

Synthesis of Biotinylated Episilvestrol: Highly Selective Targeting of the Translation Factors eIF4A1/II

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Supporting Information

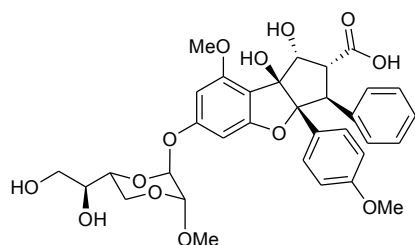
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General

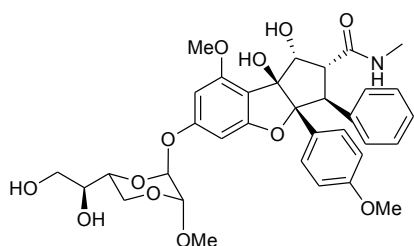
Proton nuclear magnetic resonance spectra (^1H NMR, 500 MHz and 600 MHz) and proton decoupled carbon nuclear magnetic resonance spectra (^{13}C NMR, 125 MHz and 150 MHz) were obtained in deuteriochloroform with residual chloroform as internal standard unless otherwise noted. Chemical shifts are followed by multiplicity, coupling constant(s) (J , Hz), integration, and assignments where possible. Optical rotations were recorded for a 1 mL solution and units are $\text{deg} \cdot \text{cm}^2 \cdot \text{g}^{-1}$. Flash chromatography was carried out on silica gel 60. Analytical thin layer chromatography (TLC) was conducted on aluminium-backed 2 mm thick silica gel 60 GF₂₅₄ and chromatograms were visualized with 20% w/w phosphomolybdic acid in ethanol. High resolution mass spectra (HRMS) were obtained by ionizing samples via electron spray ionization (ESI). Anhydrous THF and CH_2Cl_2 were used from a solvent cartridge system. Dry methanol was distilled from magnesium methoxide. All other solvents were purified by standard methods. Petrol used refers to petroleum ether 40–60°C boiling range. All other commercially available reagents were used as received. The standard workup refers to extraction with a particular solvent (3x), washing with water and brine, drying with MgSO_4 , and concentration under reduced pressure.



Episilvestric acid 5. To episilvestrol **2** (28.2 mg, 0.431 mmol) in was added 15 ml of 0.4% KOH in 1:2 MeOH: H_2O . The reaction was allowed to stir at 50 °C for 2.5 hr. The reaction was then cooled to 0 °C and diethyl ether and sat. NaCl was added. 1M HCl was added until pH ~2 and the reaction was allowed to warm to rt and stir for 30 min.

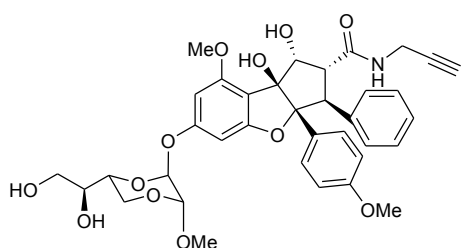
The reaction was extracted 4x with diethyl ether, dried over Na_2SO_4 , filtered, and solvent was evaporated. Product as a white solid (27.5 mg, quantitative yield) was used without further purification: $[\alpha]_D^{23} -109.9$ (c 0.1520, CH_2Cl_2); IR ν_{max} (film): 3407, 2917, 2849, 1712, 1603, 1514, 1498, 1454, 1430, 1378, 1299, 1251, 1218, 1169, 1132, 1118, 1060, 1029, 964, 901, 884, 826, 770, 733, 699 cm^{-1} ; ^1H NMR (600 MHz) δ 7.08–7.05 (m, 5H), 6.90 (d, J = 5.4 Hz, 2H), 6.65 (d, J = 8.7 Hz, 2H), 6.41 (brs, 1H), 6.26 (brs, 1H), 5.31 (s, 1H), 5.03 (brs, 1H), 4.60 (s, 1H), 4.29 (d, J = 10.6 Hz, 1H), 4.08 (brs, 1H), 3.97 (t, J = 10.9 Hz, 1H), 3.88–3.78 (m, 2H), 3.84 (s, 3H), 3.70 (s, 3H), 3.65–3.54 (m, 3H), 3.51 (s, 3H); ^{13}C NMR (150MHz) δ 173.5, 160.7, 159.9, 158.9, 157.4, 136.9, 129.0, 128.1, 128.0, 126.8, 126.5, 112.9, 108.7, 102.0, 95.4, 94.9, 93.6, 93.3, 92.6, 79.8, 76.7, 60.1, 56.1, 55.29, 55.25, 55.21, 50.2; HRMS

(ESI): Calculated for $C_{33}H_{36}NaO_{13}$ $[M+Na]^+$ 663.2048, found 663.2047. Silvestric acid was made in the same manner and spectroscopically identical to previously reported compound.³



Methyl amide 6. To a solution of episilvestric acid **5** (3.4 mg, 0.005 mmol) in CH_2Cl_2 (1.5 mL) at 0 °C was added DCC (7.4 mg, 0.036 mmol) and methyl amine hydrochloride (3.1 mg, 0.046 mmol), the resulting mixture was stirred under an Ar atmosphere for 5 min.

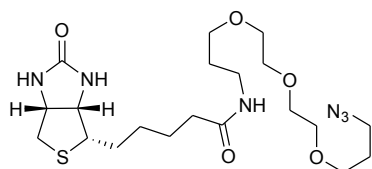
DMAP (9.6 mg, 0.079 mmol) was added and the reaction was allowed to stir at rt for 2 d. CH_2Cl_2 and H_2O were added and the reaction was cooled to 0 °C. 1M HCl was added until pH ~2 and the reaction was allowed to warm to rt and stir for 30 min. The reaction was extracted 4x with CH_2Cl_2 , washed with sat. $NaHCO_3$, H_2O , and sat. NaCl. The mixture was then dried over $MgSO_4$, filtered, and solvent was evaporated. The filtrate was purified by flash chromatography using a gradient elution of 100% EtOAc to 5% → 10% MeOH/EtOAc to give the methyl amide episilvestrol **6** (2.1 mg, 61%) as a white solid: $[\alpha]_D^{26} -173.8^\circ$ (c 0.11, CH_2Cl_2); IR ν_{max} (film): 3407, 2932, 1612, 1513, 1498, 1465, 1452, 1430, 1332, 1299, 1248, 1220, 1167, 1132, 1093, 1065, 1031, 985, 943, 902, 884, 827, 700 cm^{-1} ; 1H NMR (600 MHz) δ 7.10-7.04 (m, 5H), 6.96 (d, J = 7.0 Hz, 2H), 6.63 (d, J = 8.9 Hz, 2H), 6.43 (d, J = 1.6 Hz, 1H), 6.28 (d, J = 1.6 Hz, 1H), 6.00 (dd, J = 9.5, 4.9 Hz, 1H), 5.30 (s, 1H), 4.96 (d, J = 6.1 Hz, 1H), 4.60 (s, 1H), 4.35 (d, J = 12.3 Hz, 1H), 4.13 (ddd, J = 10.4, 7.6, 2.5 Hz, 1H), 4.00 (t, J = 11.2 Hz, 2H), 3.86 (s, 3H), 3.81 (dd, J = 11.6, 2.3 Hz, 1H), 3.69 (s, 3H), 3.68-3.61 (m, 4H), 3.51 (s, 3H), 2.67 (d, J = 4.8 Hz, 3H); ^{13}C NMR (150MHz) δ 171.1, 161.0, 159.9, 158.9, 157.4, 137.0, 129.0, 128.4, 128.1, 126.9, 126.8, 112.8, 108.7, 101.9, 95.4, 94.4, 93.7, 92.9, 92.5, 79.7, 71.6, 67.2, 62.0, 56.1, 55.8, 55.3, 51.2, 29.9, 26.6; HRMS (ESI): Calculated for $C_{34}H_{39}NNaO_{12}$ $[M+Na]^+$ 676.2364, found 676.2361.



Propargyl amide 7. To a solution of episilvestric acid **5** (20.0 mg, 0.031 mmol) in CH_2Cl_2 (7 mL) at 0 °C was added DCC (44.5 mg, 0.216 mmol) and propargyl amine (15 μ L, 0.234 mmol), the resulting mixture was stirred under an Ar atmosphere for 5 min.

DMAP (24.5 mg, 0.201 mmol) was added and the reaction was allowed to stir at rt for 2 d. CH_2Cl_2 and H_2O were added and the reaction was cooled to 0 °C. 1M HCl was added until pH ~2 and the reaction was allowed to warm to rt and stir for 30 min. The reaction was

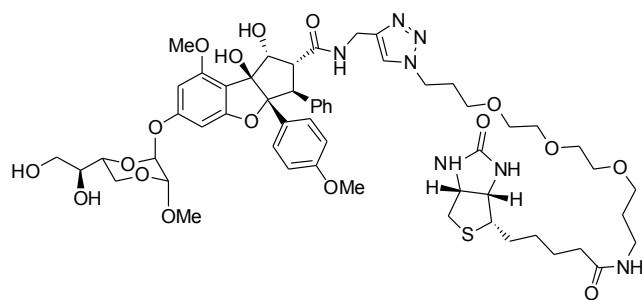
extracted 4x with CH₂Cl₂, washed with sat. NaHCO₃, H₂O, and sat. NaCl. The mixture was then dried over MgSO₄, filtered, and solvent was evaporated. The filtrate was purified by flash chromatography with 80% EtOAc/petrol as eluent to give the propargyl amide **7** (13.8 mg, 65%) as a white solid: $[\alpha]_D^{23}$ -88.1° (*c* 0.40, CH₂Cl₂); IR $\nu_{\max}$ (film): 3426, 2970, 2924, 1739, 1607, 1514, 1498, 1454, 1428, 1366, 1299, 1228, 1217, 1170, 1132, 1094, 1063, 1031, 986, 946, 904, 886, 825, 751, 734, 700, 660 cm⁻¹; ¹H NMR (600 MHz) δ 7.09-7.05 (m, 5H), 6.95 (d, *J* = 6.9 Hz, 2H), 6.63 (d, *J* = 8.9 Hz, 2H), 6.44 (d, *J* = 1.7 Hz, 1H), 6.34 (t, *J* = 5.0 Hz, 1H), 6.27 (d, *J* = 1.7, 1H), 5.29 (s, 1H), 4.98 (dd, *J* = 6.1, 2.1 Hz, 1H), 4.60 (s, 1H), 4.35 (d, *J* = 12.1 Hz, 1H), 4.12 (ddd, *J* = 10.6, 7.5, 2.7 Hz, 1H), 3.99 (t, *J* = 11.3 Hz, 1H), 3.95 (brs, 1H), 3.94 (ddd, *J* = 17.6, 6.8, 2.6 Hz, 1H), 3.87 (s, 3H), 3.84 (dd, *J* = 4.9, 2.6 Hz, 1H), 3.82-3.79 (m, 1H), 3.70 (dd, *J* = 12.8, 6.1 Hz, 1H), 3.69 (s, 3H), 3.67-3.64 (m, 2H), 3.63-3.60 (m, 1H), 3.50 (s, 3H), 2.54-2.50 (m, 2H), 2.15 (t, *J* = 2.5 Hz, 1H); ¹³C NMR (150MHz) δ 170.2, 161.0, 160.0, 158.9, 157.4, 136.8, 129.0, 128.4, 128.1, 126.9, 126.7, 112.8, 108.5, 101.8, 95.4, 94.4, 93.7, 92.9, 92.5, 79.5, 79.3, 71.9, 71.5, 67.2, 62.0, 60.2, 56.1, 55.8, 55.25, 55.23, 51.1, 29.6; HRMS (ESI): Calculated for C₃₆H₄₀NO₁₂ [M+H]⁺ 678.2545, found 678.2553. Propargyl amide **7** was pure by HPLC (*R*_t = 9.26 mins. 5 μ m Phenomenex Lux Cellulose-1 10x250mm column, 50% MeCN/H₂O eluent, flow rate: 2.00 mL/min/).



Azide biotin linker 8. Azide biotin linker **8** was prepared

in 3 steps from biotin as previously reported¹ with a modification as detailed below. Biotin (1.00 g, 4.093 mmol) was dissolved in 20 mL DMF at 70 °C and allowed to cool to rt. EtN₃ (0.73g, 1.00 mL, 7.175 mmol) was added, followed by pentafluorophenyl trifluoroacetate (1.63 g, 1.00 mL, 5.820 mmol). The reaction was allowed to stir for 30 min at rt and became pink. Solvent was removed in vacuo and the crude material was triturated with diethyl ether. The product biotin-pFp ester was recovered as a white solid (1.59 g, 95%). Biotin-pFp ester (1.20 g, 2.924 mmol) was dissolved in 40 mL DMF and cooled to 0 °C. A flask containing 4,7,10-tioxa-1,13-tridecanediamine (3.76 g, 3.75 mL, 17.107 mmol) and EtN₃ (0.58 g, 800 μ L, 5.740 mmol) was also cooled to 0 °C. Biotin-pFp ester was then transferred dropwise via cannula over 15 min into the diamine flask. The reaction was allowed to stir at rt for 1 h and became a pale pink. Solvent was removed in vacuo and the crude material was triturated with diethyl ether rather than purified by column chromatography as reported. This gave very pure biotin-amine as a white solid (1.23 g, 94%).

The biotin-amine (179.3 mg, 0.402 mmol) was dissolved in 7.0 mL MeOH. K_2CO_3 (83.4 mg, 0.603 mmol), $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, and imidazole-1-sulfonyl azide hydrochloride² (105.0 mg, 0.501 mmol) were added. The reaction was allowed to stir at rt for 16 h. Solvent was removed in vacuo and the crude material was purified by flash chromatography using a gradient elution of 15% $\rightarrow$ 25% MeOH/EtOAc to give the biotin azide linker **8** (103 mg, 55%, 58% bsrn) as a white, waxy solid: $[\alpha]_D^{25} +34.9^\circ$ (c 1.60, MeOH); IR ν_{max} (film): 3738, 3299, 2936, 2095, 1740, 1706, 1366, 1275, 1262, 1217, 1120, 764, 751 cm^{-1} ; ^1H NMR (500 MHz, d_4 -methanol) δ 4.49 (ddd, $J = 7.8, 4.9, 0.6$ Hz, 1H), 4.31 (dd, $J = 7.9, 4.5$ Hz, 1H), 3.65-3.63 (m, 4H), 3.61-3.58 (m, 4H), 3.56 (t, $J = 6.1$ Hz, 2H), 3.52 (t, $J = 6.2$ Hz, 2H), 3.40 (t, $J = 6.7$ Hz, 2H), 3.26 (t, $J = 6.8$ Hz, 2H), 3.21 (ddd, $J = 7.9, 4.6, 3.5$ Hz, 1H), 2.71 (d, $J = 12.7$ Hz, 1H), 2.20 (t, $J = 7.4$ Hz, 2H), 1.85-1.56 (m, 8H), 1.47-1.41 (m, 2H); ^{13}C NMR (125MHz) δ 175.9, 166.0, 71.52, 71.51, 71.26, 71.22, 69.9, 68.9, 63.3, 61.6, 57.0, 49.5, 41.0, 39.7, 37.8 36.9, 30.4, 30.2, 29.8, 29.5, 26.9; HRMS (ESI): Calculated for $\text{C}_{20}\text{H}_{36}\text{N}_6\text{NaO}_5\text{S}$ $[\text{M}+\text{Na}]^+$, 495.2360, found 495.2348. This compound was spectroscopically identical to that previously reported.¹



Biotinylated episilvestrol 9. To propargyl amide **7** (3.5 mg, 0.005 mmol) in 2:1 DMSO: H_2O (1.5 mL) was added biotin azide **8** (3.2 mg, 0.007 mmol), TBTA (0.072 mg, 0.00014 mmol), and sodium ascorbate (0.276 mg, 0.0014

mmol). The reaction was wrapped in foil and CuSO_4 (0.02 mg, 0.00014 mmol) was added and the reaction was allowed to stir at 40 $^\circ\text{C}$ for 2 d. The solvent was evaporated and the mixture was purified via flash chromatography using a gradient elution of 100% EtOAc to 10% $\rightarrow$ 30% MeOH/EtOAc to give biotinylated episilvestrol **9** (5.1 mg, 86%, 95% bsrn) as a white solid: $[\alpha]_D^{25} -79.4^\circ$ (c 0.11, CH_2Cl_2); IR ν_{max} (film): 3310, 3083, 2970, 2928, 2875, 1739, 1700, 1647, 1623, 1541, 1515, 1498, 1455, 1434, 1366, 1301, 1228, 1217, 1169, 1133, 1119, 1097, 1067, 1031, 974, 946, 909, 887, 827, 731, 702 cm^{-1} ; ^1H NMR (500 MHz) δ 7.75 (t, $J = 5.2$ Hz, 1H), 7.36 (s, 1H), 7.09 (d, $J = 8.8$ Hz, 3H), 7.05-6.99 (m, 6H), 6.73 (t, $J = 5.0$ Hz, 1H), 6.61 (d, $J = 13.5$ Hz, 2H), 6.43 (d, $J = 1.6$ Hz, 1H), 6.34 (brs, 1H), 6.24 (d, $J = 1.6$ Hz, 1H), 5.30 (s, 1H), 5.13 (brs, 1H), 4.86 (dd, $J = 5.0, 2.1$ Hz, 1H), 4.60 (s, 1H), 4.51 (brs, 1H), 4.47 (dd, $J = 15.8, 6.1$ Hz, 1H), 4.43 (dd, $J = 7.0, 4.7$ Hz, 1H), 4.41 (d, $J = 14.0$ Hz, 1H), 4.34, (t, $J = 6.9$ Hz, 3H), 4.28 (dd, $J = 7.4, 4.7$ Hz, 1H), 4.09 (ddd, $J = 10.6, 7.9, 2.5$

Hz, 1H), 3.97 (t, J = 11.3, 1H), 3.87 (dd, J = 13.8, 5.2 Hz, 1H), 3.84-3.79 (m, 2H), 3.81 (s, 3H), 3.74 (m, 1H), 3.69-3.65 (m, 2H), 3.67 (s, 3H), 3.62-3.51 (m, 16H), 3.50 (s, 3H), 3.40-3.25 (m, 6H), 3.12 (ddd, J = 11.7, 7.3, 4.6 Hz, 1H), 2.86 (dd, J = 12.9, 5.0 Hz, 1H), 2.65 (d, J = 12.8 Hz, 1H), 2.45 (brs, 1H), 2.10-2.02 (m 5H), 1.73-1.54 (m, 21 H), 1.45-1.32 (m, 3H), 1.25 (s, 3H); ^{13}C NMR (125MHz) δ 173.2, 171.2, 163.8, 161.0, 159.6 158.6, 157.6, 144.87, 144.85, 137.0, 128.9, 128.4, 127.8, 127.0, 126.5, 123.0, 112.6, 108.5, 101.9, 95.4, 94.6, 93.7, 93.5, 92.1, 79.0, 71.5, 70.5, 70.4, 70.2, 70.0, 69.9, 67.2, 67.1, 62.2, 62.1, 60.4, 60.1, 56.1, 55.8, 55.7, 55.10, 55.09, 51.8, 47.0, 40.6, 37.7, 35.6, 35.0, 30.1, 29.7, 28.8, 28.21, 28.16, 25.5; HRMS (ESI): Calculated for $\text{C}_{56}\text{H}_{75}\text{N}_7\text{NaO}_{17}\text{S}$ $[\text{M}+\text{Na}]^+$ 1172.4832, found 1172.4846. Biotinylated episilvestrol **9** was pure by HPLC (R_t = 8.43 mins. 5 μm , Phenomenex Lux cellulose-1 10 x 250mm column, 40% MeCN/ H_2O eluent, flow rate: 2.00 mL/min).

In vitro translations

In vitro translations were performed for 1 h at 30 °C in rabbit reticulocyte lysate essentially as described.³ The Dual Glo Luciferase Assay kit (Promega, Madison, WI, USA) was used to measure Firefly and Renilla luciferase activity, translated from capped mRNA transcribed from pSP/(CAG)₃₃/FF/HCV/Ren.pA51. Data are represented as Firefly luciferase activity/Renilla luciferase activity relative to vehicle (DMSO-treated) controls. Renilla luciferase serves as an internal control since HCV IRES-driven translation is resistant to silvestrol.⁴

Cell viability assay

Mouse embryonic fibroblasts (MEFs) immortalized with SV40 large T antigen (1000 cells/well in a 96 well opaque plate) were seeded into serial dilutions of compound in Dulbecco's modified Eagle's medium supplemented with 10% fetal calf serum (FCS; Bovogen, East Keilor, Australia), 50 μM 2-mercaptoethanol (Sigma, Castle Hill, Australia) and 100 μM asparagine (Sigma). After 72 h at 37 °C/10 % CO_2 , the number of viable cells was measured as a function of ATP concentration using the CellTiter-Glo Luminescent Cell Viability Assay (Promega, Alexandria, Australia).

Rate of translation in MEFs

MEFs (45 000 cells/well) were seed in 24h well plates. Once cells adhered, media was replaced with indicated concentrations of compound for 40 minutes at 37 °C/10 % CO_2 , after

which 5 μ L of [35 S]Easy Tag Express Protein Labeling mix (1175 Ci/mmol) (Perkin Elmer, Waltham, MA, USA) was added for an additional 20 minutes. Cells were then washed with PBS, and subsequently lysed in Ripa buffer. Half the lysate was spotted onto Whattman paper preblocked with L-methionine and protein was precipitated with TCA before quantitation by Scintillation counting.⁴ The rate of translation was standardised to protein content using the Micro BCA protein assay (Pierce, Scoresby, Australia).

Streptavidin pulldowns

MEFs (10 million cells per sample) were washed in PBS and lysed in 0.5 mL of IP buffer [50 mM Tris pH 7.5, 120mM NaCl, 2 mM EDTA, 2 mM KCl, 1% Triton X-100, protease inhibitors (complete mini EDTA-free protease inhibitor cocktail tablet; Roche)] and membranes were cleared by centrifugation. RNase A (Sigma) was added (10 μ g) to the lysates and were incubated at room temperature for 10 min to reduce non-specific pulldown of RNA-binding proteins. Samples were precleared with streptavidin sepharose high performance beads (GE Healthcare, Uppsala, Sweden) for 30 min at 4 °C. Biotinylated episilvestrol (9) or biotin alone (AK Scientific) (20 μ M) was then added to lysates with fresh streptavidin sepharose beads and rotated end-over-end overnight at 4 °C. Pulldowns were washed in IP buffer 5 times at 4 °C and eluted with successive treatments of 50 μ M silvestrol, 25mM glycine pH 2.5, at room temperature and finally in LDS (NuPAGE® LDS Sample Buffer 1X, Invitrogen, CA, USA) at 95 °C. Equal volumes of the samples were separated on 4-12% NuPAGE® gels, transferred to PVDF and probed using the following antibodies: eIF4AI (ab31217; Abcam), eIF4AII (ab31218; Abcam), eIF4AIII (ab32485; Abcam), eIF4G (C45A4; Cell Signaling), and eIF4E (87; BD Transduction Laboratories), DDX3 (D19B4; Cell Signalling), DHX29 (D19E10; Cell Signalling). Alternatively, samples were silver stained essentially as described.⁵

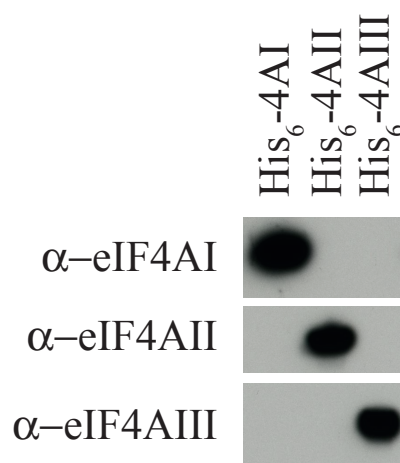


Figure 1. Specificity of indicated antibodies. Recombinant His₆-tagged protein (100ng) was separated by NuPAGE®, transferred to PVDF, and probed with antibodies against eIF4AI (ab31217; Abcam), eIF4AII (ab31218; Abcam), and eIF4AIII (ab32485; Abcam). Recombinant proteins were purified as previously described.

Protein Mass spectroscopy

Eluted proteins were digested by the filter-aided sample preparation method.⁶ Briefly, the eluate was added to SDS-containing buffer and loaded onto a Vivaspın 500 30 K device (Sartorius Stedman). SDS was removed by urea exchange followed by alkylation with 50 mM iodoacetamide for 20 min. Urea was then replaced with 20 mM ammonium bicarbonate before the proteins were digested overnight at 37 °C with trypsin (Gold, Promega) (1 µg of trypsin:100 µg of protein). The peptides were collected from the filter by centrifugation followed by two additional elutions with 20 mM ammonium bicarbonate. Peptide eluates were then quantified on a Nanodrop 2000 at a wavelength of 280 nm and acidified to 1% formic acid prior to MS analysis.

MS data were acquired on an LTQ Orbitrap XL mass spectrometer (Thermo Fisher Scientific) fitted with a Nano-ESI source (Proxeon; Thermo Fisher Scientific) coupled to a nano-HPLC system (Agilent Technologies). Approximately 1 µg of total digested peptide was loaded onto a 20 mm long nanoACQUITY pre-column with 180 µm I.D. and 5 µm C18 silica bead (Waters) in 5% buffer B at a flow rate of 10 µl/min (Buffer A - 0.1% formic acid. Buffer B - 90% ACN, 0.1% formic acid) and then resolved on a 100 mm nanoACQUITY column with 100 µm I.D. and 1.7 µm C18 silica bead (Waters) using a 70 min gradient (5% to 45% buffer B) at a flow rate of 1.2 µl/min. The Orbitrap was then run in a data-dependent

acquisition mode with the Orbitrap resolution set at 60,000 and the top-five multiply charged species selected for fragmentation in the linear ion trap by collision-induced dissociation (single charged species were ignored). The ion threshold was set to 15,000 counts for MS/MS. The activation time was set to 30 ms. Raw files consisting of full-scan MS and ion-trap spectra were converted to the MGF data format and searched against an in-house generated target/decoy database (LudwigNR-Q412, from WEHI Bioinformatics) and searched using our in-house Mascot Cluster (WEHI Systems Biology Mascot Server, Matrix Science). Spectra were searched with a mass tolerance of 10 ppm in MS mode and 0.7 Da in MS/MS mode, allowing up to 3 missed cleavage sites. Cysteine carbamidomethylation was included as a fixed modification, while oxidized Methionine and Lysine acetylation were set to variable. Peptides were identified at a 1% false discovery rate and were visualized using Scaffold 3.0 (Proteome Software).

Silvestrol Elutions, Samples report created on 11/12/2012

Experiment: Silvestrol Elutions
Peak List Generator: unknown
Version: unknown
Charge States Calculated: unknown
Deisotoped: unknown
Textual Annotation: unknown
Database Set: 1 Database
Database Name: the LudwigNR_Q312_generic_forward database
Version: unknown
Taxonomy: Mus musculus
Number of Proteins: 96518
Does database contain common contaminants?: unknown
Search Engine Set: 1 Search Engine
Search Engine: Mascot
Version: 2.3.02.05
Samples: All Samples
Fragment Tolerance: 0.70 Da (Monoisotopic)
Parent Tolerance: 10.0 PPM (Monoisotopic)
Fixed Modifications: +57 on C (Carbamidomethyl)
Variable Modifications: +16 on M (Oxidation)
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Digestion Enzyme: Trypsin
Max Missed Cleavages: 3
Scaffold Version: Scaffold.3.6.1
Peptide Thresholds: 90.0% minimum
Protein Thresholds: 95.0% minimum and 1 peptides minimum

Elution #	Number of Unique Peptides Value?	Starred?	Identified Proteins (80)	Accession Number	Molecular Weight	Protein Grouping Antibody	Quantitative Variance	Taxonomy	Uncategorized Sample							
									Blank 1	scotin only, silvestrol elution	Blank 2	9, silvestrol elution	Blank 3	only, glycine elution	Blank 4	9, glycine elution
2.1	TRUE	FALSE	spP60843:Eukaryotic initiation factor 4A-1 Tax. Id=10090 [Mus musculus]	P60843	46 kDa			unknown	0	0	15	0	0	0	26	
1.1	TRUE	FALSE	trQ4FZL1:EIF4a1 protein (Fragment) Tax. Id=10090 [Mus musculus]	Q4FZL1	46 kDa			unknown	0	0	0	0	0	0	26	
2	TRUE	FALSE	spP60710:Actin, cytoplasmic 1 Tax. Id=10090 [Mus musculus]	P60710	42 kDa	TRUE		unknown	0	10	0	2	0	6	0	10
2.1	TRUE	FALSE	spP63260:Actin, cytoplasmic 2 Tax. Id=10090 [Mus musculus]	P63260	42 kDa			unknown	0	10	0	2	0	6	0	10
2.2	TRUE	FALSE	trQ3U5B4:Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3U5B4	42 kDa	TRUE		unknown	0	10	0	2	0	6	0	10
2.3	TRUE	FALSE	trQ3UAF6:Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3UAF6	42 kDa	TRUE		unknown	0	10	0	2	0	6	0	10
2.4	TRUE	FALSE	trQ3UAF7:Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3UAF7	42 kDa	TRUE		unknown	0	10	0	2	0	6	0	10
3	TRUE	FALSE	trD3Z3R0:Uncharacterized protein Tax. Id=10090 [Mus musculus]	D3Z3R0	30 kDa			unknown	0	4	0	0	0	8	0	11
3.1	TRUE	FALSE	trF6TJZ4:Uncharacterized protein (Fragment) Tax. Id=10090 [Mus musculus]	F6TJZ4	30 kDa			unknown	0	4	0	0	0	8	0	11
3.2	TRUE	FALSE	spP12970:60S ribosomal protein L7a Tax. Id=10090 [Mus musculus]	P12970	30 kDa			unknown	0	4	0	0	0	8	0	11
3.3	TRUE	FALSE	trQ6P1A9:Ribosomal protein L7a Tax. Id=10090 [Mus musculus]	Q6P1A9	30 kDa			unknown	0	4	0	0	0	8	0	11
3.4	TRUE	FALSE	trQ80U17:Rp17a protein (Fragment) Tax. Id=10090 [Mus musculus]	Q80U17	30 kDa			unknown	0	4	0	0	0	8	0	11
4	TRUE	FALSE	spP62702:40S ribosomal protein S4, X isoform Tax. Id=10090 [Mus musculus]	P62702	30 kDa			unknown	0	10	0	2	0	5	0	7
4.1	TRUE	FALSE	trQ545F8:Uncharacterized protein Tax. Id=10090 [Mus musculus]	Q545F8	27 kDa			unknown	0	10	0	2	0	5	0	7
5	TRUE	FALSE	spP34377:Histone H1.3 Tax. Id=10090 [Mus musculus]	P34377	22 kDa	TRUE		unknown	0	5	0	1	0	10	0	7
5.1	TRUE	FALSE	trQ3U292:Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3U292	22 kDa	TRUE		unknown	0	5	0	1	0	10	0	7
6	TRUE	FALSE	trD3Z6C3:Uncharacterized protein Tax. Id=10090 [Mus musculus]	D3Z6C3	30 kDa			unknown	0	10	0	0	0	4	0	8
6.1	TRUE	FALSE	spP97351:40S ribosomal protein S3a Tax. Id=10090 [Mus musculus]	P97351	30 kDa			unknown	0	10	0	0	0	4	0	8
6.2	TRUE	FALSE	trQ3UAC2:Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3UAC2	30 kDa			unknown	0	10	0	0	0	4	0	8
7	TRUE	FALSE	spQ8VD58:Myosin-9 Tax. Id=10090 [Mus musculus]	Q8VD58	226 kDa			unknown	0	2	0	0	0	13	0	9
8	TRUE	FALSE	trP62720:40S ribosomal protein S18 Tax. Id=10090 [Mus musculus]	P62720	18 kDa			unknown	0	5	0	1	0	6	0	8
8.1	TRUE	FALSE	trQ5SVZ5:MG116671 Tax. Id=10090 [Mus musculus]	Q5SVZ5	18 kDa			unknown	0	5	0	1	0	6	0	8
9	TRUE	FALSE	spP62301:40S ribosomal protein S13 Tax. Id=10090 [Mus musculus]	P62301	17 kDa			unknown	0	6	0	1	0	4	0	6
10	TRUE	FALSE	trD3YWP3:MG1034428 Tax. Id=10090 [Mus musculus]	D3YWP3	18 kDa			unknown	0	6	0	0	0	7	0	5
10.1	TRUE	FALSE	spP62751:60S ribosomal protein L23a Tax. Id=10090 [Mus musculus]	P62751	18 kDa			unknown	0	6	0	0	0	7	0	5
10.2	TRUE	FALSE	trQ4YX93:Rp23a protein (Fragment) Tax. Id=10090 [Mus musculus]	Q4YX93	18 kDa			unknown	0	6	0	0	0	7	0	5
10.3	TRUE	FALSE	trQ91YK6:Rp23a protein (Fragment) Tax. Id=10090 [Mus musculus]	Q91YK6	17 kDa			unknown	0	6	0	0	0	7	0	5
10.4	TRUE	FALSE	trEXP_001476183.1: PREDICTED: 60S ribosomal protein L23a-like Tax. Id=10090 [Mus musculus]	XP_001476183.1	18 kDa			unknown	0	6	0	0	0	7	0	5
11	TRUE	FALSE	trQ5U438:Nucleophosmin 1 Tax. Id=10090 [Mus musculus]	Q5U438	33 kDa			unknown	0	8	0	1	0	4	0	3
11.1	TRUE	FALSE	spQ61937:Nucleophosmin Tax. Id=10090 [Mus musculus]	Q61937	33 kDa			unknown	0	8	0	1	0	4	0	3
11.2	TRUE	FALSE	trEXP_001476579.1: PREDICTED: nucleophosmin-like Tax. Id=10090 [Mus musculus]	XP_001476579.1	33 kDa			unknown	0	8	0	1	0	4	0	3
12	TRUE	FALSE	spP47962:60S ribosomal protein L5 Tax. Id=10090 [Mus musculus]	P47962	34 kDa			unknown	0	8	0	2	0	3	0	3
12.1	TRUE	FALSE	trQ3TKR5:Ribosomal protein L5 Tax. Id=10090 [Mus musculus]	Q3TKR5	34 kDa			unknown	0	8	0	2	0	3	0	3
12.2	TRUE	FALSE	trQ3U850:Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3U850	34 kDa			unknown	0	8	0	2	0	3	0	3
13	TRUE	FALSE	spP61255:60S ribosomal protein L26 Tax. Id=10090 [Mus musculus]	P61255	17 kDa			unknown	0	4	0	1	0	5	0	4
14	TRUE	FALSE	trQ9U2X4:60S ribosomal protein L6 Tax. Id=10090 [Mus musculus]	Q9U2X4	34 kDa			unknown	0	7	0	1	0	8	0	3
14.1	TRUE	FALSE	spP47911:60S ribosomal protein L6 Tax. Id=10090 [Mus musculus]	P47911	33 kDa			unknown	0	7	0	1	0	8	0	3
14.2	TRUE	FALSE	trEXP_483949.3: PREDICTED: 60S ribosomal protein L6-like Tax. Id=10090 [Mus musculus]	XP_483949.3	35 kDa			unknown	0	7	0	1	0	8	0	3
15	TRUE	FALSE	trQ3TW40:Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3TW40	74 kDa			unknown	0	0	0	0	0	11	0	4
15.1	TRUE	FALSE	spP57020:MKAA4195 protein (Fragment) Tax. Id=10090 [Mus musculus]	Q57020	75 kDa			unknown	0	0	0	0	0	11	0	4
15.2	TRUE	FALSE	trQ9Q0E1:Histone H2B type 1-E Tax. Id=10090 [Mus musculus]	Q9Q0E1	16 kDa			unknown	0	6	0	0	0	11	0	4
15.3	TRUE	FALSE	sp_s09DDE1-2(Histone)isoform 2 of Q9DDE1 Tax. Id=10090 [Mus musculus]	Q9DDE1-2	74 kDa			unknown	0	0	0	0	0	11	0	4
16	TRUE	FALSE	trE9Q5A0:Uncharacterized protein Tax. Id=10090 [Mus musculus]	E9Q5A0	48 kDa			unknown	0	5	0	1	0	2	0	3
16.1	TRUE	FALSE	spP19253:60S ribosomal protein L13a Tax. Id=10090 [Mus musculus]	P19253	23 kDa			unknown	0	5	0	1	0	2	0	3
17	TRUE	FALSE	spP62717:60S ribosomal protein L18a Tax. Id=10090 [Mus musculus]	P62717	21 kDa			unknown	0	4	0	1	0	5	0	2
18	TRUE	FALSE	spP62911:60S ribosomal protein L32 Tax. Id=10090 [Mus musculus]	P62911	16 kDa			unknown	0	3	0	1	0	4	0	4
18.1	TRUE	FALSE	trEXP_00086045.1: PREDICTED: 60S ribosomal protein L32-like Tax. Id=10090 [Mus musculus]	XP_00086045.1	16 kDa			unknown	0	3	0	0	0	4	0	4
19	TRUE	FALSE	trD3YX54:60S ribosomal protein L13 Tax. Id=10090 [Mus musculus]	D3YX54	24 kDa			unknown	0	4	0	2	0	5	0	3
19.1	TRUE	FALSE	spP47963:60S ribosomal protein L13 Tax. Id=10090 [Mus musculus]	P47963	24 kDa			unknown	0	4	0	2	0	5	0	3
19.2	TRUE	FALSE	trEXP_001474740.1: PREDICTED: 60S ribosomal protein L13-like Tax. Id=10090 [Mus musculus]	XP_001474740.1	24 kDa			unknown	0	4	0	2	0	5	0	3
20	TRUE	FALSE	spP62900:60S ribosomal protein L31 Tax. Id=10090 [Mus musculus]	P62900	14 kDa			unknown	0	3	0	1	0	3	0	5
20.1	TRUE	FALSE	trQ9CY93:Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q9CY93	14 kDa			unknown	0	3	0	1	0	3	0	5
20.2	TRUE	FALSE	trEXP_922988.1: PREDICTED: 60S ribosomal protein L31-like isoform 1 Tax. Id=10090 [Mus musculus]	XP_922988.1	14 kDa			unknown	0	3	0	1	0	3	0	5
21	TRUE	FALSE	trD3YW41:60S ribosomal protein L36 Tax. Id=10090 [Mus musculus]	D3YW41	12 kDa			unknown	0	3	0	0	0	3	0	4
21.1	TRUE	FALSE	trD3Z3R1:60S ribosomal protein L36 Tax. Id=10090 [Mus musculus]	D3Z3R1	12 kDa			unknown	0	3	0	0	0	3	0	4
21.2	TRUE	FALSE	trQ5M9L1:60S ribosomal protein L36 Tax. Id=10090 [Mus musculus]	Q5M9L1	12 kDa			unknown	0	3	0	0	0	3	0	4
21.3	TRUE	FALSE	trQ6ZWZ4:60S ribosomal protein L36 Tax. Id=10090 [Mus musculus]	Q6ZWZ4	12 kDa			unknown	0	3	0	0	0	3	0	4
22	TRUE	FALSE	spQ6ZWY7:60S ribosomal protein L35 Tax. Id=10090 [Mus musculus]	Q6ZWY7	15 kDa			unknown	0	4	0	1	0	2	0	4
23	TRUE	FALSE	trQ3U561:Ribosomal protein Tax. Id=10090 [Mus musculus]	Q3U561	25 kDa			unknown	0	1	0	0	0	4	0	4
23.1	TRUE	FALSE	trQ5XJF6:Ribosomal protein Tax. Id=10090 [Mus musculus]	Q5XJF6	25 kDa			unknown	0	1	0	0	0	4	0	4
24	TRUE	FALSE	spQ55142:60S ribosomal protein L35a Tax. Id=10090 [Mus musculus]	Q55142	13 kDa			unknown	0	3	0	0	0	3	0	3
24.1	TRUE	FALSE	trQ8BQV7:Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q8BQV7	13 kDa			unknown	0	3	0	0	0	3	0	3
25	TRUE	FALSE	spP61358:60S ribosomal protein L27 Tax. Id=10090 [Mus musculus]	P61358	16 kDa			unknown	0	5	0	0	0	2	0	4
26	TRUE	FALSE	spP41056:60S ribosomal protein L28 Tax. Id=10090 [Mus musculus]	P41056	16 kDa			unknown	0	3	0	1	0	3	0	2
26.1	TRUE	FALSE	trQ5M9N5:Ribosomal protein L28 Tax. Id=10090 [Mus musculus]	Q5M9N5	16 kDa			unknown	0	3	0	1	0	3	0	2
26.2	TRUE	FALSE	trEXP_001473974.1: PREDICTED: 60S ribosomal protein L28-like Tax. Id=10090 [Mus musculus]	XP_001473974.1	16 kDa			unknown	0	3	0	1	0	3	0	2
27	TRUE	FALSE	trE9PW19:Ribosomal protein L15 Tax. Id=10090 [Mus musculus]	E9PW19	24 kDa			unknown	0	7	0	0	0	0	0	2
27.1	TRUE	FALSE	trE9QAZ2:Ribosomal protein L15 Tax. Id=10090 [Mus musculus]	E9QAZ2	24 kDa			unknown	0	7	0	0	0	0	0	2
27.2	TRUE	FALSE	trQ3U7D2:Ribosomal protein L15 Tax. Id=10090 [Mus musculus]	Q3U7D2	24 kDa			unknown	0	7	0	0	0	0	0	2
27.3	TRUE	FALSE	spQ9CZM2:60S ribosomal protein L15 Tax. Id=10090 [Mus musculus]	Q9CZM2	24 kDa			unknown	0	7	0	0	0	0	0	2
28	TRUE	FALSE	trQ4VAZ8:Ribosomal protein L21 Tax. Id=10090 [Mus musculus]	Q4VAZ8	19 kDa			unknown	0	5	0	0	0	1	0	2
28.1	TRUE	FALSE	trQ9CQMB:MG12646 Tax. Id=10090 [Mus musculus]	Q9CQMB	19 kDa			unknown	0	5	0	0	0	1	0	2
29	TRUE	FALSE	spP14869:60S acidic ribosomal protein P0 Tax. Id=10090 [Mus musculus]	P14869	34 kDa			unknown	0	4	0	2	0	2	0	2
29.1	TRUE	FALSE	trQ5FWB6:MG17387, isoform CRA, a Tax. Id=10090 [Mus musculus]	Q5FWB6	34 kDa			unknown	0	4	0	2	0	2	0	2
30	TRUE	FALSE	spP62918:60S ribosomal protein L8 Tax. Id=10090 [Mus musculus]	P62918	28 kDa			unknown	0	6	0	1	0	1	0	1
30.1	TRUE	FALSE	trQ3U1S0:Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3U1S0	28 kDa			unknown	0	6	0	1	0	1	0	1
31	TRUE	FALSE	trA01LV3:Histone H2B (Fragment) Tax. Id=10090 [Mus musculus]	A01LV3	14 kDa			unknown	0	3	0	0	0	2	0	2
31.1	TRUE	FALSE	spP10853:Histone H2B type 1-E Tax. Id=10090 [Mus musculus]	P10853	14 kDa			unknown	0	3	0	0	0	2	0	2
31.2	TRUE	FALSE	spP10854:Histone H2B type 1-M Tax. Id=10090 [Mus musculus]	P10854	14 kDa			unknown	0	3	0	0				

37.3	TRUE	FALSE	ens ENSMUSP00000126334 ENSMUSG00000090544 transcript ENSMUST00000126334	ENSMUSP00000126334	30 kDa	unknown	0	6	0	0	0	2	0	1
37.4	TRUE	FALSE	tr F6Y1Z4 Uncharacterized protein (Fragment) Tax. Id=10090 [Mus musculus]	F6Y1Z4	30 kDa	unknown	0	6	0	0	0	2	0	1
37.5	TRUE	FALSE	sp P25444 40S ribosomal protein S2 Tax. Id=10090 [Mus musculus]	P25444	31 kDa	unknown	0	6	0	0	0	2	0	1
37.6	TRUE	FALSE	tr Q31LE5 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q31LE5	31 kDa	unknown	0	6	0	0	0	2	0	1
37.7	TRUE	FALSE	tr Q31LE5 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q31LE5	31 kDa	unknown	0	6	0	0	0	2	0	1
37.8	TRUE	FALSE	tr Q31XR5 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q31XR5	24 kDa	unknown	0	6	0	0	0	2	0	1
37.9	TRUE	FALSE	tr Q31XS9 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q31XS9	31 kDa	unknown	0	6	0	0	0	2	0	1
37.1	TRUE	FALSE	tr fXP_003086745.1 PREDICTED: 40S ribosomal protein S2-like Tax. Id=10090 [Mus musculus]	fXP_003086745.1	31 kDa	unknown	0	6	0	0	0	2	0	1
38	TRUE	FALSE	sp Q9J8E6 60S ribosomal protein L4 Tax. Id=10090 [Mus musculus]	Q9J8E6	47 kDa	unknown	0	8	0	0	0	0	0	0
39	TRUE	FALSE	tr P61514 60S ribosomal protein L37a Tax. Id=10090 [Mus musculus]	P61514	10 kDa	unknown	0	7	0	0	0	2	0	2
39.1	TRUE	FALSE	tr Q5M9N6 Rpl37a protein Tax. Id=10090 [Mus musculus]	Q5M9N6	9 kDa	unknown	0	3	0	0	0	2	0	2
39.2	TRUE	FALSE	tr Q9CYW3 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q9CYW3	10 kDa	unknown	0	3	0	0	0	2	0	2
40	TRUE	FALSE	sp P62889 60S ribosomal protein L30 Tax. Id=10090 [Mus musculus]	P62889	13 kDa	unknown	0	2	0	0	0	4	0	4
41	TRUE	FALSE	ens ENSMUSP00000102200 ENSMUSG0000008683 transcript ENSMUST00000102200	ENSMUSP00000102200	12 kDa	unknown	0	3	0	0	0	2	0	2
41.1	TRUE	FALSE	tr P8WJ41 Ribosomal protein S15A (Fragment) Tax. Id=10090 [Mus musculus]	P8WJ41	12 kDa	unknown	0	3	0	0	0	2	0	2
41.2	TRUE	FALSE	sp P62245 40S ribosomal protein S15a Tax. Id=10090 [Mus musculus]	P62245	15 kDa	unknown	0	3	0	0	0	2	0	2
42	TRUE	FALSE	tr E9Q132 Uncharacterized protein Tax. Id=10090 [Mus musculus]	E9Q132	15 kDa	unknown	0	4	0	0	0	2	0	1
42.1	TRUE	FALSE	tr E9QNJ0 Uncharacterized protein Tax. Id=10090 [Mus musculus]	E9QNJ0	18 kDa	unknown	0	4	0	0	0	2	0	1
42.2	TRUE	FALSE	tr Q3UW40 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3UW40	18 kDa	unknown	0	4	0	0	0	2	0	1
42.3	TRUE	FALSE	tr Q8HP67 60S ribosomal protein L24 Tax. Id=10090 [Mus musculus]	Q8HP67	18 kDa	unknown	0	4	0	0	0	2	0	1
43	TRUE	FALSE	tr G3XA10 Histone nuclear ribonucleoprotein L1, isoform CRA b Tax. Id=10090 [Mus musculus]	G3XA10	87 kDa	unknown	0	5	0	0	0	1	0	0
43.1	TRUE	FALSE	tr Q3TVV6 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3TVV6	88 kDa	unknown	0	5	0	0	0	1	0	0
43.2	TRUE	FALSE	tr Q3TWN5 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3TWN5	88 kDa	unknown	0	5	0	0	0	1	0	0
43.3	TRUE	FALSE	tr Q3TXW2 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3TXW2	88 kDa	unknown	0	5	0	0	0	1	0	0
43.4	TRUE	FALSE	tr Q3ULH5 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3ULH5	88 kDa	unknown	0	5	0	0	0	1	0	0
43.5	TRUE	FALSE	tr Q8C990 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q8C990	88 kDa	unknown	0	5	0	0	0	1	0	0
43.6	TRUE	FALSE	tr Q8VEK3 Heterogeneous nuclear ribonucleoprotein U1 Tax. Id=10090 [Mus musculus]	Q8VEK3	88 kDa	unknown	0	5	0	0	0	1	0	0
44	TRUE	FALSE	tr D3YY00 Uncharacterized protein Tax. Id=10090 [Mus musculus]	D3YY00	22 kDa	unknown	0	4	0	0	0	3	0	1
44.1	TRUE	FALSE	sp P51410 60S ribosomal protein L9 Tax. Id=10090 [Mus musculus]	P51410	22 kDa	unknown	0	4	0	0	0	3	0	1
44.2	TRUE	FALSE	tr Q5M9J5 Ribosomal protein L9 Tax. Id=10090 [Mus musculus]	Q5M9J5	22 kDa	unknown	0	4	0	0	0	3	0	1
45	TRUE	FALSE	tr Q6PHZ1 Rpl17 protein Tax. Id=10090 [Mus musculus]	Q6PHZ1	21 kDa	unknown	0	6	0	0	0	2	0	0
46	TRUE	FALSE	tr P35979 60S ribosomal protein L12 Tax. Id=10090 [Mus musculus]	P35979	18 kDa	unknown	0	3	0	0	0	1	0	0
46.1	TRUE	FALSE	tr Q3TQ2 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3TQ2	18 kDa	unknown	0	3	0	0	0	1	0	2
46.2	TRUE	FALSE	tr Q8C2K0 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q8C2K0	18 kDa	unknown	0	3	0	0	0	1	0	2
46.3	TRUE	FALSE	tr fXP_001003212.1 PREDICTED: 60S ribosomal protein L12-like Tax. Id=10090 [Mus musculus]	fXP_001003212.1	18 kDa	unknown	0	3	0	0	0	1	0	2
47	TRUE	FALSE	tr A2A547 Ribosomal protein L19 Tax. Id=10090 [Mus musculus]	A2A547	23 kDa	unknown	0	4	0	0	0	1	0	0
47.1	TRUE	FALSE	sp P89496 60S ribosomal protein L19 Tax. Id=10090 [Mus musculus]	P89496	23 kDa	unknown	0	4	0	0	0	1	0	0
48	TRUE	FALSE	tr E9PXE7 Uncharacterized protein Tax. Id=10090 [Mus musculus]	E9PXE7	19 kDa	unknown	0	5	0	0	0	0	0	0
48.1	TRUE	FALSE	sp P62281 40S ribosomal protein S11 Tax. Id=10090 [Mus musculus]	P62281	18 kDa	unknown	0	5	0	0	0	0	0	0
48.2	TRUE	FALSE	tr Q9DB79 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q9DB79	19 kDa	unknown	0	5	0	0	0	0	0	0
49	TRUE	FALSE	sp P62806 Histone H4 Tax. Id=10090 [Mus musculus]	P62806	11 kDa	unknown	0	3	0	0	0	3	0	2
50	TRUE	FALSE	tr A0A1V1 Histone H2A (Fragment) Tax. Id=10090 [Mus musculus]	A0A1V1	14 kDa	unknown	0	3	0	0	0	1	0	1
50.1	TRUE	FALSE	tr P8WJ41 Ribosomal protein S15A (Fragment) Tax. Id=10090 [Mus musculus]	P8WJ41	12 kDa	unknown	0	3	0	0	0	1	0	1
50.2	TRUE	FALSE	sp P27273 Histone H2A type 1 Tax. Id=10090 [Mus musculus]	P27273	14 kDa	unknown	0	3	0	0	0	1	0	1
50.3	TRUE	FALSE	tr Q64426 Histone H2A (Fragment) Tax. Id=10092 [Mus musculus domesticus]	Q64426	15 kDa	unknown	0	3	0	0	0	1	0	1
50.4	TRUE	FALSE	tr Q64523 Histone H2A type 2-C Tax. Id=10090 [Mus musculus]	Q64523	14 kDa	unknown	0	3	0	0	0	1	0	1
50.5	TRUE	FALSE	sp Q6G8S7 Histone H2A type 2-A Tax. Id=10090 [Mus musculus]	Q6G8S7	14 kDa	unknown	0	3	0	0	0	1	0	1
50.6	TRUE	FALSE	tr Q8HFI2 Histone H2A type 3 Tax. Id=10090 [Mus musculus]	Q8HFI2	14 kDa	unknown	0	3	0	0	0	1	0	1
50.7	TRUE	FALSE	tr Q8CGP4 Histone H2A Tax. Id=10090 [Mus musculus]	Q8CGP4	14 kDa	unknown	0	3	0	0	0	1	0	1
50.8	TRUE	FALSE	tr Q8CGP5 Histone H2A type 1-F Tax. Id=10090 [Mus musculus]	Q8CGP5	14 kDa	unknown	0	3	0	0	0	1	0	1
50.9	TRUE	FALSE	tr Q8CGP6 Histone H2A type 1-H Tax. Id=10090 [Mus musculus]	Q8CGP6	14 kDa	unknown	0	3	0	0	0	1	0	1
51	TRUE	FALSE	tr Q8CGP7 Histone H2A type 1-K Tax. Id=10090 [Mus musculus]	Q8CGP7	14 kDa	unknown	0	3	0	0	0	1	0	1
50.11	TRUE	FALSE	tr Q8R1M2 Histone H2A J Tax. Id=10090 [Mus musculus]	Q8R1M2	14 kDa	unknown	0	3	0	0	0	1	0	1
50.12	TRUE	FALSE	tr fXP_003086745.1 PREDICTED: substrate corticoin Tax. Id=10090 [Mus musculus]	fXP_003086745.1	32 kDa	unknown	0	6	0	0	0	1	0	1
51	TRUE	FALSE	tr P14131 40S ribosomal protein S16 Tax. Id=10090 [Mus musculus]	P14131	16 kDa	unknown	0	6	0	0	0	0	0	0
51.1	TRUE	FALSE	tr Q5CYZ9 Rpl6 protein Tax. Id=10090 [Mus musculus]	Q5CYZ9	19 kDa	unknown	0	6	0	0	0	1	0	0
51.2	TRUE	FALSE	tr Q641N3 Rpl6 protein (Fragment) Tax. Id=10090 [Mus musculus]	Q641N3	18 kDa	unknown	0	6	0	0	0	1	0	0
52	TRUE	FALSE	sp P62830 60S ribosomal protein L23 Tax. Id=10090 [Mus musculus]	P62830	15 kDa	unknown	0	4	0	0	0	1	0	1
53	TRUE	FALSE	sp P67984 60S ribosomal protein L22 Tax. Id=10090 [Mus musculus]	P67984	15 kDa	unknown	0	2	0	0	0	2	0	2
54	TRUE	FALSE	tr Q3TH2 28S rRNA regulatory light chain 12P Tax. Id=10090 [Mus musculus]	Q3TH2	23 kDa	unknown	0	0	0	0	0	0	0	0
55	TRUE	FALSE	tr D3Z4H3 Uncharacterized protein Tax. Id=10090 [Mus musculus]	D3Z4H3	13 kDa	unknown	0	0	0	0	0	3	0	1
55.1	TRUE	FALSE	sp Q9D1R9 60S ribosomal protein L34 Tax. Id=10090 [Mus musculus]	Q9D1R9	13 kDa	unknown	0	0	0	0	0	3	0	1
56	TRUE	FALSE	sp P27659 60S ribosomal protein L3 Tax. Id=10090 [Mus musculus]	P27659	46 kDa	unknown	0	5	0	0	0	0	0	0
56.1	TRUE	FALSE	tr Q3U9L3 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3U9L3	46 kDa	unknown	0	5	0	0	0	0	0	0
56.2	TRUE	FALSE	tr Q3UB15 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3UB15	46 kDa	unknown	0	5	0	0	0	0	0	0
56.3	TRUE	FALSE	tr Q3UB67 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3UB67	46 kDa	unknown	0	5	0	0	0	0	0	0
56.4	TRUE	FALSE	tr Q3UB90 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3UB90	46 kDa	unknown	0	5	0	0	0	0	0	0
56.5	TRUE	FALSE	tr fXP_982298.1 PREDICTED: 60S ribosomal protein L3-like Tax. Id=10090 [Mus musculus]	fXP_982298.1	44 kDa	unknown	0	5	0	0	0	0	0	0
57	TRUE	FALSE	sp P35980 60S ribosomal protein L18 Tax. Id=10090 [Mus musculus]	P35980	22 kDa	unknown	0	2	0	0	0	1	0	2
57.1	TRUE	FALSE	tr Q642K1 60S ribosomal protein L18 Tax. Id=10090 [Mus musculus]	Q642K1	22 kDa	unknown	0	2	0	0	0	1	0	2
58	TRUE	FALSE	tr Q66920 60S ribosomal protein L14 Tax. Id=10090 [Mus musculus]	Q66920	23 kDa	unknown	0	1	0	0	0	1	0	1
58.1	TRUE	FALSE	sp Q9C857 60S ribosomal protein L14 Tax. Id=10090 [Mus musculus]	Q9C857	23 kDa	unknown	0	1	0	0	0	1	0	1
58.2	TRUE	FALSE	tr Q9CWK0 Uncharacterized protein Tax. Id=10090 [Mus musculus]	Q9CWK0	26 kDa	unknown	0	1	0	0	0	1	0	1
59	TRUE	FALSE	tr D3YZN6 MC6449843 Tax. Id=10090 [Mus musculus]	D3YZN6	17 kDa	unknown	0	3	0	0	0	2	0	1
60	TRUE	FALSE	sp P62267 40S ribosomal protein S23 Tax. Id=10090 [Mus musculus]	P62267	16 kDa	unknown	0	4	0	0	0	0	0	0
60.1	TRUE	FALSE	tr Q497E1 Ribosomal protein S23 Tax. Id=10090 [Mus musculus]	Q497E1	16 kDa	unknown	0	4	0	0	0	0	0	0
60.2	TRUE	FALSE	tr Q9CWV9 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q9CWV9	16 kDa	unknown	0	4	0	0	0	0	0	0
60.3	TRUE	FALSE	tr Q9CZ15 Uncharacterized protein Tax. Id=10090 [Mus musculus]	Q9CZ15	16 kDa	unknown	0	4	0	0	0	0	0	0
61	TRUE	FALSE	tr D3Z1P6 Uncharacterized protein Tax. Id=10090 [Mus musculus]	D3Z1P6	16 kDa	unknown	0	2	0	0	0	2	0	1
61.1	TRUE	FALSE	tr Q70569 Ribosomal protein S14 Tax. Id=10090 [Mus musculus]	Q70569	16 kDa	unknown	0	2	0	0	0	2	0	1
61.2	TRUE	FALSE	sp P62264 40S ribosomal protein S14 Tax. Id=10090 [Mus musculus]	P62264	16 kDa	unknown	0	2	0	0	0	2	0	1
61.3	TRUE	FALSE	tr Q3U853 Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3U853	16 kDa	unknown	0	2	0	0	0	2	0	1
62	TRUE	FALSE	tr P51881 ADP-ATP translocase 2 Tax. Id=10090 [Mus musculus]	P51881	23 kDa	unknown	0	2	0	0	0	0	0	3
63	TRUE	FALSE	tr E9Q3V8 40S ribosomal protein S24 Tax. Id=10090 [Mus musculus]	E9Q3V8	19 kDa	unknown	0	2	0	0	0	0	0	2
63.1	TRUE	FALSE	sp P62849 40S ribosomal protein S24 Tax. Id=10090 [Mus musculus]	P62849	7	unknown	0	2	0	0	0	0	0	2
63.2	TRUE	FALSE	sp P62849-2 Rps24 isoform 2 of P62849 Tax. Id=10090 [Mus musculus]	P62849-2	15 kDa	unknown	0	2	0	0	0	0	0	2
63.3	TRUE	FALSE	sp P62849-3 Rps24 isoform 3 of P62849 Tax. Id=10090 [Mus musculus]	P62849-3	15 kDa	unknown	0	2	0	0	0	0	0	2
63.4	TRUE	FALSE	tr Q3TH2 28S rRNA regulatory light chain 12P Tax. Id=10090 [Mus musculus]	Q3TH2	23 kDa	unknown	0	0	0	0	0	2	0	3
63.5	TRUE	FALSE	tr Q9CQK2 40S ribosomal protein S24 Tax. Id=10090 [Mus musculus]	Q9CQK2	16 kDa	unknown	0	2	0	0	0	0	0	2
63.6	TRUE	FALSE	tr Q9CY61 40S ribosomal protein S24 Tax. Id=10090 [Mus musculus]	Q9CY61	15 kDa	unknown	0	2	0	0	0	0	0	2
63.7	TRUE	FALSE	tr Q9D7P1 40S ribosomal protein S24 Tax. Id=10090 [Mus musculus]	Q9										

78	TRUE	FALSE	trA1L333/DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 Tax. Id=10090 [Mus mus]	A1L333	69 kDa	unknown	0	2	0	0	0	0	0	0	0	0
78.1	TRUE	FALSE	trQ3V0Z8/Putative uncharacterized protein (Fragment) Tax. Id=10090 [Mus mus]	Q3V0Z8	77 kDa	unknown	0	2	0	0	0	0	0	0	0	0
78.2	TRUE	FALSE	trQ3U222/Dab5 protein (Fragment) Tax. Id=10090 [Mus musculus]	Q3U222	73 kDa	unknown	0	2	0	0	0	0	0	0	0	0
78.3	TRUE	FALSE	trpQ61656/Possible ATP-dependent RNA helicase (DDX5) Tax. Id=10090 [Mus mus]	Q61656	69 kDa	unknown	0	2	0	0	0	0	0	0	0	0
78.4	TRUE	FALSE	trQ8BT80/DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 Tax. Id=10090 [Mus mus]	Q8BT80	69 kDa	unknown	0	2	0	0	0	0	0	0	0	0
79	TRUE	FALSE	trB7ZBW3/Elongation factor 1-alpha Tax. Id=10090 [Mus musculus]	B7ZBW3	50 kDa	unknown	0	0	0	0	0	0	1	0	0	0
79.1	TRUE	FALSE	trp10126/Elongation factor 1-alpha 1 Tax. Id=10090 [Mus musculus]	P10126	50 kDa	unknown	0	0	0	0	0	0	1	0	0	0
79.2	TRUE	FALSE	trp62831/Elongation factor 1-alpha 2 Tax. Id=10090 [Mus musculus]	P62831	50 kDa	unknown	0	0	0	0	0	0	1	0	0	0
79.3	TRUE	FALSE	trQ3TIE3/Elongation factor 1-alpha Tax. Id=10090 [Mus musculus]	Q3TIE3	50 kDa	unknown	0	0	0	0	0	0	1	0	0	0
79.4	TRUE	FALSE	trQ3UA81/Elongation factor 1-alpha Tax. Id=10090 [Mus musculus]	Q3UA81	50 kDa	unknown	0	0	0	0	0	0	1	0	0	0
79.5	TRUE	FALSE	trQ3UZQ3/Elongation factor 1-alpha Tax. Id=10090 [Mus musculus]	Q3UZQ3	50 kDa	unknown	0	0	0	0	0	0	1	0	0	0
80	TRUE	FALSE	trD3YTQ9/Uncharacterized protein Tax. Id=10090 [Mus musculus]	D3YTQ9	14 kDa	unknown	0	1	0	0	0	0	0	0	0	0
80.1	TRUE	FALSE	trp62843/40S ribosomal protein S15 Tax. Id=10090 [Mus musculus]	P62843	17 kDa	unknown	0	1	0	0	0	0	0	0	0	0
80.2	TRUE	FALSE	trQ3UK70/Putative uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3UK70	17 kDa	unknown	0	1	0	0	0	0	0	0	0	0
80.3	TRUE	FALSE	trQ3UXS6/Uncharacterized protein Tax. Id=10090 [Mus musculus]	Q3UXS6	15 kDa	unknown	0	1	0	0	0	0	0	0	0	0
80.4	TRUE	FALSE	trXP_003086515.1/PREDICTED: 40S ribosomal protein S15-like Tax. Id=10090 [Mus musculus]	XP_003086515.1	17 kDa	unknown	0	1	0	0	0	0	0	0	0	0

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Figure 2. Analysis of the silvestrol and glycine elutions of pulldown assay using biotinylated episilvestrol (**9**) by mass spectrometry.

eLF4AI

Query	Start	End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
625	46	61	914.4726	1826.9306	1826.9315	-0.47	1	40	0.00018	1	U	R.GIYAYGFKEKPSAIQQR.A
626	46	61	914.4736	1826.9326	1826.9315	0.63	1	45	6.00E-05	1	U	R.GIYAYGFKEKPSAIQQR.A
627	46	61	609.9849	1826.9329	1826.9315	0.75	1	36	0.00056	1	U	R.GIYAYGFKEKPSAIQQR.A
628	46	61	609.985	1826.9332	1826.9315	0.91	1	34	0.0029	1	U	R.GIYAYGFKEKPSAIQQR.A
56	62	68	407.7463	813.478	813.4782	-0.22	0	4	0.39	1	U	R.AILPCIK.G
57	62	68	407.7466	813.4786	813.4782	0.52	0	3	0.5	1	U	R.AILPCIK.G
548	69	82	697.8491	1393.6836	1393.6838	-0.082	0	115	1.40E-10	1	U	K.GYDVIAQAQSGTGK.T
549	69	82	697.8494	1393.6842	1393.6838	0.35	0	92	7.70E-09	1	U	K.GYDVIAQAQSGTGK.T
361	100	110	570.8405	1139.6664	1139.6662	0.18	0	31	0.014	1	U	K.ATQALVLAPTR.E
362	100	110	570.8405	1139.6664	1139.6662	0.18	0	36	0.0044	1	U	K.ATQALVLAPTR.E
170	111	118	479.2716	956.5286	956.5291	-0.44	0	29	0.035	1	U	R.ELAQQIQK.V
171	111	118	479.2719	956.5292	956.5291	0.19	0	35	0.0092	1	U	R.ELAQQIQK.V
606	147	161	540.2956	1617.865	1617.8661	-0.69	0	45	0.0016	1	U	K.LQMEAPHIIVGTPGR.V
607	147	161	540.2959	1617.8659	1617.8661	-0.13	0	31	0.014	1	U	K.LQMEAPHIIVGTPGR.V
608	147	161	809.9404	1617.8662	1617.8661	0.098	0	41	0.00035	1	U	K.LQMEAPHIIVGTPGR.V
609	147	161	809.9405	1617.8664	1617.8661	0.22	0	61	4.00E-06	1	U	K.LQMEAPHIIVGTPGR.V
110	162	168	447.7287	893.4428	893.4429	-0.077	0	25	0.015	1	U	R.VFDMLNR.R
111	162	168	447.7288	893.443	893.4429	0.15	0	26	0.018	1	U	R.VFDMLNR.R
260	162	169	525.7791	1049.5436	1049.544	-0.36	1	11	0.53	1	U	R.VFDMLNRR.Y
584	178	190	778.3596	1554.7046	1554.7058	-0.74	0	61	6.00E-06	1	U	K.MFVLDEADEMLSR.G
585	178	190	778.3598	1554.705	1554.7058	-0.48	0	69	2.40E-06	1	U	K.MFVLDEADEMLSR.G
579	191	202	751.3873	1500.76	1500.7613	-0.82	1	64	2.60E-06	1	U	R.GFKDQIYDIFQK.L
580	191	202	751.3879	1500.7612	1500.7613	-0.019	1	59	1.70E-05	1	U	R.GFKDQIYDIFQK.L
386	194	202	585.2953	1168.576	1168.5764	-0.33	0	27	0.011	1	U	K.DQIYAFQK.L
387	194	202	585.2955	1168.5764	1168.5764	0.015	0	35	0.0078	1	U	K.DQIYAFQK.L
145	227	233	467.7496	933.4846	933.4854	-0.85	1	11	3.5	6	U	K.FMRDPIR.I
146	227	233	467.75	933.4854	933.4854	0.0054	1	9	5.7	5	U	K.FMRDPIR.I
400	238	247	594.3345	1186.6544	1186.6557	-1.07	1	29	0.061	1	U	K.KEELTLEGIR.Q
401	238	247	396.559	1186.6552	1186.6557	-0.46	1	22	0.27	2	U	K.KEELTLEGIR.Q
402	238	247	594.335	1186.6554	1186.6557	-0.23	1	43	0.0023	1	U	K.KEELTLEGIR.Q

403	238	247	396.5593	1186.6561	1186.6557	0.3	1	22	0.3	3	U	K.KEELTLEGIR.Q
267	239	247	530.2869	1058.5592	1058.5608	-1.43	0	32	0.0085	1	U	K.KEELTLEGIR.Q
268	239	247	530.288	1058.5614	1058.5608	0.65	0	35	0.0059	1	U	K.KEELTLEGIR.Q
280	248	255	534.7767	1067.5388	1067.54	-1.06	0	12	0.26	1	U	R.QFYINVER.E
225	284	291	509.7816	1017.5486	1017.5495	-0.82	1	22	0.089	1	U	R.KVDWLTEK.M
226	284	291	509.7821	1017.5496	1017.5495	0.16	1	19	0.093	1	U	R.KVDWLTEK.M
108	285	291	445.7346	889.4546	889.4545	0.13	0	9	0.22	1	U	K.VDWLTEK.M
109	285	291	445.7347	889.4548	889.4545	0.36	0	18	0.18	1	U	K.VDWLTEK.M
589	296	309	791.3364	1580.6582	1580.6599	-1.07	0	55	7.20E-06	1	U	R.DFTVSAMHGMDQK.E
590	296	309	527.8936	1580.659	1580.6599	-0.61	0	3	0.62	1	U	R.DFTVSAMHGMDQK.E
591	296	309	527.8939	1580.6599	1580.6599	-0.045	0	9	0.15	1	U	R.DFTVSAMHGMDQK.E
592	296	309	791.3373	1580.66	1580.6599	0.066	0	56	5.00E-06	1	U	R.DFTVSAMHGMDQK.E
326	325	334	557.8445	1113.6744	1113.6758	-1.17	0	65	6.00E-06	1	U	R.VLITDILLAR.G
327	325	334	557.8448	1113.675	1113.6758	-0.63	0	39	0.00044	1	U	R.VLITDILLAR.G
69	354	359	416.2089	830.4032	830.4035	-0.27	0	27	0.044	1	U	R.ENYIHR.I
70	354	359	416.209	830.4034	830.4035	-0.03	0	26	0.045	1	U	R.ENYIHR.I
597	369	382	530.6152	1588.8238	1588.8243	-0.31	2	57	4.00E-05	1	U	R.KGVAINMVTEEDKR.T
598	369	382	530.6153	1588.8241	1588.8243	-0.12	2	48	0.00018	1	U	R.KGVAINMVTEEDKR.T
599	369	382	795.4195	1588.8244	1588.8243	0.12	2	50	2.60E-05	1	U	R.KGVAINMVTEEDKR.T
566	370	382	731.3718	1460.729	1460.7293	-0.18	1	44	7.90E-05	1	U	K.GVAINMVTEEDKR.T
567	370	382	731.3722	1460.7298	1460.7293	0.37	1	33	0.0021	1	U	K.GVAINMVTEEDKR.T

elF4A II

Query	Start	End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
625	47	62	914.4726	1826.9306	1826.9315	-0.47	1	40	0.00018	1	U	R.GIYAYGFEKPSAIQQR.A
626	47	62	914.4736	1826.9326	1826.9315	0.63	1	45	6.00E-05	1	U	R.GIYAYGFEKPSAIQQR.A
627	47	62	609.9849	1826.9329	1826.9315	0.75	1	36	0.00056	1	U	R.GIYAYGFEKPSAIQQR.A
628	47	62	609.985	1826.9332	1826.9315	0.91	1	34	0.0029	1	U	R.GIYAYGFEKPSAIQQR.A
56	63	69	407.7463	813.478	813.4782	-0.22	0	4	0.39	1	U	R.AIIPCIG
57	63	69	407.7466	813.4786	813.4782	0.52	0	3	0.5	1	U	R.AIIPCIG
548	70	83	697.8491	1393.6836	1393.6838	-0.082	0	115	1.40E-10	1	U	K.GYDVIAQAQSGTGK.T
549	70	83	697.8494	1393.6842	1393.6838	0.35	0	92	7.70E-09	1	U	K.GYDVIAQAQSGTGK.T
170	112	119	479.2716	956.5286	956.5291	-0.44	0	29	0.035	1	U	R.ELAQQIQK.V
171	112	119	479.2719	956.5292	956.5291	0.19	0	35	0.0092	1	U	R.ELAQQIQK.V
110	163	169	447.7287	893.4428	893.4429	-0.077	0	25	0.015	1	U	R.VFDMLNRR
111	163	169	447.7288	893.443	893.4429	0.15	0	26	0.018	1	U	R.VFDMLNRR
260	163	170	525.7791	1049.5436	1049.544	-0.36	1	11	0.53	1	U	R.VFDMLNRR.Y
584	179	191	778.3596	1554.7046	1554.7058	-0.74	0	61	6.00E-06	1	U	K.MFVLDEADEMLSR.G
585	179	191	778.3598	1554.705	1554.7058	-0.48	0	69	2.40E-06	1	U	K.MFVLDEADEMLSR.G
280	249	256	534.7767	1067.5388	1067.54	-1.06	0	12	0.26	1	U	R.QFYINVER.E
225	285	292	509.7816	1017.5486	1017.5495	-0.82	1	22	0.089	1	U	R.KVDWLTEK.M
226	285	292	509.7821	1017.5496	1017.5495	0.16	1	19	0.093	1	U	R.KVDWLTEK.M

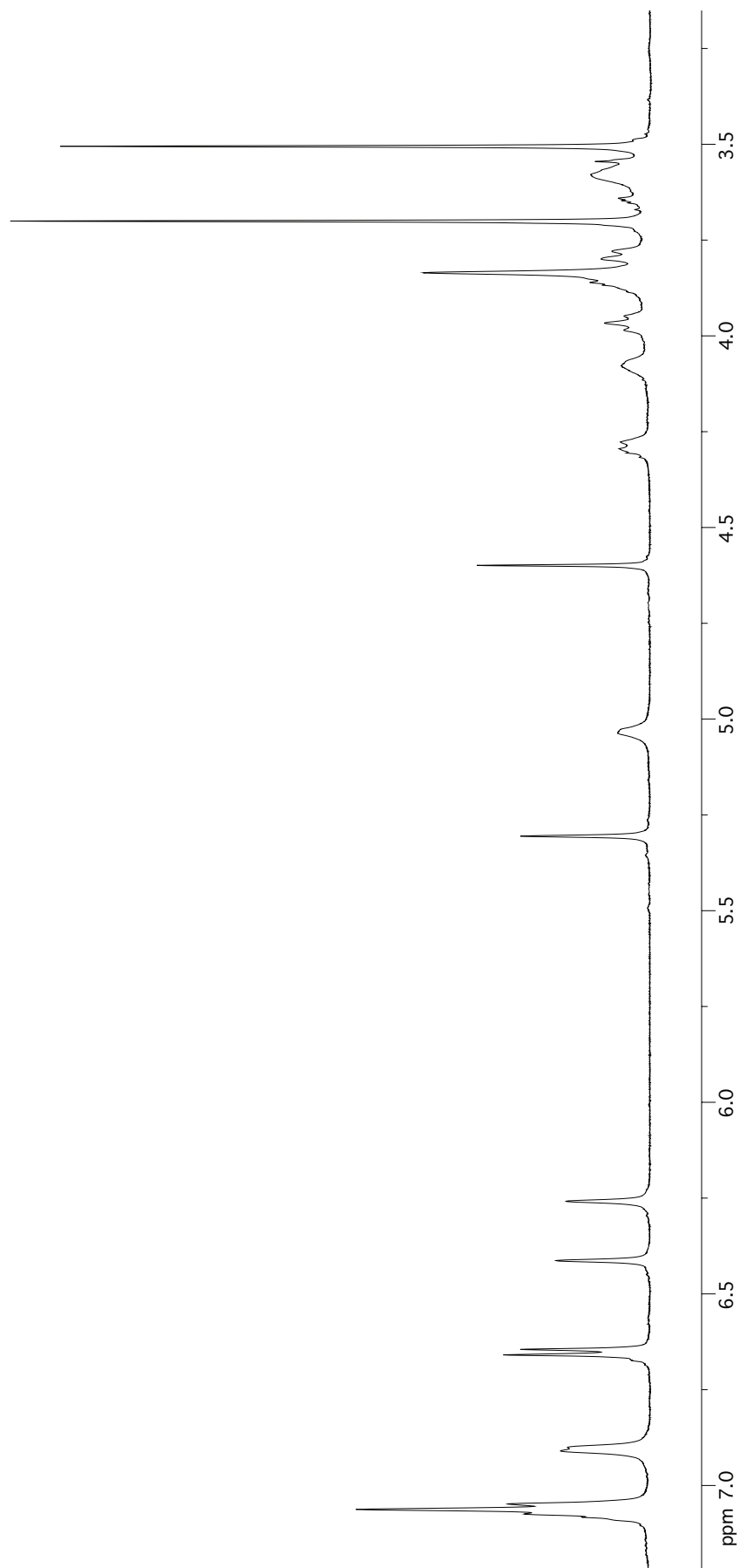
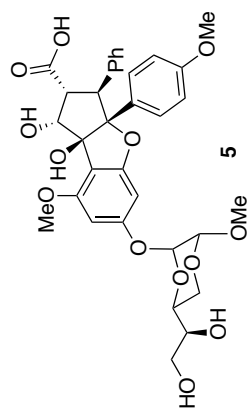
108	286	292	445.7346	889.4546	889.4545	0.13	0	9	0.22	1	U	K.VDWLTEK.M
109	286	292	445.7347	889.4548	889.4545	0.36	0	18	0.18	1	U	K.VDWLTEK.M
326	326	335	557.8445	1113.6744	1113.6758	-1.17	0	65	6.00E-06	1	U	R.VLITDILLAR.G
327	326	335	557.8448	1113.675	1113.6758	-0.63	0	39	0.00044	1	U	R.VLITDILLAR.G
69	355	360	416.2089	830.4032	830.4035	-0.27	0	27	0.044	1	U	R.ENYIHR.I
70	355	360	416.209	830.4034	830.4035	-0.03	0	26	0.045	1	U	R.ENYIHR.I

Figure 3. eIF4A isoform comparison by mass spectrometry. Peptides in *italics* are eIF4AI specific.

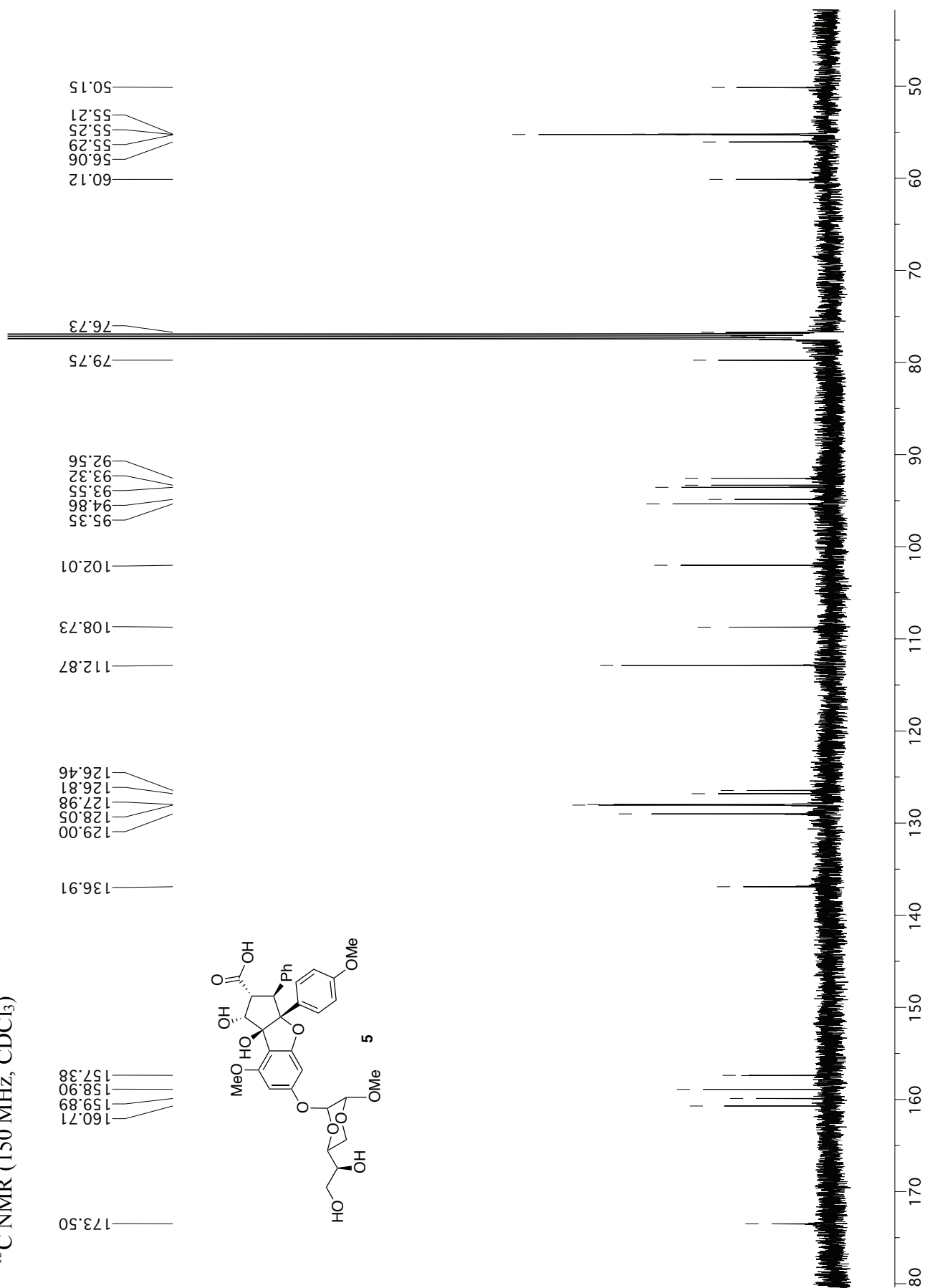
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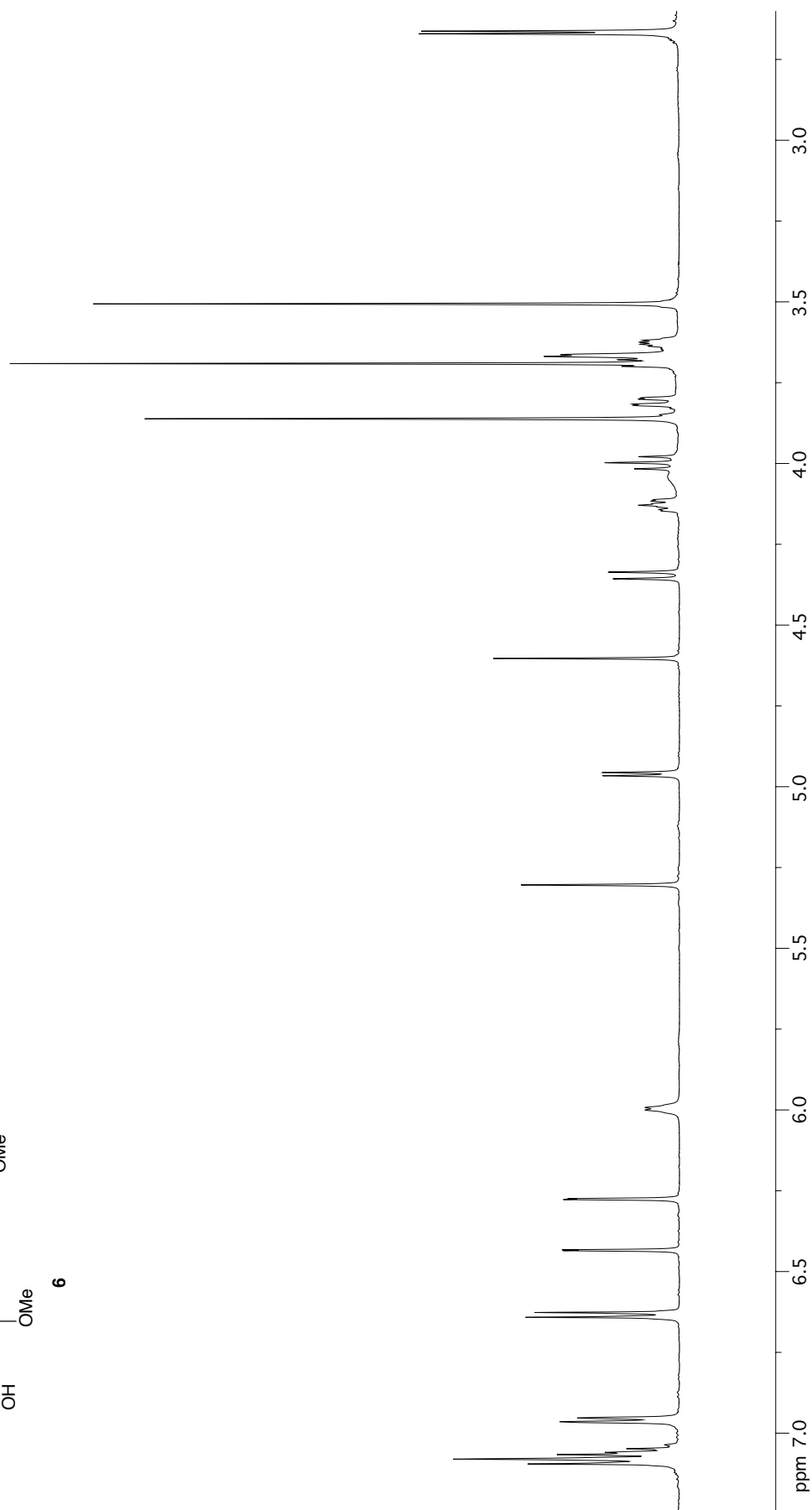
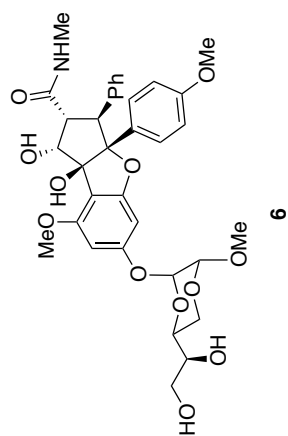
¹H NMR (600 MHz, CDCl₃)



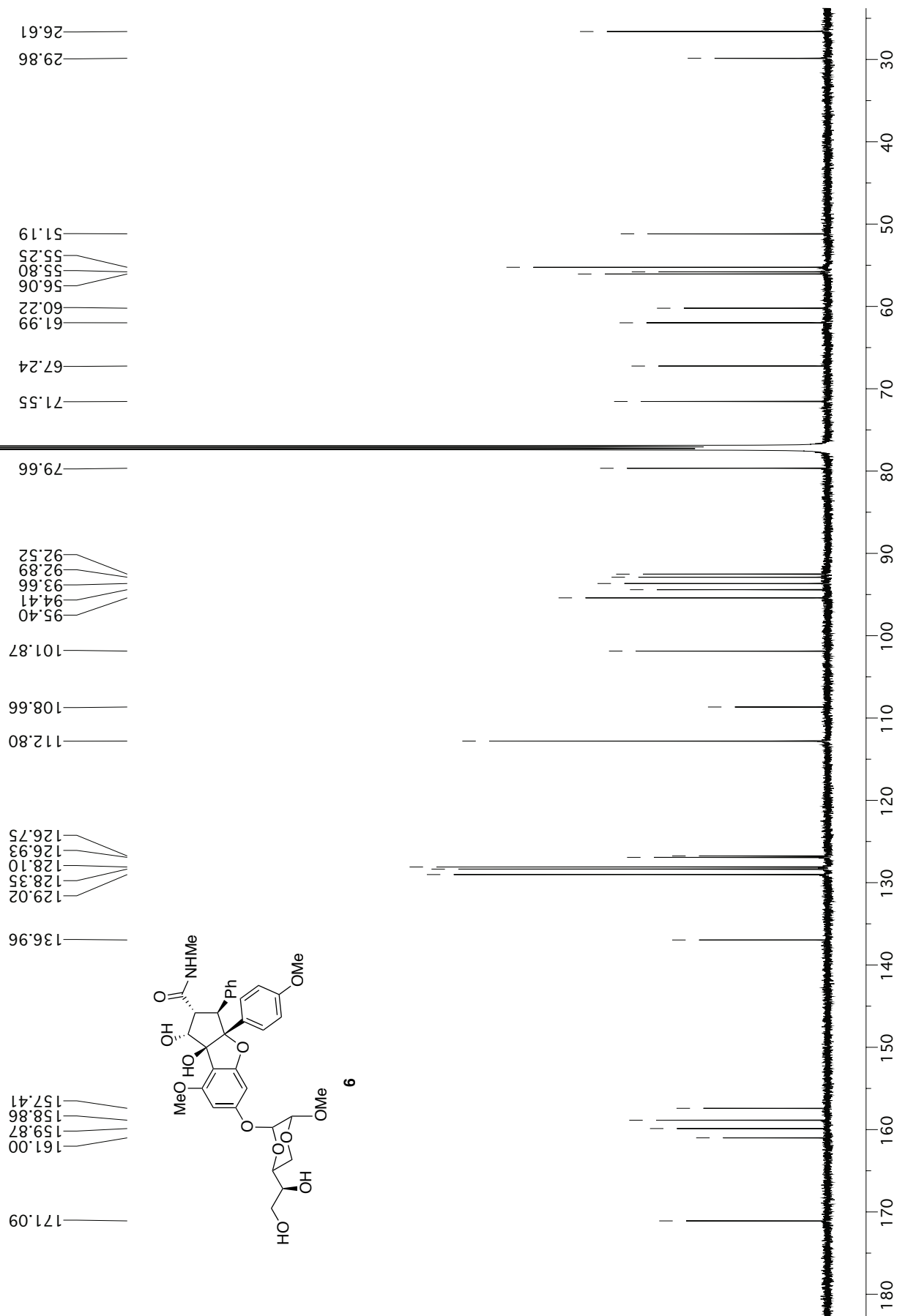
^{13}C NMR (150 MHz, CDCl_3)



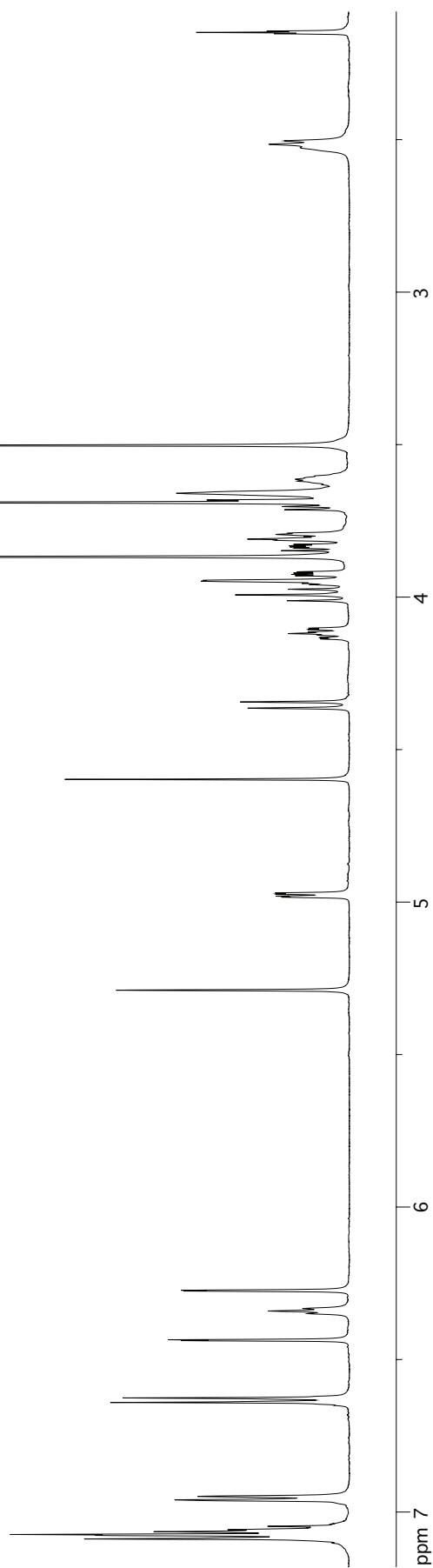
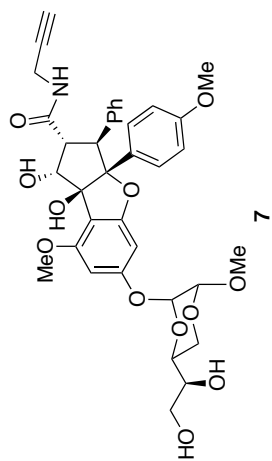
¹H NMR (600 MHz, CDCl₃)



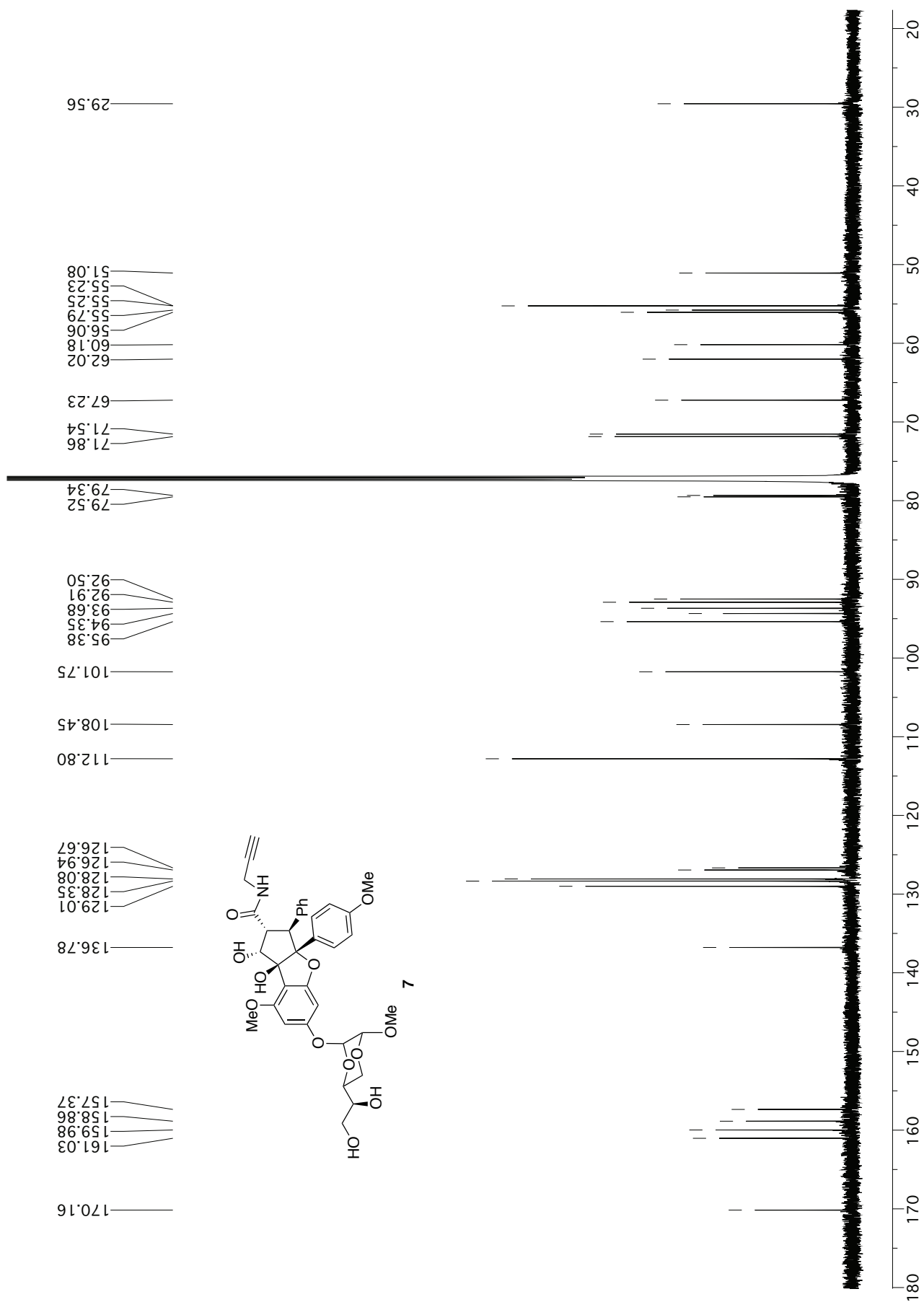
^{13}C NMR (150 MHz, CDCl_3)



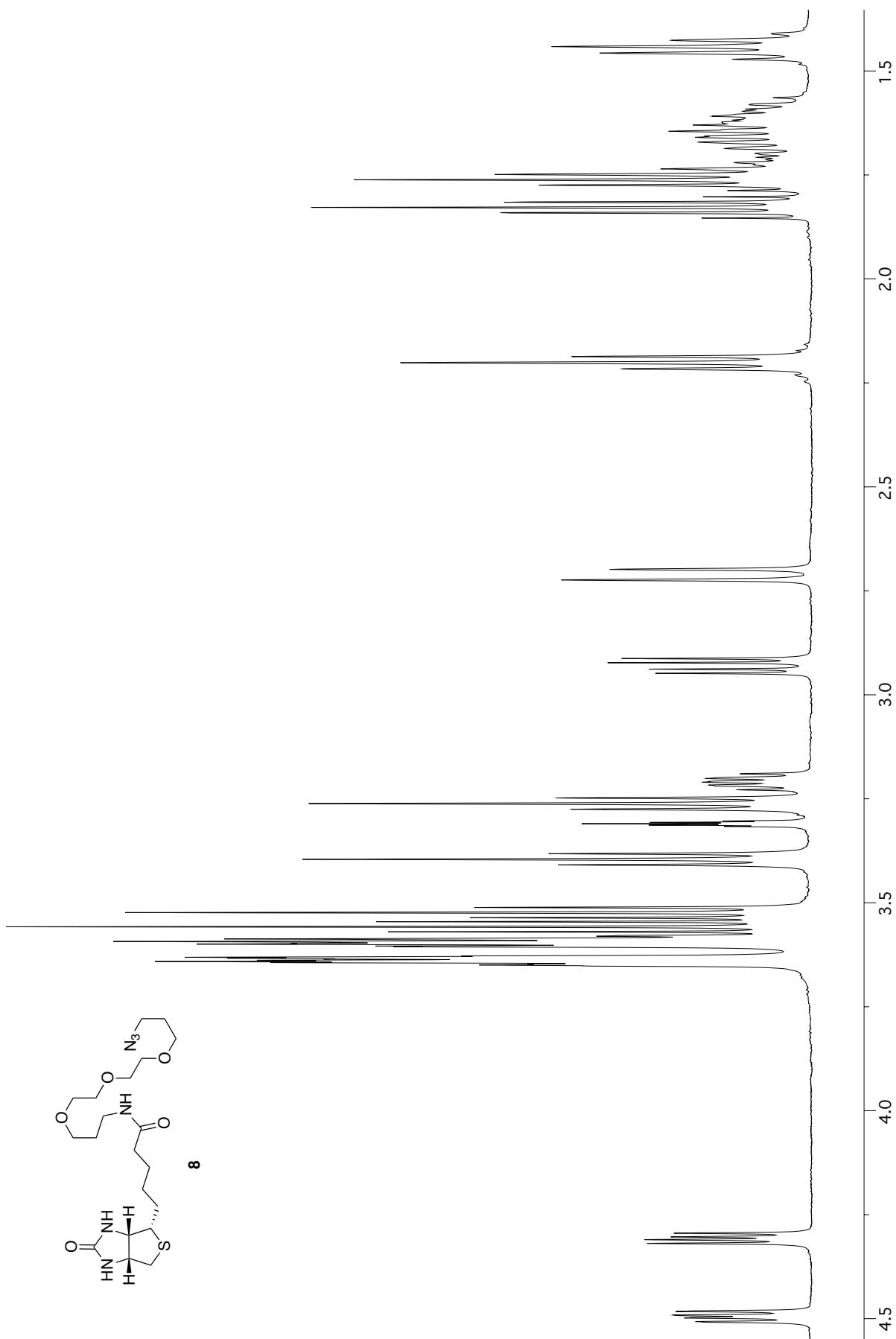
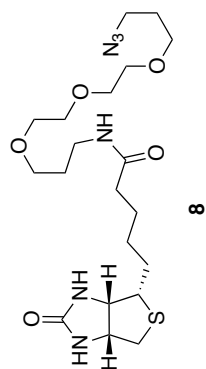
¹H NMR (600 MHz, CDCl₃)



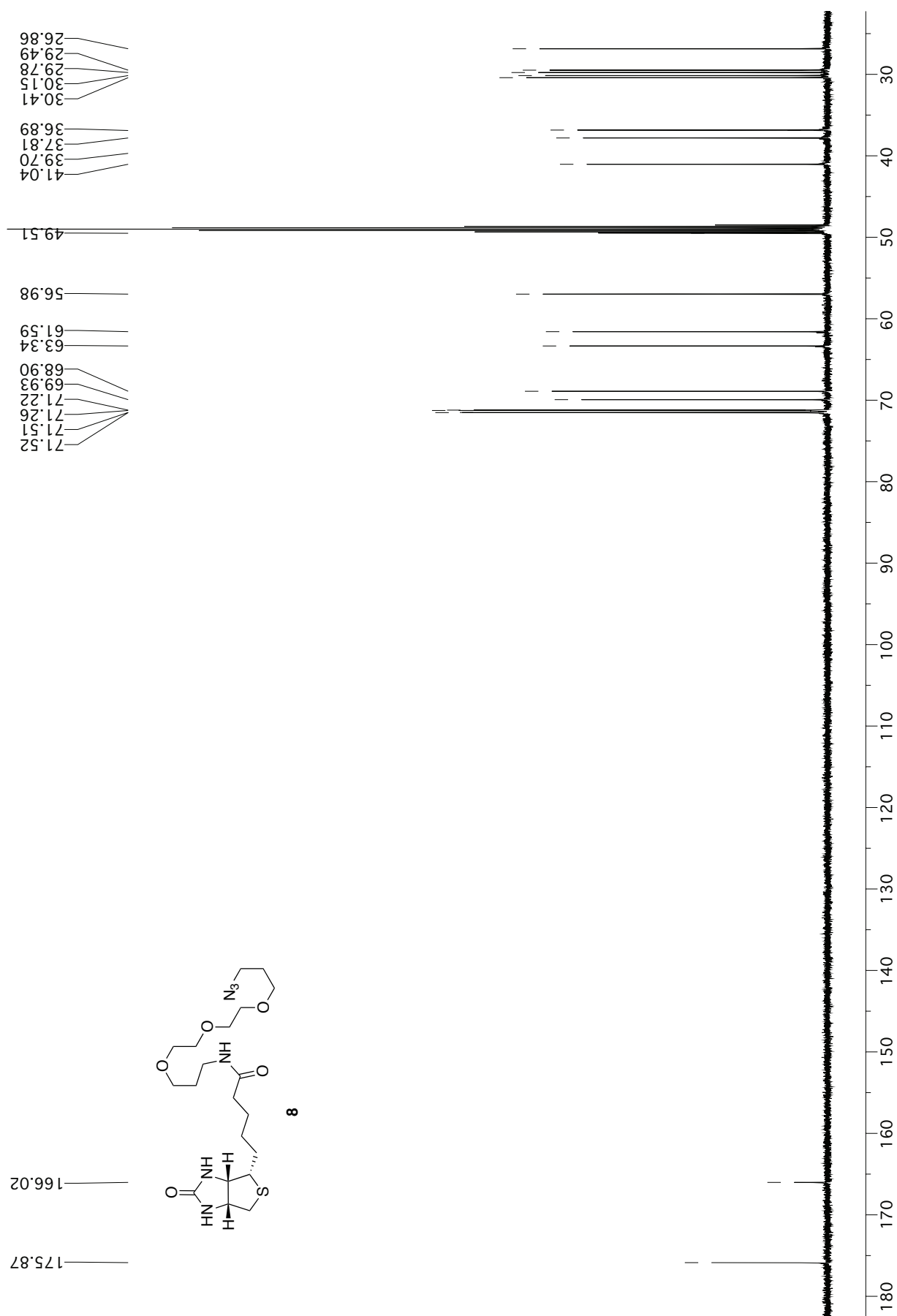
^{13}C NMR (150 MHz, CDCl_3)



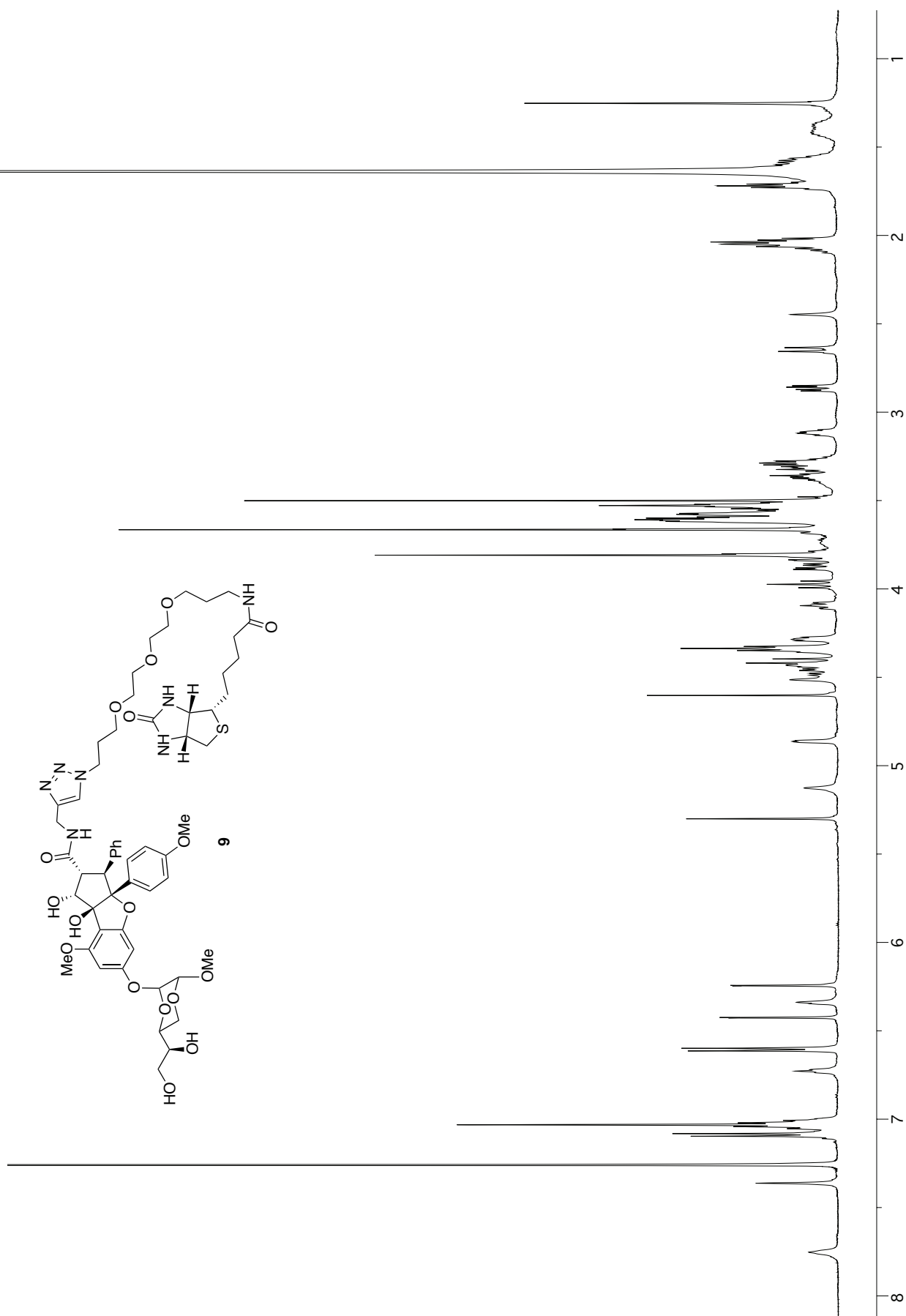
^1H NMR (500 MHz, CDCl_3)



^{13}C NMR (125 MHz, CDCl_3)



^1H NMR (600 MHz, CDCl_3)



¹³C NMR (150 MHz, CDCl₃)

