1 Introduction

2 Methods

The sequence for the domain Tau-5 of Human Androgen Receptor-1 (AR1) and mutant $W393A, W433A$ are shown in Table 1.

Table 1: Primary Residue Sequence for AR1 Tau-5* domain. Mutationed residues are displayed in red.

Peptide	Sequence
WT	GPAAGSSGTLELPSTLSLYKSGALDEAAAYQSRDYYNFPLALAGPPPPPPPP HPHARIKLENPLDYGSAWAAAAAQCRYGDLASLHGAGAAGPGSGSPSAAAS SSWHTLFTAEEGQLYGPC
$W393A, W433A$	GPAAGSSGTLELPSTLSLYKSGALDEAAAYQSRDYYNFPLALAGPPPPPPPP HPHARIKLENPLDYGSAAAAAAAQCRYGDLASLHGAGAAGPGSGSPSAAAS SSAHTLFTAEEGQLYGPC

2.1 Sample Expression

We need to add the cell line, plasmid insertion conditions, expression conditions, isolation, up to SEC purification.

2.2 Sample Purification

The sample was purified with an AKTA pure 25 FPLC. Size exclusion chromatography was carried out at room temperature using a Superdex 75 Increase 10/300 GL to isolate monomeric species of our expressed peptide. A minimal buffer containing 0.1 M ..... Following purification, the samples were

3 Results

4 Discussion

5 Conclusion

From the NMR chemical shifts and there differences insight into the physiochemical influence of EPI-001 on the Tau-5 domain of Human Androgen Receptor-1. The changes to the conformational sampling of the Tau-5 domain are assessed via the NMR chemical shift differences. From the CS differences we conclude that EPI-001 changes the helical propensity of two regions, R2 and R3. The helicity sampling is increased for R2, while it is deminished in R3, albiet the CS differences of R3 are less than those observed in R2. Thus EPI-001, influences helical propensity shifting sampling of helical content, deminishing structural organization.