Figure S1. (A) Scattering profiles of RXRα full-length without DNA (green) and ~~and~~ RXRα-*Ramp2* DR1 (red). The profiles are arbitrary displaced in logarithmic scale for better visualization. **(B)** Distance distribution functions computed from the X-ray scattering patterns using the program GNOM.

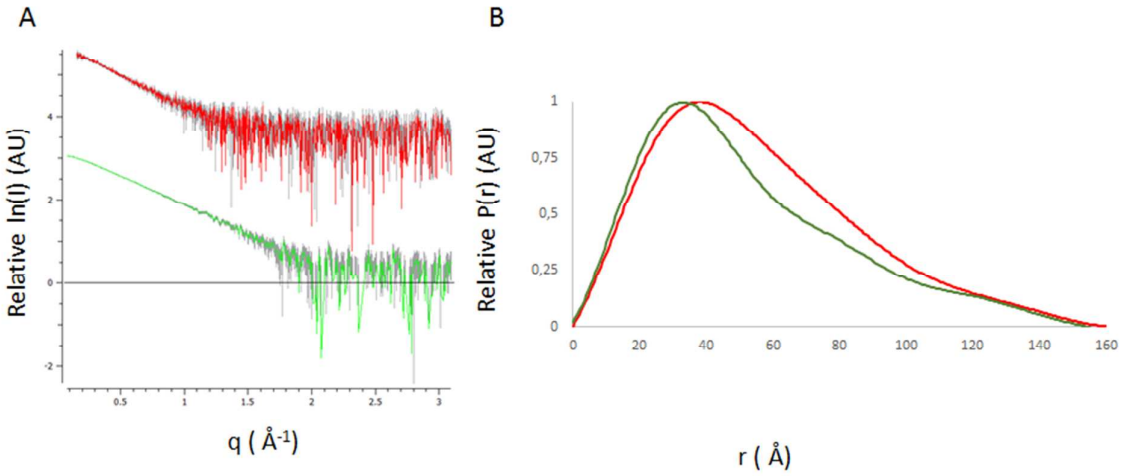
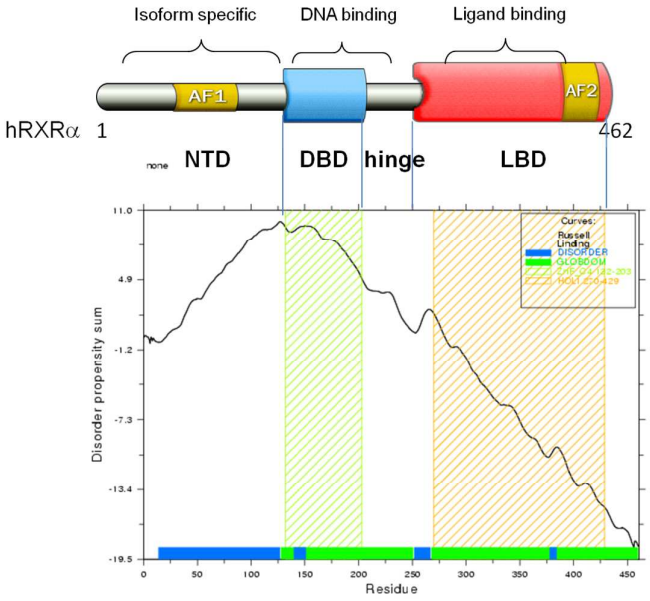


Figure S2. In silico analysis of the RXRα NTD sequence composition and disorder predictions. (A) Domain organization of hRXRα together with the GlobPlot analysis (http://globplot.embl.de) of the primary sequence of hRXRα that indicates that the NTD is disordered. (B) Primary sequence of hRXRα. The NTD, DBD and LBD are shown in grey, blue and red respectively. (C) Unified view of the outputs of disorder predictors of the RXRα NTD-DBD and results of Hydrophobic Cluster Analysis (HCA) using the MeDor metaserver (Lieutaud et al., 2008). α-helices are drawn in red, -strands are represented by blue arrows. Predicted disordered regions are represented by bidirectional arrows of different colours for different predictor algorithms, IUPred (Dosztanyi et al., 2005), Globplot (Linding et al., 2003), DisEMBL (Linding et al., 2003), FoldIndex (Prilusky et al., 2005) and RONN (Yang et al.,2005). Code: red star: proline; black losange: glycine; square: threonine; dotted square: serine.

A



B

MSTQVNSSLTSPTGRGSMAAPSLHPSLGPGIGSPGQLHSPISTLSSPINGMGPPFSVISSPMGPHSMSVPTTPTLGFSTGSPQLSSPMNPVSSS
EDIKPPLGLNGVLKVPAHPSGNMASFTKHICAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRYQKCLAM
GMKREAVQEERQRGKDRNENEVESTSSANEDMPVERILEAELAVEPKTETYVEANMGLNPSSPNDPVTNICQAADKQLFTLVEWAKRIPHFSEL
PLDDQVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSAGVGAIFDRVLTELVSKMRDMQMDKTELGCLRAIVLFNPDSKGLSNP
AEVEALREKVYASLEAYCKHKYPEQPGRFAKLLLRLPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEAPHQMT

C