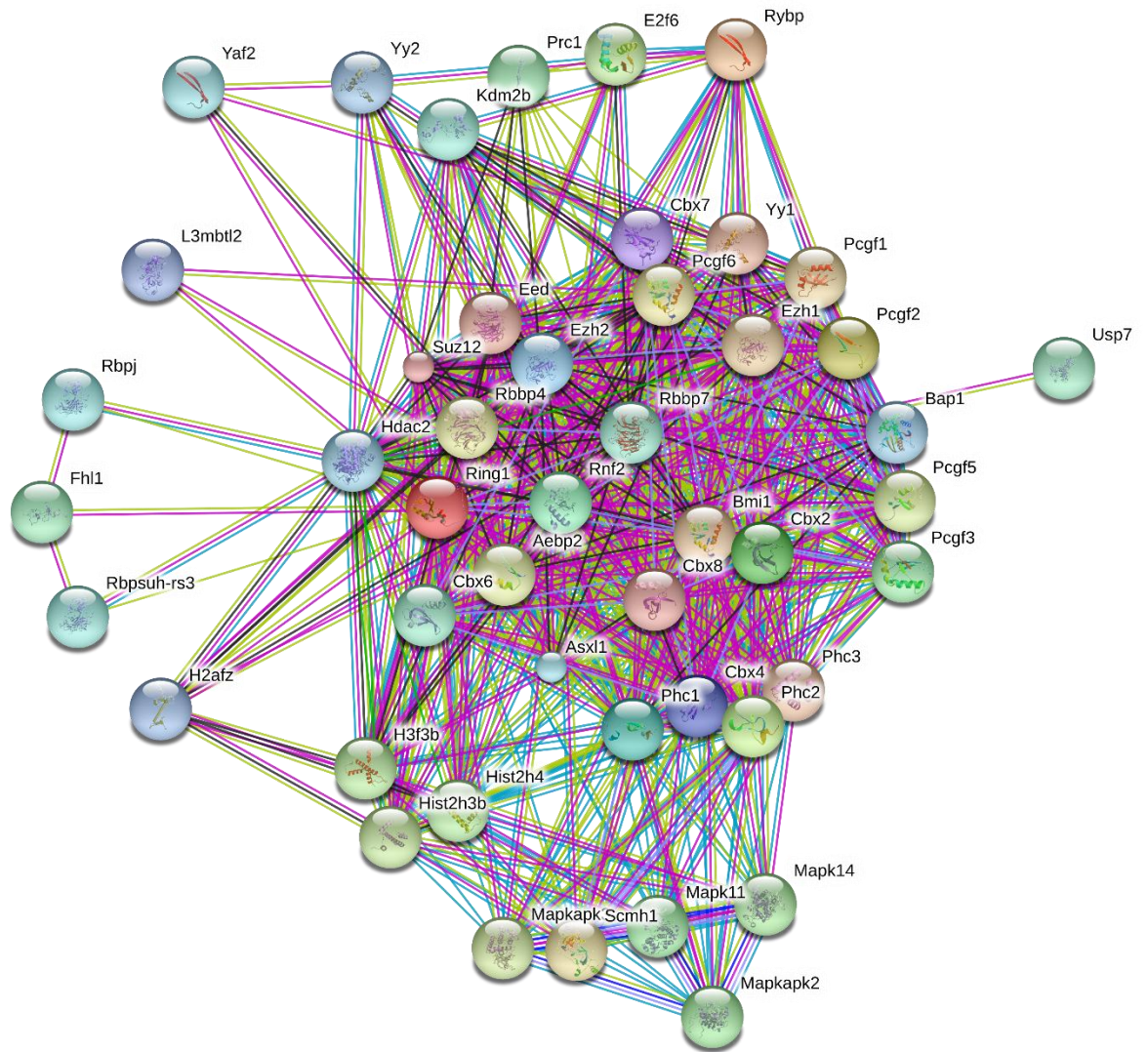
- Espritz-D
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- Espritz-N
- IUPred-L
- IUPred-S
- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

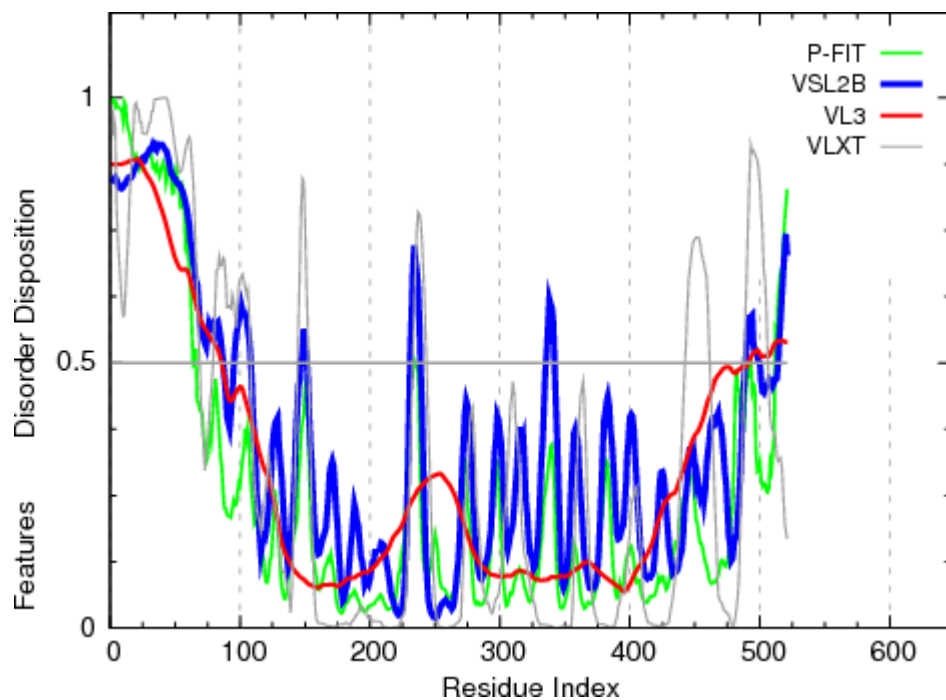
- [1] RING/U-box

Pfams:

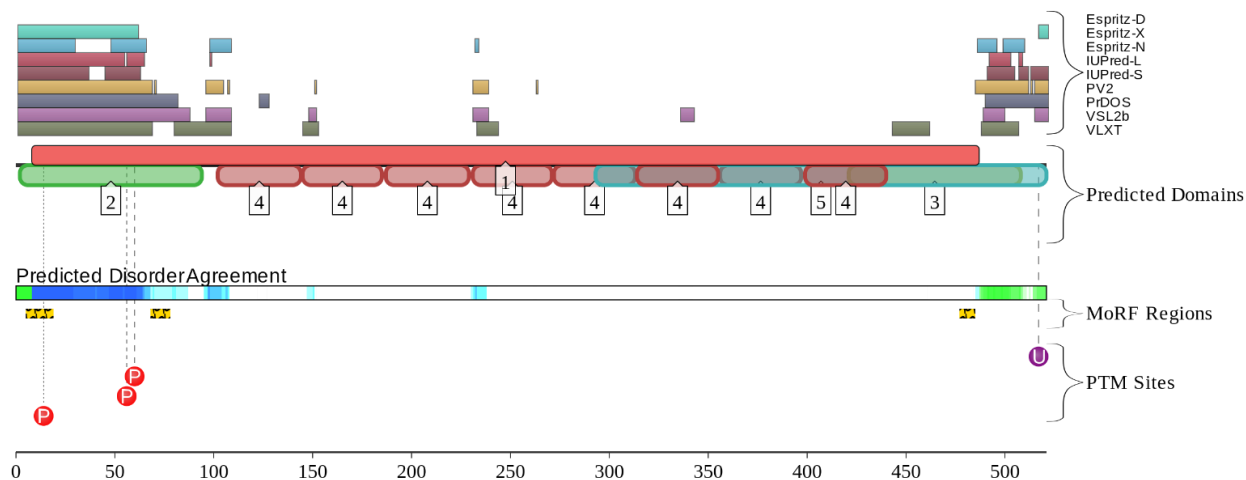
- [2] PB011743 (Pfam-B)
- [3] PB006760 (Pfam-B)
- [4] Zinc finger, C3HC4 type (RING finger)
- [5] PB013488 (Pfam-B)
- [6] PB013905 (Pfam-B)
- [7] PB000586 (Pfam-B)
- [8] PB004800 (Pfam-B)
- [9] PB006829 (Pfam-B)



Supplementary Figure S6. Abundance and functionality of intrinsic disorder in RING1 (O35730).



ENSRNOP00000032371, ENSMUSP00000022496



Key:

- Predicted SCOP Structure
- Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- Predicted MoRFs
- Curated PTM Site

Disorder:

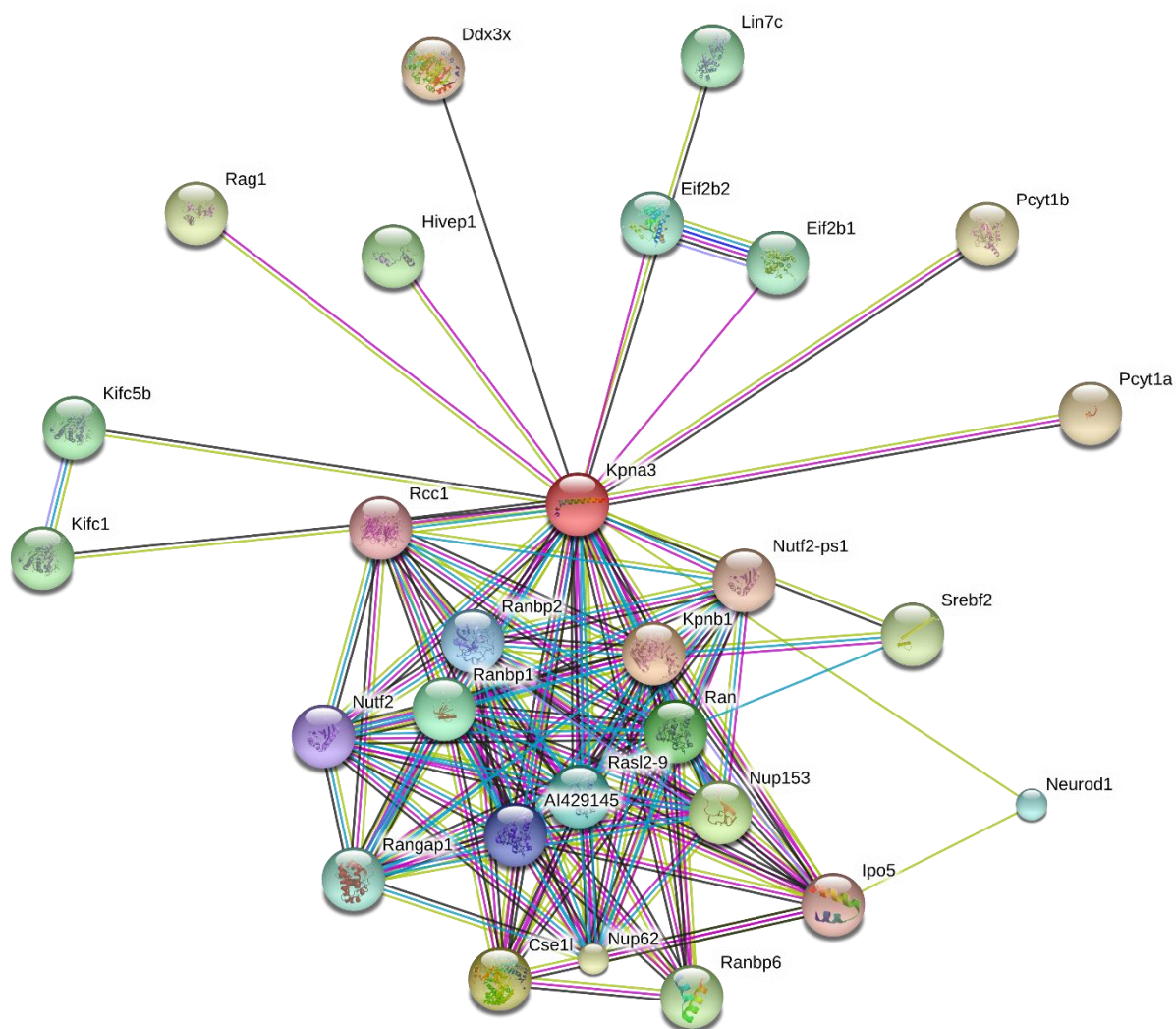
- Espritz-D
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- IUPred-L
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- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

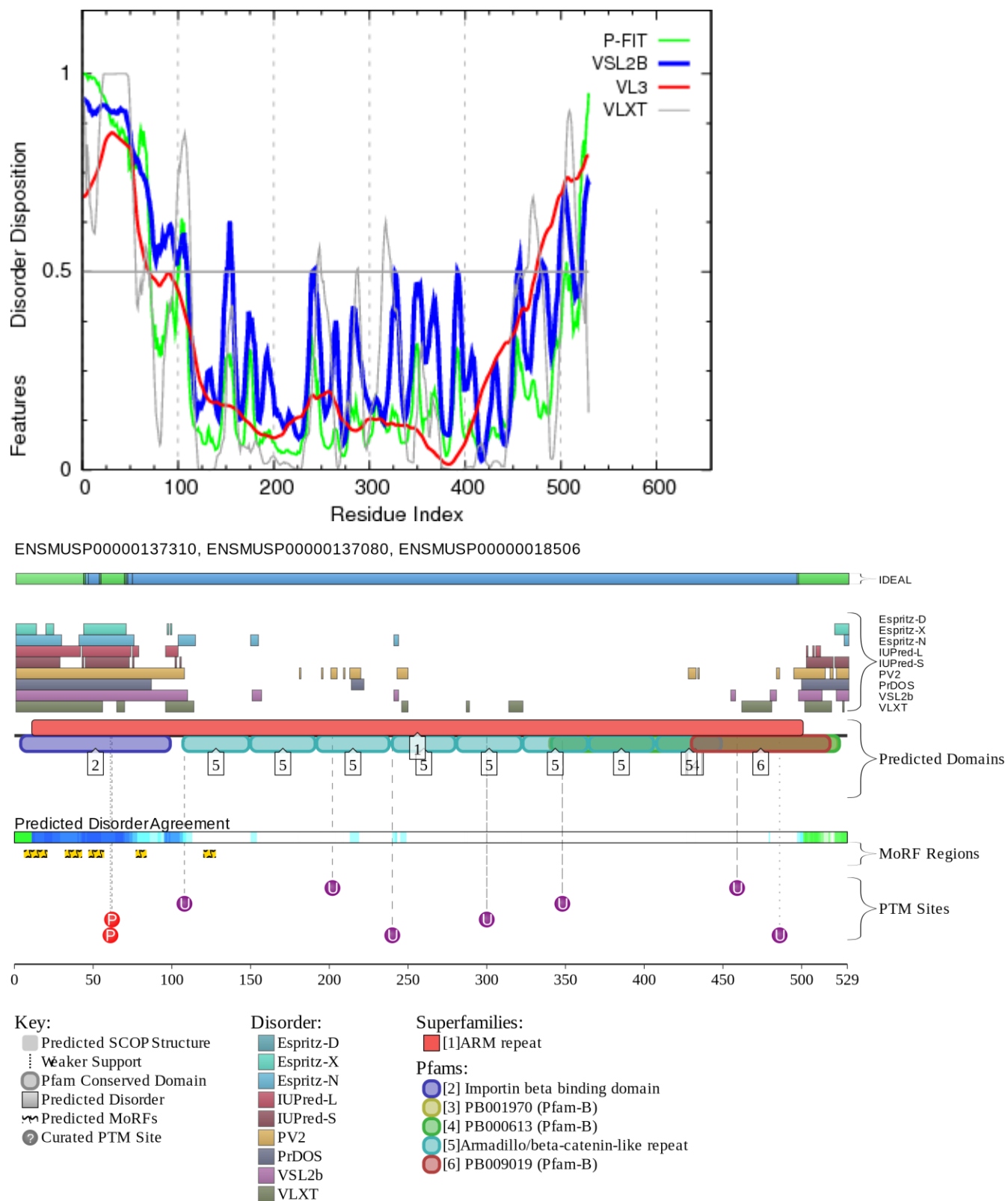
- [1] ARM repeat

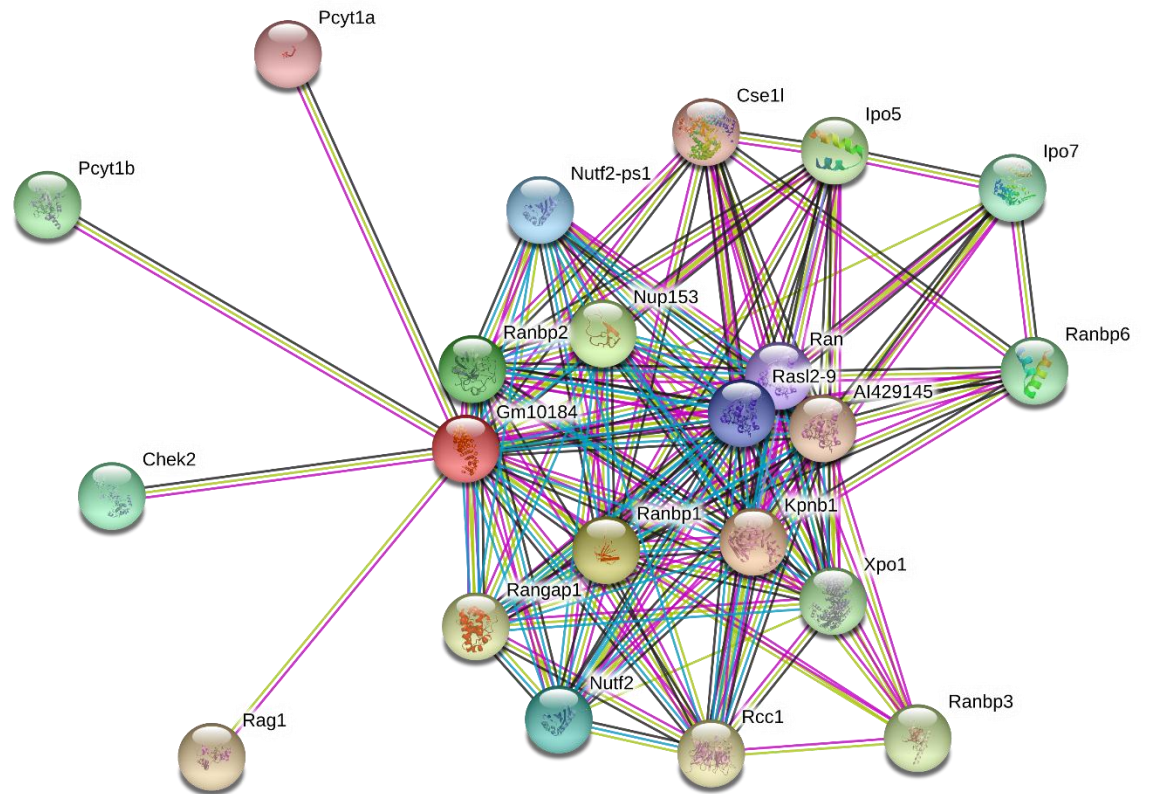
Pfams:

- [2] Importin beta binding domain
- [3] PB009019 (Pfam-B)
- [4] Armadillo/beta-catenin-like repeat
- [5] PB001970 (Pfam-B)

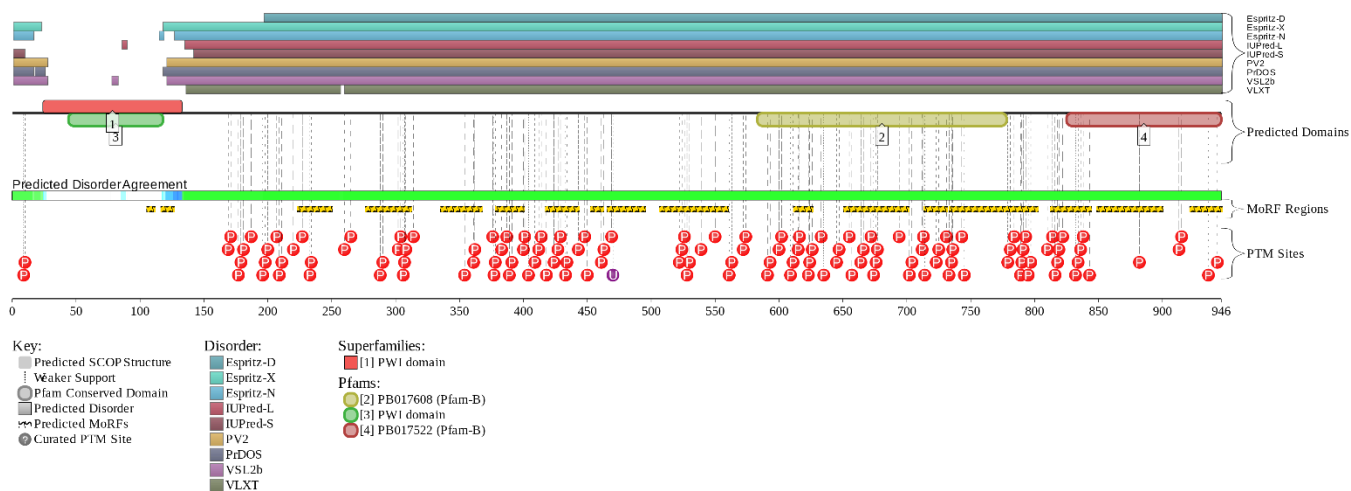
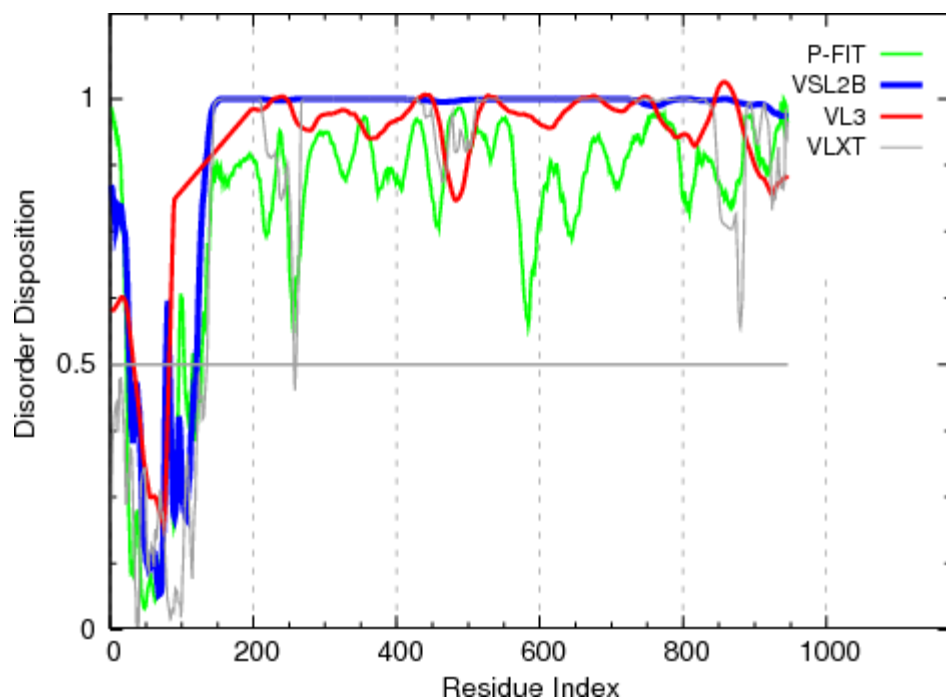


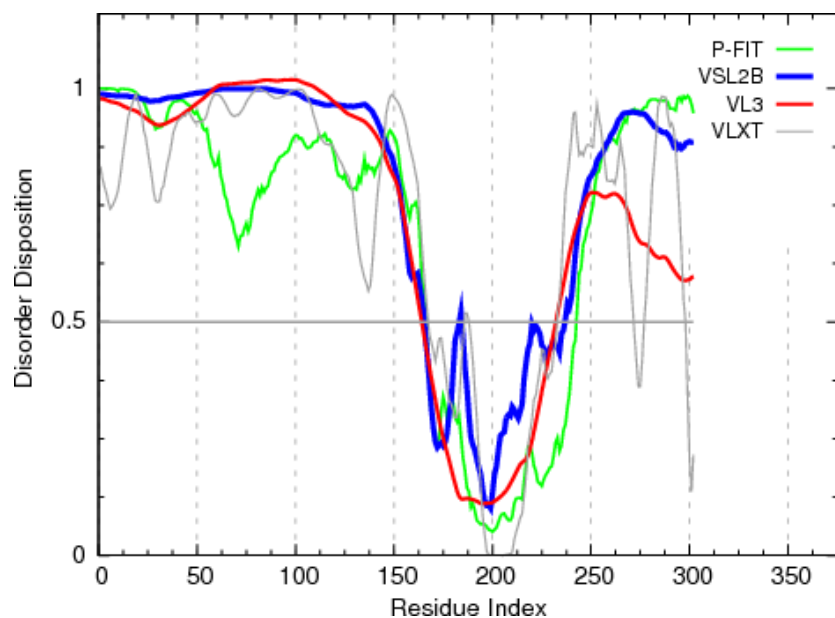
Supplementary Figure S7. Abundance and functionality of intrinsic disorder in Qip2 (O35344).



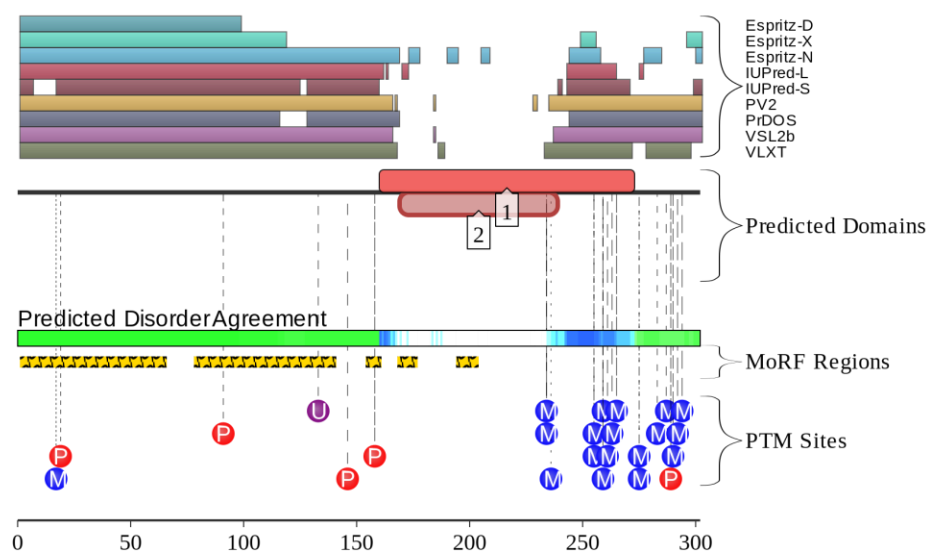


Supplementary Figure S8. Abundance and functionality of intrinsic disorder in Pendulin (P52293).





ENSMUSP00000022808



Key:

- Predicted SCOP Structure
- Weaker Support
- Pfam Conserved Domain
- Predicted Disorder
- Predicted MoRFs
- Curated PTM Site

Disorder:

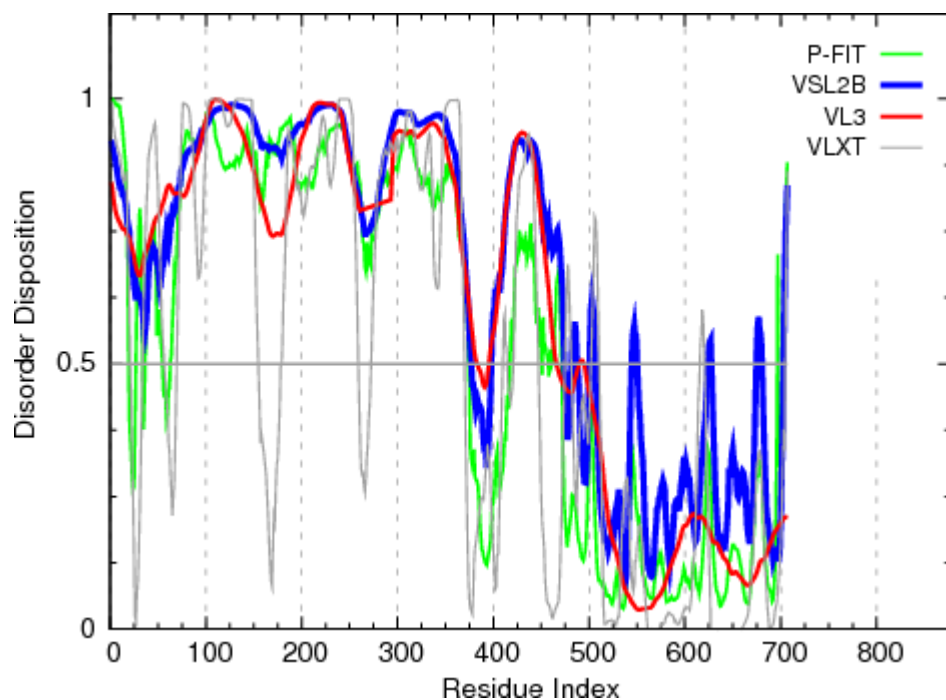
- Espritz-D
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- IUPred-L
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- PV2
- PrDOS
- VSL2b
- VLXT

Superfamilies:

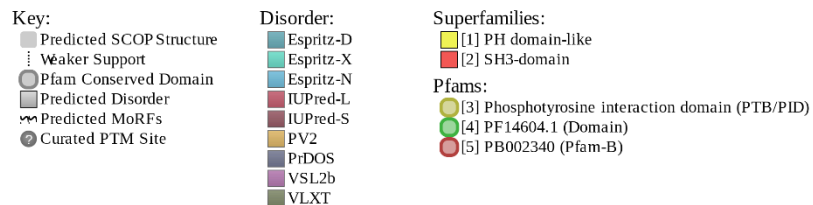
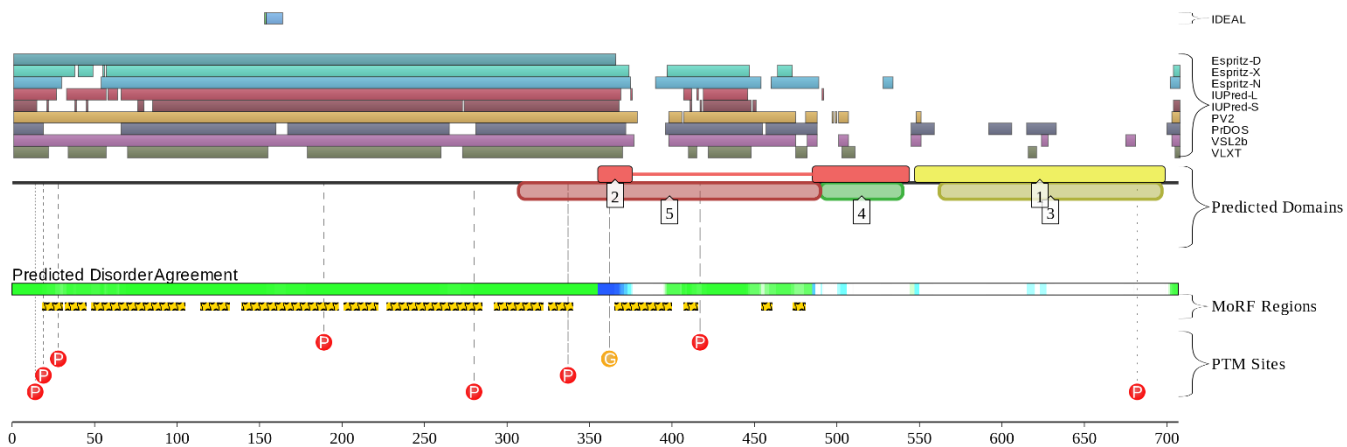
- [1] RNA-binding domain, RBD

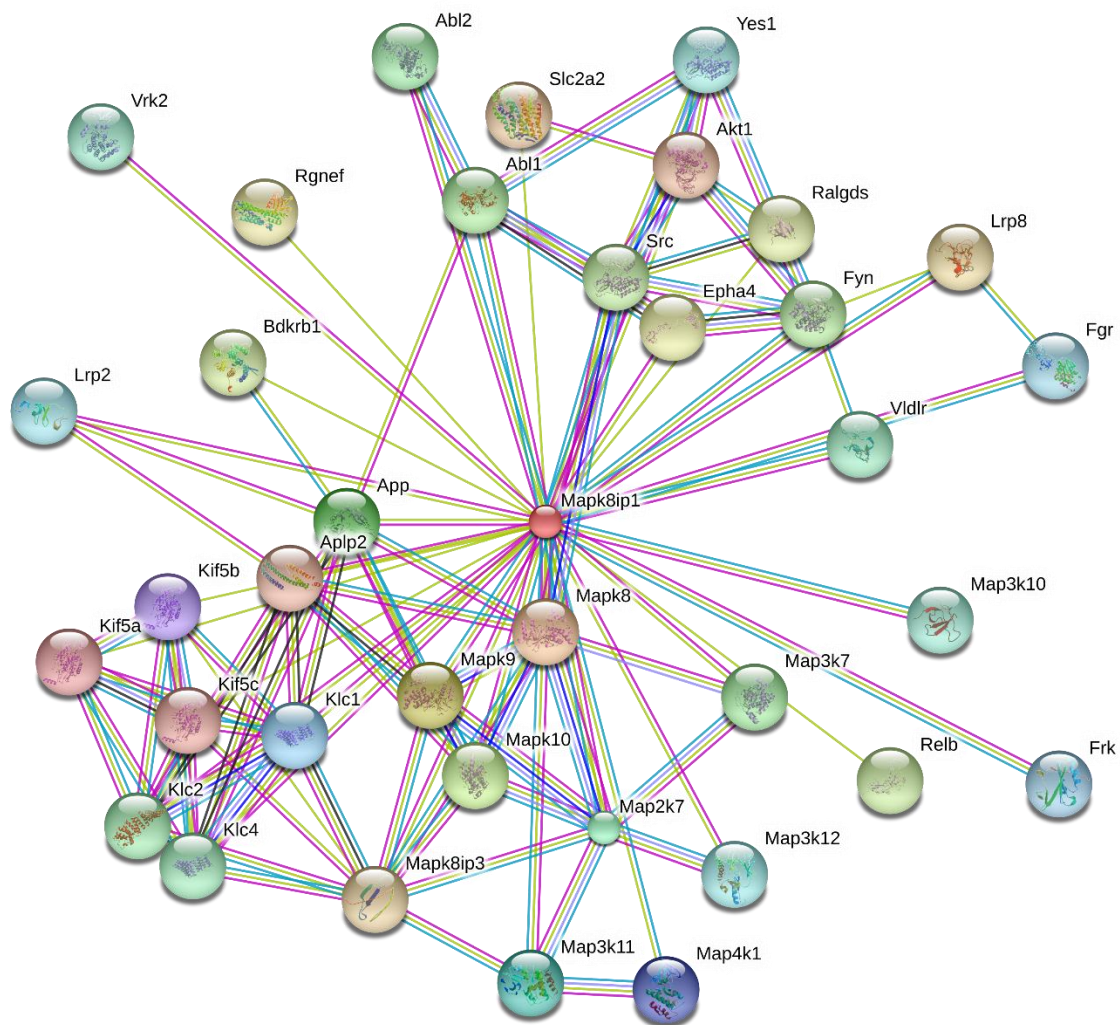
Pfams:

- [2] RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

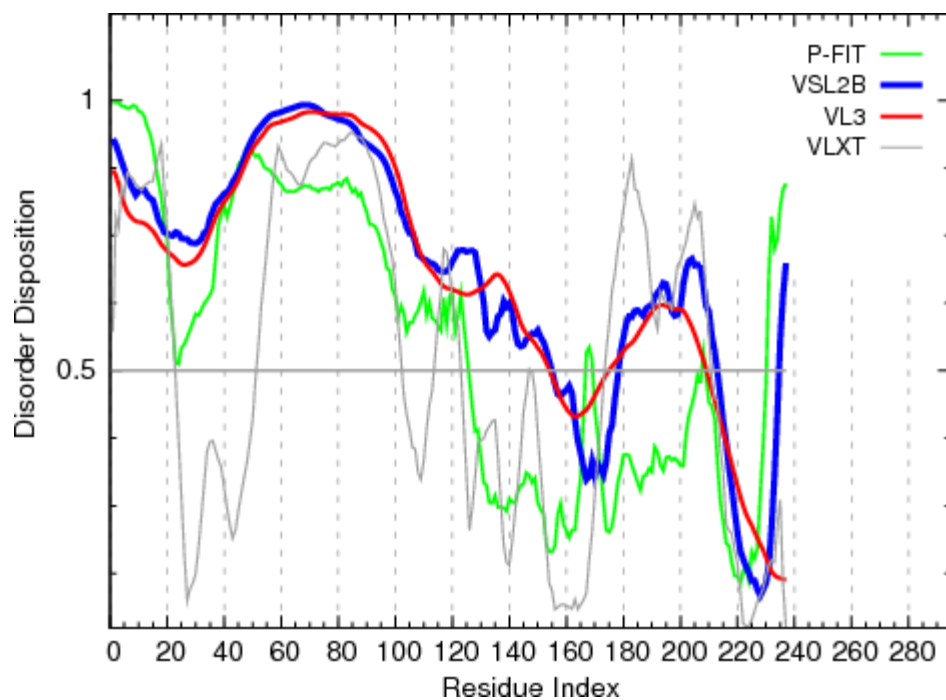


ENSMUSP00000050773

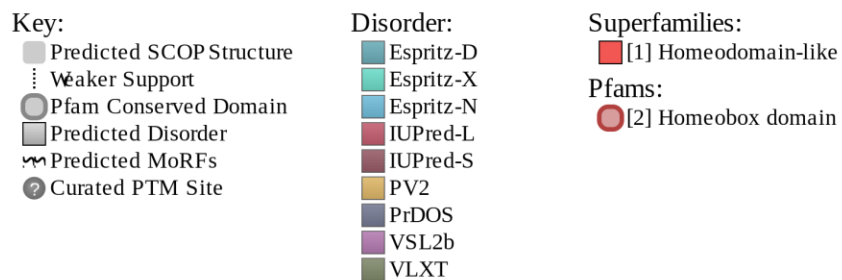
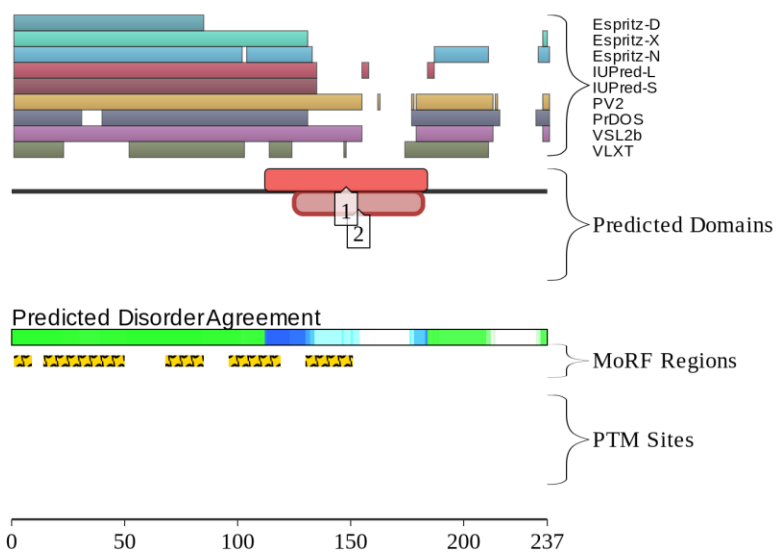


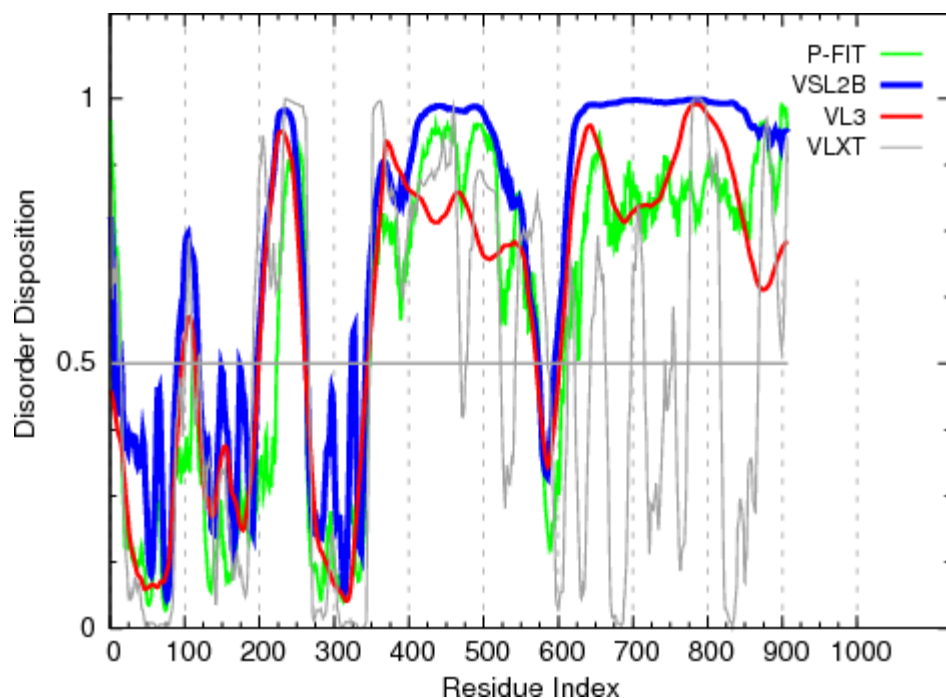


Supplementary Figure S11. Abundance and functionality of intrinsic disorder in Jip1 (Q9WVI9).

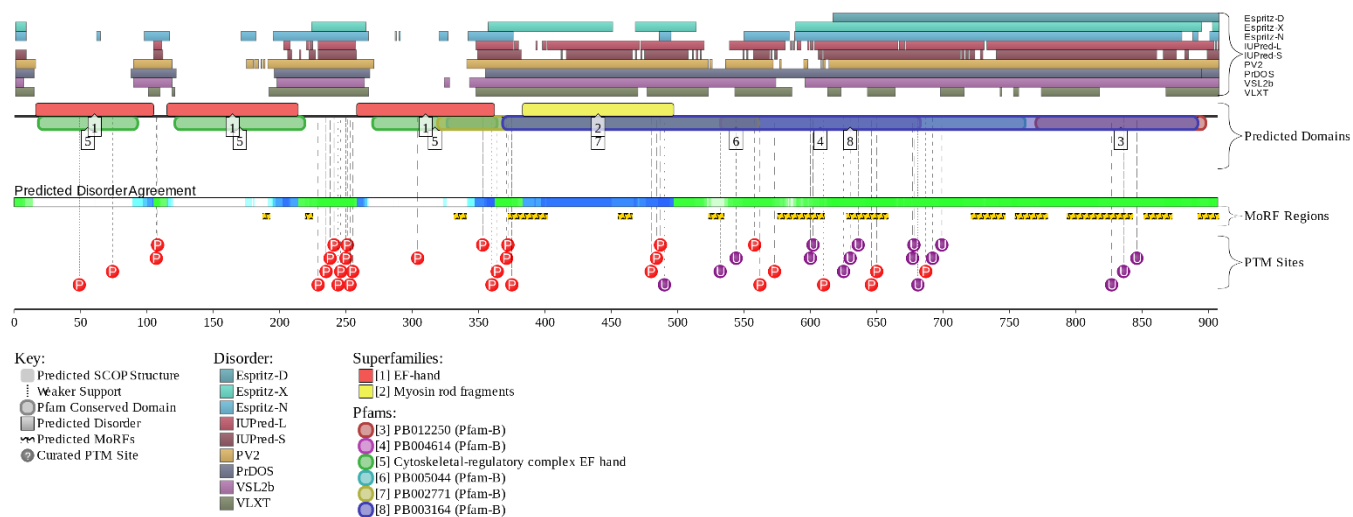


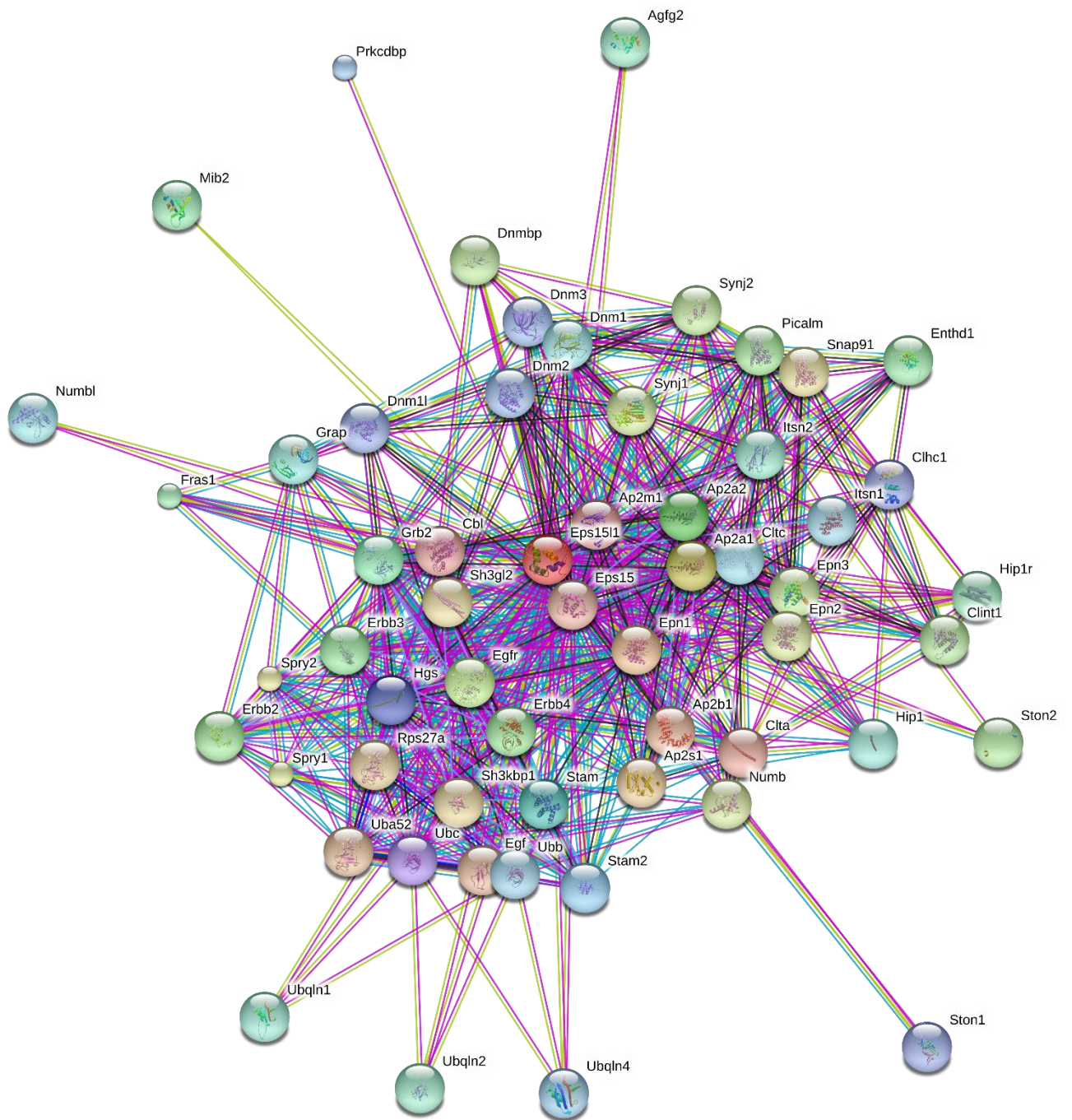
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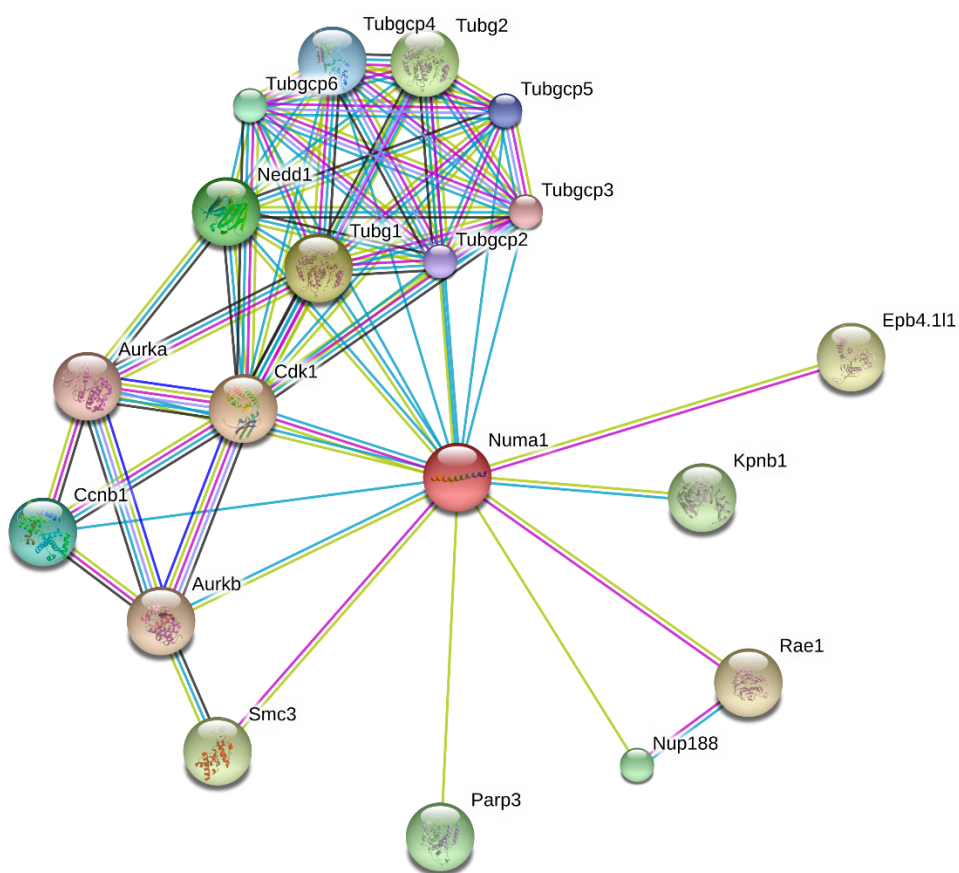
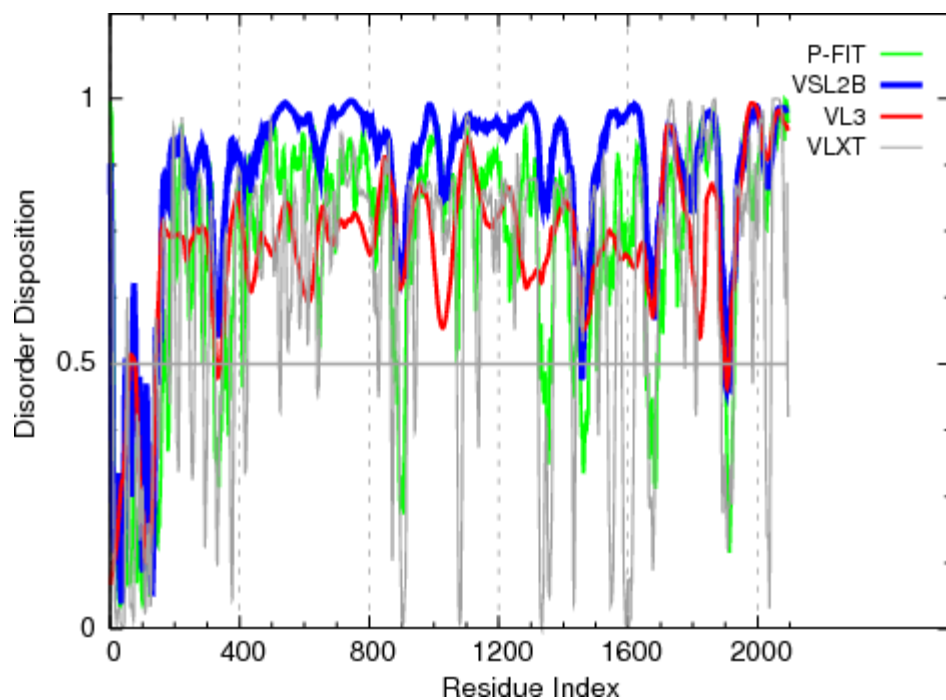


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Supplementary Figure S13. Abundance and functionality of intrinsic disorder in Eps15R (Q60902).



Supplementary Figure S14. Abundance and functionality of intrinsic disorder in Numa1 (Q80Y35).