RXRα LBD/R-DHRA /NCoA2	
Data processing	
Resolution (Å)	25-1.8 (1.86-1.80)
Crystal space group	$P4_32_12$
Cell parameters (Å)	$a = b = 64.014$; $c = 112.066$
Unique reflections	22407
Mean redundancy	7.9 (3.8)
R_{sym} (%)[a]	5.2 (48.1)
Completeness (%)	99.2 (97.2)
Mean I/σ	34.7(2.3)
Refinement	
Resolution (Å)	24-1.8
Number of non-hydrogen atoms	
RXR-LBD	1680
Coactivator peptide	98
Ligand	22
Water molecules	181
RMSD bond length (Å)	0.006
RMSD bond angles (°)	1.065
R_{cryst} (%)[b]	17.9
R_{free} (%)[c]	22.1
Averaged *B* factor for non-hydrogen atoms (Å^2)	
RXR-LBD	37.6
Coactivator peptide	44.6
R-DHRA	31.2
Water	44.5

SupportingTable 1 Data collection and refinement statistics.