

Supplementary Materials

Improved Synthesis and Determination of Biologically Active Diastereomer of YK11

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Experimental section

Luciferase reporter assay

Cells of the human embryonic kidney cell line HEK293 were cultured in Dulbecco's modified Eagle's medium (DMEM; WAKO) containing 10% fetal bovine serum (FBS) and penicillin-streptomycin in a humidified atmosphere containing 5 % CO₂ at 37 °C. The cells maintained in phenol red-free DMEM containing 5% charcoal-stripped FBS (csFBS) were seeded in 48-well plates and transfected with AR expression plasmids, the ARE-luciferase reporter plasmids¹, and a Renilla pGL4.74 (hRluc/TK; Promega) as an internal standard using the reverse-transfection method with the PEI Max Reagent (Polysciences Inc.). After incubation overnight, the cells were treated with one of the AR ligands for 24 h prior to measuring the luciferase activity using the Dual-Luciferase Reporter Assay System (Promega).

Crystallographic parameters for structures of **YK-11 (2a)**.

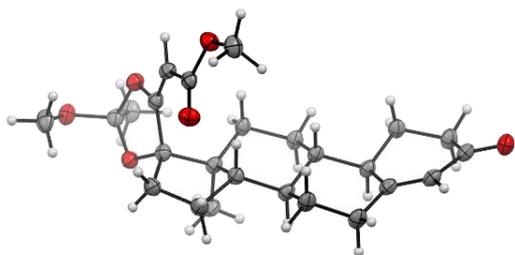
X-ray data were collected on a Rigaku XtaLAB P200 diffractometer with multi-layer mirror monochromated $\text{CuK}\alpha$ ($\lambda = 1.54187 \text{ \AA}$) and a hybrid photon counting detector (PILATUS 200K). The crystal structure was solved by direct methods (SHELXT Version 2014/5)² and refined by full-matrix least-squares SHELXL-2014/7.³ All non-hydrogen atoms were refined anisotropically. All hydrogen atoms were generated theoretically added. The absolute configuration of the molecule was reasonable in terms of the Flack parameter⁴ **YK-11 (2a)** contains two crystallographically independent molecules in the asymmetric unit. Highly disordered solvent, which located in channels along [010], was unable to be modeled. As the identification of disordered solvent molecules riding on the center of symmetry was failed in the refinement of void space, PLATON/SQUEEZE program⁵ was applied. PLATON/SQUEEZE shows the total potential solvent accessible void volume is 270 \AA^3 and residual electrons count 76 in the unit cell. CCDC-1974030 contains the supplementary crystallographic data for this paper. These data can be obtained free of charge from The Cambridge Crystallographic Data Centre via www.ccdc.cam.ac.uk/data_request/cif.

Table S1 Crystallographic data and refinement parameters for **YK-11 (2a)**

Compound	YK11 (2a)
Empirical formula	C ₂₅ H ₃₄ O ₆
Formula weight	430.54
Crystal system	monoclinic
Space group	<i>P</i> 2 ₁
<i>a</i> / Å	15.7937(3)
<i>b</i> / Å	7.49440(10)
<i>c</i> / Å	20.8812(2)
α / deg	90.0000
β / deg	97.4360(13)
γ / deg	90.0000
<i>V</i> / Å ³	2450.80(6)
<i>Z</i>	4
Temperature / <i>K</i>	93
Goodness-of-fit on <i>F</i> ² [a]	1.056
<i>R</i> ₁ [<i>I</i> > 2σ(<i>I</i>)] on <i>F</i> [b]	0.0408
<i>wR</i> ₂ (all data) on <i>F</i> ² [c]	0.1136
Reflection collected (all data)	29206
Independent reflections [<i>I</i> > 2σ(<i>I</i>)]	8505
<i>R</i> _{int}	0.0310
Flack parameter	0.03(6)
<i>T</i> _{max}	0.849
<i>T</i> _{min}	0.954
2θ _{max}	68.249
<i>D</i> _{calcd} ./ gcm ⁻³	1.167
μ / mm ⁻¹	0.670
CCDC code	1974030

[a] Goodness of fit = $[\sum w(F_o^2 - F_c^2)^2 / (N_o - N_v)]^{1/2}$ (*N*_o = number of observations, *N*_v = number of variables). [b] $R_1 = \sum ||F_o| - |F_c|| / \sum |F_o|$ [c] $wR_2 = [\sum (w(F_o^2 - F_c^2)^2) / \sum w(F_o^2)^2]^{1/2}$

(a)



(b)

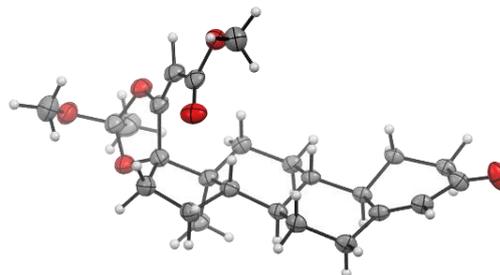


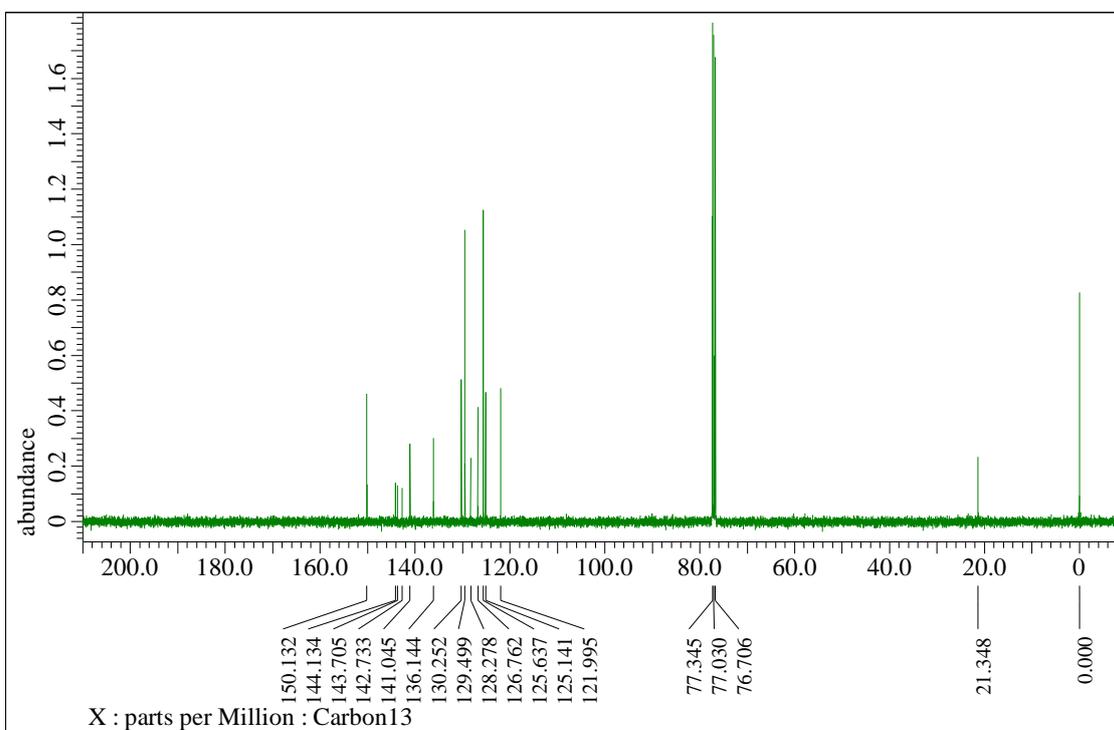
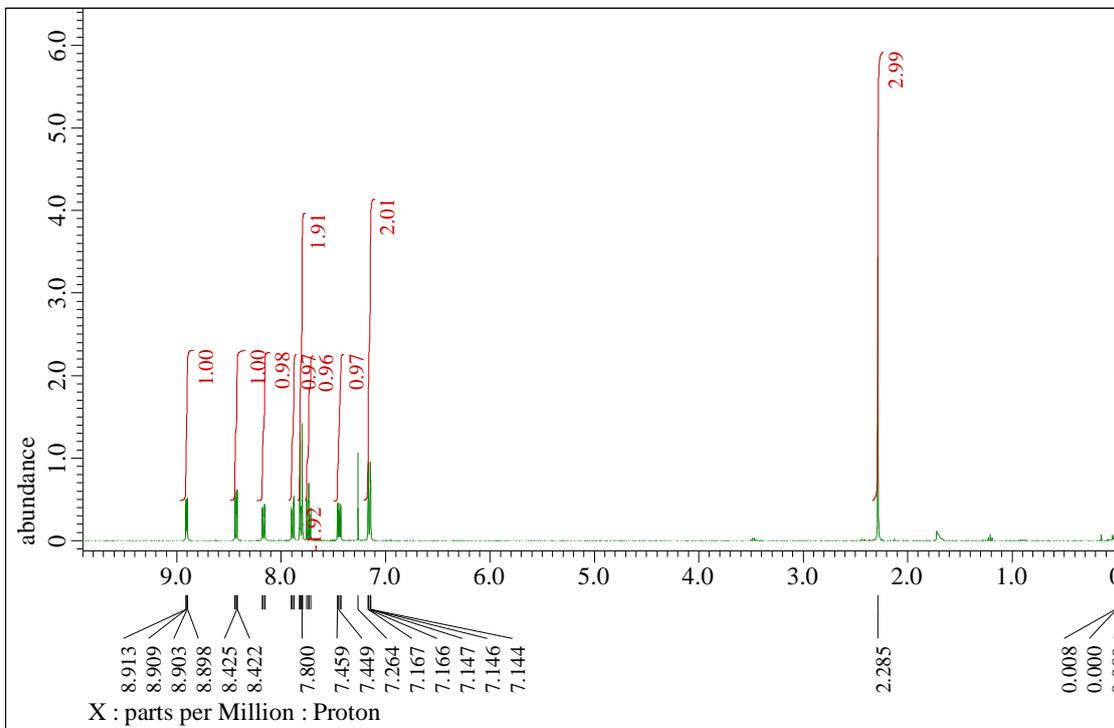
Figure S1 X-ray structure of **YK-11 (2a)**. **YK-11 (2a)** contains two crystallographically independent molecules (a and b) in the asymmetric unit. Colors of atoms: C, gray spheres; O, red spheres; H, light gray spheres.

References

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- (2) G. M. Sheldrick, *Acta Crystallogr.* **2014**, *A70*, C1437.
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- (4) a) H. D. Flack, G. Bernardinelli, *Acta Crystallogr.* **1999**, *A55*, 908-915. b) H.D. Flack, G. Bernardinelli, *J. Appl. Crystallogr.* **2000**, *33*, 1143-1148.
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^1H NMR and ^{13}C NMR spectra

L3



YK11 (2a)

