

Ligand binding and heterodimerization with retinoid X receptor  $\alpha$  (RXR $\alpha$ ) induce farnesoid X receptor (FXR) conformational changes affecting co-activator binding

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Running title: Allosteric signal transduction in FXR/RXR heterodimer

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**Keywords:** Farnesoid X receptor (FXR), Retinoid X receptor (RXR), transcription factor, signal transduction, X-ray crystallography, metabolism, allostery, conformational change

## SUPPORTING INFORMATION

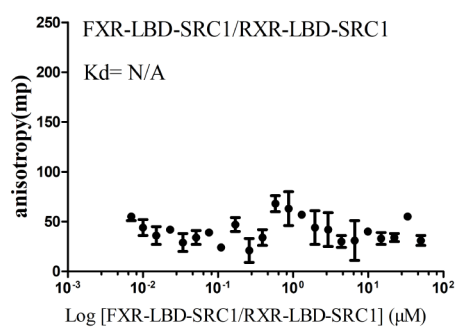
Table S1. Peptide binding by fluorescence anisotropy

Receptors	FXR/RXR ligands	Dissociation constants ( $\mu\text{M}$ )
FXR-LBD	apo	6.60 $\pm$ 0.33
FXR-LBD/RXR-LBD•SRC1	apo/apo	2.42 $\pm$ 0.27
	HNC143	0.71 $\pm$ 0.07
	HNC143/9cRA	0.58 $\pm$ 0.06
	HNC180	0.51 $\pm$ 0.04
	HNC180/9cRA	0.46 $\pm$ 0.05
	GW4064	0.73 $\pm$ 0.07
	GW4064/9cRA	0.43 $\pm$ 0.05
RXR-LBD	apo	4.30 $\pm$ 0.64
FXR-LBD•SRC1/RXR-LBD	apo/apo	2.12 $\pm$ 0.08
	9cRA	0.70 $\pm$ 0.01
	HNC143/9cRA	0.48 $\pm$ 0.24
	HNC180/9cRA	0.31 $\pm$ 0.16
	GW4064/9cRA	0.50 $\pm$ 0.10

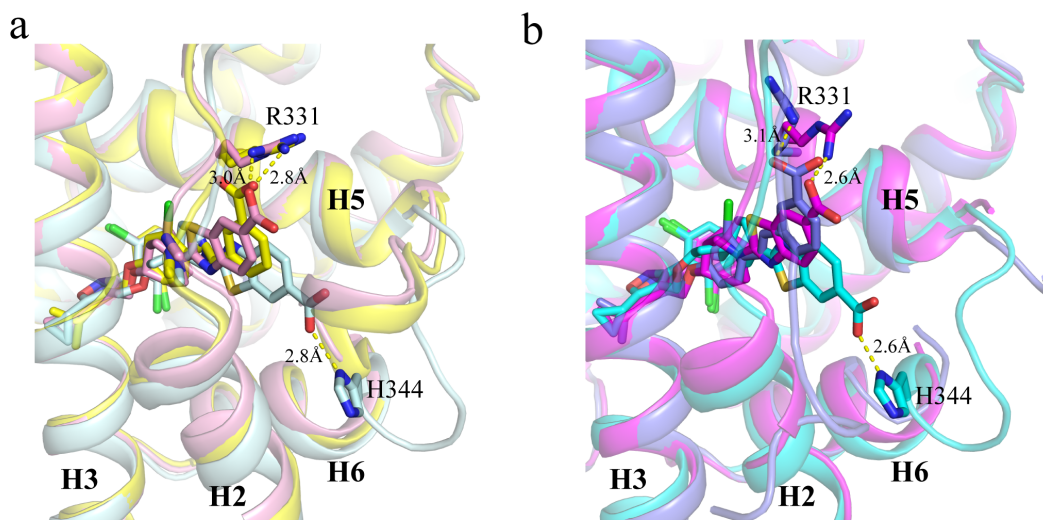
Table S2. Interactions in the RXR $\alpha$ /FXR dimer interface

Non-polar interactions			Polar interactions		
RXR $\alpha$		FXR	RXR $\alpha$		FXR
(H9)	Y397-A431	(H11)	(H7)	D379-R436	(H11)
(H9)	Y397-R436	(H11)	(H7)	K356-E405	(H9)
(H9)	A398-Q428	(L9)	(H11)	R426-T442	(H11)
(H11)	F415-A431	(H11)	(H11)	S427-R441	(H11)
(H11)	A416-F430	(H11)	(H11)	K417-E405	(H9)
(H11)	L419-L434	(H11)	(H11)	K417-E409	(H9)
(H11)	L420-L434	(H11)	(H11)	R421-D394	(L8)
(H11)	L420-L412	(H9)	(H11)	R426-E439	(H11)
(H11)	L420-L437	(H11)	(H11)	E434-H445	(H11)
(H11)	P423-T438	(H11)			
(H11)	L430-T442	(H11)			

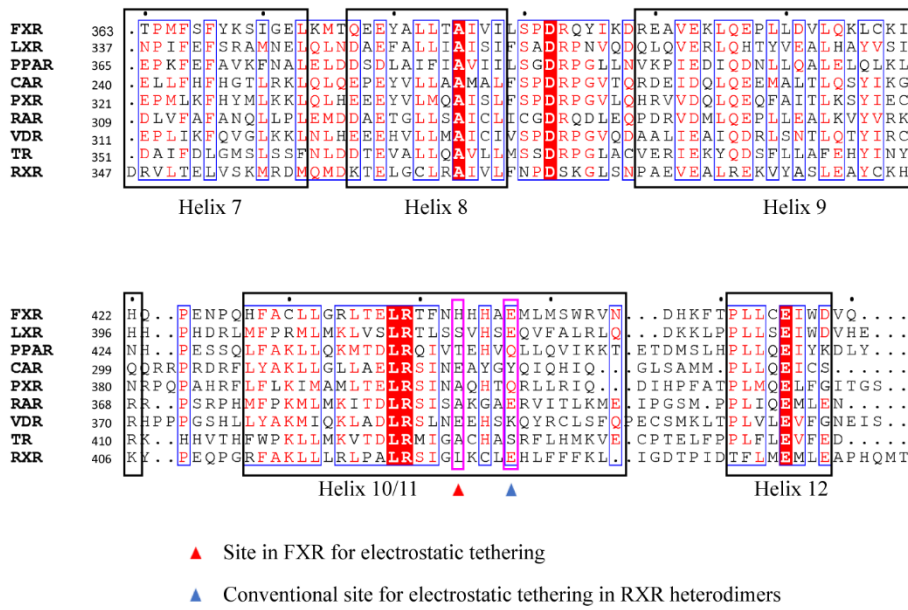
Residues involved in dimerization are listed along with the secondary structures. The intermolecular interactions are grouped into polar and nonpolar interactions. The nonpolar interactions include Vander Waals contacts and hydrophobic interactions with a distance cutoff 4.5 Å, and the polar interactions include charged interactions (4 Å cutoff) and hydrogen bonds (3.5 Å cutoff)



**Supporting Fig. 1. Characterization of the interaction between coactivator and FXR-LBD•SRC1/RXR-LBD•SRC1.** No interaction was observed between the fluorescein-labeled peptide and FXR-LBD•SRC1/RXR-LBD•SRC1.

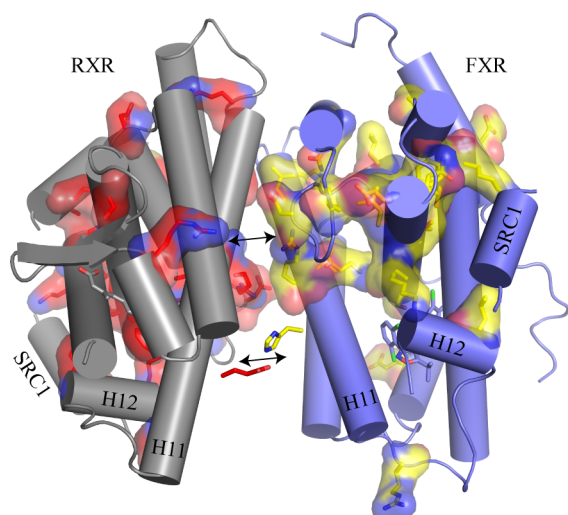


**Supporting Fig. 2. Conformation induced by ligands in FXR-LBD and FXR/RXR-LBD structure.** (a) Alignment of FXR-LBD structures with three different ligands show the conformation difference between helix 5 and helix 6. (HNC143-FXR-LBD, pale cyan; HNC180-FXR-LBD, pink; GW4064-FXR-LBD, yellow). (b) Alignment of three FXR/RXR-LBD structures. (HNC143-FXR/9cRA-RXR, cyan; HNC180-FXR/9cRA-RXR, magenta; GW4064-FXR/9cRA-RXR, slate). Hydrogen bond is labeled as dashed line, colored yellow.

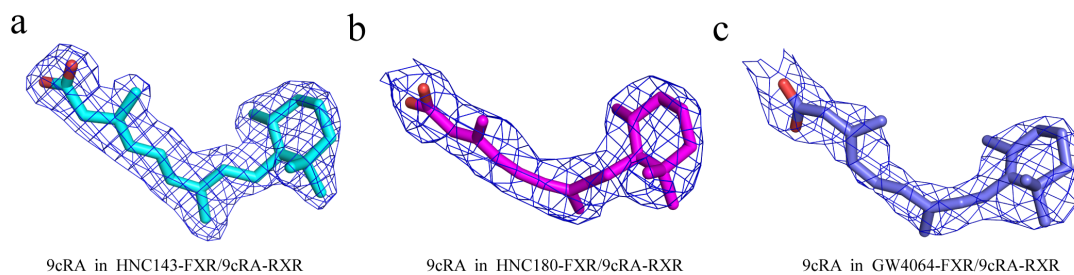


**Supporting Fig. 3. Structure-based sequence alignment of RXR nuclear receptor partners**

Only the regions that are involved in the dimerization interface are shown. The secondary structures are noted under the sequences.

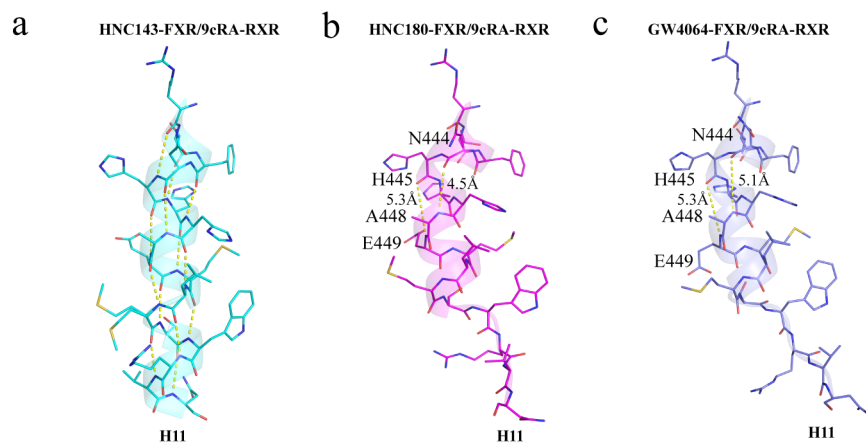


**Supporting Fig. 4. Schematic diagram summarizing the signal pathway through the heterodimer interface.** The SCA network residues are plotted on FXR and RXR using the GW4064-FXR/9cRA-RXR crystal structure as a model. Residues participated in electrostatic tethering are shown as sticks. Arrows indicate the signal transduction pathway through the heterodimer interface.

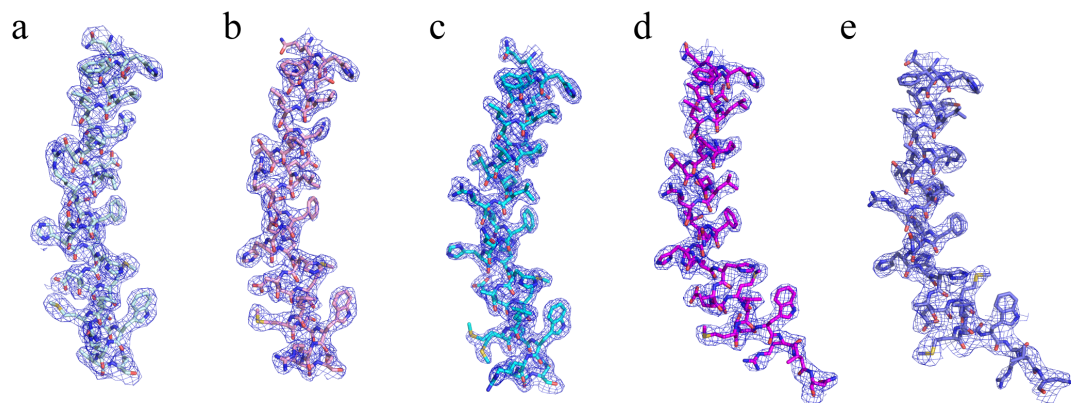


**Supporting Fig. 5. Electron density maps for 9cRA in the three FXR/RXR heterodimers.** (a-c) Electron density maps for 9cRA within the RXR pockets in the three heterodimers as labeled in the figure. The maps were calculated with  $\sigma_A$ -weighted 2Fo-Fc coefficients and contoured at  $1.0\sigma$ .

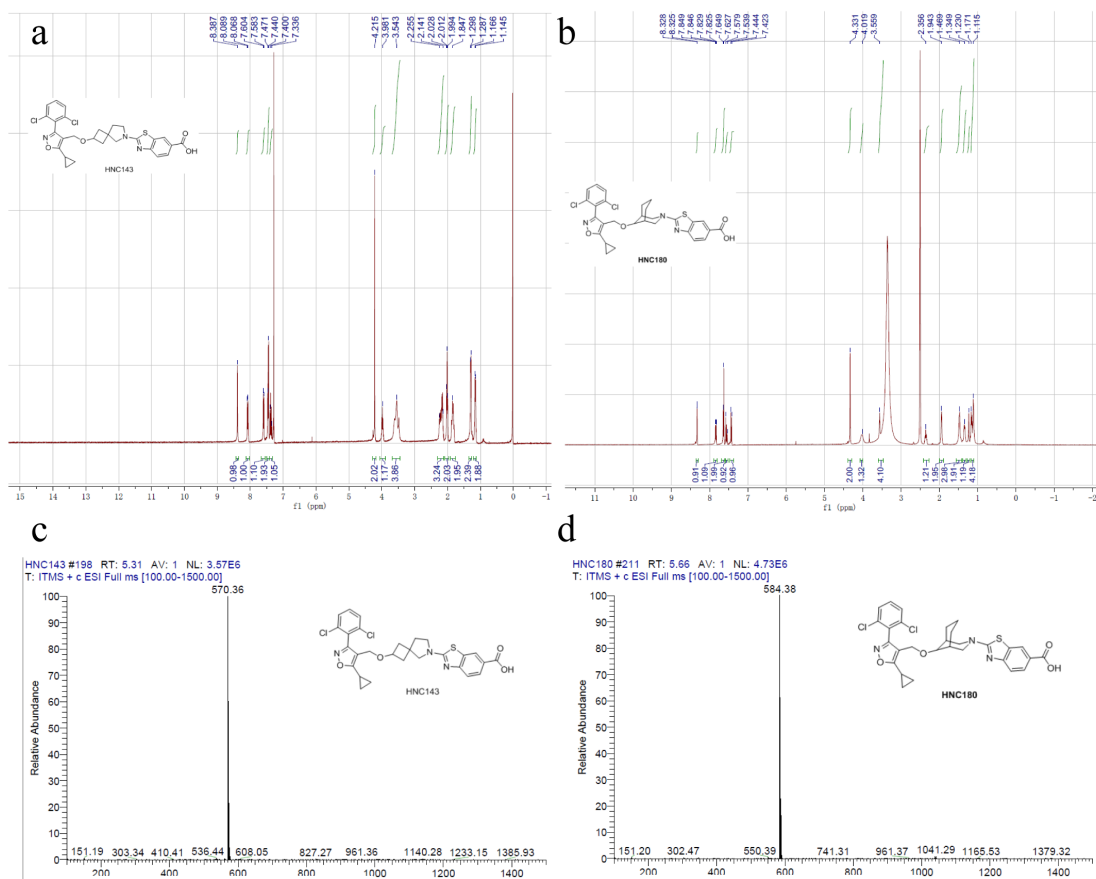




**Supporting Fig. 6. Secondary structure changes in the C terminus of H11 in FXR in three ligands bound heterodimers.** (a) In HNC143 bound heterodimer, the C terminus of H11 has a normal hydrogen bond network, while main chain hydrogen bonds formed by N444-E448, H445-E449 are lost in (b) HNC180 and (c) GW4064 bound heterodimers.



**Supporting Fig. 7. Electron density maps for FXR Helix 11 in two FXR monomers and three FXR/RXR heterodimers.** (a-e) Electron density maps for FXR Helix11 (a) in HNC143-FXR (pale cyan), (b) HNC180-RXR (pink), (c) HNC143-FXR/9cRA-RXR (cyan), (d) HNC180-FXR/9cRA-RXR (magenta), (e) GW4064-FXR/9cRA-RXR (slate). The maps were calculated with 2Fo-Fc coefficients and contoured at  $1.0\sigma$ .



**Supporting Fig. 8.  $^1\text{H-NMR}$  spectra and Mass Spectra data. (a-b)  $^1\text{H-NMR}$  spectra of HNC143 and HNC180. (c-d) Mass Spectra data of HNC143 and HNC180.**