

P036 Identifying androgen receptor cofactors using oligonucleotide scaffolds

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The Androgen Receptor (AR) is a ligand activated transcription factor which plays important roles in development and prostate cancer. We recently published a genome-wide location analysis for AR promoter binding sites. The majority of these binding sites lacked the consensus 15bp AR binding sequence. We identified a highly enriched 6bp AR 'half-site' which was sufficient to recruit the AR both *in vitro* and *in vivo*. However, current models suggest that the AR binds as a homodimer to two adjacent 'half-sites'. Therefore, the identification of single AR 'half-sites' suggests an alternative mechanism for AR recruitment. In addition these 6bp AR binding sequences occur frequently in the genome, suggesting that other factors are involved in AR binding site selection. Using unbiased motif searches we found significant co-enrichment of ETS transcription factor binding sites with these 6bp AR 'half-sites' in AR bound regions of the genome. This suggests that ETS factors may contribute to AR genomic binding site selection. To identify cooperating transcription factors and cofactors we have used a biotinylated oligonucleotide pull-down assay coupled with Western blotting. This approach has allowed the identification of proteins which bind to sequences containing both AR and ETS binding sites, but not to scrambled control sequences. By combining these existing approaches it is possible identify cooperating transcription factors and cofactors, assess co-dependency for DNA binding and provides candidates for future functional studies.