

Development and Synthesis of Utrophin Actin Binding Domain 1 (ABD1)

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Introduction

Duchenne Muscular Dystrophy (DMD) is an X-linked recessive genetic disease resulting in the absence or dysfunction of the muscle protein dystrophin. Dystrophin is proposed to dissipate mechanical stress placed on the muscle cell membrane (sarcolemma) during muscle contraction. In patients with DMD this mechanical stress is left unchecked producing lesions within the cell membrane which leads to cell death and muscle deterioration.

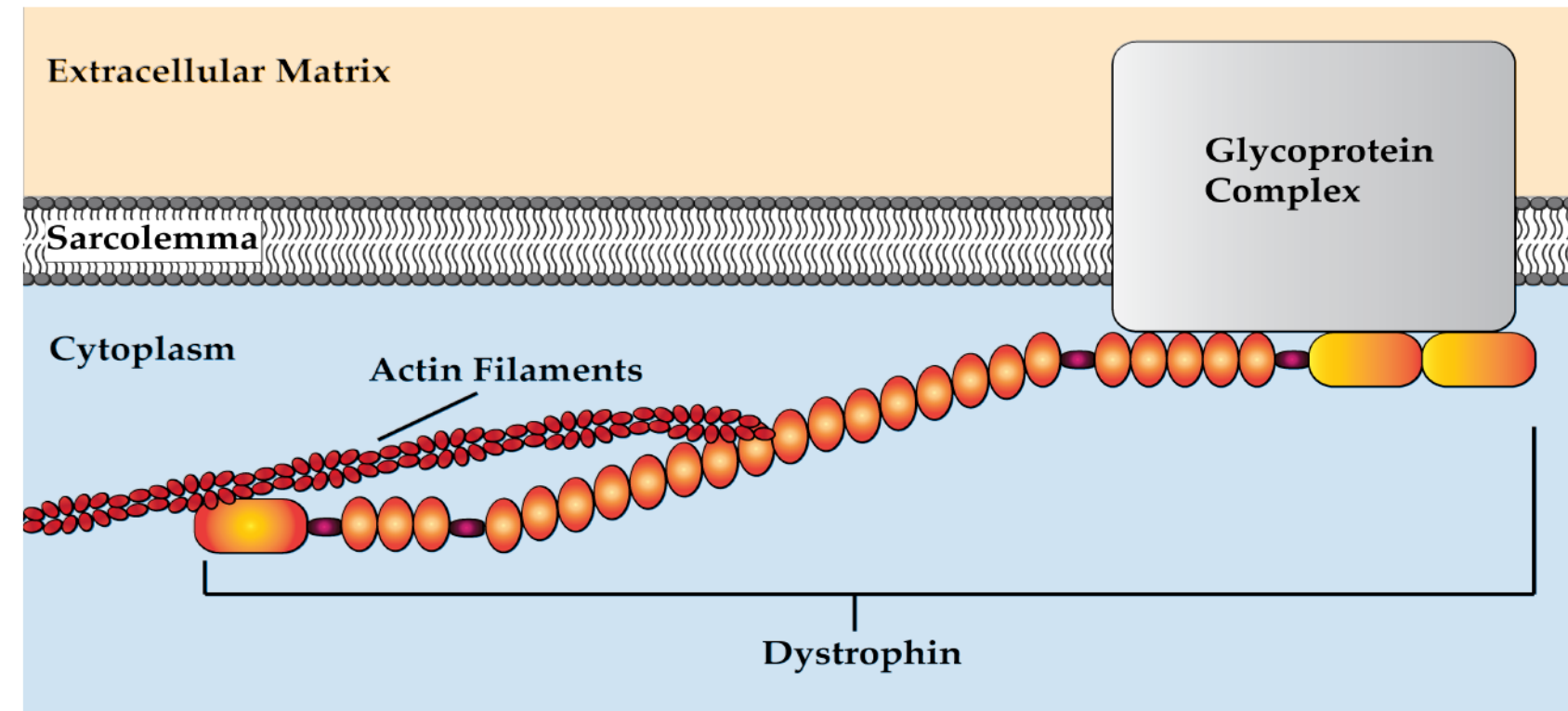


Figure 1: Dystrophin in Muscle cells. Dystrophin connects the sarcolemma to the actin filaments and is critical in dissipating stress placed on muscle.

In patients with DMD it has been observed that the expression of dystrophin's fetal homolog, utrophin, is upregulated. However, utrophin is unable to fully compensate for the lack of dystrophin resulting in patient mortality in mid to late twenties.

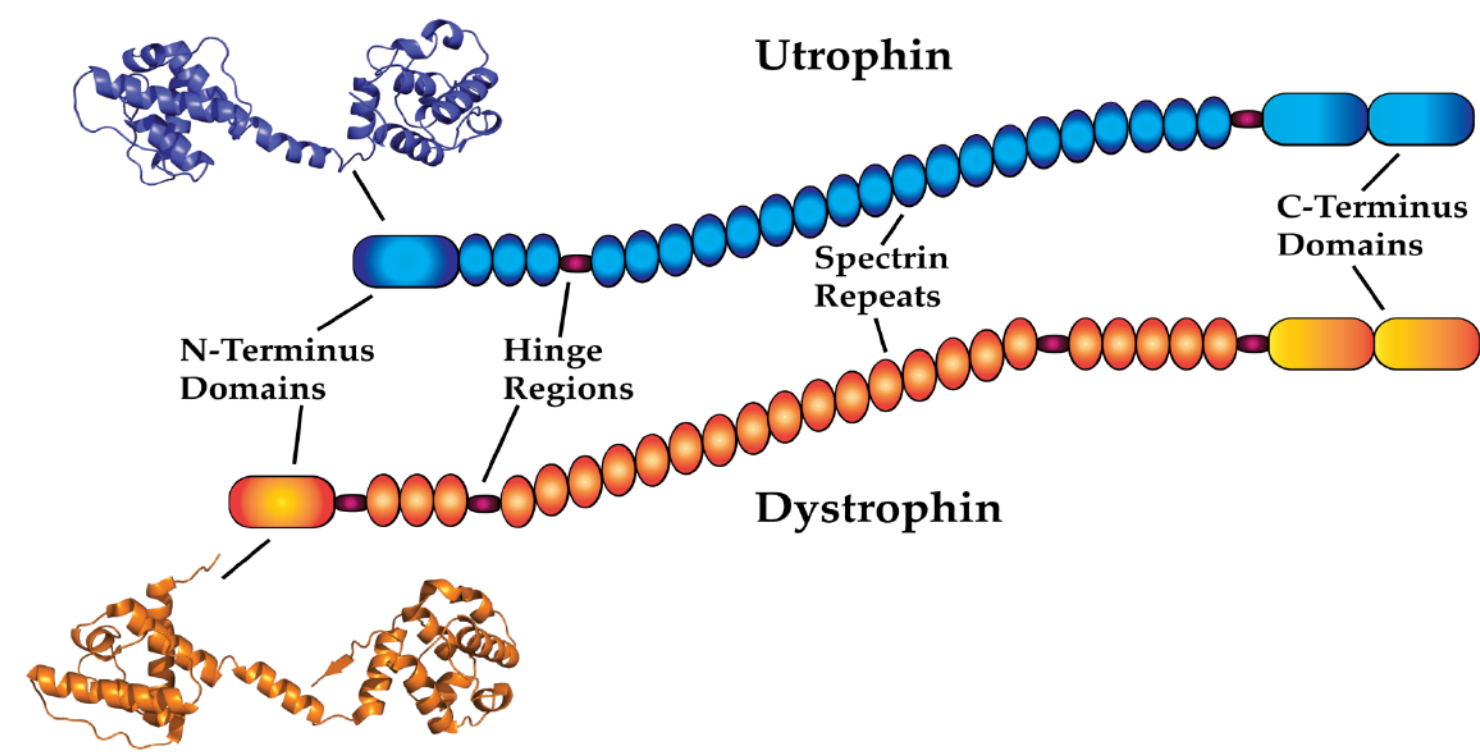


Figure 2: Structural Comparison of Utrophin and Dystrophin. Utrophin and Dystrophin share 85% homology in their actin binding domains.

We seek to make clear the characteristic differences between dystrophin and utrophin beginning with their first actin binding domains (ABD1). We hypothesize that the difference in function between dystrophin and utrophin lies within these characteristics. This project aims to design an expression vector containing utrophin ABD1.

Methods

The Utrophin ABD1 amino acid sequence (Universal Protein Resource) was used in the design of the plasmid. The sequence was codon optimized for expression in *E. coli* and inserted into pUC57 plasmid using restriction enzymes. The gene segment was amplified using polymerase chain reaction and inserted into an expression vector containing components necessary for effective protein expression and purification in *E. coli* cells.

Plasmid Design

Gene Development

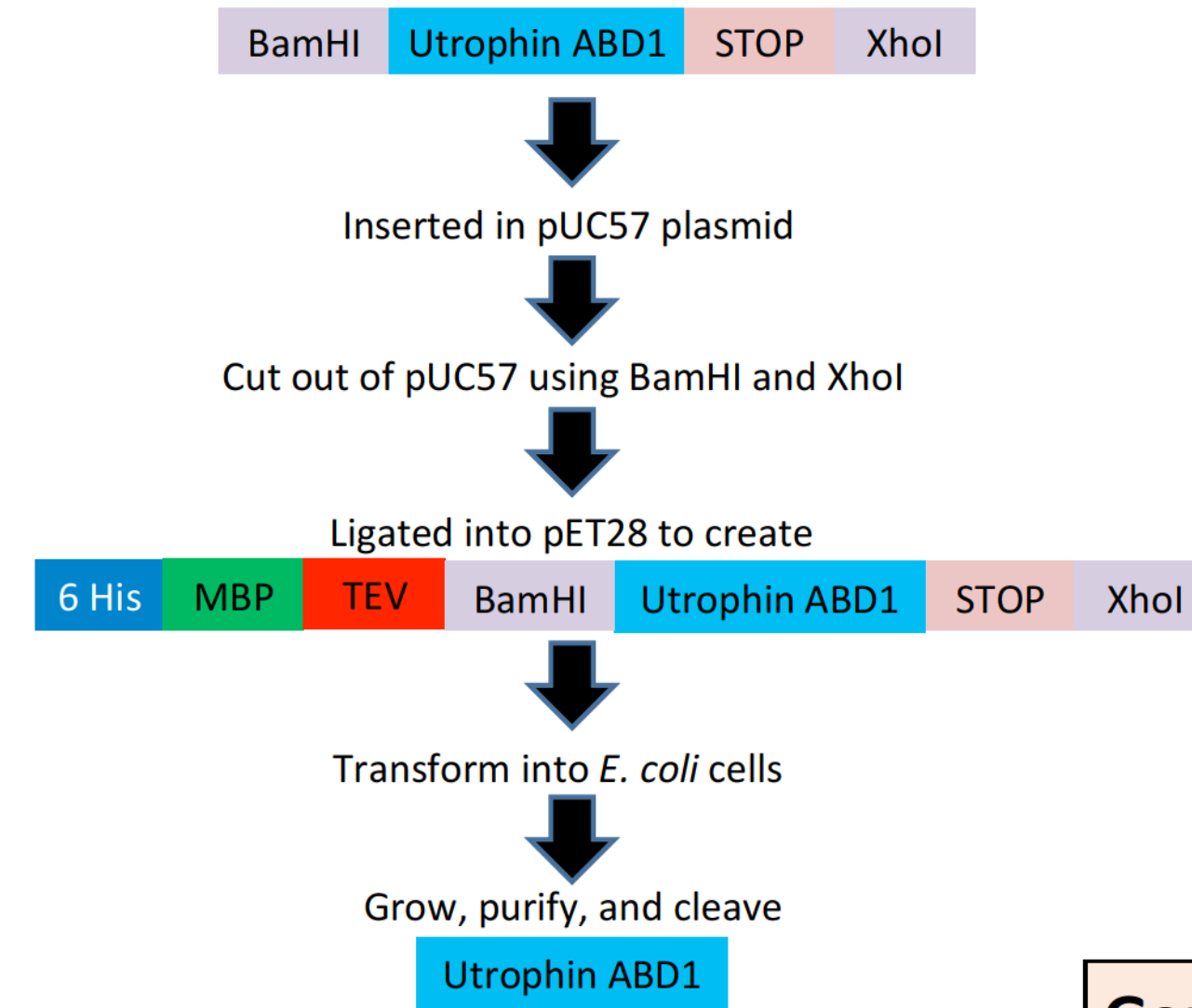


Figure 3: Map of Gene Development. The development and synthesis of utrophin ABD1 proceeded through a series of steps to obtain pure Utrophin ABD1. Each step was purposeful and specifically designed to obtain pure utrophin ABD1.

Table 1: Codon Optimization Provides Enhanced Sequencing. Example of codon optimization and the specificity when transitioning between organisms.

Gene	TTA	GTA
Amino Acid	Leucine	Valine
Codon Optimized	CTG	GTC

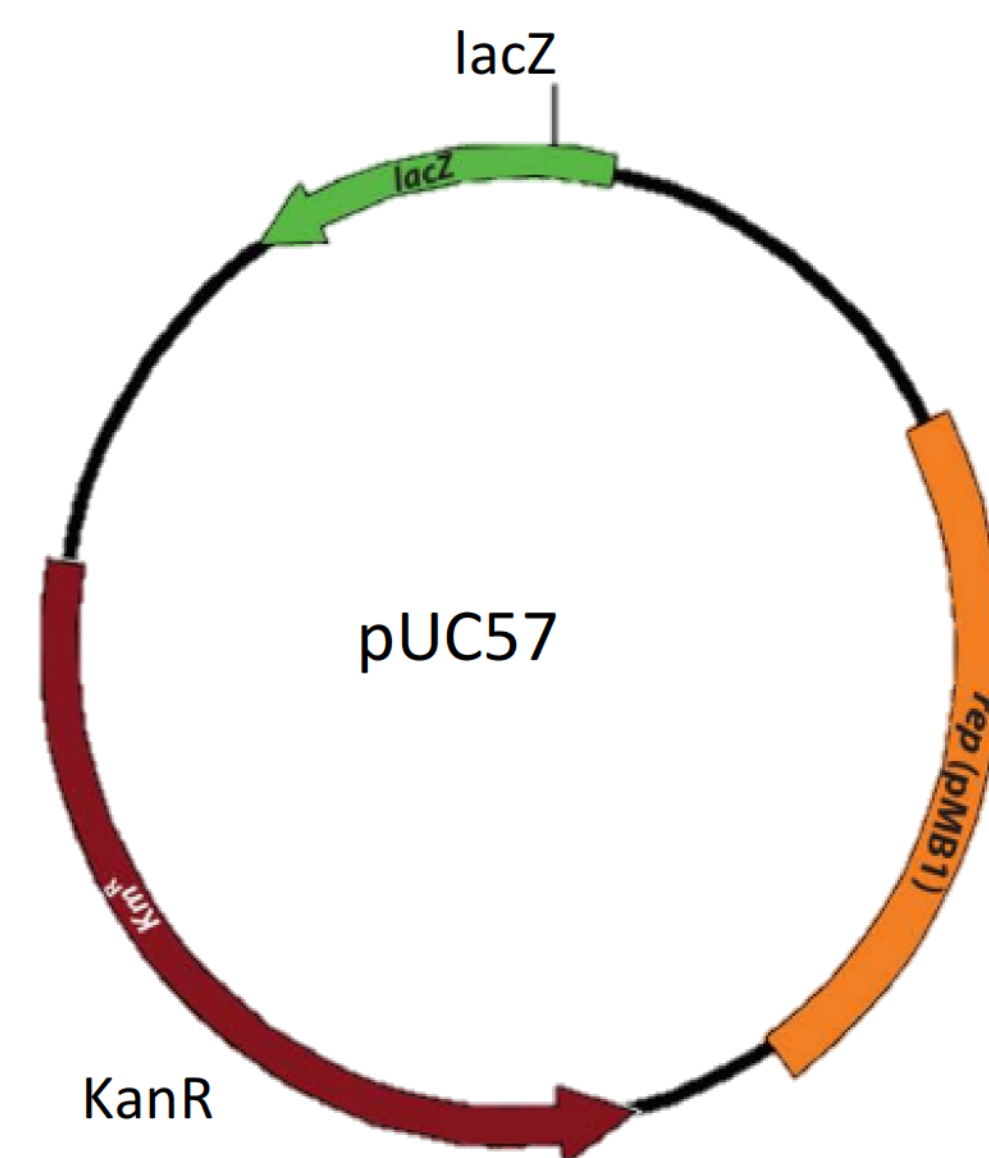


Figure 4: pUC57 *E. coli* Plasmid. *E. coli* plasmid for insertion of utrophin ABD1 containing selectable and screenable markers for visual analysis. These markers include a visual indicator and bacterial resistance.

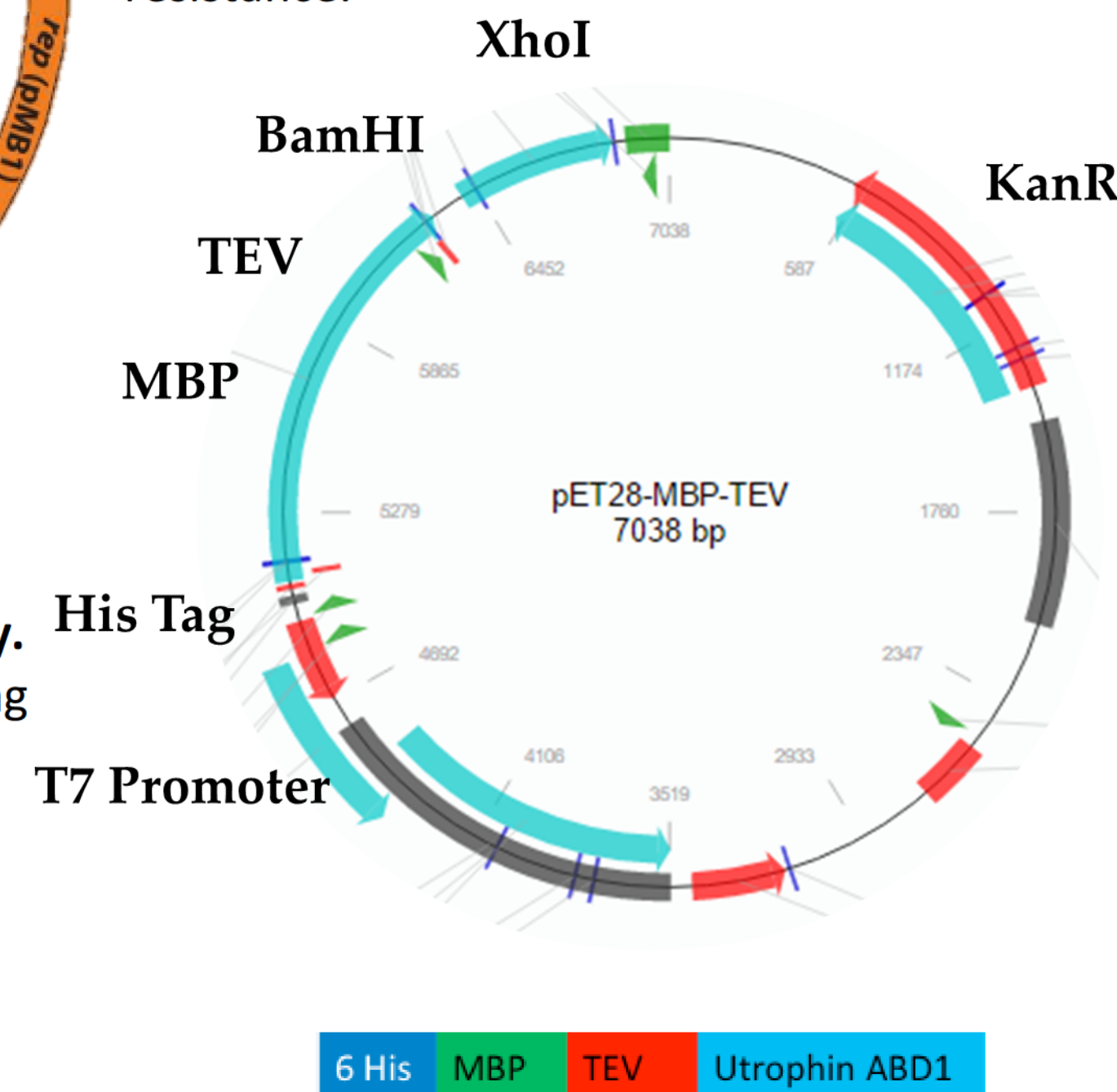


Figure 5: Expression Vector for Nickel Affinity Chromatography. The expression vector containing all necessary components for nickel column chromatography and the resulting construct for purification.

Protein Purification

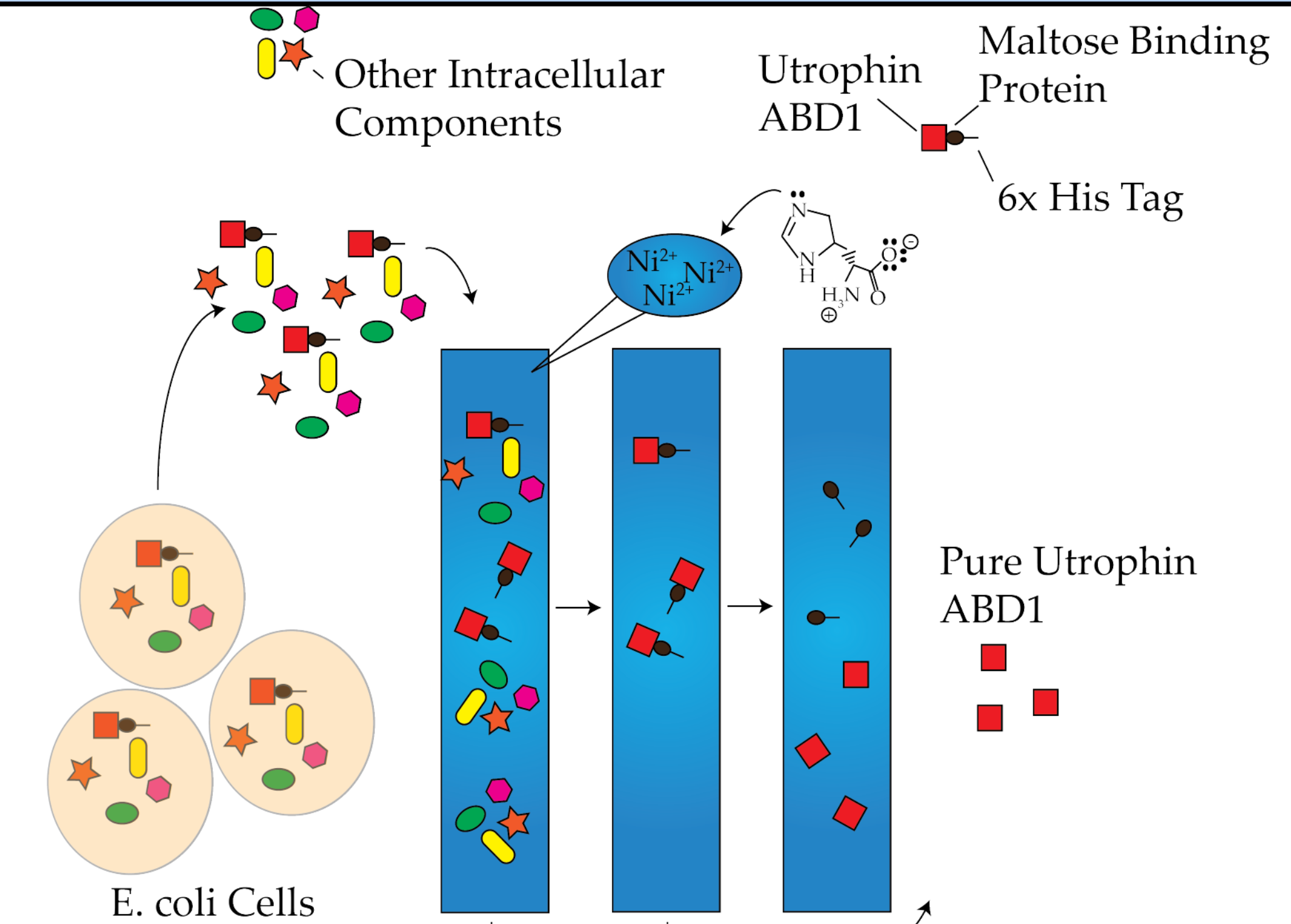


Figure 5: High Yield in Purity From Nickel Chromatography. The tight binding of the lone pair electrons on histidine to the nickel enables the selected release of utrophin ABD1.

Conclusion

Duchenne Muscular Dystrophy is characterized by the failure to dissipate mechanical stress in the muscle. In order to create a potential therapeutic target, utrophin ABD1 was developed and synthesized for future parameterization of the first actin binding domain. The construct was designed using the *E. coli*, codon optimized gene flanked by two restriction enzymes for excision of the construct from the pUC57 plasmid into the expression vector. The expression vector added a histidine tag, maltose binding protein, and TEV protease for high yield purification.

References

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