Supplementary information

Structural Basis of Natural Promoter Recognition by Retinoid X Nuclear Receptor

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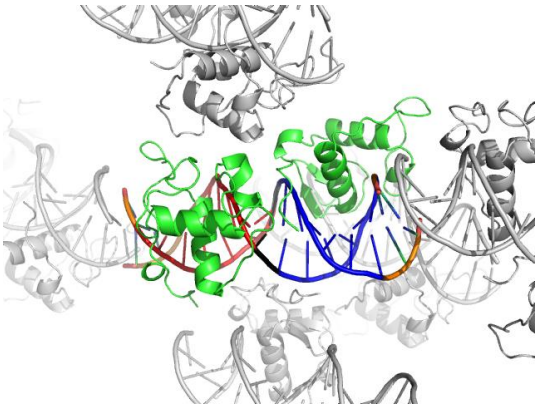
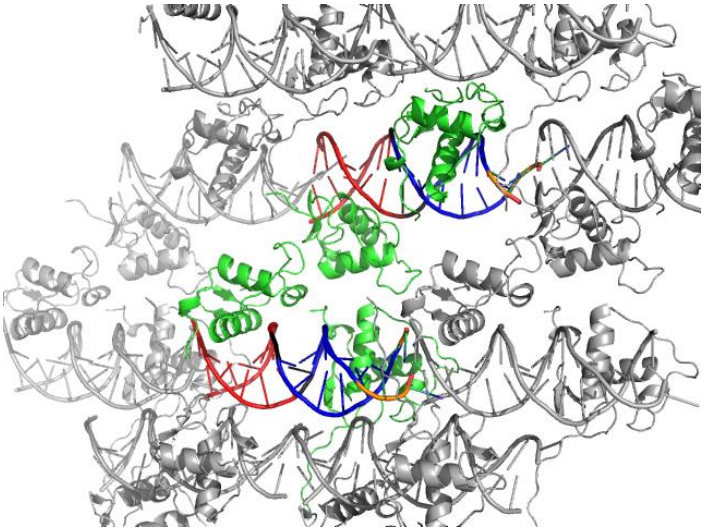
Supplementary Fig. S1. Crystal packing of RXR-DBD-DNA complexes. The asymmetric unit content is shown in green for (**a)** the dimeric RXR DBD-*Ramp2,* (**b**) the dimeric RXR-DBD-*Gde1SpA* and (**c**) the dimeric RXR-DBD-idDR1.

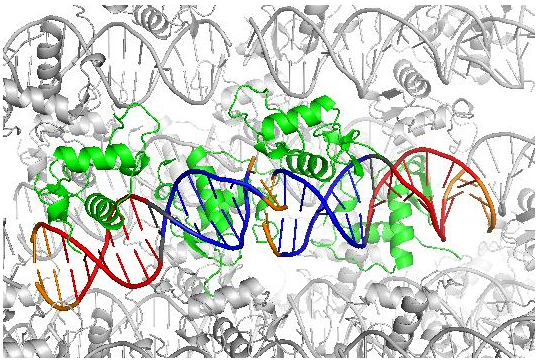
a



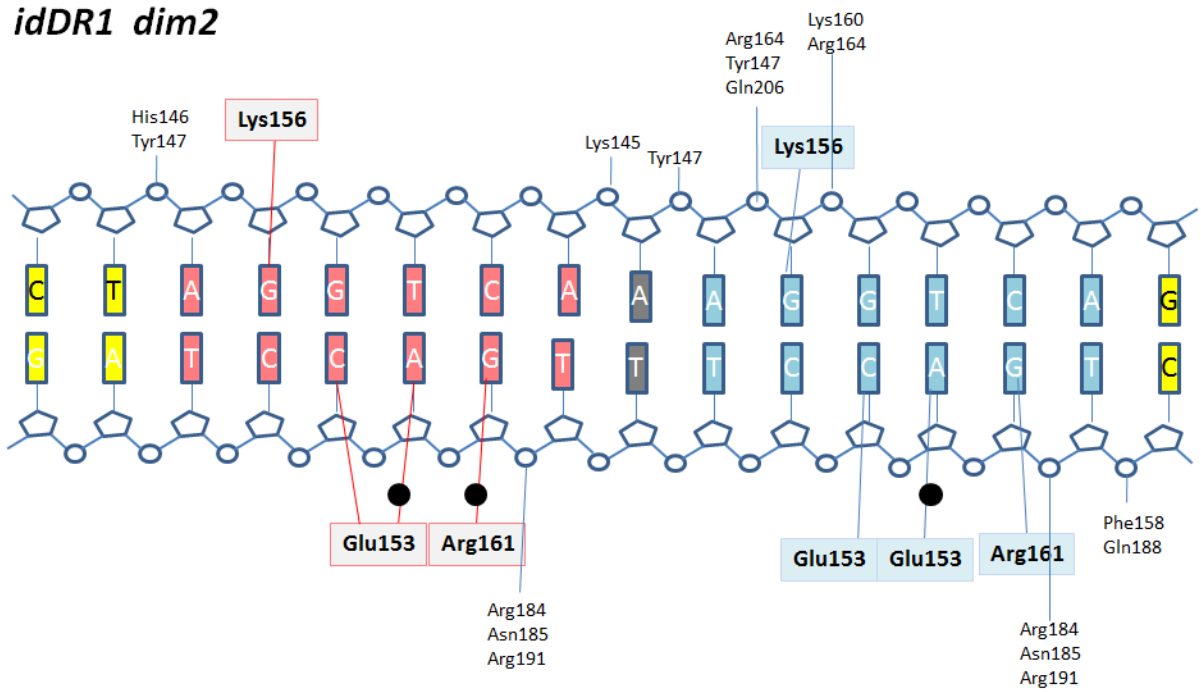
b



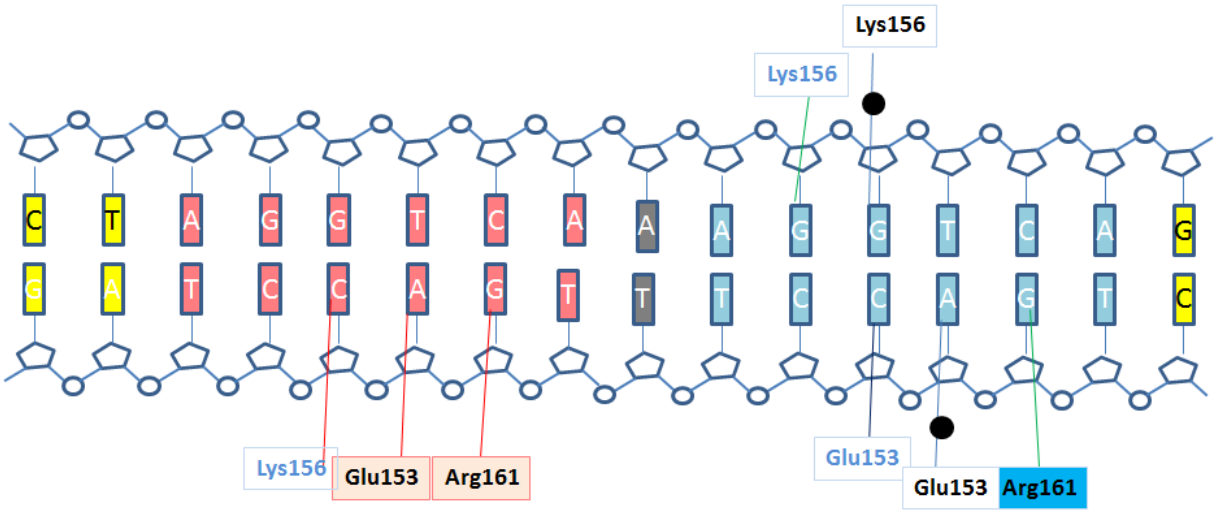
c



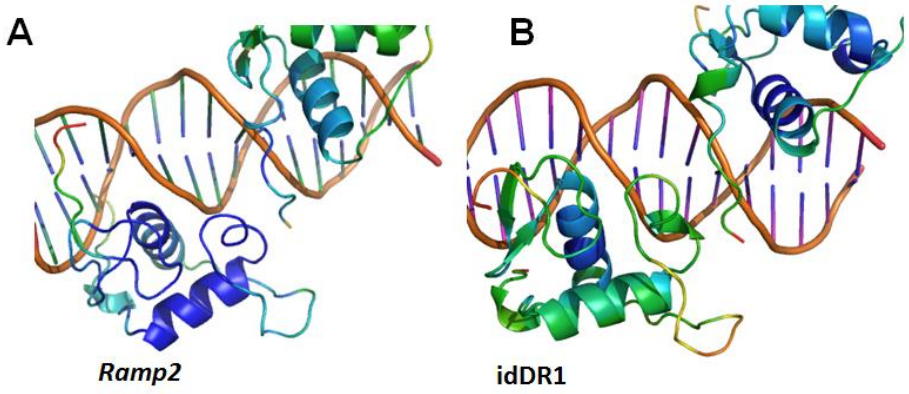
Supplementary Fig. S2. Schematic representations of the protein-DNA contacts for the second dimer of the RXR-DBD-idDR1 complex. Bridging water molecules are shown as black circles. The hydrogen-bond interactions with the 5' subunit and 3'subunit are highlighted in light grey and cyan, respectively. The first hexanucleotide is shown in salmon, the second one in blue and the interspacer nucleotide in grey. The gray circles indicate the DNA phosphates and the labeled residues their contacts with RXR.



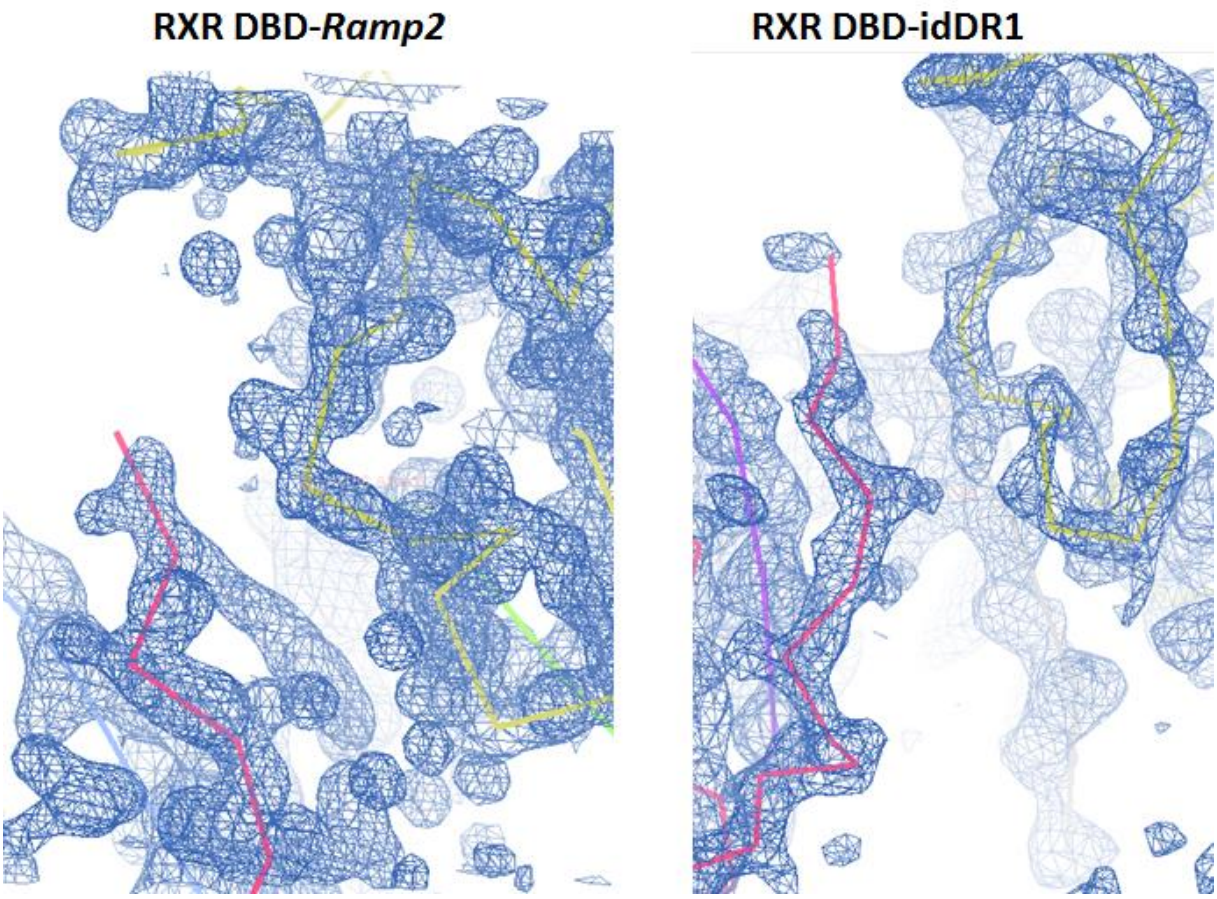
idDR1 (PDB: 1BY4)



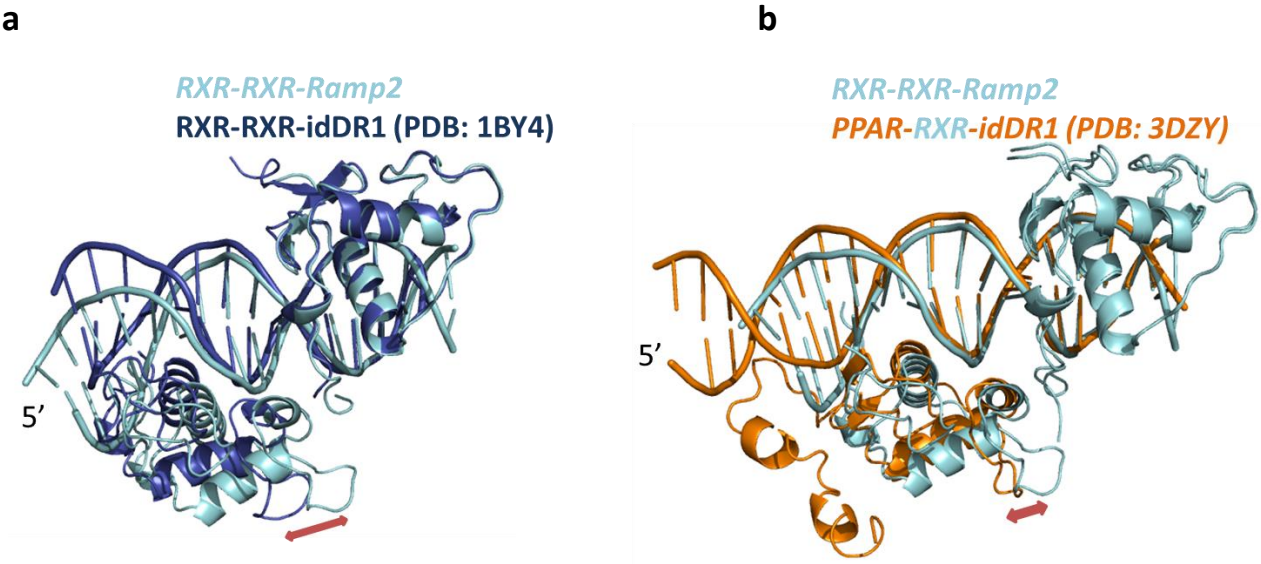
Supplementary Fig. S3: Overall stabilization of the complexes as shown by the B-factor plot on the overall structure of the RXR-DBD-*Ramp2* (a) and RXR-DBD-idDR1 (b) complexes. The protein secondary structural elements are colored by B-factors on a relative scale: highest B-factor, red; lowest B-factor, blue.



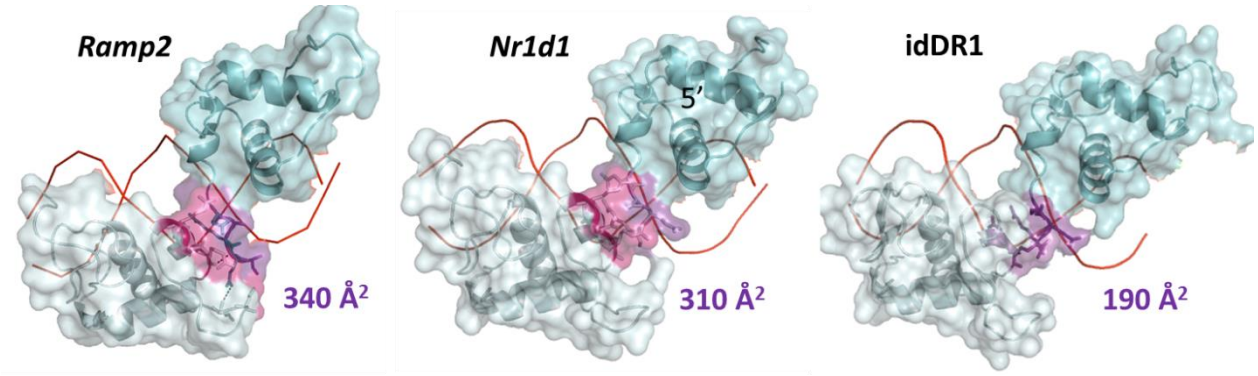
Supplementary Fig. S4. 2Fo-Fc electron density maps of the dimerization interface of the RXR DBD complexes at 1σ. The Cα chain is shown in yellow and pink for the RXR DBD monomers.



Supplementary Fig. S5. Comparison of RXR-DBD-*Ramp2* structure with RXR dimer-idDR1. (**a**) Superimposed crystal structures of RXR DBD-*Ramp2* (cyan) with RXR DBD-idDR1 (PDB ID: 1BY4, grey). Superposition was performed on the 3' bound RXR DBD. The largest differences are observed for the idDR1 as indicated by arrows and a zoomed view of the dimerization region. (**b**) Superimposed crystal structures of RXR DBD-*Ramp2* (cyan) with PPAR-RXR-idDR1 (PDB ID: 3DZY, orange).



Supplementary Fig. S6. Comparison of the dimerization interface. Surface representation of the dimerization interfaces of *Ramp2*, *Nr1d1* and idDR1 RXR-DBDs complexes. The complexes with the natural DR1s show the largest dimerization interactions (highlighted in violet) compared to the complex with idDR1.



Supplementary Table S1. X-ray data collection and refinement statistics of RXR-DBD complexes.

	Ramp2	*Nr1d1*	*Gde1SpA*	*idDR1*
PDB ID	4CN2	4CN5	4CN3	4CN7
Data Collection				
X ray source	ESRF ID23-1	ESRF BM30A	ESRF ID23-2	ESRF ID23-2
Detector	ADSC Q315R	ADSC Q315R	MAR CCD 225	MAR CCD 225
Wavelength (Å)	1,283	1,283	0,873	0,873
Temperature	100K	100K	100K	100K
Resolution (Å)	25 – 2.06 (2.10 – 2.06)	43.0 – 2.0 (2.05 – 2.00)	69.6 – 2.30 (2.42 – 2.30)	40.8 – 2.34 (2.42 – 2.35)
Space Group	C2	C2	P212121	P212121
Unit cell parameters	a = 113.234Å b = 43.952Å c = 63.316Å α = 90°, β = 106.016°, γ = 90°	a = 103.286Å b = 44.327Å c = 63.915Å α = 90°, β = 98.950°, γ = 90°	a = 53.07Å b = 69.47Å c = 139.13Å α = 90°, β = 90°, γ = 90°	A = 37.63Å b = 65.35Å c = 209.12Å α = 90°, β = 90°, γ = 90°
Total reflections	32567	67786	135293	97410
Unique reflections	17566	19176	23573	22310
Completeness (%)	95.3 (70.8)	98.3 (98.9)	95.1 (86.8)	98.4 (86.7)
Rmerge (%)	8.1 (21.9)	2.8 (11.8)	14.3 (46.6)	6.7 (102.4
Mean I/σ(I)	15.9 (4.2)	27.2 (9.4)	9.7 (3.5)	11.3 (1.1)
Multiplicity	3.1 (1.8)	3.5 (3.4)	6.0 (5.6)	4.4 (3.9)
Wilson B	29,64	22,78	38,55	36,5
Model Refinement				
Rwork/Rfree	0.154/0.202	0.167/0.228	0.183/0.249	0.173/0.209
No. of non-H atoms	2260	2298	4311	3925
Protein/DNA	2022	1970	3980	3771
Water	222	315	323	151
Ligand/ion	12/4	13	8	3
Average *B* factor (Å²)				
Protein/DNA	37,87	35,6	27,96	67,46
Water	41,55	38,55	30,174	53,94
Ligand/Ion	44.14/45.87	48,08	26,85	81,88
R.m.s. Deviations				
Bond lengths (Å)	0,01	0,006	0,01	0,009
Bond angles (°)	1,11	1,187	1,23	1,192
Ramachandran plots				
Favoured (%)	92,4	94,7	91,5	96,4
Allowed (%)	7,6	5,3	8,4	3,6
Outliers (%)	0	0	0	0