

Fig. S1a.

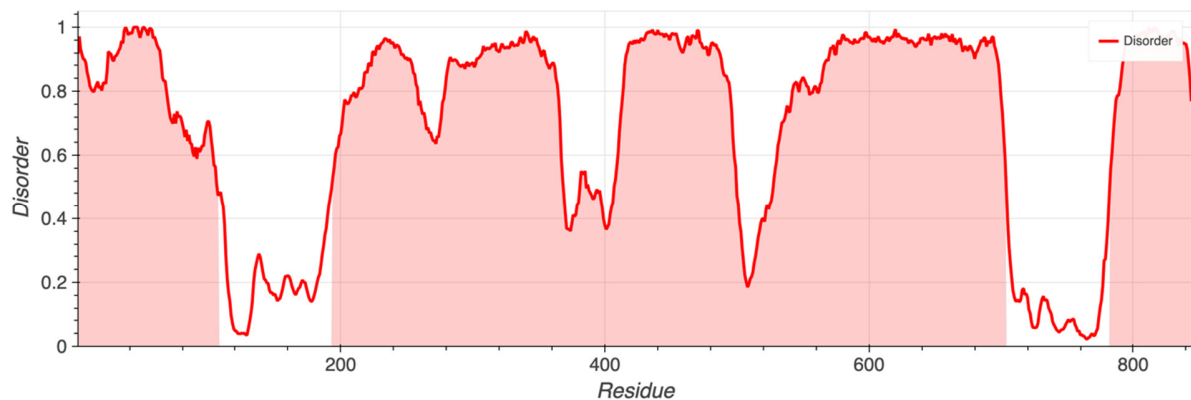


Fig. S1b.

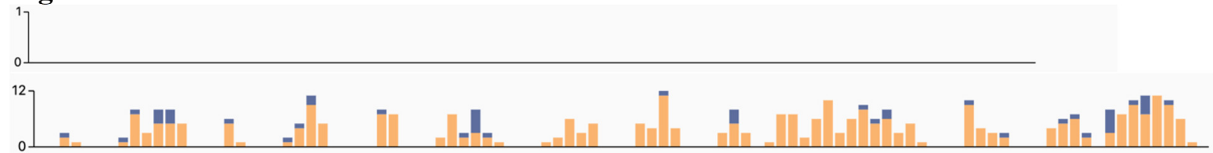


Figure S1. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue **(b)** overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for SAMD11.

Fig. S2a.

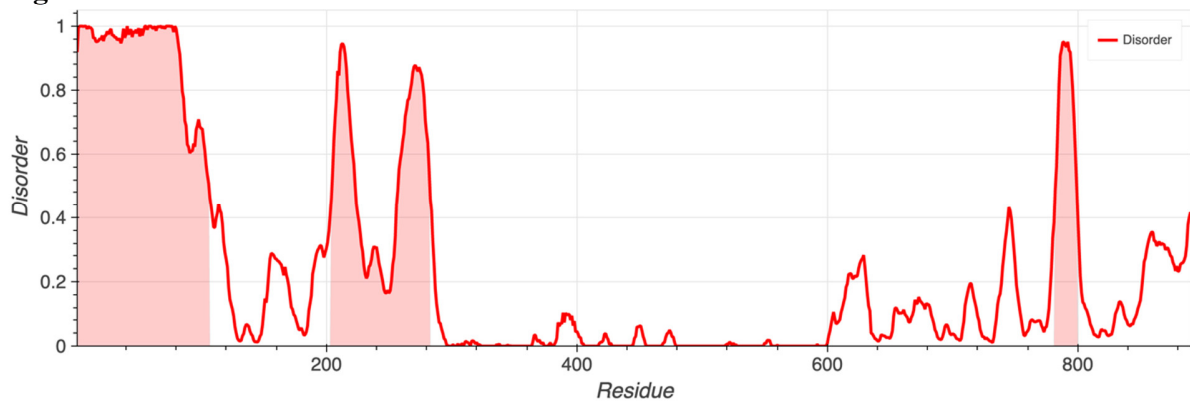


Fig. S2b.

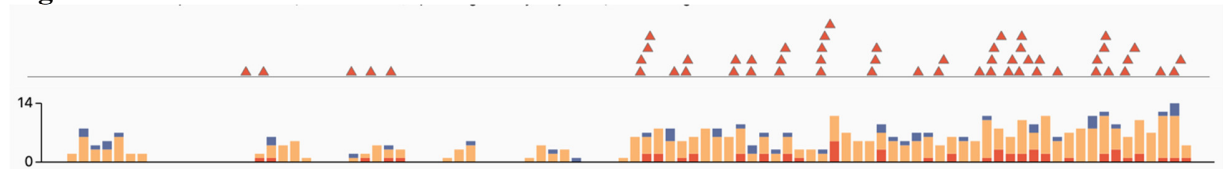


Figure S2. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue **(b)** overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for WFS1.

Fig. S3a.

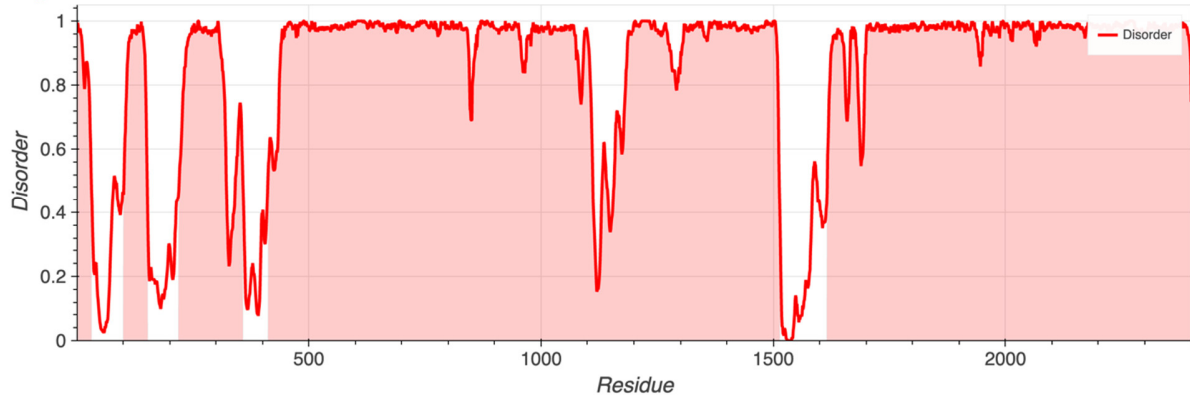


Fig. S3b.

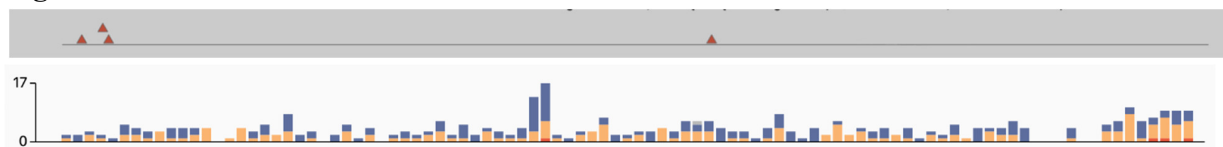


Figure S3. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue **(b)** overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for RP1L1.

Fig. S4a.

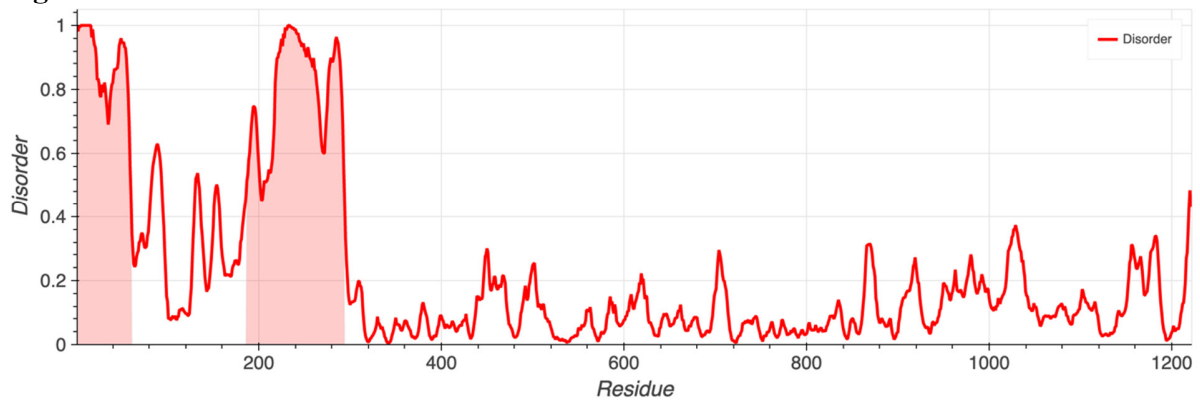


Fig. S4b.

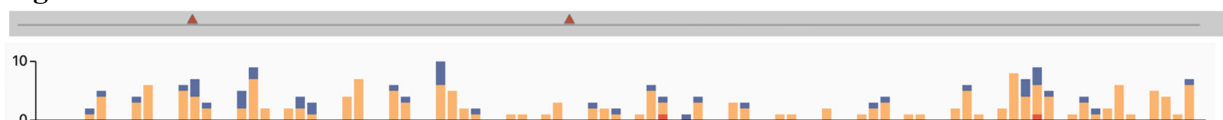


Figure S4. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue **(b)** overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for ADAMTS18.

Fig. S5a.

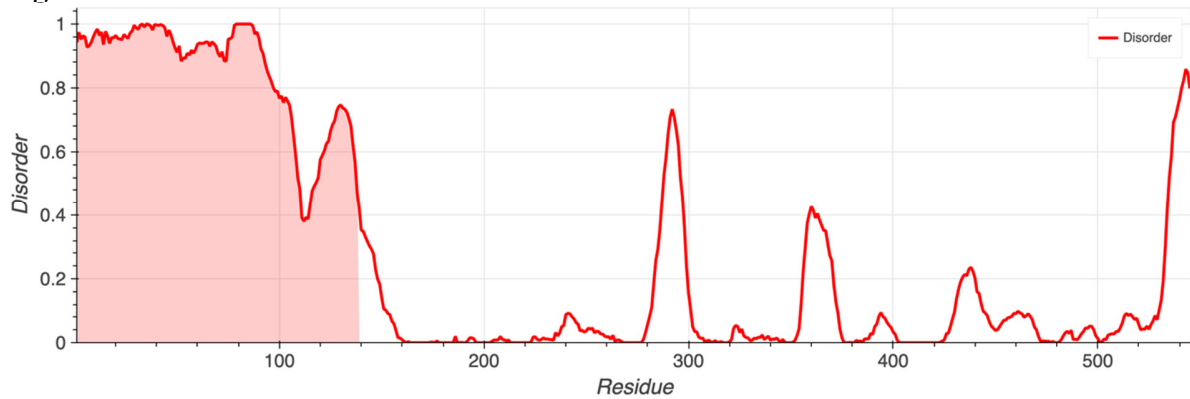


Fig. S5b.

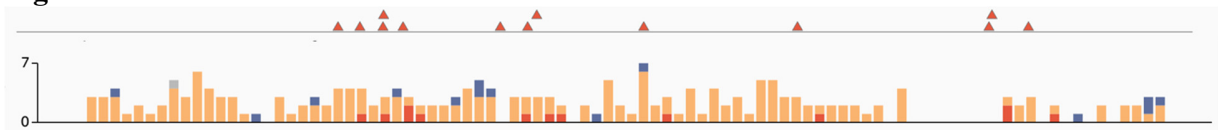


Figure S5. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue **(b)** overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for KCNV2.

Fig. S6a.

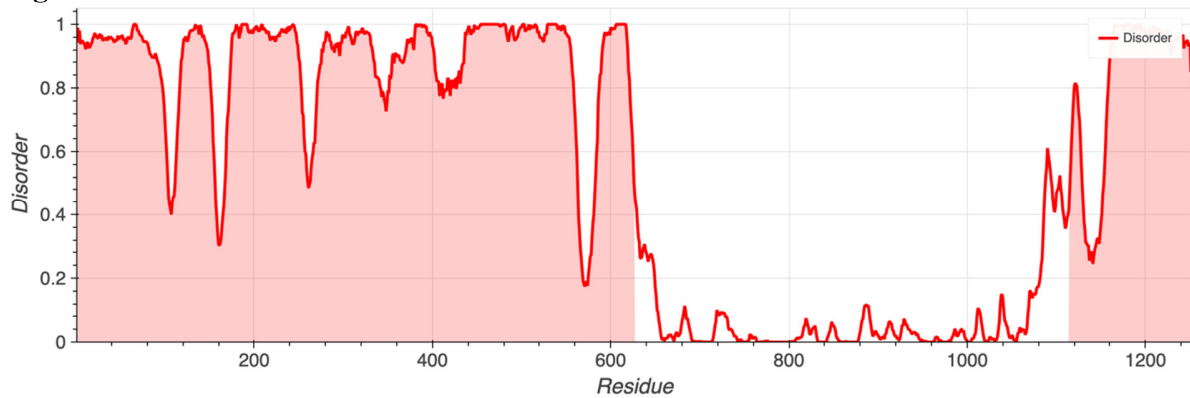


Fig. S6b.

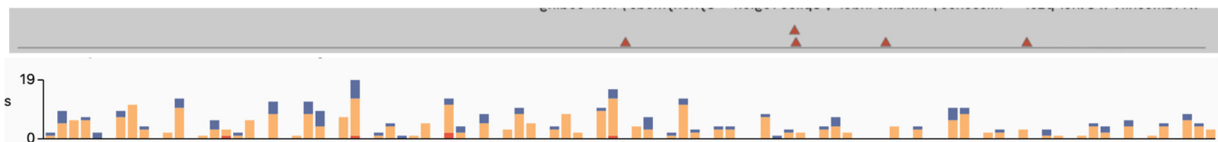


Figure S6. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue **(b)** overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for CNGB1.

Fig. S7a.

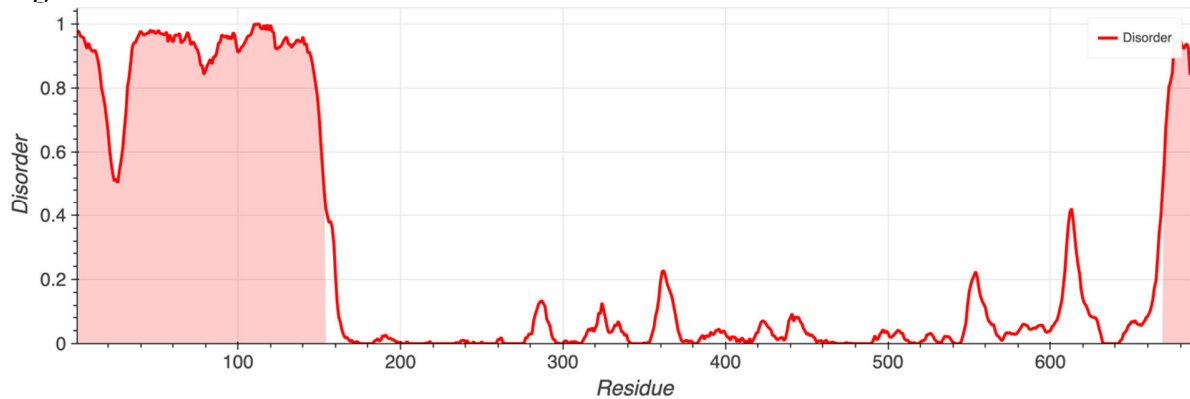


Fig. S7b.

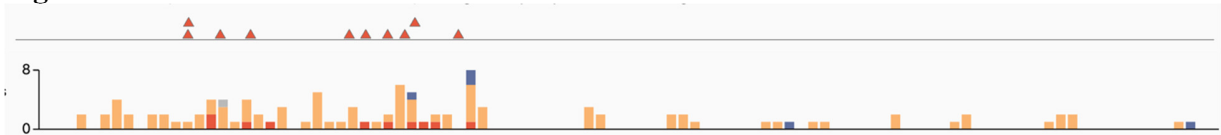


Figure S7. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue **(b)** overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for CNGA1.

Fig. S8a.

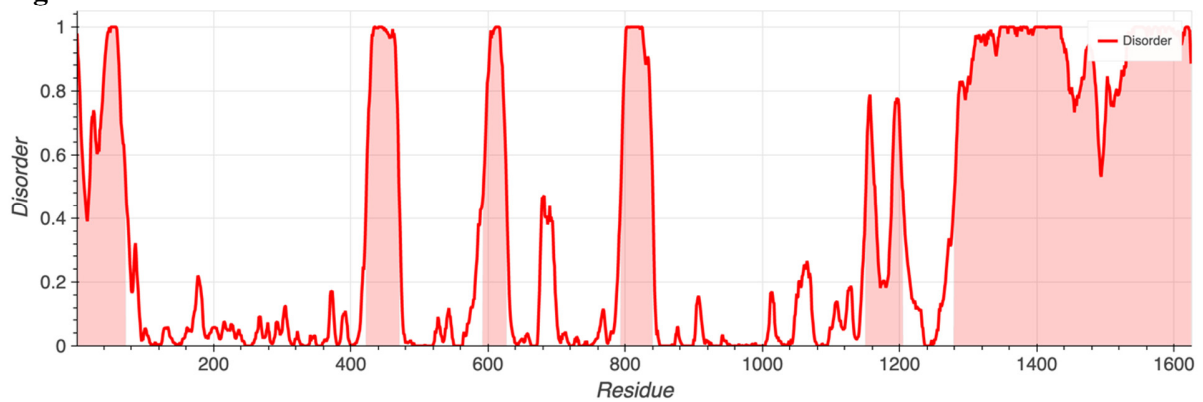


Fig S8b.

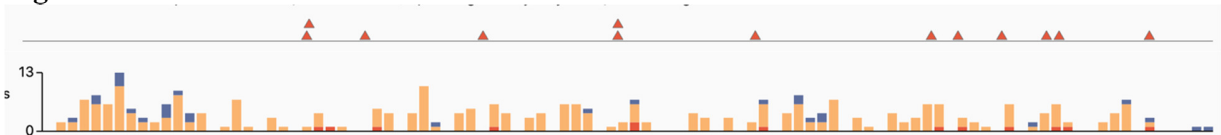


Figure S8. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue **(b)** overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for TRPM1.

Fig. S9a.

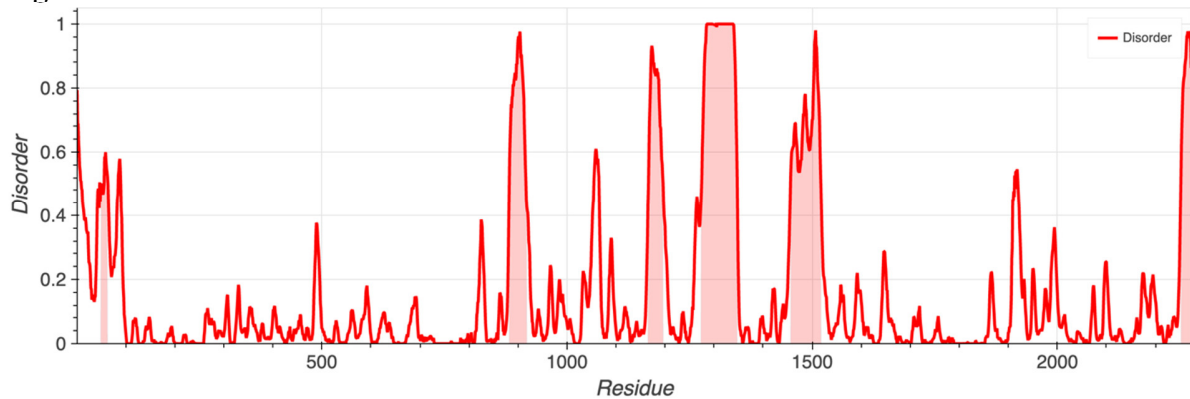


Fig. S9b.

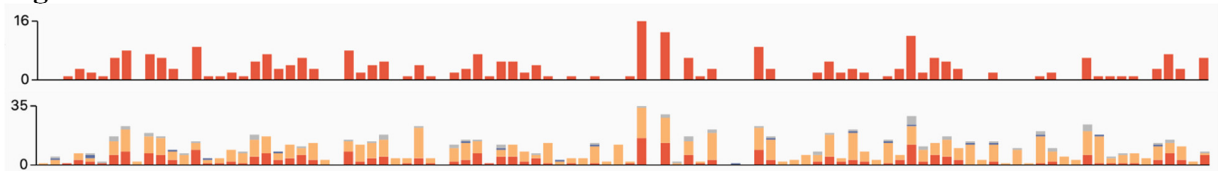


Figure S9. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue (b) overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for ABCA4.

Fig. S10a.

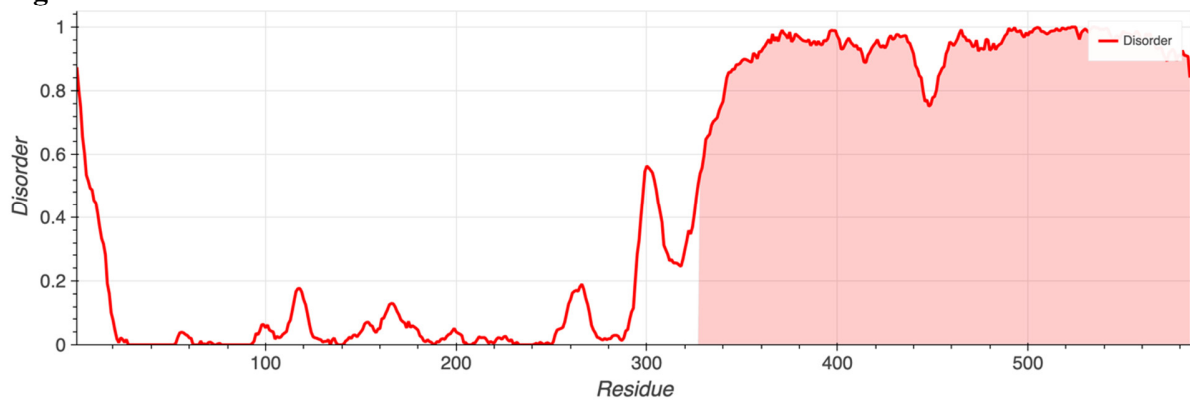


Fig. S10b.

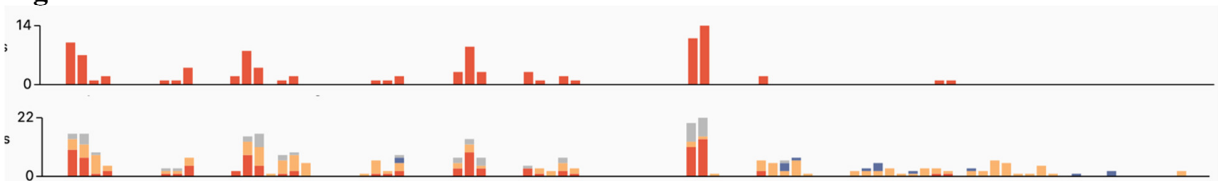


Figure S10. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue (b) overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for BEST1

Fig. S11a.

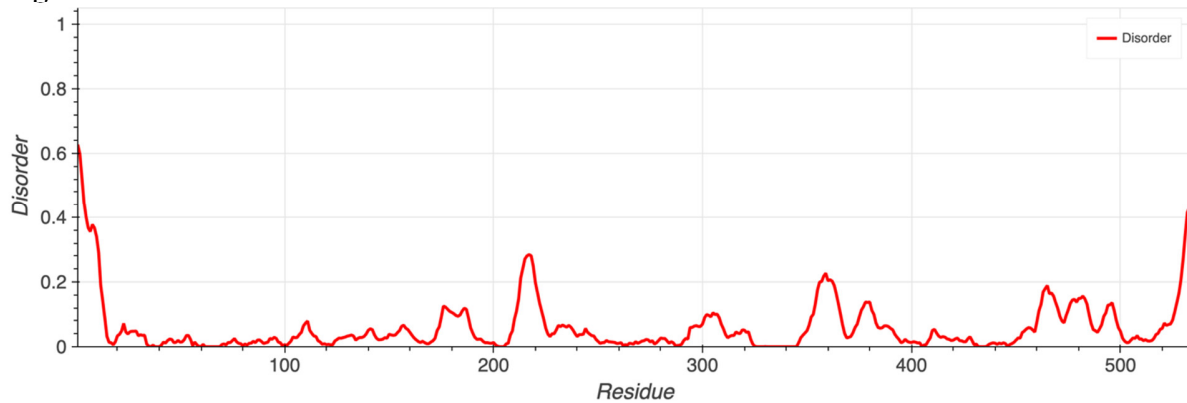


Fig. S11b.

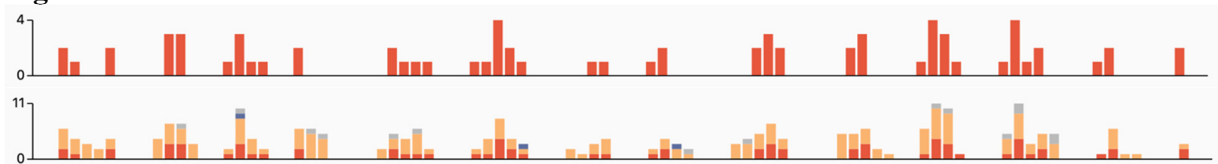


Figure S11. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue (b) overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for RPE65.

Fig. S12a.

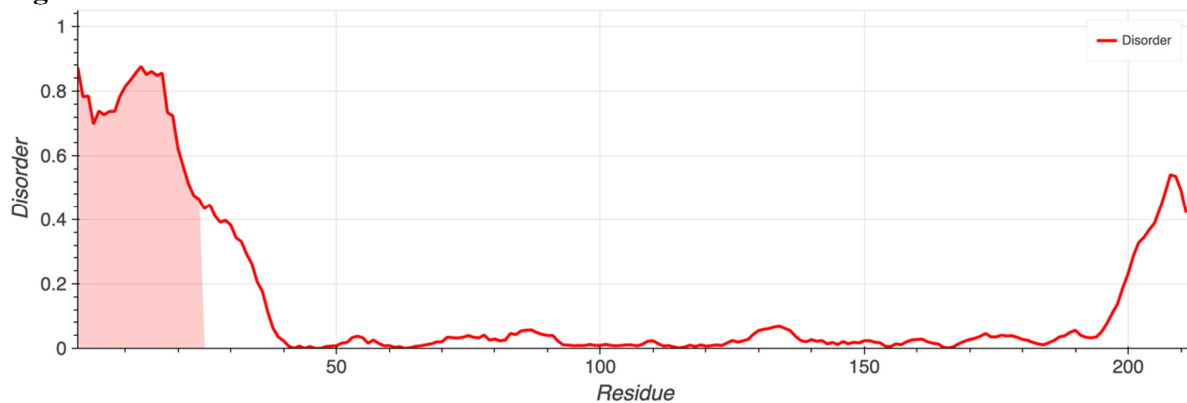


Fig. S12b.

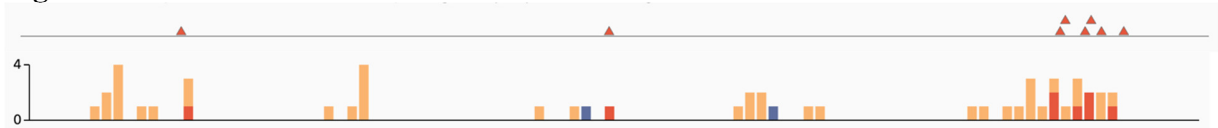


Figure 12. (a) Metapredict generated plots of intrinsically disordered regions as a function of amino acid residue (b) overlay of pathogenic missense variants (top panel) and total missense variants (bottom panel) for TIMP3.