

## Supporting Information

### Structure-Guided Design of *N*-Phenyl Tertiary Amines as Transrepression-Selective Liver X Receptor Modulators with Anti-inflammatory Activity

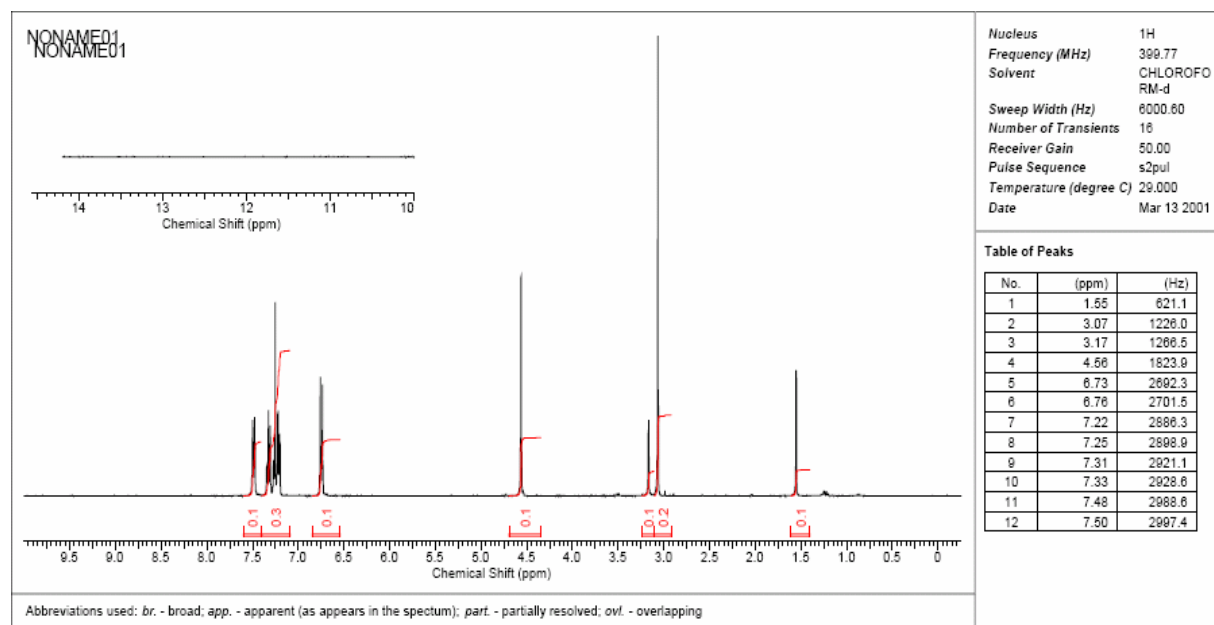
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#### Contents:

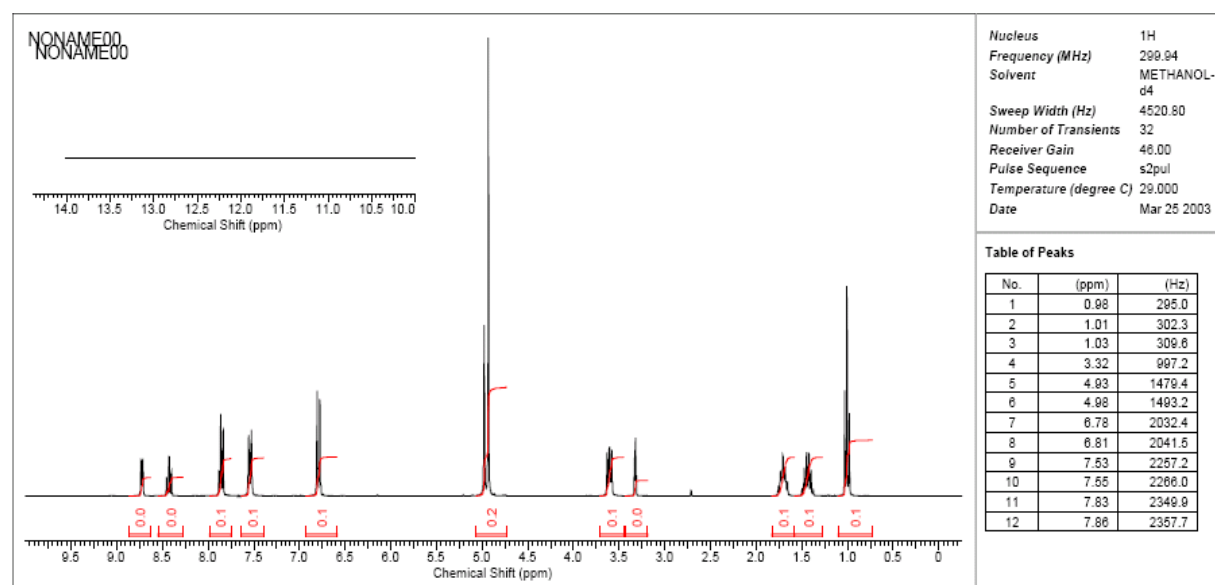
1. S2-S12: NMR spectra for compounds **4-5** and **7-22**
2. S13-S15: co-crystallization of GSK2186 (**19**) with murine LXR $\alpha$  and human RXR $\alpha$ :

## 1) NMR Spectra

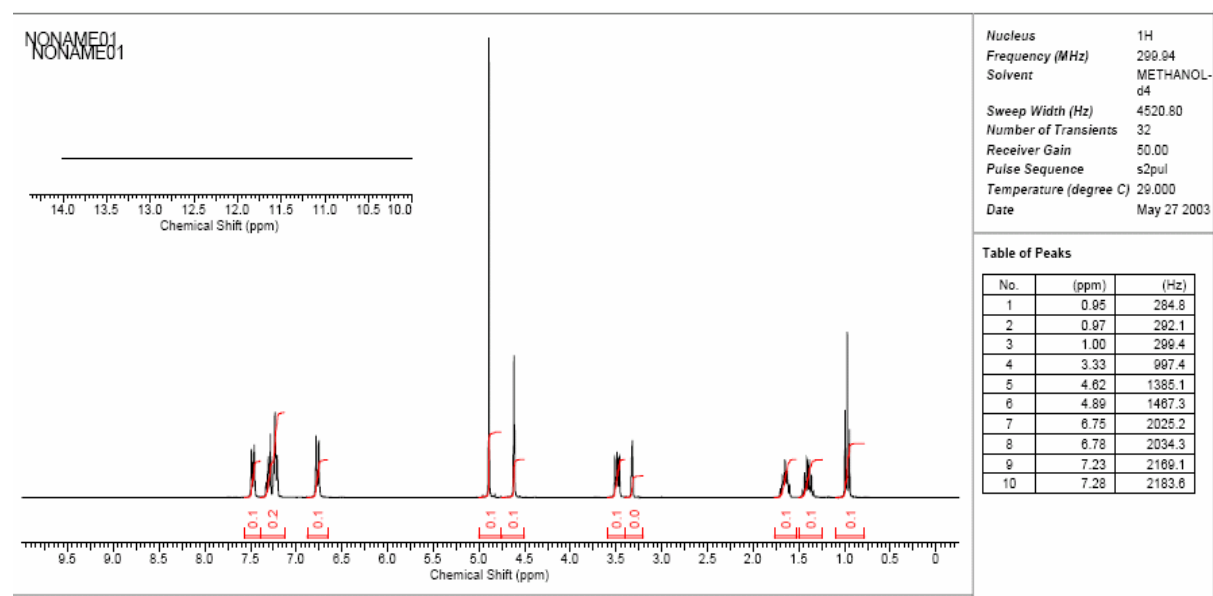
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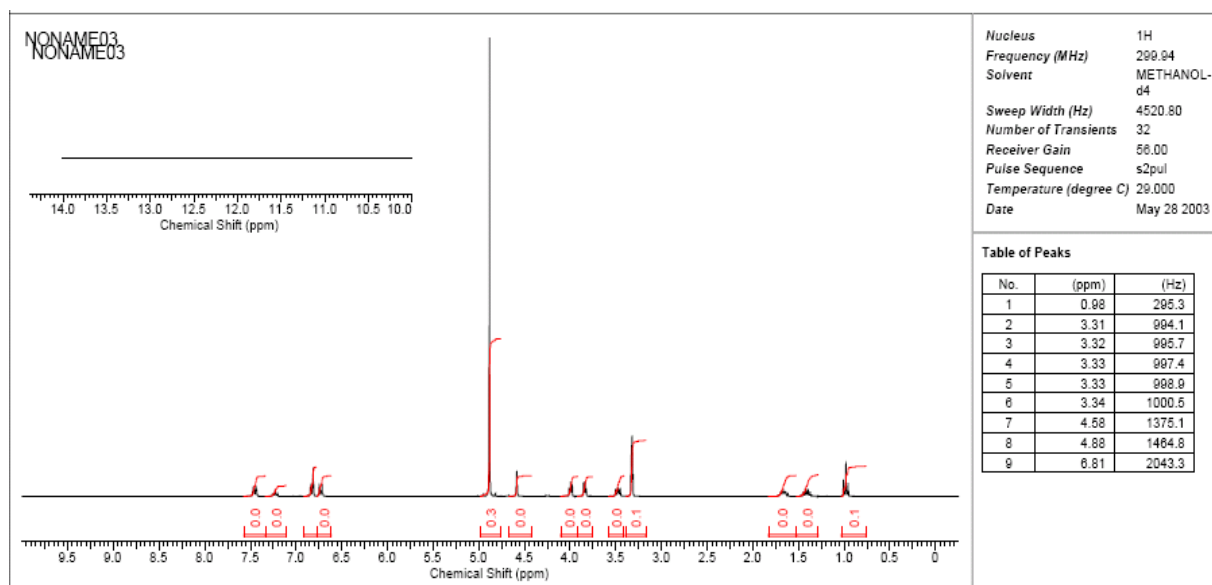
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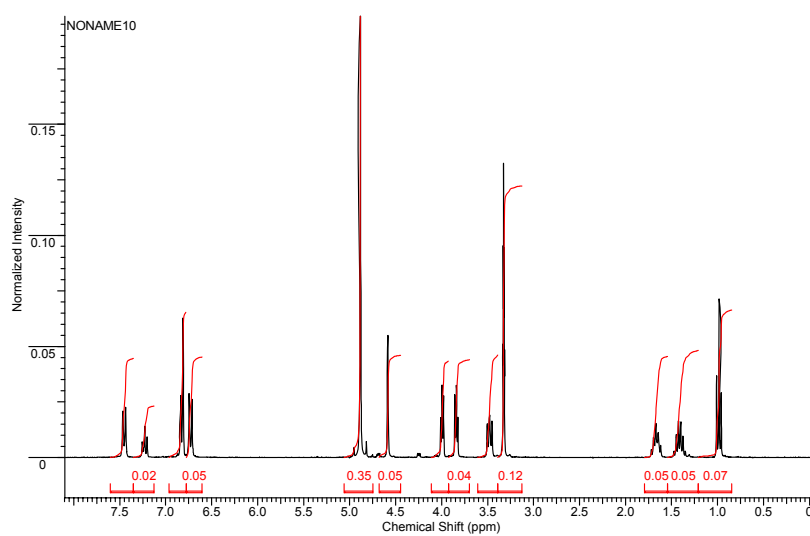
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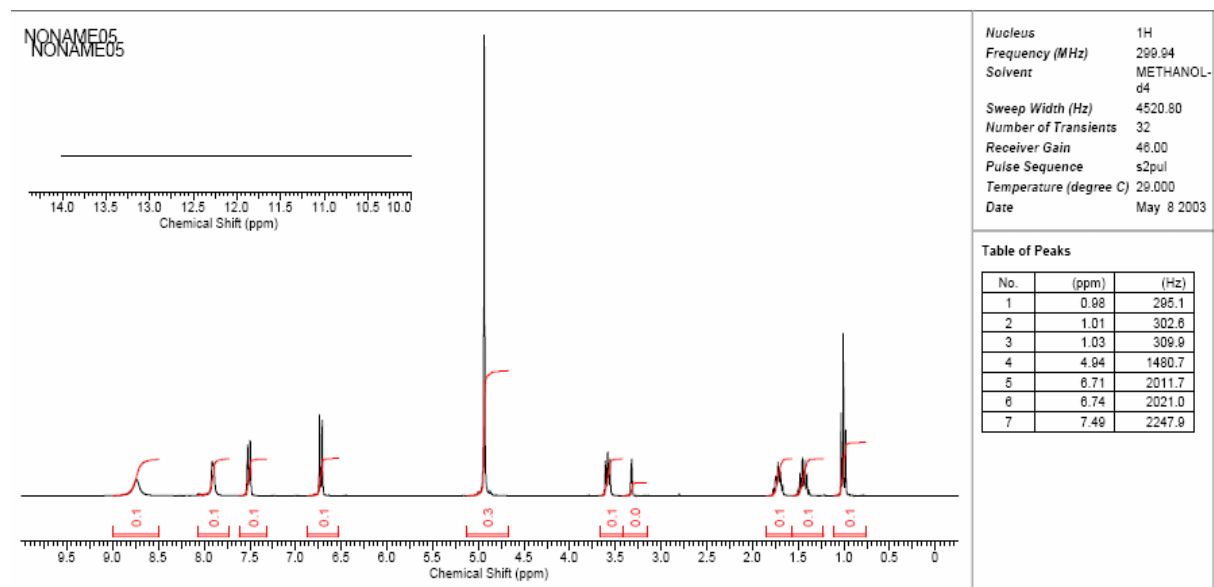
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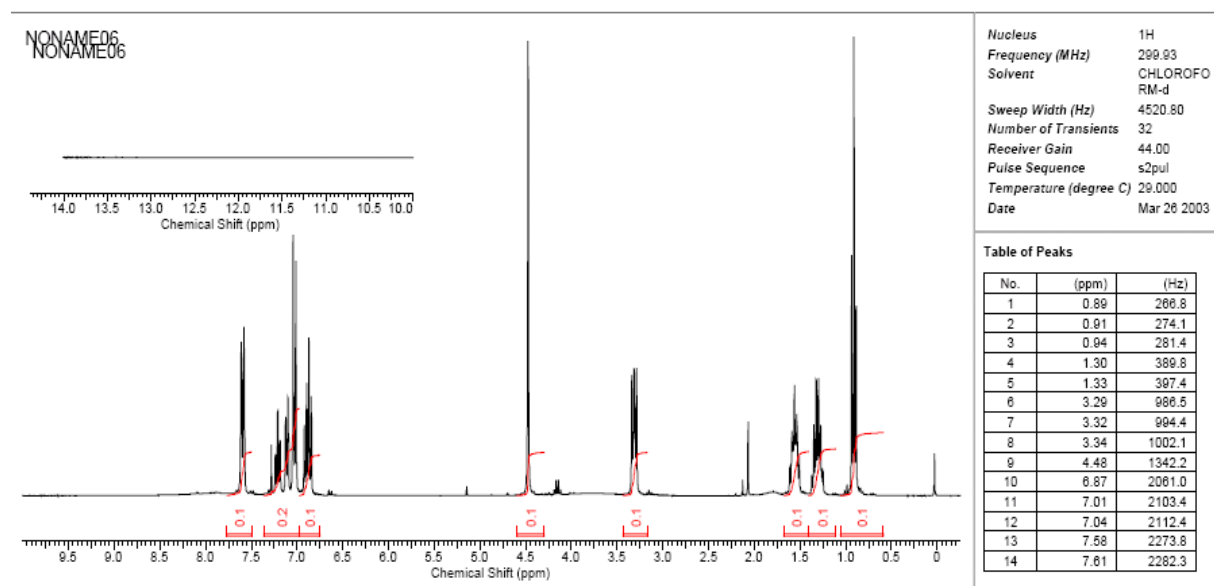
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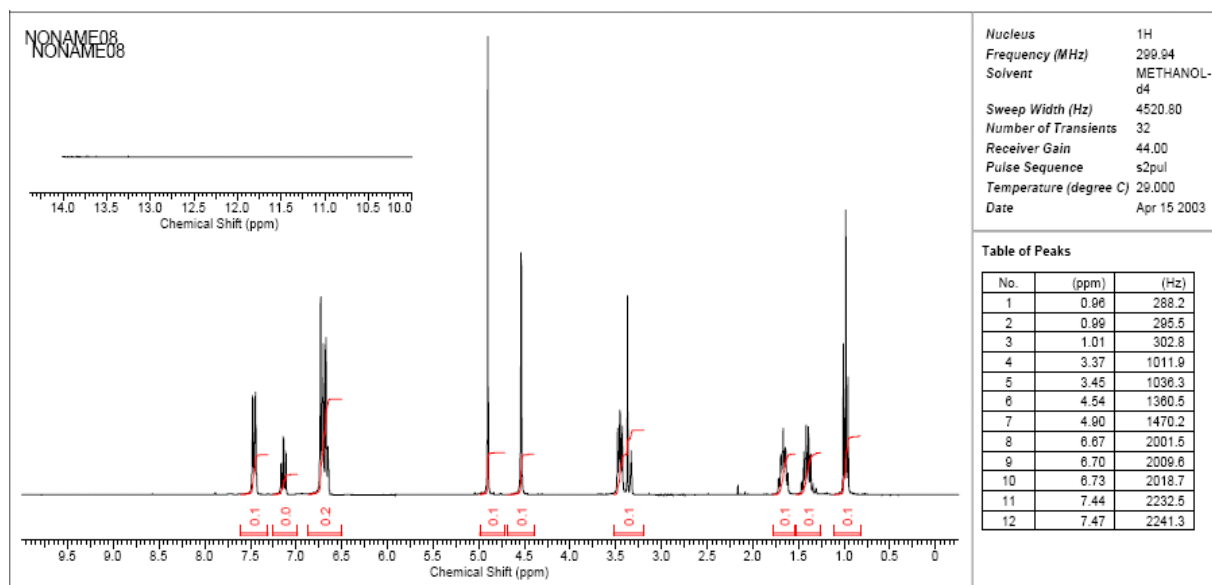
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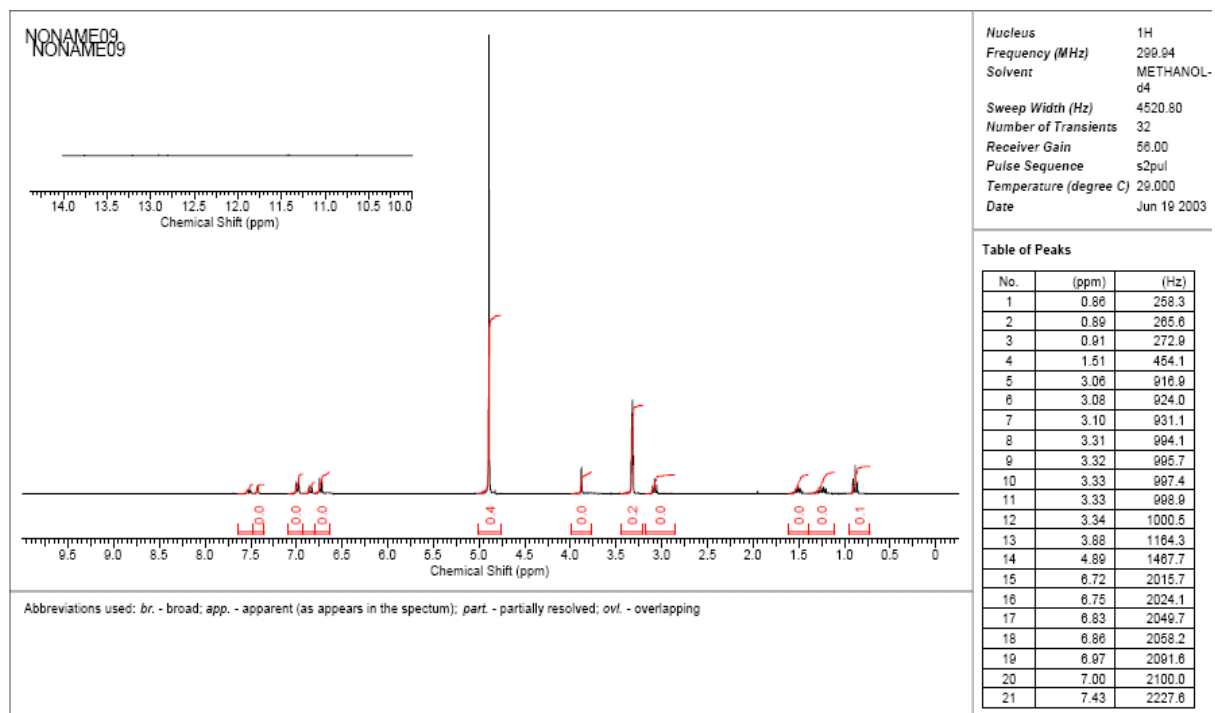
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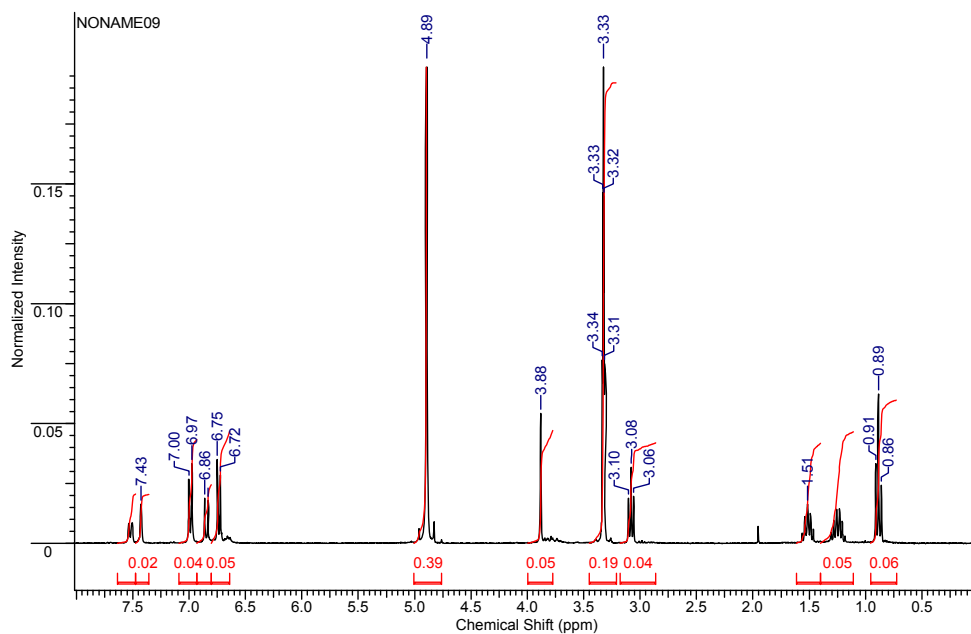
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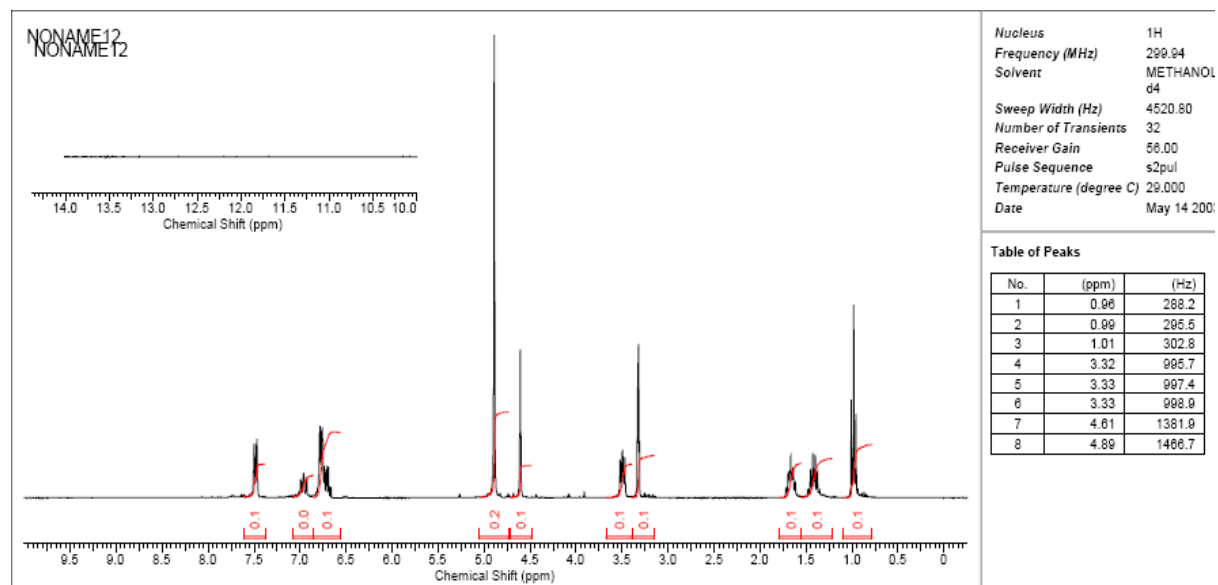
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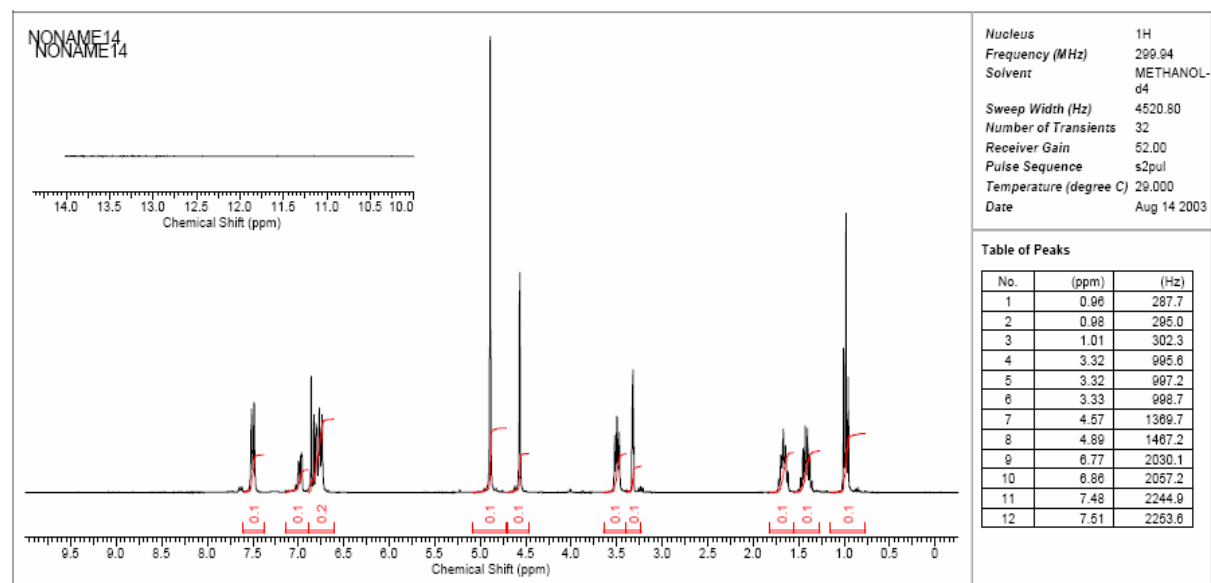
Expanded vertical axis:



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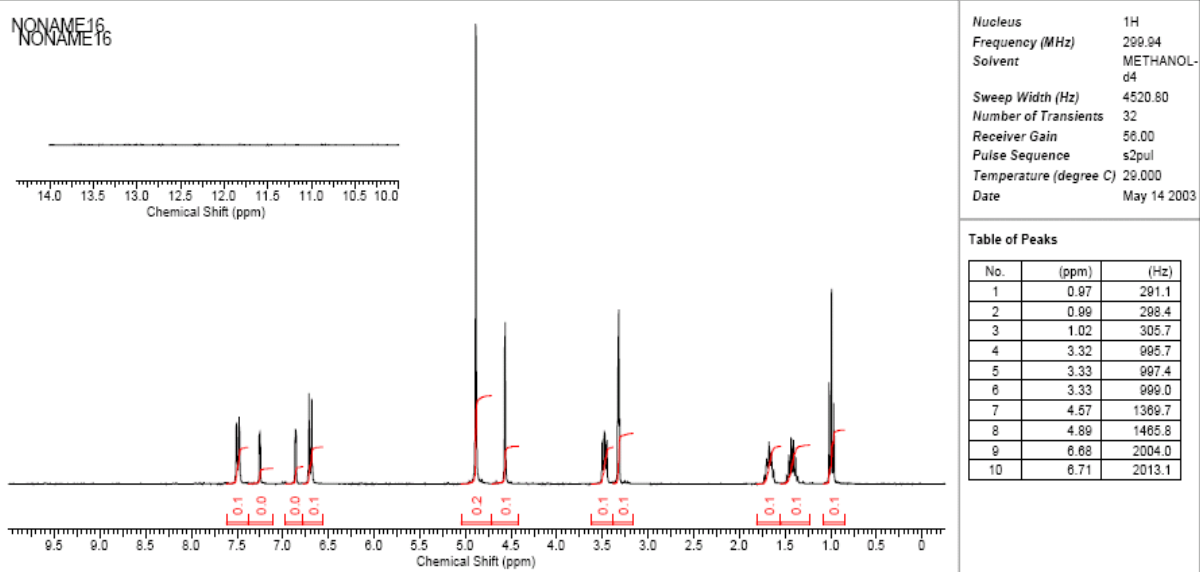


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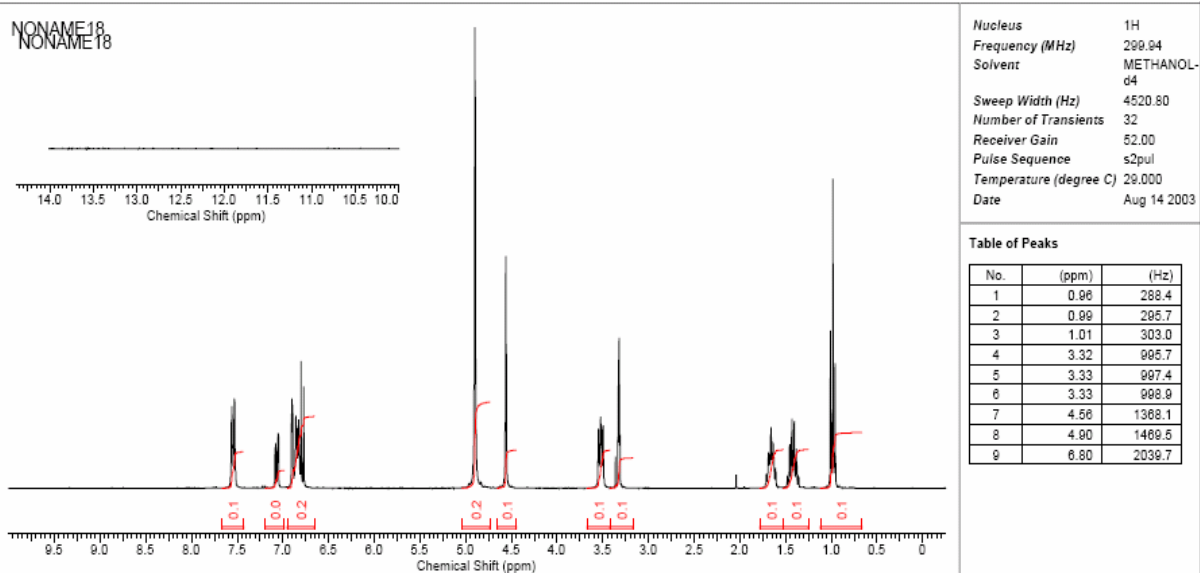




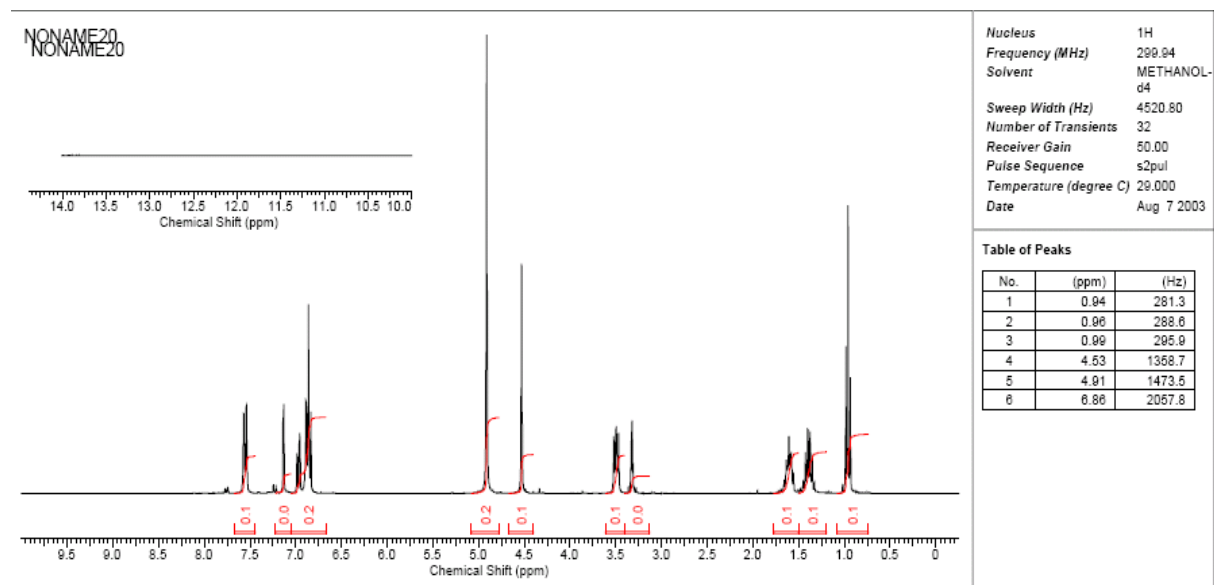
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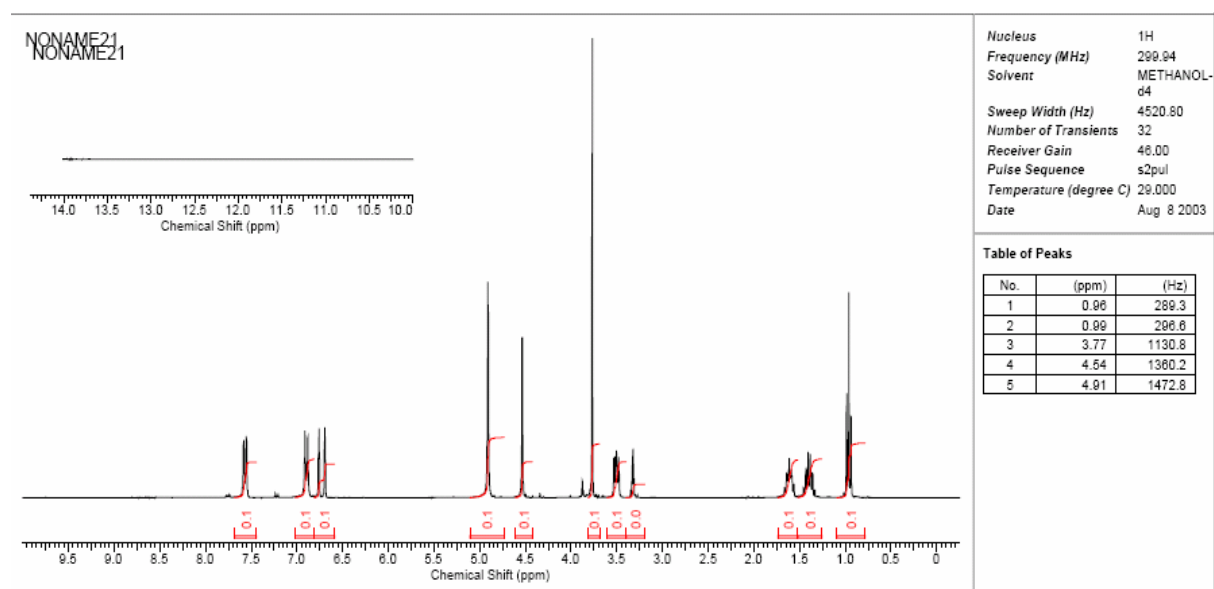
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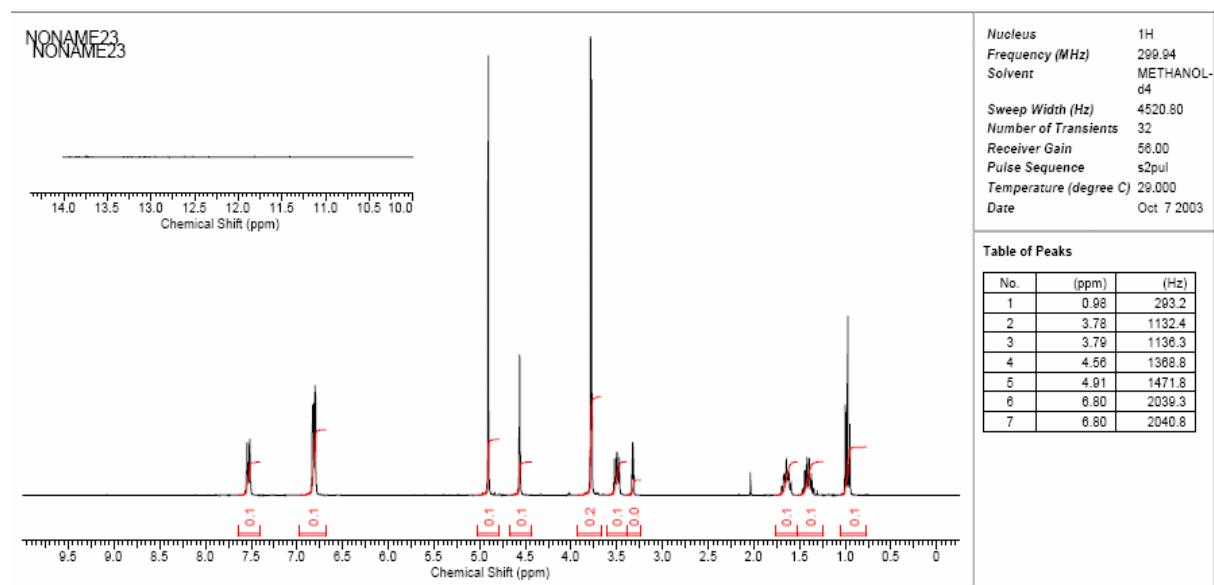
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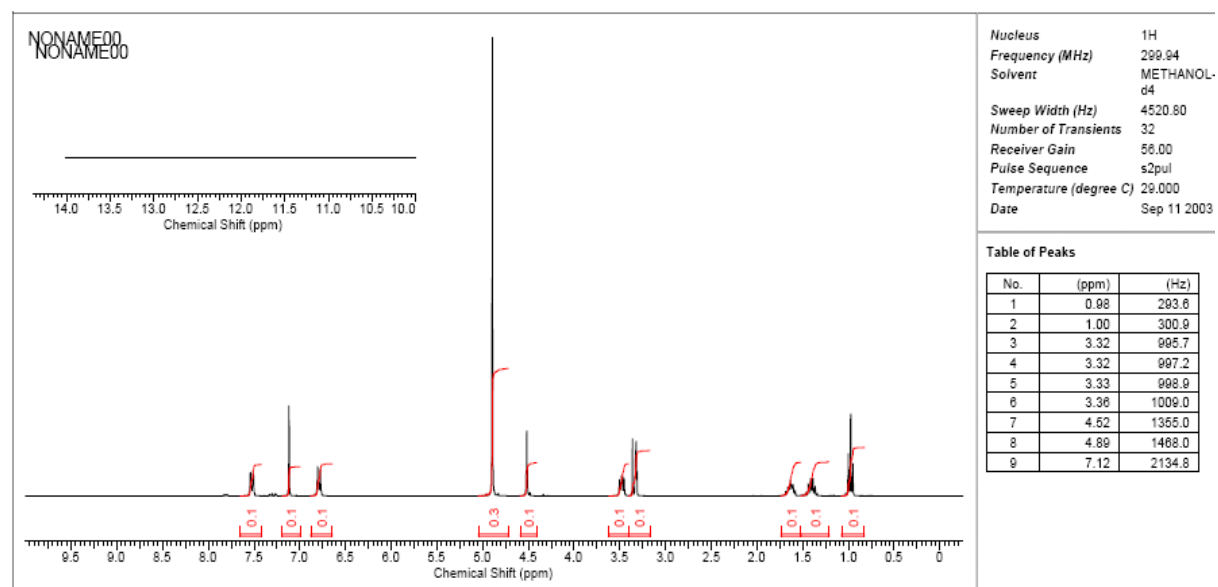
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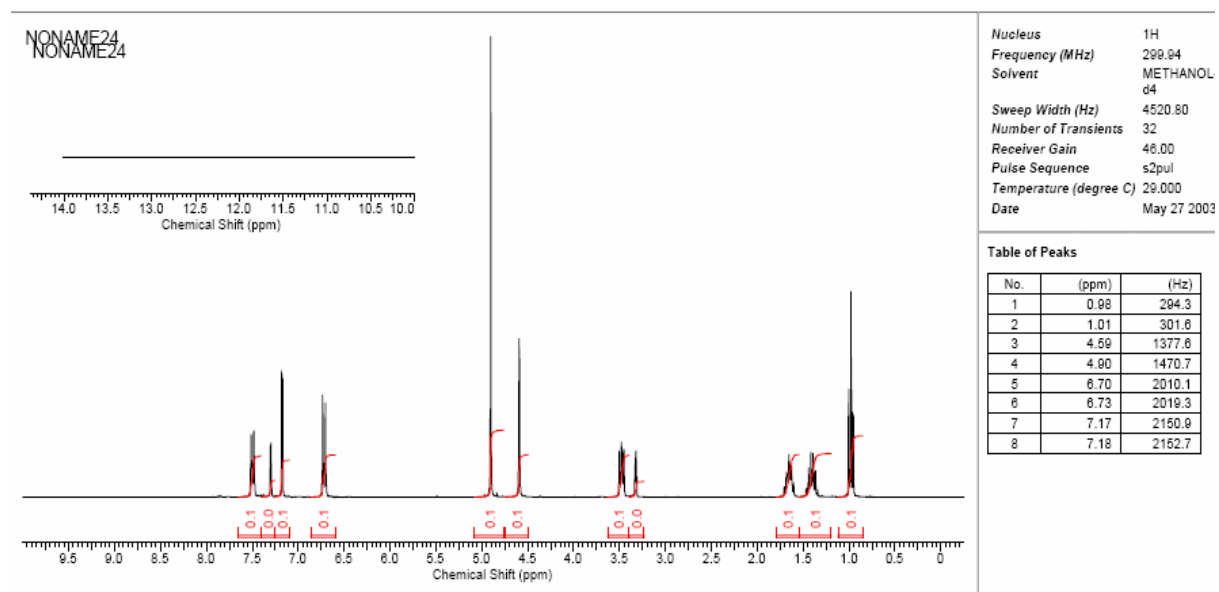
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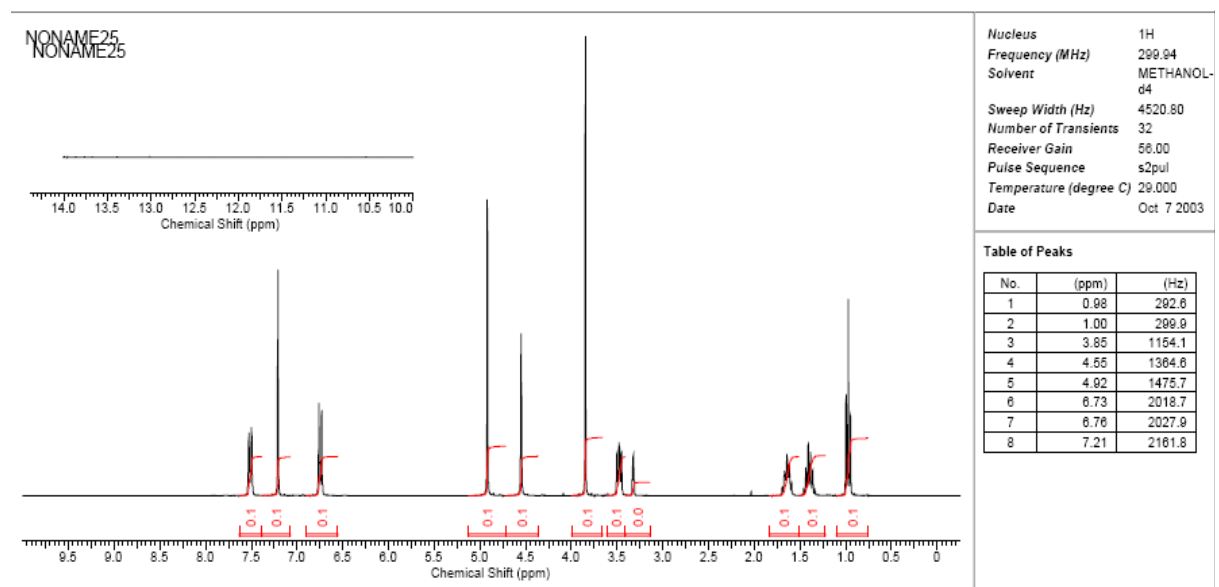
## Compound 20:



## Compound 21:



## Compound 22:



## **2) Co-crystallization of GSK2186 (19) with murine LXR $\alpha$ and human RXR $\alpha$ :**

The mLXR $\alpha$ (200-445)/hRXR $\alpha$ (225-462) co-expression strain was made by transforming two plasmid vectors into the E. coli K12 strain HMS174(DE3) (Novagene, Madison, WI). Plasmid pLXR $\alpha$ (200-445) was made by inserting a PCR fragment containing the human LXR $\alpha$ LBD(aa200-445) ORF into the Nhe/BamHI sites of pRSETa vector (Invitrogen, Calsbad, CA). The resulting construct expresses LXR $\alpha$ LBD as a H6-thrombin-LXR $\alpha$ LBD fusion protein. Plasmid pRXRa(225-462) was constructed previously (Gampe et al., 2000, Mol. Cell 5:545-555) and is described below. The ORF containing the human RXR $\alpha$ LBD(225-462) was inserted into the NdeI/HindIII sites of pET24a (Novagen) and from which the T7-lacO-RXR $\alpha$ LBD expression cassette was further subcloned between the BamHI/HindIII sites of pACYC184 (New England Biolabs). The resulting plasmid expresses untagged RXR $\alpha$ LBD.

To prepare N-terminal His tagged mLXR $\alpha$ (200-445)/hRXR $\alpha$ (225-462), E.Coli HMS174 cells were grown overnight at 30°C in 1L of Luria-Bertani Broth(Tryptone, 10g/L; Yeast Extract, 5g/L; NaCl, 5g/L) plus 1% Glucose. As selection agents, 3.4ml of Chloramphenicol(10mg/ml) and 10ml of Carbenicillin(10mg/ml) were added. The 1L overnight was then used to inoculate a reactor for an 8L production. The reactor equipment used was a 10L Biostat B. (8L working volume(B. Braun Biotech) glass vessel with water-jacketed temperature control. Dissolved Oxygen (DO) was monitored at a setpoint of 40%. pH was controlled at 6.5 using a dropwise addition of a 30% solution of Ammonium Hydroxide. The media contained: (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 5g/L; K<sub>2</sub>HPO<sub>4</sub>, 6g/L; KH<sub>2</sub>PO<sub>4</sub>, 3g/L; Tryptone, 10g/L; Yeast Extract, 5g/L; NaCl, 5g/L.

Components added post sterilization are 200ml of 60% Glucose, 1M  $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ , 5ml/L; 1000X Trace metals ( $\text{FeCl}_2 \cdot 6\text{H}_2\text{O}$ , 37.8g/L;  $\text{Na}_2\text{MoO}_4 \cdot \text{H}_2\text{O}$ , 0.7g/L;  $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$ , 0.4g/L;  $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$ , 0.5g/L;  $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ , 0.8g/L;  $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$ , 0.8g/L;  $\text{H}_3\text{BO}_3$ , 0.2g/L,) 1ml/L. The cells grew at 37°C to an optical density of about 5, the temperature was then dropped to 25°C and induced with 0.1mM IPTG. Induction occurred overnight for about 19hrs at which time the cell paste was recovered through centrifugation using a CARR Powerfuge.

All the purification steps were performed at 4°C. Ten grams of bacterial cells were lysed by two passages at 12,000 psi through a high pressure homogenizer (Avestin, Ottawa, Canada) in 100 mL of buffer A (50 mM Tris-HCl, pH 8.0, 200 mM NaCl, and 5% ethylene glycol) plus 1 mM DTT and 25 mM imidazole. Cell debris was removed by centrifugation at 34,000 x *g* for 1 h. The supernatant was loaded onto a Ni-NTA Agarose (Qiagen) column (bed volume 25 mL). The column was washed with buffer A plus 1 mM DTT, buffer A Plus 1 mM DTT and 50 mM imidazole, and eluted with 250 mM imidazole in buffer B (50 mM Tris-HCl, pH 8.0, and 5% ethylene glycol) plus 1 mM DTT. The Ni-NTA pool was diluted 8-fold with buffer B plus 1 mM DTT and then treated with thrombin (E/S=1/50) overnight at 4° C. The digestion mixture was loaded onto a Mono Q HR 10/10 column (Amersham Biosciences) equilibrated with buffer buffer B plus 5 mM DTT. Bound proteins were eluted with a linear gradient from 0 to 500 mM NaCl over 10 CV in buffer B plus 5 mM DTT. The Mono Q pool was applied onto a HiLoad 26/60 Superdex 200 column (Amersham Biosciences) equilibrated with buffer A plus 5 mM DTT. The column was eluted with the equilibration buffer to yield 20 mg of > 95% pure heterodimer.

The crystals were grown by vapor diffusion in sitting drops with 3  $\mu$ l 6.6mg/ml protein and 3  $\mu$ l well solution containing from 21%-23% PEG 3,550, 200 mM Ammonium Acetate, 100 mM Bis Tris pH 6.5 and 10 mM DTT. All operations were carried out at 4 °C. The crystals were small, 0.1 mm long rods, and took 3 weeks to appear. Data were collected at beam line 32 ID on a MAR CCD detector with support from the Industrial Macromolecular Crystallographic Association Collaborative Access Team (IMCA CAT). The data were processed with HKL2000 (Otwinowski, Z. and Minor, W. (1997) *Methods Enzymol.* **276**, 307-326). The Rmerge and completeness of the data were 6.4 % and 97 %, respectively. Crystals belonged to the space group C2 with cell dimensions  $a = 123.21$ ,  $b = 90.00$ ,  $c = 101.31$ ,  $\alpha = 90.00$ ,  $\beta = 111.88$ ,  $\gamma = 90.00$  and 2 heterodimers per asymmetric unit. The structure was solved by molecular replacement using Amore (Navaza, J. (1994) *Acta Crystallogr. A* **50**, 157-163) and using starting coordinates generated from a homology model created from LXR $\beta$  (PDB id = 1P8D) and RXR $\alpha$  (PDB id = 1FM9). The structure was rebuilt with multiple rounds of refinement using O (Jones, T. A., Zou, J.-Y., Cowan, S. W., and Kjeldgaard, M. (1991) *Acta Crystallogr. A* **47**, 110-119) and CNX (Brunger, A. T., Adams, P. D., Clore, G. M., Delano, W. L., Gros, P., Grosse-Kunstleve, R. W., Jiang, J. S., Kuszewski, J., Nilges, M., Pannu, N. S., Read, R. J., Rice, L. M., Simonson, T., and Warren, G. L. (1998) *Acta Crystallogr. D* **54**, 905-921). The model was refined to an R factor of 24 % and an R-free of 29 %. Subsequent refinement with Phenix.refine (Afonine, P.V., Grosse-Kunstleve, R.W. & Adams, P.D. (2005). CCP4 Newsl. 42, contribution 8 ) and model rebuilding with Coot (Emsley, P. & Cowtan, K. (2004) *Acta Crystallogr. D* **60**, 2126- 2132 ) improved the R factor and R-free to 22 % and 28 %, respectively.