

Figure 1. Micrographs of an AR/ERG complex bound to DNA with and without continuous support.

A) Representative micrograph imaged on a K2-equipped Krios at NYSBC (Graphene oxide on Au Quantifoil 1.2/1.3).

B) Sample in (A) 6X-concentrated (Au Quantifoil 1.2/1.3), imaged on a K3-equipped Krios at MSK.

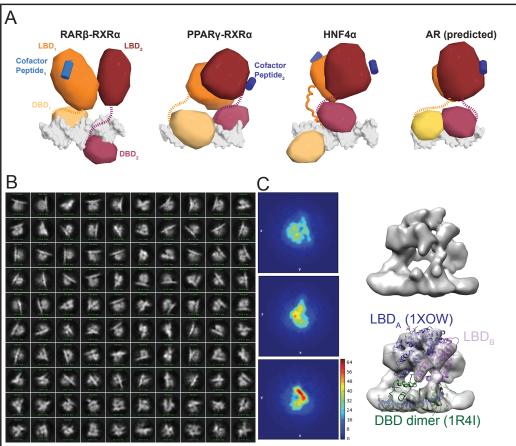


Figure 2. 2D class averages and 3D ab initio model of the AR/ERG complex bound to DNA. A) Crystal structures of the DNA-bound type II NRs RARβ-RXRα (PBD: 5UAN), PPAR γ-RXRα (PBD: 3E00), HNF4α (PDB: 4IQR), and a predicted model of Δ NTD-AR bound to DNA (Ligand binding domain [LBD] PBD: 1XOW; DNA binding domain [DBD] PBD: 1R4I) reveal conformational flexibility, depicted as Gaussian blobs, and generated with Pymol. Placement of the AR LBD homodimer is based on alignments with LBDs of the DNA-bound type II NR heterodimers. B) Third round of 2D classification using Cryosparc 2. 38,000 particles total. C) Left: ab initio model generated in Cryosparc 2 using particles in (B), with crystal structures of individual domains of AR docked into model using Chimera (bottom right).