



Supporting Information

Developing Isoxazole as a Native Photo-Cross-Linker for Photoaffinity Labeling and Chemoproteomics

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1. General Information

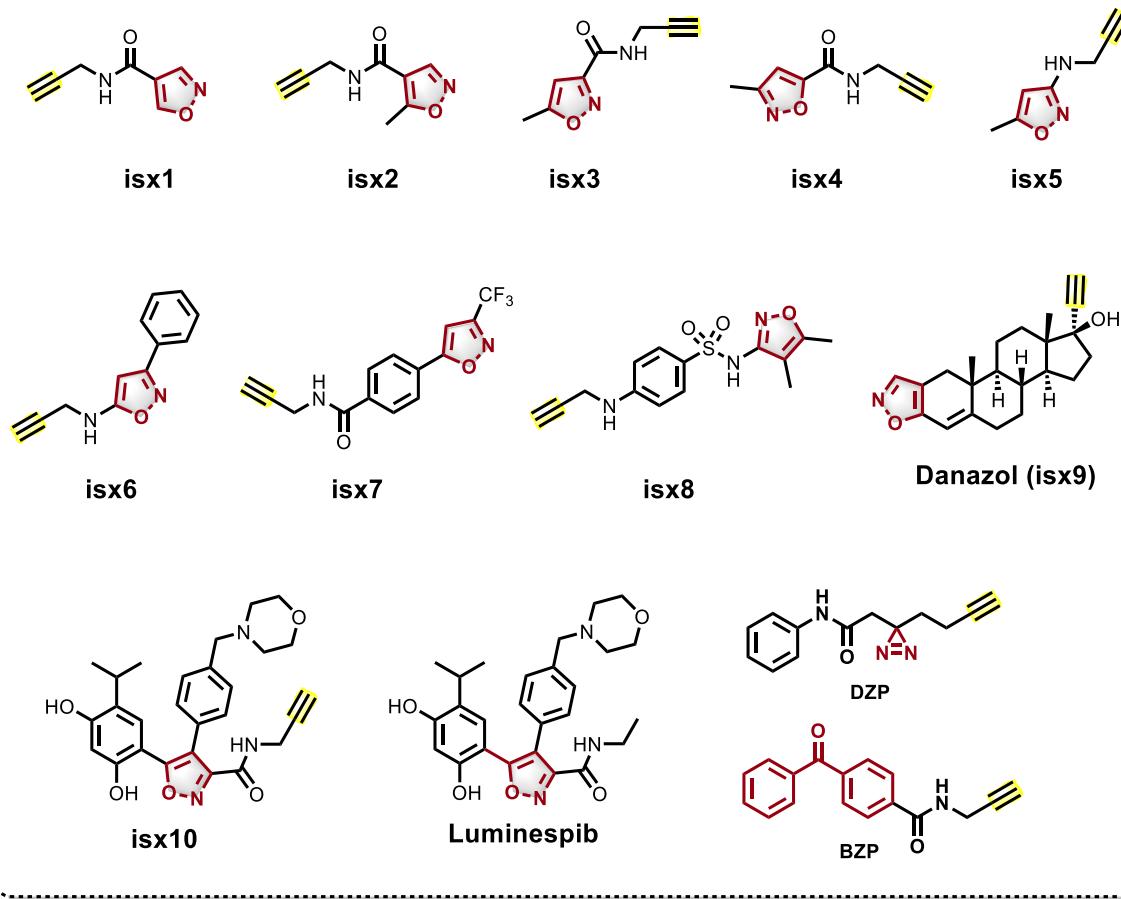
All chemicals were purchased from commercial vendors and used without further purification, unless indicated otherwise. Reaction progress was monitored by TLC on pre-coated silica plates (Merck TLC Silica gel 60 F₂₅₄), and spots were visualized by UV, iodine, or other suitable stains. All NMR spectra were recorded on Bruker spectrometers. Mass spectra were tested with the SCIEX LC-MS system (API-3200). HPLC analysis was performed on the 1525 Waters HPLC system equipped with a 2489 UV/Visible detector. Water with 0.1% TFA and acetonitrile with 0.1% TFA were used as eluents, and the flow rate was set at 1 mL/min. Chemical shifts were reported in parts per million (ppm) referenced with respect to appropriate internal standards or residual solvent peaks ($\text{CDCl}_3 = 7.26 \text{ ppm}$, $\text{DMSO}-d_6 = 2.50 \text{ ppm}$). The following abbreviations were used in reporting spectra, br s (broad singlet), s (singlet), d (doublet), t (triplet), q (quartet), m (multiplets), dd (doublet of doublets). Density functional theory (DFT) calculations were conducted with Gaussian 09. The geometry optimizations were performed in acetonitrile, using the B3LYP functional and combined with 6-311G+(d, p) basis set. The frequency and IRC (intrinsic reaction coordinate) calculations were performed at the same level.

2. Cell Culture and Western Blot

Cells were obtained from the National Cancer Institute Developmental Therapeutics Program (NCI-60). HeLa, HCT116, A549, and HEK 293T cells were cultured in DMEM or RPMI 1640 medium (Gibco) containing 10% heat-inactivated fetal bovine serum (FBS, Gibco), 100 units/mL penicillin (Gibco), 100 $\mu\text{g}/\text{mL}$ streptomycin (Gibco) and maintained in a humidified 37°C incubator under 5% CO₂. For western blotting (WB), protein samples were separated by SDS-PAGE and transferred to PVDF membranes. Membranes were blocked with 5% bovine serum albumin (BSA) in TBST (0.1% Tween 20 in tris-buffered saline) or 5% milk in TBST at r.t. for 1 h. After blocking, membranes were incubated with the corresponding primary antibodies at r.t. for 1 h or 4°C overnight. Then, membranes were washed with TBST (3 \times 15 min) and incubated with appropriate secondary antibodies at r.t. for 1 h. Finally, membranes were washed with TBST and developed by the ChemiDoc imaging systems (Bio-Rad).

3. Chemical Synthesis

Photoaffinity Probes:



Reporters:

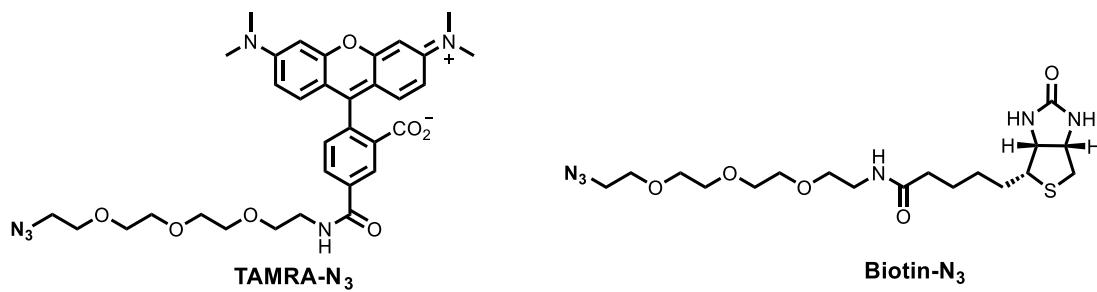
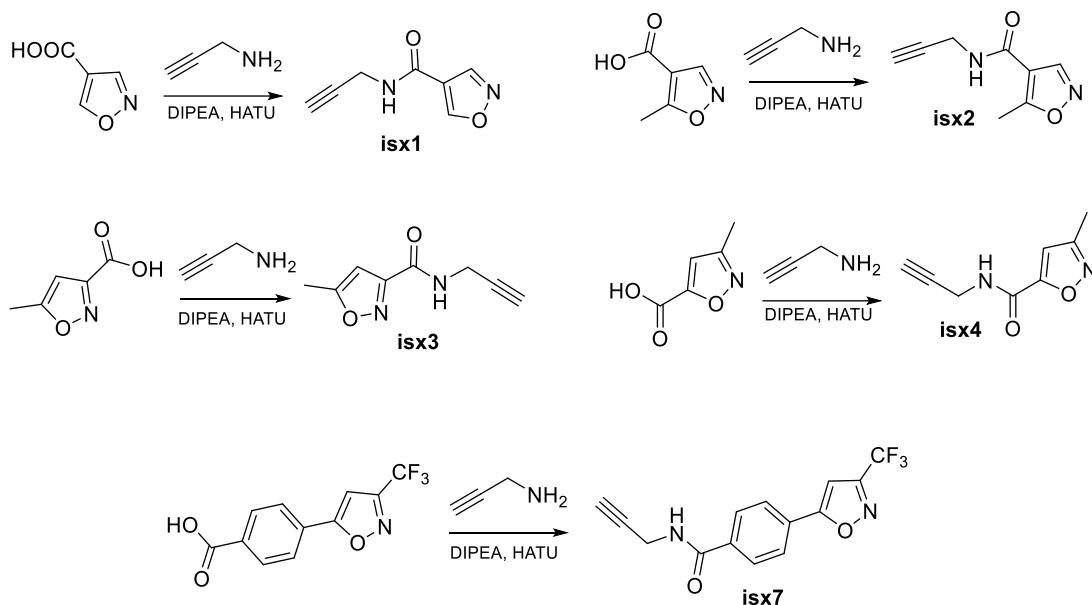


Figure S1. Photoaffinity probes and reporters used in this study.

Danazol and reporters were obtained from the commercial vendors. **DZP** and **BZP** were synthesized based on previous procedures^[1]. Other probes were synthesized via the following schemes (**Scheme S1~S4**).

3.1 Synthetic Scheme S1



Scheme S1. Synthesis of **isx1~4** and **isx7**.

N-(prop-2-yn-1-yl) isoxazole-4-carboxamide (isx1). HATU (6.7 g, 17.7 mmol) and DIPEA (2.28 g, 17.7 mmol) were added to a solution of isoxazole-4-carboxylic acid (1.0 g, 8.85 mmol) in 10 mL of DCM. The reaction mixture was stirred for 30 min before propargyl amine (1.05 g, 8.85 mmol) was added, and the mixture was further stirred at r.t. overnight. The next day, the solvent was removed, and the residue was purified with column chromatography to offer **isx1** as a white solid (1.2 g, 90.5%). ¹H NMR (400 MHz, CDCl₃) δ 8.96 (s, 1H), 8.62 (s, 1H), 6.71 (s, 1H), 4.20 (s, 2H), 2.28 (s, 1H). ¹³C NMR (101 MHz, CDCl₃) δ 159.61, 159.21, 147.79, 117.30, 78.79, 72.30, 29.44. HRMS m/z [M+H]⁺ calcd 151.0508; Found 151.0544.

The synthesis of **isx2**, **isx3**, **isx4**, and **isx7** was followed the synthesis of **isx1**.

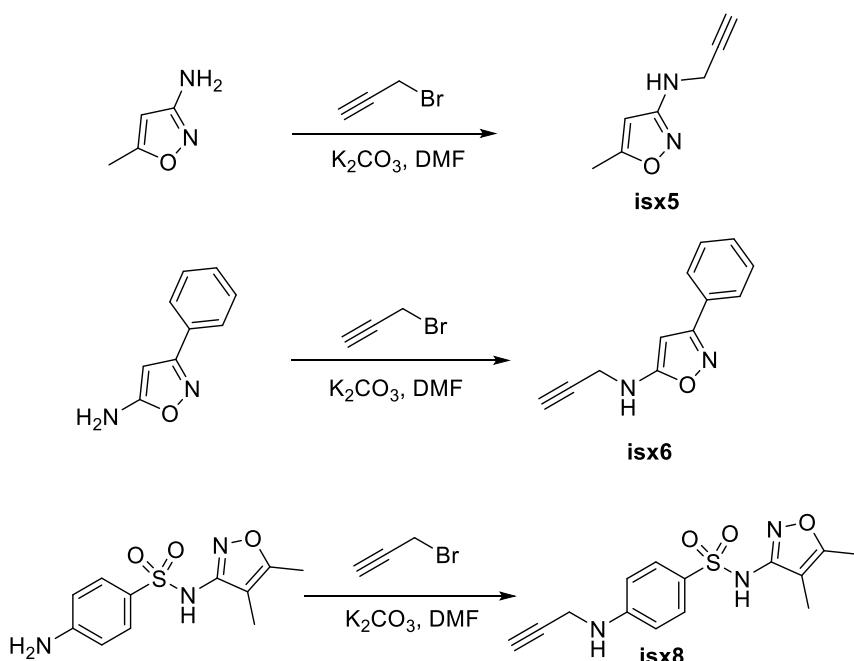
5-methyl-N-(prop-2-yn-1-yl)isoxazole-4-carboxamide (isx2) was obtained as a white power. ¹H NMR (400 MHz, CDCl₃) δ 8.41 (s, 1H), 6.23 (s, 1H), 4.18 (dd, *J* = 5.1, 2.3 Hz, 2H), 2.71 (s, 3H), 2.27 (s, 1H). ¹³C NMR (101 MHz, CDCl₃) δ 173.05, 160.79, 147.84, 111.17, 79.03, 72.09, 29.26, 12.53. HRMS m/z [M+H]⁺ calcd 165.0664; Found 165.0653.

5-methyl-N-(prop-2-yn-1-yl)isoxazole-3-carboxamide (isx3) was obtained as a white power. ¹H NMR (400 MHz, CDCl₃) δ 7.09 (s, 1H), 6.43 (s, 1H), 4.21 (d, *J* = 2.4 Hz, 2H), 2.46 (s, 3H), 2.26 (s, 1H). ¹³C NMR (101 MHz, CDCl₃) δ 171.38, 158.82, 158.26, 101.44, 78.68, 72.06, 29.10, 12.35. HRMS m/z [M+H]⁺ calcd 165.0664; Found 165.0662.

3-methyl-N-(prop-2-yn-1-yl)isoxazole-5-carboxamide (sx4) was obtained as a white powder. ^1H NMR (400 MHz, CDCl_3) δ 6.87 (s, 1H), 6.79 (s, 1H), 4.25 (d, $J = 2.2$ Hz, 2H), 2.37 (s, 3H), 2.32 (s, 1H). ^{13}C NMR (101 MHz, CDCl_3) δ 162.48, 160.94, 155.64, 108.10, 78.33, 72.43, 29.20, 11.45. HRMS m/z [M+H] $^+$ calcd 165.0664; Found 165.0676.

N-(prop-2-yn-1-yl)-4-(3-(trifluoromethyl)isoxazol-5-yl)benzamide (sx7) was obtained as a yellow solid. ^1H NMR (400 MHz, CDCl_3) δ 7.93 (d, $J = 8.3$ Hz, 2H), 7.88 (d, $J = 8.2$ Hz, 2H), 6.84 (s, 1H), 6.47 (s, 1H), 4.28 (dd, $J = 4.7, 2.3$ Hz, 2H), 2.31 (s, 1H). ^{13}C NMR (101 MHz, CDCl_3) δ 171.13, 165.86, 156.38, 135.99, 128.87, 128.07, 126.29, 120.90, 98.07, 79.08, 72.29, 30.01. HRMS m/z [M+H] $^+$ calcd 295.0694; Found 295.0699.

3.2 Synthetic Scheme S2



Scheme S2. Synthesis of **sx5**, **sx6**, and **sx8**.

5-methyl-N-(prop-2-yn-1-yl) isoxazol-3-amine (sx5). Propargyl bromide (236 mg, 2 mmol) was slowly added to a solution of 5-methylisoxazol-3-amine (200 mg, 2 mmol) and potassium carbonate (690 mg, 5 mmol) in 5 mL of DMF. The reaction mixture was subsequently stirred at 50°C. After TLC indicated no starting materials were left, 20 mL of water was added to quench the reaction, followed by extraction with ethyl acetate (15 mL \times 3). The organic phase was combined and dried over anhydrous sodium sulfate and concentrated in vacuo. The residue was then purified with column chromatography to offer the desired compound **sx5** as a yellow oil (136 mg, 51.7%). ^1H NMR (400 MHz, CDCl_3) δ 5.55 (d, $J = 0.7$ Hz, 1H), 3.96 (d, $J = 2.4$ Hz, 2H), 2.30 – 2.27 (m, 3H), 2.26 – 2.23 (m, 1H). ^{13}C NMR (101 MHz, CDCl_3) δ 169.20,

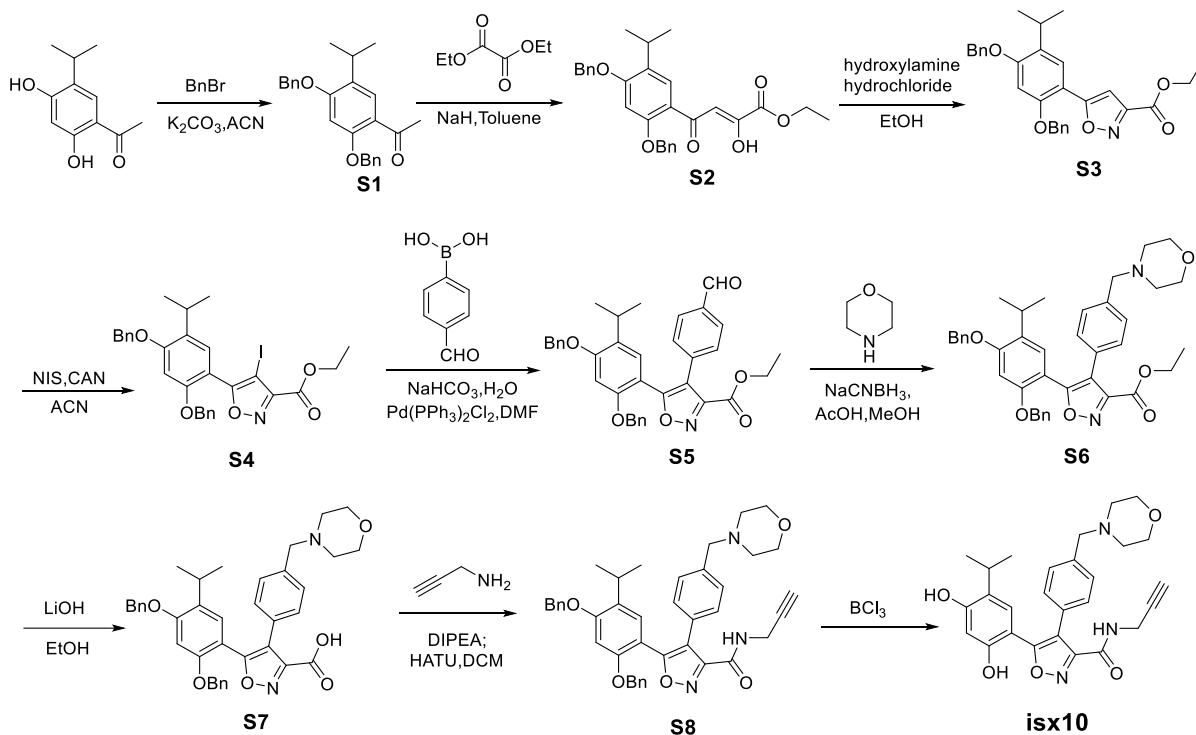
164.04, 93.28, 80.46, 71.65, 33.55, 12.53. HRMS m/z [M+H]⁺ calcd 137.0715; Found 137.0710.

Synthesis of **isx6** and **isx8** was followed the synthetic procedures of **isx5**.

3-phenyl-N-(prop-2-yn-1-yl)isoxazol-5-amine (isx6) was obtained as a colourless oil. ¹H NMR (300 MHz, DMSO) δ 7.82 – 7.65 (m, 3H), 7.50 – 7.41 (m, 3H), 5.66 (s, 1H), 3.97 (dd, J = 6.0, 2.3 Hz, 2H), 3.23 (t, J = 2.3 Hz, 1H). ¹³C NMR (75 MHz, CDCl₃) δ 169.44, 163.65, 129.84, 129.64, 128.75, 126.69, 78.94, 72.50, 34.10. HRMS m/z [M+H]⁺ calcd 199.0871; Found 199.0873.

N-(4,5-dimethylisoxazol-3-yl)-4-(prop-2-yn-1-ylamino)benzenesulfonamide (isx8) was obtained as a yellow solid. ¹H NMR (400 MHz, CDCl₃) δ 7.52 (d, J = 7.4 Hz, 2H), 6.66 (d, J = 7.0 Hz, 2H), 4.23 (d, J = 1.7 Hz, 2H), 3.55 (s, 2H), 2.24 (s, 3H), 2.19 (s, 1H), 1.98 (s, 3H). ¹³C NMR (101 MHz, CDCl₃) δ 161.99, 157.44, 151.48, 130.17, 125.44, 114.16, 111.85, 76.66, 74.03, 39.66, 11.08, 7.01. HRMS m/z [M+H]⁺ calcd 306.0912; Found 306.0917.

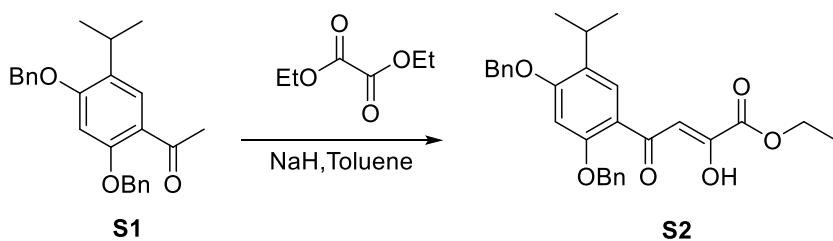
3.3 Synthetic Scheme S3



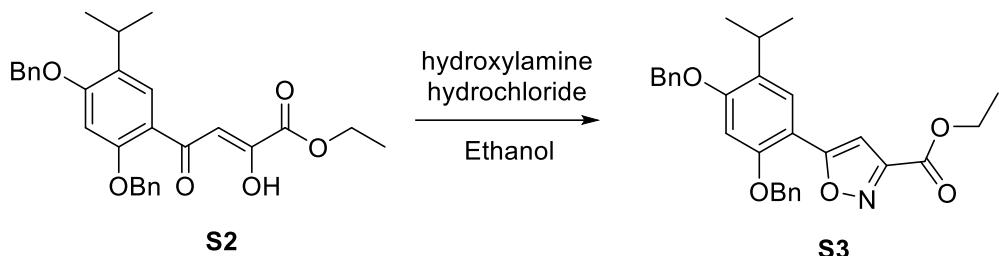
Scheme S3. Synthesis of **isx10**.

Synthesis of **isx10** and Luminespib was based on the previous schemes^[2].

1-(2,4-bis(benzyloxy)-5-isopropylphenyl)ethan-1-one (S1). Potassium carbonate (7.11 g, 51.55 mmol) was added to a solution of 1-(2,4-dihydroxy-5-isopropylphenyl)ethan-1-one (5.00 g, 25.77 mmol) in 80 mL of acetonitrile. The mixture was stirred at r.t. for 5 min. Subsequently, benzyl bromide (9.70 g, 56.69 mmol) was added dropwise over 10 min. Then the mixture was heated at reflux overnight. Then the mixture was cooled and concentrated in vacuo to obtain a slurry, which was partitioned between water (50 mL) and EA (50 mL), and the phases were separated. The organic extracts were dried over anhydrous Na₂SO₄ and evaporated in vacuo. The residue was purified with column chromatography (PE : EA = 5:1) to offer the title compound (1.56 g, 81%) as a white powder. ¹H NMR (400 MHz, CDCl₃) δ 7.78 (s, 1H), 7.47 – 7.33 (m, 10H), 6.52 (s, 1H), 5.10 (d, *J* = 4.5 Hz, 4H), 3.36 – 3.22 (m, 1H), 2.57 (s, 3H), 1.23 (d, *J* = 6.9 Hz, 6H). ¹³C NMR (101 MHz, CDCl₃) δ 198.08, 160.48, 158.42, 136.55, 136.32, 129.94, 128.77, 128.73, 128.29, 128.11, 127.57, 127.08, 120.64, 97.34, 70.96, 70.17, 32.33, 26.58, 22.63. ESI-MS Calcd for [M+H]⁺ 375.5; Found 375.2.

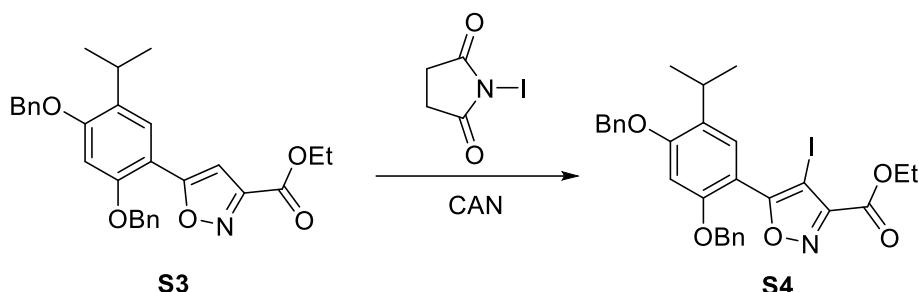


Ethyl (Z)-4-(2,4-bis(benzyloxy)-5-isopropylphenyl)-2-hydroxy-4-oxobut-2-enoate (S2). Sodium hydride (60% in mineral oil) (320 mg, 13.9 mmol) was added to an ice-cold solution of S1 (2.0 g, 5.35 mmol) in dry toluene (30 mL). Diethyl oxalate (860 mg, 5.81 mmol) was added, and the reaction mixture was heated to 80°C for 30 min. The mixture was cooled to r.t. and 50 mL of cold acetic acid was added to precipitate the product. The crude product was then washed with cold hexane and dried in vacuo to offer S2 (2.05 g, 81%) as a yellow solid. ¹H NMR (400 MHz, CDCl₃) δ 15.63 (s, 1H), 7.87 (s, 1H), 7.49 – 7.32 (m, 11H), 6.53 (s, 1H), 5.12 (d, *J* = 10.4 Hz, 4H), 4.28 (q, *J* = 7.1 Hz, 2H), 3.37 – 3.25 (m, 1H), 1.32 – 1.19 (m, 9H). ¹³C NMR (101 MHz, CDCl₃) δ 190.00, 167.75, 162.80, 161.43, 158.78, 136.26, 135.90, 130.59, 128.79, 128.76, 128.28, 128.24, 127.47, 127.10, 117.26, 103.37, 97.63, 71.14, 70.27, 62.12, 26.61, 22.58, 14.07. ESI-MS Calcd for [M+H]⁺ 475.6; Found 475.5.

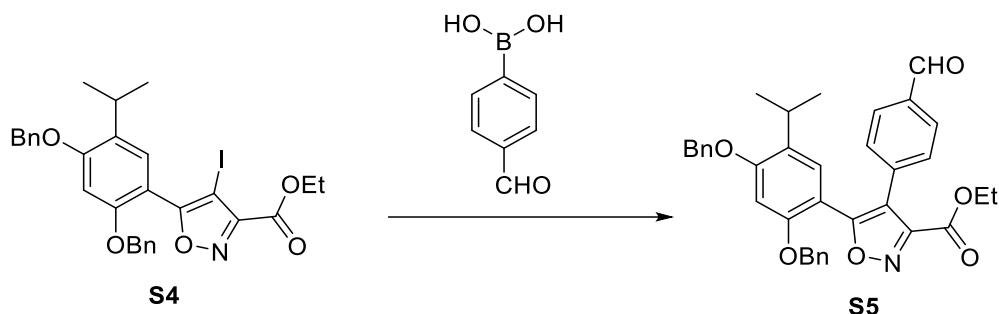


Ethyl 5-(2,4-bis(benzyloxy)-5-isopropylphenyl)isoxazole-3-carboxylate (S3).

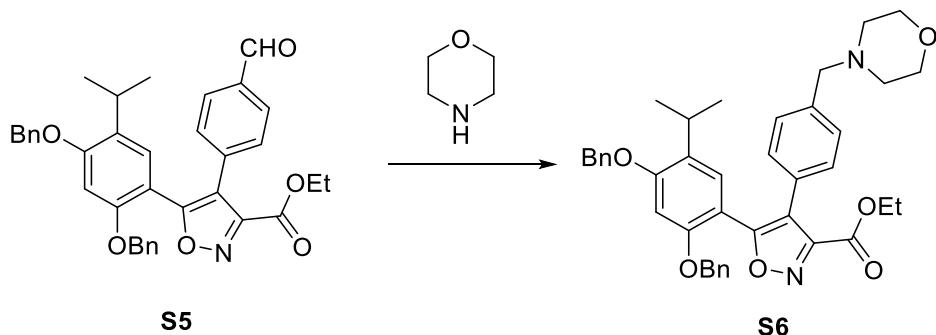
Hydroxylamine hydrochloride (291 mg, 4.2 mmol) and S2 (1 g, 2.1 mmol) were added to 30 mL of ethanol. The mixture was heated to reflux for 2 h and then cooled in an ice bath. The precipitate was filtered, washed with cold ethanol and dried in vacuo to offer S3 (820 mg, 83%) as a yellow solid. ¹H NMR (400 MHz, CDCl₃) δ 7.85 (s, 1H), 7.46 – 7.35 (m, 10H), 7.02 (s, 1H), 6.59 (s, 1H), 5.17 (s, 2H), 5.08 (s, 2H), 4.43 (q, *J* = 7.1 Hz, 2H), 3.44 – 3.27 (m, 1H), 1.41 (t, *J* = 7.1 Hz, 3H), 1.27 (d, *J* = 6.9 Hz, 6H). ¹³C NMR (101 MHz, CDCl₃) δ 168.34, 160.53, 158.61, 156.96, 154.85, 136.60, 136.23, 130.41, 128.84, 128.73, 128.37, 128.11, 127.44, 127.10, 125.28, 108.57, 102.22, 97.79, 70.84, 70.19, 61.94, 26.65, 22.72, 14.19. ESI-MS Calcd for [M+H]⁺ 472.6; Found 472.2.



Ethyl 5-(2,4-bis(benzyloxy)-5-isopropylphenyl)-4-iodoisoxazole-3-carboxylate (S4). S3 (200 mg, 0.43 mmol) was dissolved in 20 mL of anhydrous acetonitrile and dichloromethane (2 : 1), *N*-iodosuccinimide (190 mg, 0.86 mmol) was added followed by ceric ammonium nitrate (11.6 mg, 0.0215 mmol), and the solution was stirred at r.t. overnight. The reaction mixture was concentrated in vacuo to offer an orange oil, which will slowly be crystallized. The residue was triturated with hexane and filtered to provide the desired compound S4 (192.7 mg, 75%) as a light-yellow solid. ¹H NMR (400 MHz, CDCl₃) δ 7.48 – 7.27 (m, 11H), 6.61 (s, 1H), 5.10 (s, 2H), 5.07 (s, 2H), 4.49 (q, *J* = 7.1 Hz, 2H), 3.41 – 3.29 (m, 1H), 1.46 (t, *J* = 7.1 Hz, 3H), 1.24 (d, *J* = 6.9 Hz, 6H). ¹³C NMR (101 MHz, CDCl₃) δ 172.44, 159.56, 159.17, 155.92, 155.88, 136.57, 136.49, 129.99, 129.04, 128.73, 128.65, 128.12, 127.98, 127.15, 127.11, 107.78, 98.48, 70.98, 70.20, 62.39, 57.97, 26.50, 22.70, 14.19. ESI-MS Calcd for [M+H]⁺ 598.5; Found 598.8.

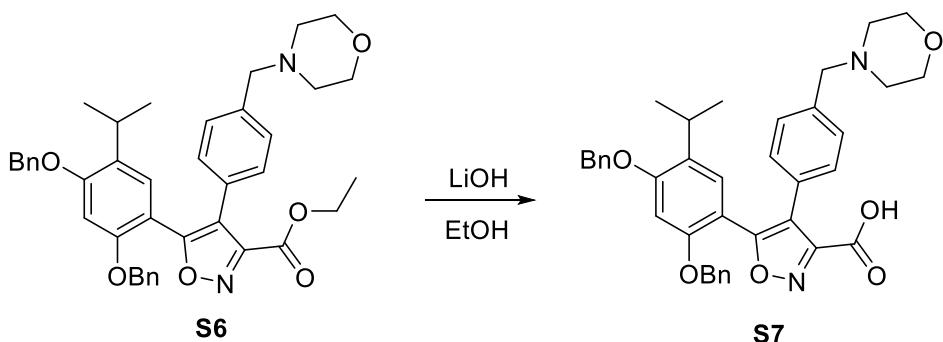


Ethyl 5-(2,4-bis(benzyloxy)-5-isopropylphenyl)-4-(4-formylphenyl) isoxazole-3-carboxylate (S5). To a solution of S4 (200 mg, 0.335 mmol), 4-(formylphenyl) boronic acid (60 mg, 0.4 mmol), sodium bicarbonate (85 mg, 1 mmol) in a mixture of 5 mL of DMF and 1 mL of water, [1,1'-bis(diphenylphosphino)ferrocene]-dichloropalladium(II) (12 mg, 0.016 mmol) was added before the mixture was degassed. After heating to 80°C for 3 h, the reaction was quenched with 50 mL of water, extracted with DCM and washed with saline, dried over Na₂SO₄ and then purified with column chromatography (hexane : EA = 3:1) to offer the desired compound S5 (121.3 mg, 63%) as brown oil. ¹H NMR (400 MHz, CDCl₃) δ 9.98 (s, 1H), 7.72 (d, *J* = 8.3 Hz, 2H), 7.40 – 7.32 (m, 7H), 7.30 – 7.24 (m, 4H), 7.02 (dd, *J* = 6.5, 2.9 Hz, 2H), 6.47 (s, 1H), 5.02 (s, 2H), 4.70 (s, 2H), 4.37 (q, *J* = 7.1 Hz, 2H), 3.33 – 3.20 (m, 1H), 1.33 (t, *J* = 7.1 Hz, 3H), 1.14 (d, *J* = 6.9 Hz, 6H). ¹³C NMR (101 MHz, CDCl₃) δ 191.90, 167.73, 160.39, 159.04, 155.23, 154.21, 136.65, 136.51, 136.21, 135.29, 130.40, 130.22, 129.24, 128.71, 128.49, 128.40, 128.12, 128.06, 128.01, 127.15, 127.06, 116.71, 107.84, 98.18, 70.53, 70.14, 62.19, 26.37, 22.57, 14.06. ESI-MS Calcd for [M+H]⁺ 576.7; Found 576.8.

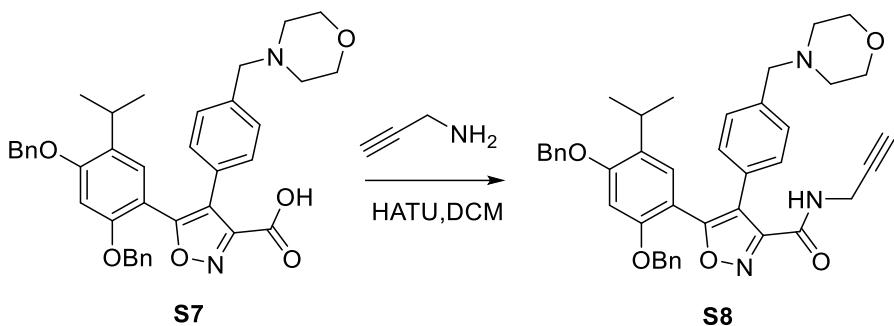


Ethyl 5-(2,4-bis(benzyloxy)-5-isopropylphenyl)-4-(4-(morpholinomethyl)phenyl)isoxazole-3-carboxylate (S6). Acetic acid (260 mg) was added dropwise to a mixture of S5 (500 mg, 0.869 mmol), morpholine (227 mg, 2.607 mmol), NaCNBH₃ (110 mg, 1.74 mmol) and 3 Å molecular sieves (1 g) in DCM (30 mL). The reaction mixture was stirred at r.t. under nitrogen atmosphere overnight. The mixture was then filtered through a sintered funnel, and the filtrate was washed with saturated NaHCO₃ solution (20 mL). The aqueous phase was

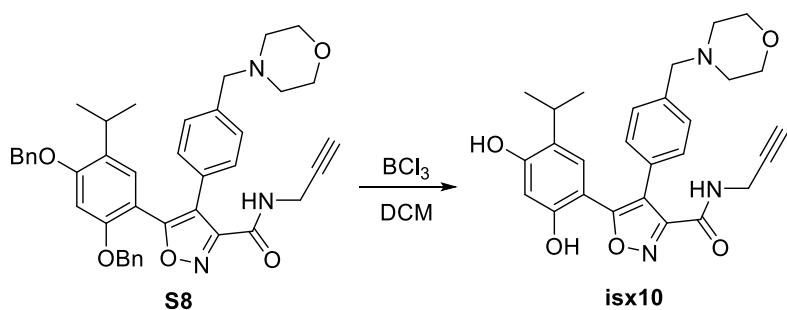
extracted further with DCM (2×15 mL). The combined organic layers were dried over Na_2SO_4 and evaporated in vacuo to give a crude product, which was purified by column chromatography, eluting with a gradient of 50% EA/hexane to 100% EA to offer the desired compound S6 (415 mg, 74%) as a colourless oil. ^1H NMR (400 MHz, CDCl_3) δ 7.44 – 7.27 (m, 10H), 7.22 (dd, $J = 7.8, 5.4$ Hz, 4H), 7.09 (s, 1H), 6.50 (s, 1H), 5.01 (s, 2H), 4.87 (s, 2H), 4.40 (q, $J = 7.1$ Hz, 2H), 3.74 – 3.70 (m, 4H), 3.51 (s, 2H), 3.30 – 3.17 (m, 1H), 2.46 (s, 4H), 1.35 (t, $J = 7.1$ Hz, 3H), 1.05 (d, $J = 6.9$ Hz, 6H). ^{13}C NMR (101 MHz, CDCl_3) δ 167.32, 160.63, 158.49, 155.63, 154.38, 136.66, 136.60, 129.91, 128.89, 128.67, 128.57, 128.53, 128.06, 127.85, 127.14, 126.88, 117.56, 108.60, 98.59, 70.78, 70.09, 67.00, 63.19, 61.93, 53.62, 26.14, 22.50, 14.06. ESI-MS Calcd for $[\text{M}+\text{H}]^+$ 647.8; Found 648.0.



5-(2,4-bis(benzyloxy)-5-isopropylphenyl)-4-(4(morpholinomethyl) phenyl) isoxazole-3-carboxylic acid (S7). S6 (100 mg, 0.155 mmol) was dissolved in 10 mL of EtOH/H₂O (1:1). Next, LiOH (22.2 mg, 0.93 mmol) in 2 mL of water was added dropwise under an ice-water bath. The mixture was then warmed up to r.t. and stirred for another 1 hour. 2 N HCl was added to acidify the solution to pH = 4. The aqueous phase was then extracted with 30 mL of DCM. The organic phase was combined and dried over Na_2SO_4 and evaporated in vacuo to give the crude product, which was purified by column chromatography to offer S7 as a white power (89 mg, 93%). ^1H NMR (400 MHz, DMSO) δ 7.48 – 7.39 (m, 6H), 7.38 – 7.29 (m, 4H), 7.27 – 7.19 (m, 4H), 6.99 (s, 1H), 6.95 (s, 1H), 5.17 (s, 2H), 5.07 (s, 2H), 4.02 (s, 2H), 3.73 (s, 4H), 3.18 – 3.05 (m, 1H), 2.84 (s, 4H), 0.96 (d, $J = 6.8$ Hz, 6H). ^{13}C NMR (101 MHz, CDCl_3) δ 166.41, 164.19, 158.68, 157.27, 155.28, 136.59, 136.45, 132.55, 130.85, 130.31, 130.06, 128.65, 128.44, 128.03, 127.84, 127.19, 127.07, 126.75, 116.08, 108.46, 98.55, 70.54, 70.13, 63.62, 60.45, 51.36, 26.26, 22.60. ESI-MS Calcd for $[\text{M}-\text{H}]^-$ 617.7; Found 617.5.



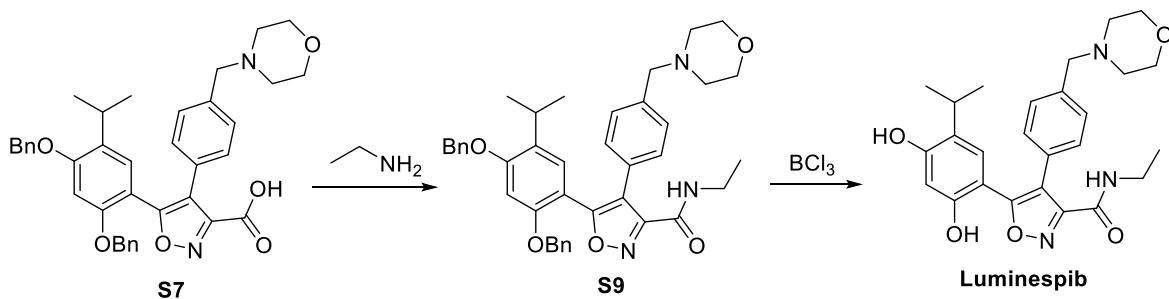
5-(2,4-bis(benzyloxy)-5-isopropylphenyl)-4-(4-(morpholinomethyl) phenyl) isoxazole-3-carboxylic acid (S8). S7 (50 mg, 0.08 mmol), HATU (92 mg, 0.24 mmol), and DIPEA (31 mg, 0.24 mmol) were dissolved in 5 mL of DCM. The reaction mixture was stirred after 30 min before propargyl amine (4.4 mg, 0.08 mmol) was added. The mixture was further stirred at r.t. overnight. The next day, the solvent was removed, and the resulting residue was purified by column chromatography to offer S8 as a white solid (46 mg, 88%). ¹H NMR (400 MHz, CDCl₃) δ 7.45 – 7.27 (m, 12H), 7.20 (d, *J* = 6.6 Hz, 2H), 7.14 – 7.06 (m, 2H), 6.50 (s, 1H), 5.01 (s, 2H), 4.87 (s, 2H), 4.22 (dd, *J* = 5.3, 2.5 Hz, 2H), 3.76 – 3.68 (m, 4H), 3.52 (s, 2H), 3.31 – 3.16 (m, 1H), 2.48 (s, 4H), 2.29 (t, *J* = 2.4 Hz, 1H), 1.05 (d, *J* = 6.9 Hz, 6H). ¹³C NMR (101 MHz, CDCl₃) δ 167.49, 159.34, 158.51, 155.63, 155.32, 136.68, 136.59, 130.14, 129.96, 128.93, 128.68, 128.58, 128.54, 128.07, 127.88, 127.15, 126.85, 117.19, 108.61, 98.62, 78.84, 72.08, 70.79, 70.10, 66.89, 63.17, 53.57, 29.08, 26.13, 22.50. ESI-MS Calcd for [M+H]⁺ 656.8; Found 657.1.



5-(2,4-dihydroxy-5-isopropylphenyl)-4-(4-(morpholinomethyl) phenyl)-N-(prop-2-yn-1-yl)isoxazole-3-carboxamide (isx10). S8 (40 mg, 0.061 mmol) was dissolved in DCM (1 mL) and the mixture was cooled to 0°C under N₂, BCl₃ (1.0 M in DCM, 5 eq.) was added subsequently. The reaction mixture was then warmed up to r.t. and stirred for another 1.5 h. Next, DCM was removed in vacuo and saturated NaHCO₃ solution (5 mL) was added. The aqueous residue was extracted with EA (4 × 10 mL), concentrated in vacuo, purified by column chromatography with silica gel eluting with MeOH : DCM (1 : 10) to obtain **isx10** (13 mg, 44%) as a yellow solid. ¹H NMR (400 MHz, DMSO) δ 9.79 (s, 1H), 9.69 (s, 1H), 9.31 (t, *J* =

5.7 Hz, 1H), 7.23 (d, J = 7.9 Hz, 2H), 7.18 (d, J = 7.9 Hz, 2H), 6.72 (s, 1H), 6.44 (s, 1H), 3.99 (dd, J = 5.6, 2.4 Hz, 2H), 3.55 (s, 4H), 3.42 (s, 2H), 3.16 (t, J = 2.4 Hz, 1H), 3.02 – 2.92 (m, 1H), 2.33 (s, 4H), 0.89 (d, J = 6.9 Hz, 6H). ^{13}C NMR (101 MHz, DMSO) δ 167.03, 160.31, 157.96, 157.55, 155.21, 137.45, 129.40, 129.19, 128.70, 128.24, 126.09, 115.27, 104.84, 103.17, 80.86, 73.66, 66.62, 62.61, 53.61, 28.66, 25.83, 22.83. HRMS m/z [M+H]⁺ calcd 476.2185; Found 476.2169.

3.4 Synthetic Scheme S4



Scheme S4. Synthesis of Luminespib.

5-(2,4-bis(benzyloxy)-5-isopropylphenyl)-N-ethyl-4(4(morpholinomethyl)phenyl)isoxazole-3 carboxamide (S9) was obtained as a yellow solid. ^1H NMR (400 MHz, CDCl₃) δ 7.45 – 7.26 (m, 12H), 7.24 – 7.17 (m, 2H), 7.08 (s, 1H), 6.85 (t, J = 5.4 Hz, 1H), 6.50 (s, 1H), 5.01 (s, 2H), 4.87 (s, 2H), 3.75 – 3.66 (m, 4H), 3.52 – 3.40 (m, 4H), 3.31 – 3.15 (m, 1H), 2.46 (s, 4H), 1.24 (t, J = 7.3 Hz, 3H), 1.04 (d, J = 6.9 Hz, 6H). ^{13}C NMR (101 MHz, CDCl₃) δ 167.18, 159.58, 158.41, 156.07, 155.63, 136.74, 136.62, 130.10, 129.92, 128.84, 128.67, 128.63, 128.53, 128.06, 127.85, 127.15, 126.86, 117.14, 108.83, 98.65, 70.80, 70.09, 67.01, 63.25, 53.63, 34.34, 26.13, 22.51, 14.70. ESI-MS Calcd for [M+H]⁺ 646.8; Found 647.1.

5-(2,4-dihydroxy-5-isopropylphenyl)-N-ethyl-4(4(morpholinomethyl)phenyl)isoxazole-3 carboxamide (Luminespib) was obtained as a yellow solid. ^1H NMR (400 MHz, DMSO) δ 9.78 (s, 1H), 9.67 (s, 1H), 8.85 (t, J = 5.5 Hz, 1H), 7.24 (d, J = 8.0 Hz, 2H), 7.19 (d, J = 8.0 Hz, 2H), 6.73 (s, 1H), 6.44 (s, 1H), 3.55 (s, 4H), 3.42 (s, 2H), 3.28 – 3.16 (m, 2H), 3.03 – 2.91 (m, 1H), 2.33 (s, 4H), 1.07 (t, J = 7.2 Hz, 3H), 0.90 (d, J = 6.8 Hz, 6H). ^{13}C NMR (101 MHz, DMSO) δ 166.74, 160.26, 158.25, 157.91, 155.19, 137.36, 129.32, 129.17, 128.94, 128.22, 126.07, 115.14, 104.97, 103.18, 66.63, 62.60, 53.61, 34.21, 25.84, 22.83, 14.87. ESI-MS Calcd for [M+H]⁺ 466.6; Found 466.8.

4. Absorption Spectrum of MPISC

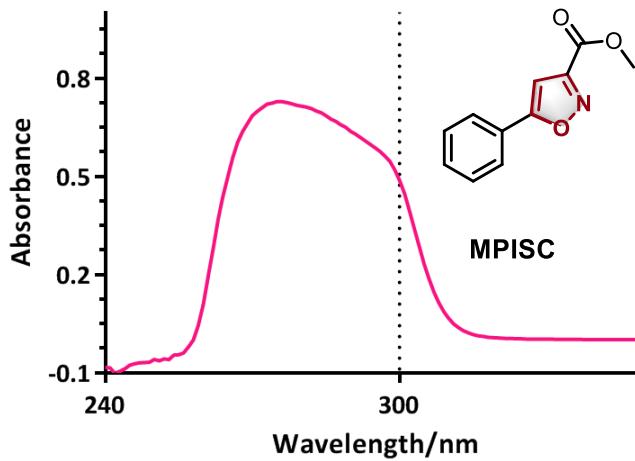


Figure S2. The absorption spectrum of **MPISC** in ACN (acetonitrile).

5. DFT Calculation

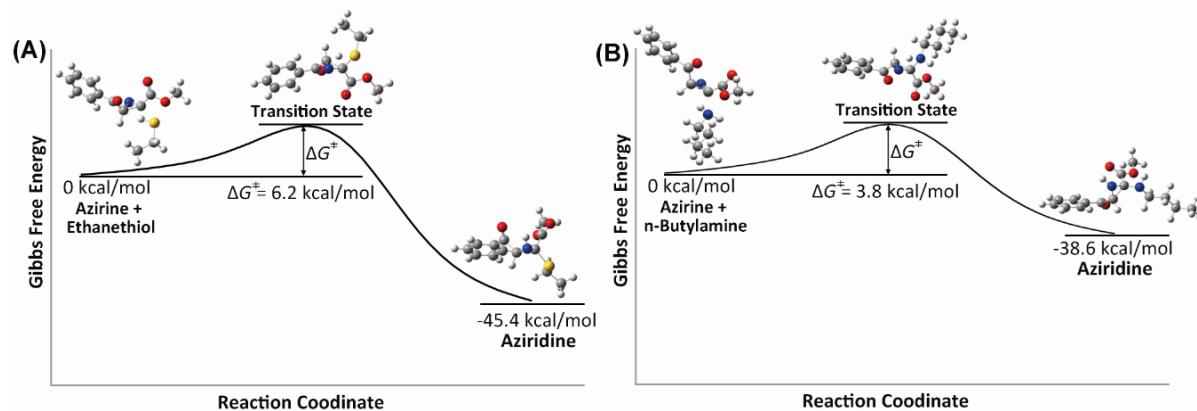


Figure S3. (A) DFT calculation of the reaction coordinates of the azirine intermediate with ethanethiol. (B) DFT calculation of the reaction coordinates of the azirine intermediate with n-butylamine.

6. Photo-Cross-Linking Reactions of Isoxazole and Amino Acids

Z-Glu-OMe ((S)-4-(((benzyloxy)carbonyl)amino)-5-methoxy-5-oxopentanoic acid) (100 μM) was mixed with **MPISC** (100 μM) in ACN/PBS (1:1, pH = 7.4) and irradiated with a handheld UV lamp (302 nm, 6 W). The reaction mixture was analyzed with HPLC at different irradiation durations (0 min, 1 min, 2 min, 5 min, respectively). The azirine product **AZD1** was isolated and validated by HRMS, $^1\text{H-NMR}$, $^{13}\text{C-NMR}$, DEPT90-NMR, DEPT135-NMR, and $^1\text{H}-^{13}\text{C}$ HSQC. ^1H NMR (400 MHz, CDCl_3) δ 8.12 (dd, $J = 7.1, 4.8 \text{ Hz}$, 2H), 7.65 (t, $J = 7.4 \text{ Hz}$, 1H),

7.54 (t, $J = 7.7$ Hz, 2H), 7.40 – 7.30 (m, 5H), 5.54 (s, 1H), 5.12 (s, 2H), 4.58 – 4.40 (m, 1H), 3.79 (s, 4H), 3.61 (d, $J = 3.7$ Hz, 3H), 3.36 (d, $J = 9.5$ Hz, 1H), 2.71 – 2.50 (m, 2H), 2.31 (m, 1H), 2.08 (m, 1H). ^{13}C NMR (101 MHz, CDCl_3) δ 189.80, 172.15, 171.96, 164.99, 155.97, 136.05, 134.81, 134.41, 128.99, 128.85, 128.57, 128.28, 128.17, 69.32, 67.20, 53.57, 53.04, 52.72, 46.75, 29.81, 27.24. HRMS m/z [M+H] $^+$ calcd 499.1717, found 499.1751.

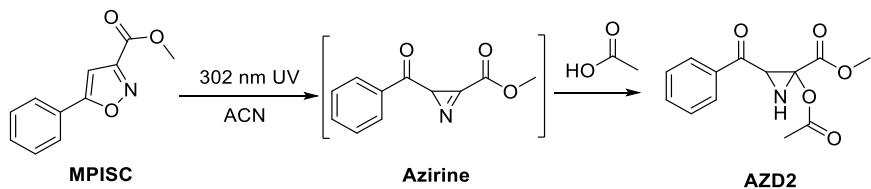


Figure S4. Photo-cross-linking of MPISC and acetic acid.

Acetic acid (0.1 mmol) was mixed with **MPISC** (0.1 mmol) in acetonitrile. The mixture was irradiated with a handheld UV lamp (302 nm) and analyzed with HPLC at different irradiation durations (0 min, 1 min, 2 min, and 5 min, respectively). The proposed azirine product **AZD2** was purified with column chromatography (DCM : MeOH = 10 : 1) and obtained as a colorless oil. The resulting product was verified by HRMS, ^1H -NMR, ^{13}C -NMR, DEPT90-NMR, DEPT135-NMR, and ^1H - ^{13}C HSQC. ^1H NMR (400 MHz, CDCl_3) δ 8.10 (d, $J = 7.5$ Hz, 2H), 7.63 (t, $J = 7.3$ Hz, 1H), 7.52 (t, $J = 7.6$ Hz, 2H), 3.76 (d, $J = 10.6$ Hz, 1H), 3.62 (s, 3H), 3.34 (d, $J = 10.4$ Hz, 1H), 2.21 (s, 3H). ^{13}C NMR (101 MHz, CDCl_3) δ 189.87, 170.21, 165.09, 134.84, 134.40, 128.99, 128.83, 69.19, 53.54, 46.74, 20.68. HRMS m/z [M+H] $^+$ calcd 264.0872, found 264.0882.

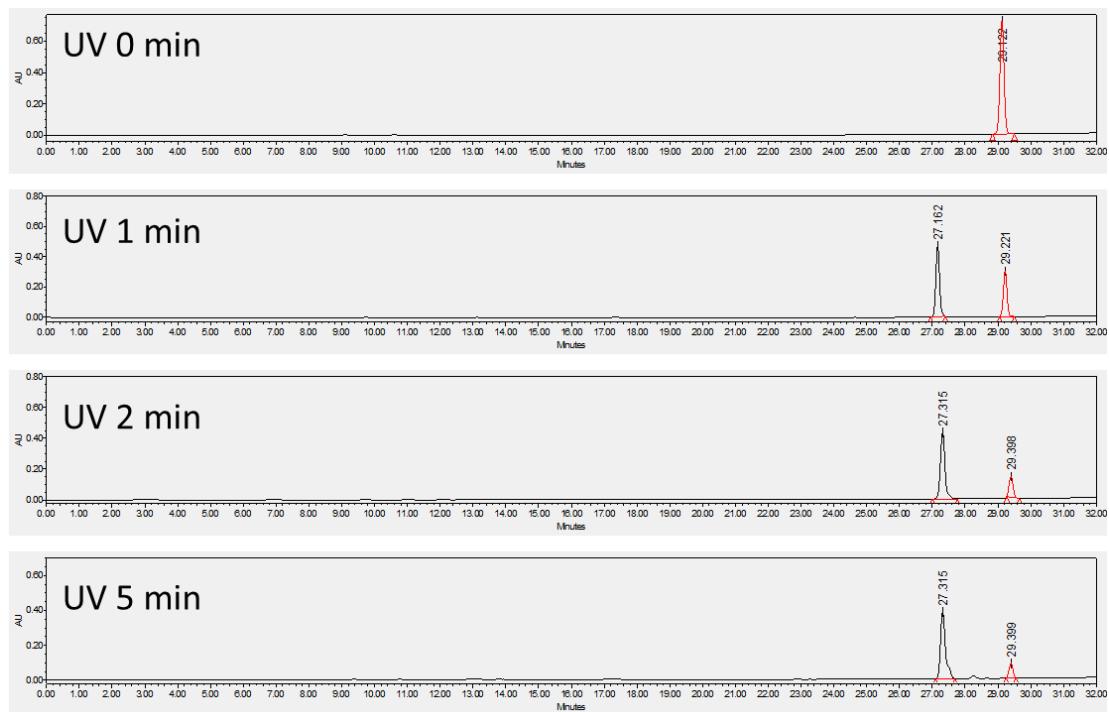


Figure S5. HPLC analysis of photoreaction of **MPISC** and acetic acid in acetonitrile (254 nm channel).

For the stability test of the aziridine products, **AZD1** was dispersed in PBS buffer (pH 7.4) and exposed to an ambient environment for 72 h. The NMR spectra were retested and compared with the original spectra.

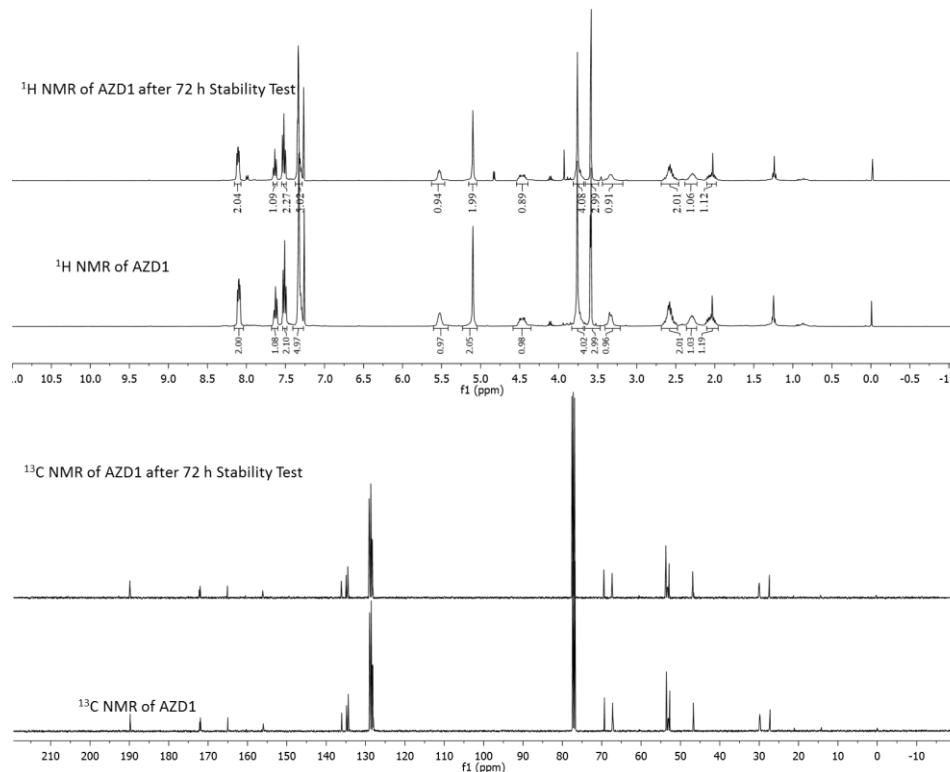


Figure S6. NMR spectra of **AZD1** after 72 h exposure under an ambient condition.

Mainchain-protected tyrosine (Boc-*Tyr*-OMe), cysteine (Ac-*Cys*-OMe), and lysine (Fmoc-*Lys*-OMe) were obtained and utilized to verify the photo-cross-linking with isoxazoles. The amino acid (100 μ M) was mixed with **MPISC** (100 μ M) in ACN/PBS (1:1; pH= 7.4) and irradiated with UV for 5 min. Subsequently, the reaction mixture was analyzed by HPLC. The peaks eluted from HPLC were collected for HRMS analysis.

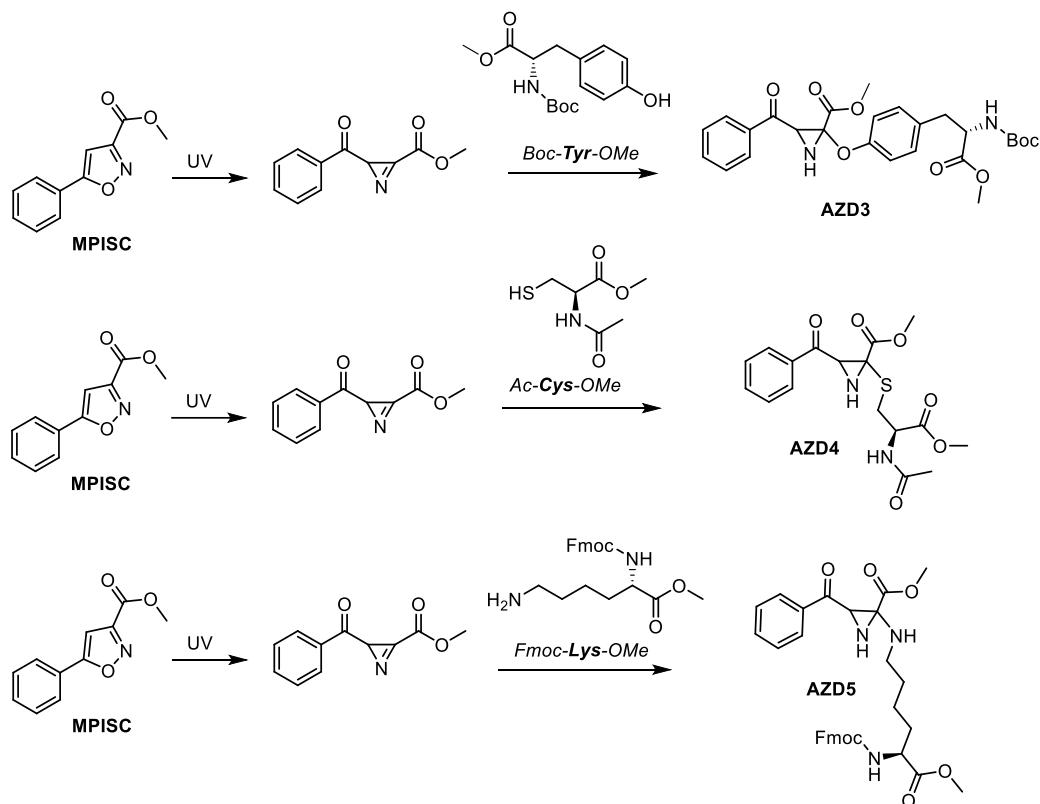


Figure S7. Proposed photo-cross-linking mechanism of **MPISC** with other nucleophilic amino acids.

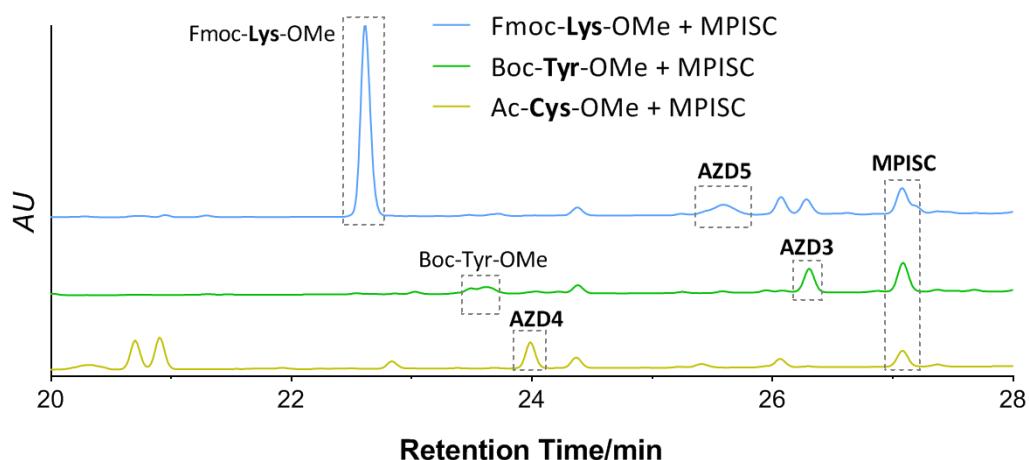
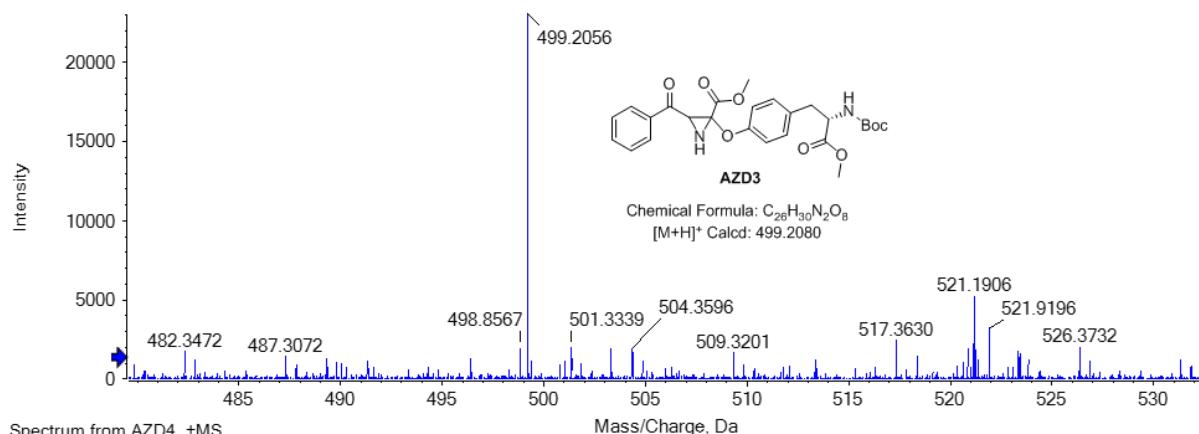
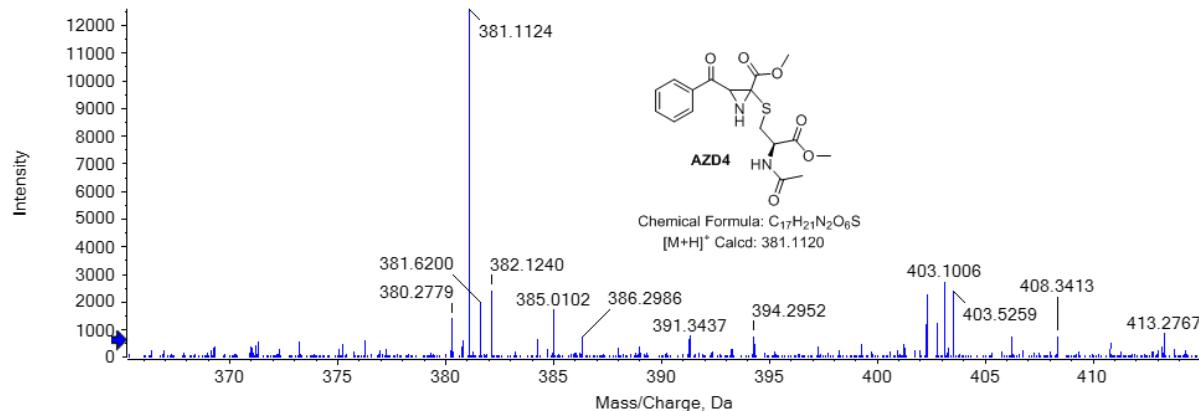


Figure S8. HPLC analysis of photoreaction of **MPISC** and other nucleophilic amino acids. (254 nm channel).

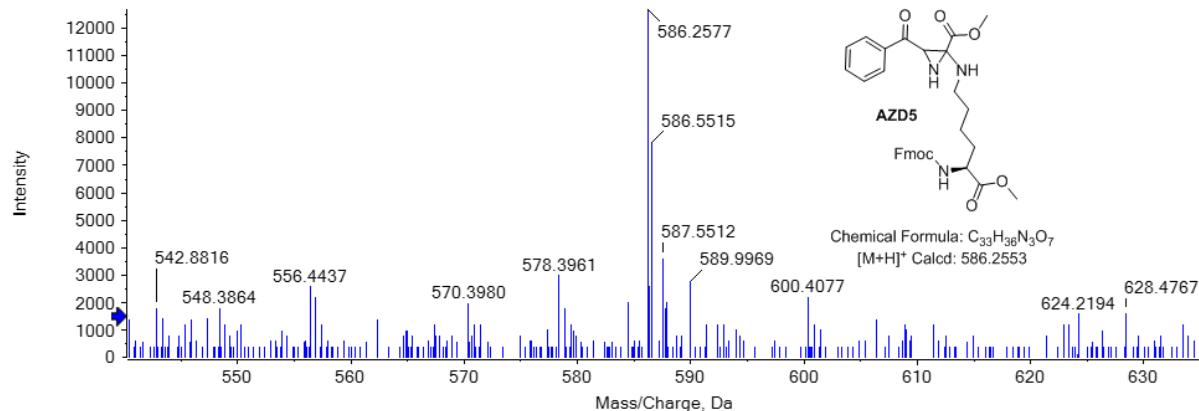
Spectrum from AZD3, +MS



Spectrum from AZD4, +MS



Spectrum from AZD5, +MS

**Figure S9.** HRMS spectra of peaks isolated from HPLC analysis.

7. Analysis of Photo-Cross-Linking Sites on Peptide

To identify the photo-cross-linking sites on peptides by **MPISC**, a free peptide, RQYAWESGFTCNHK, was obtained and utilized. **MPISC** (200 μ M) and the peptide (200 μ M) were mixed in PBS and ACN (1:1, 500 μ L). The mixture was incubated at r.t. for 30 min before irradiating with 302 nm UV on ice for 5 min. After the irradiation, the solution was diluted, desalting, and analyzed with MALDI-TOF MS and LC-MS/MS.

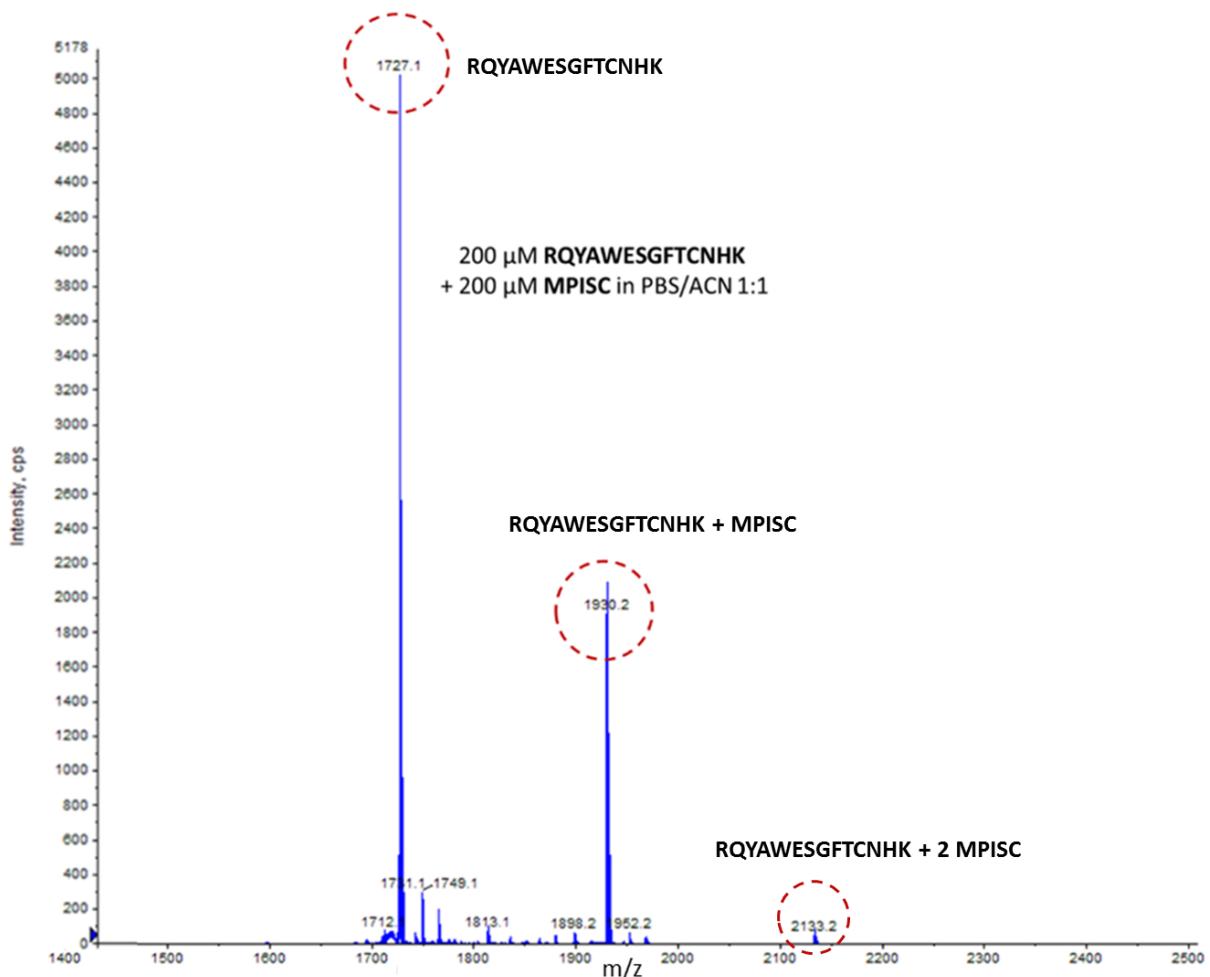
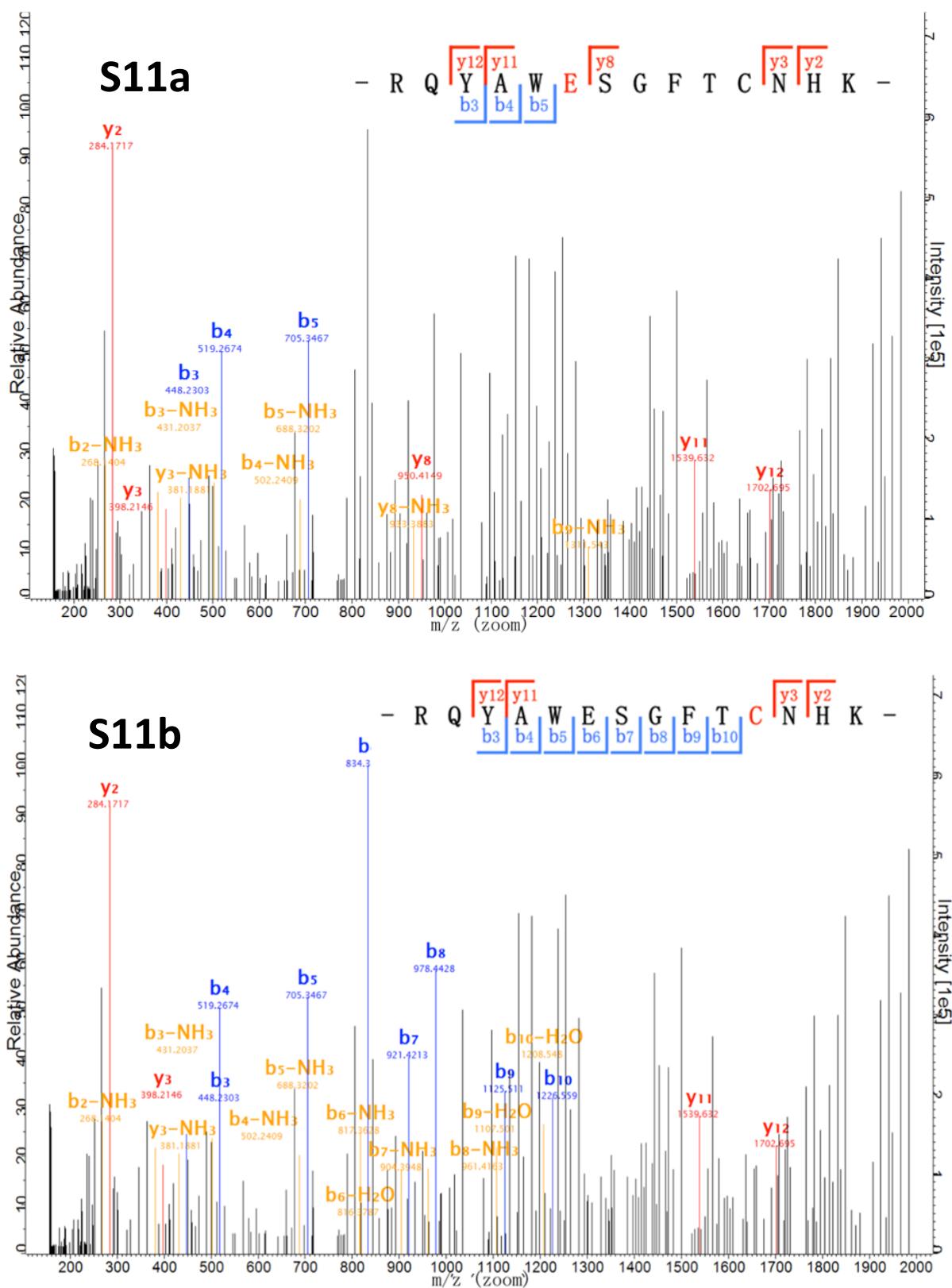


Figure S10. MALDI-TOF MS analysis of the photo-cross-linking sites of **MPISC** on the peptide.



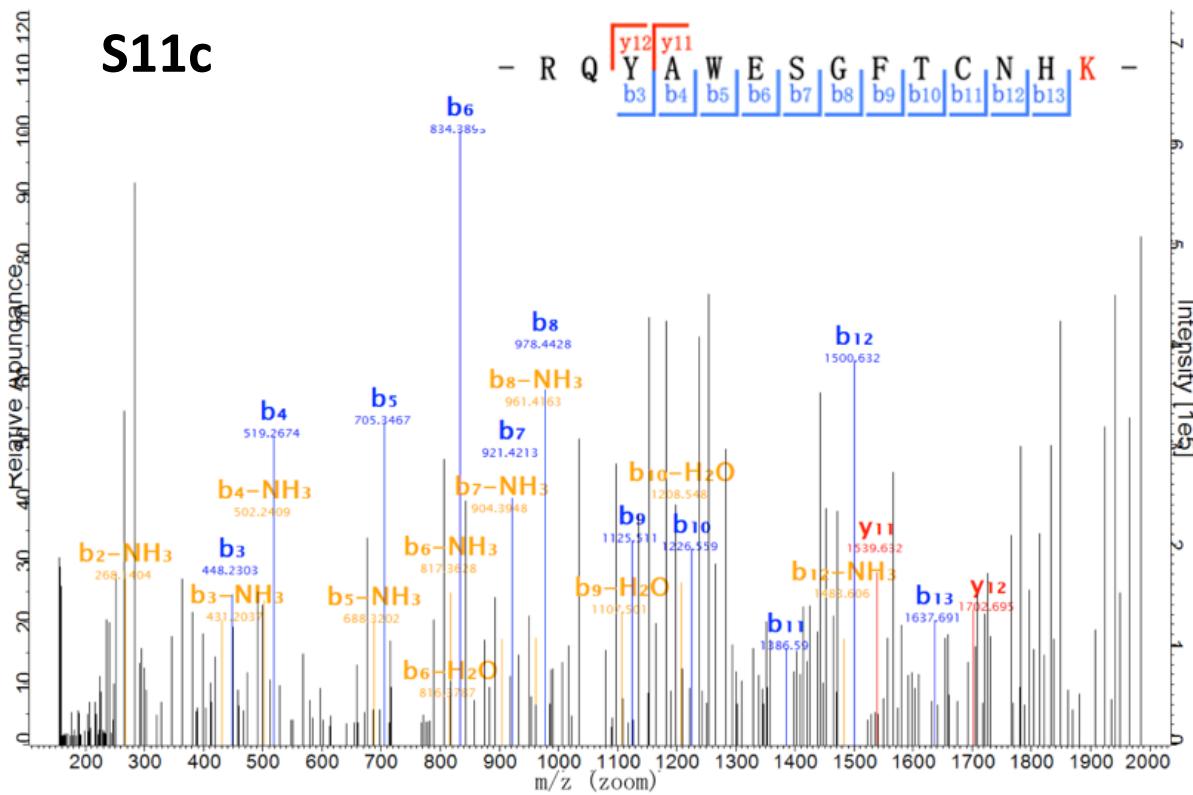
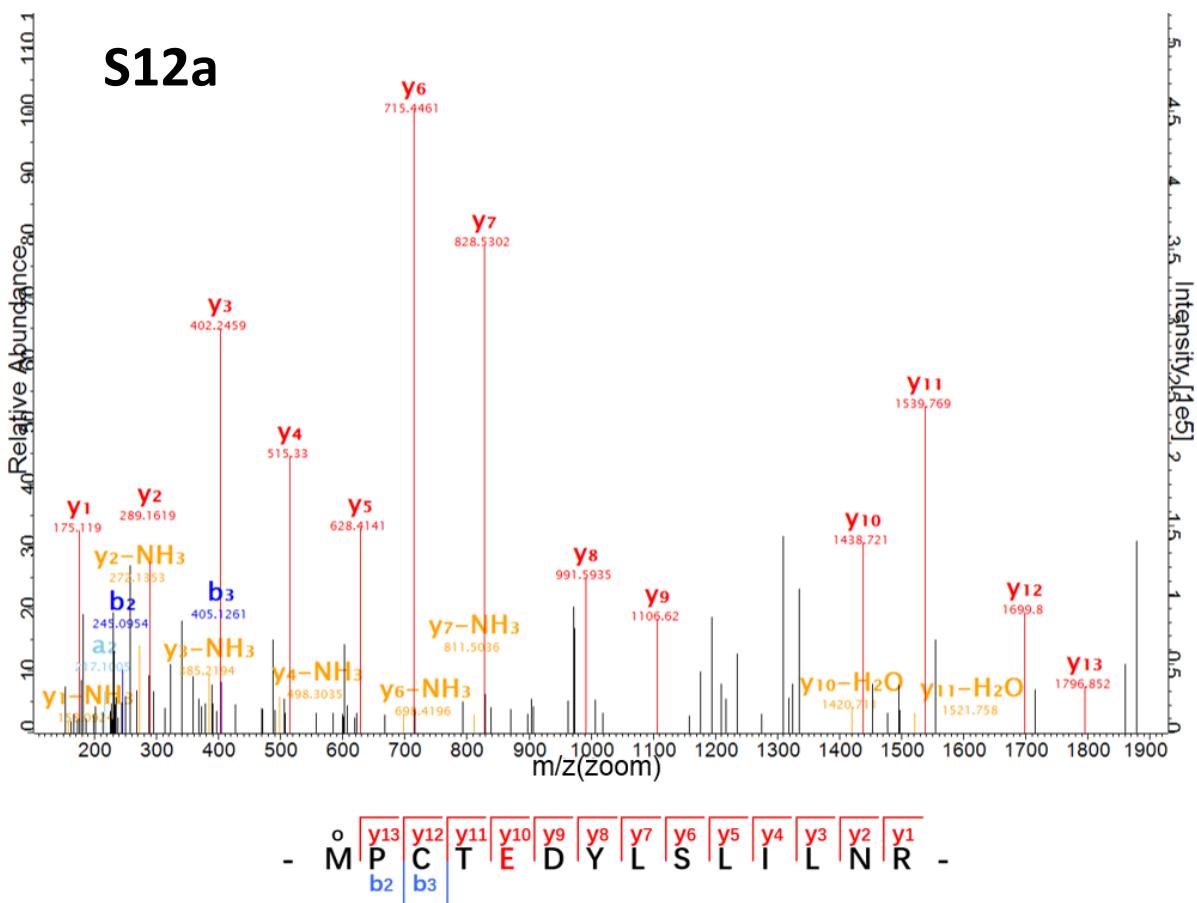


Figure S11a~c. LC-MS/MS analysis of the photo-cross-linking residue sites of **MPISC** on the peptide.

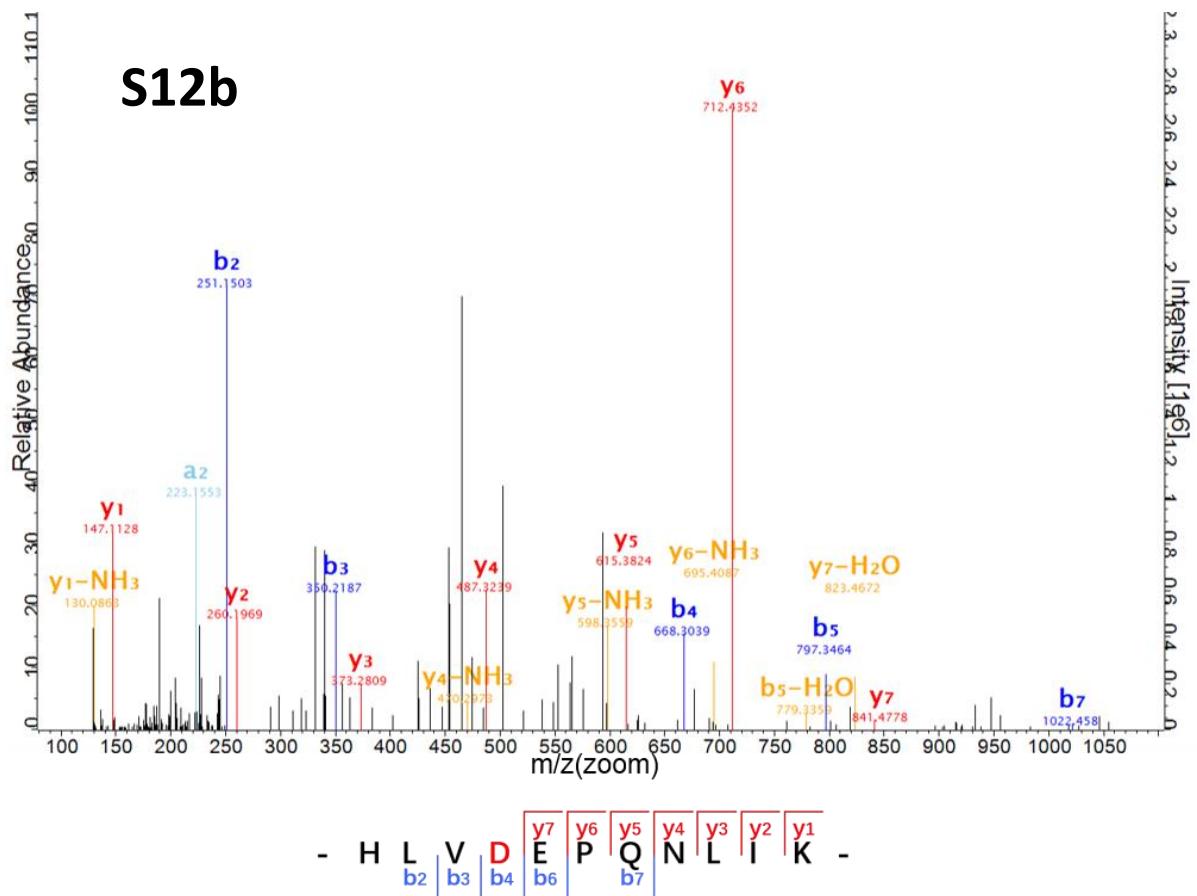
8. Analysis of Photo-Cross-Linking Sites on BSA

Generally, 7.5 μ M of BSA and 150 μ M of isoxazole probes (**MPISC** and **isx6~8**) were mixed in 200 μ L of PBS. The mixture was incubated at 37°C for 30 min before irradiating with 302 nm UV on ice for 5 min. After another 1 h incubation at r.t., BSA was precipitated by pre-chilled acetone and collected by centrifugation at 4°C. The resulting pellets were separated by SDS-PAGE and stained with coomassie brilliant blue (CBB). The stained BSA bands were cut out and collected for in-gel digestion by trypsin (Promega) before LC-MS/MS analysis.

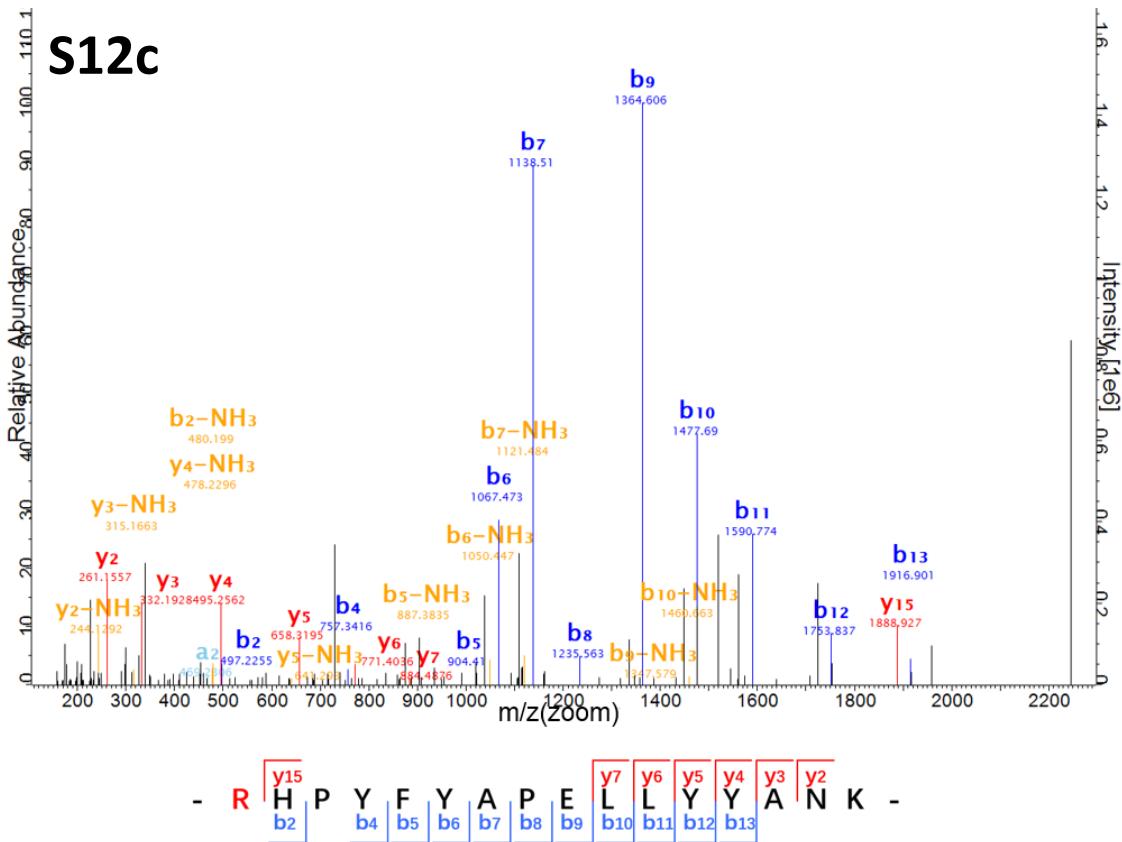
S12a



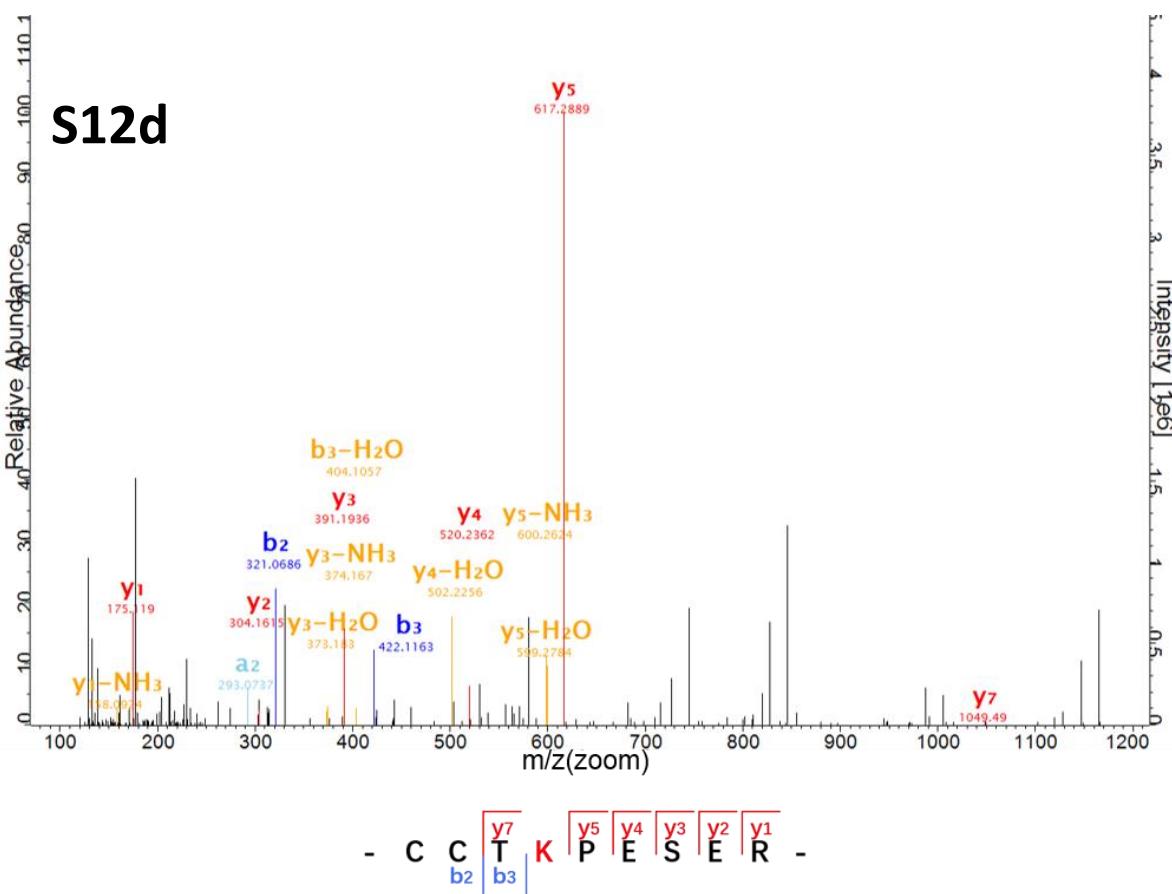
S12b

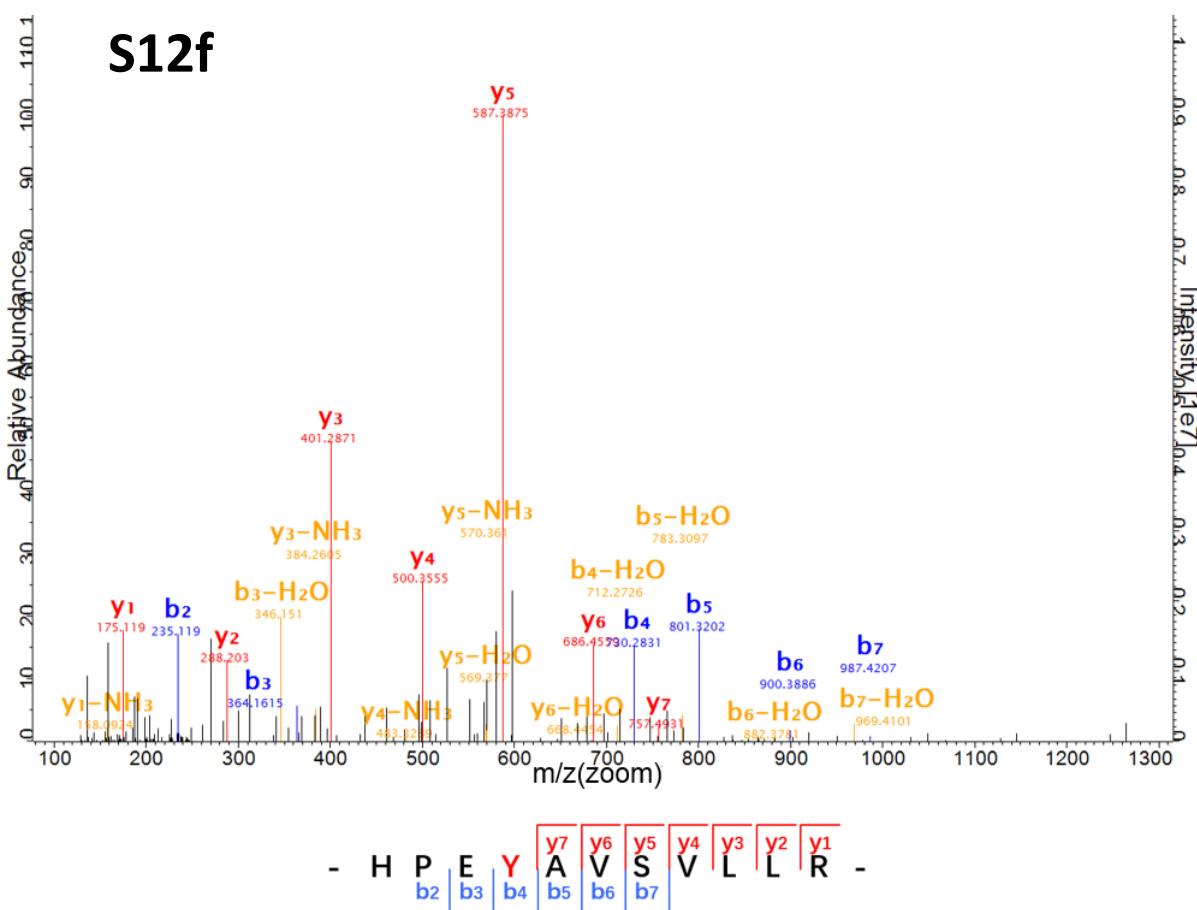
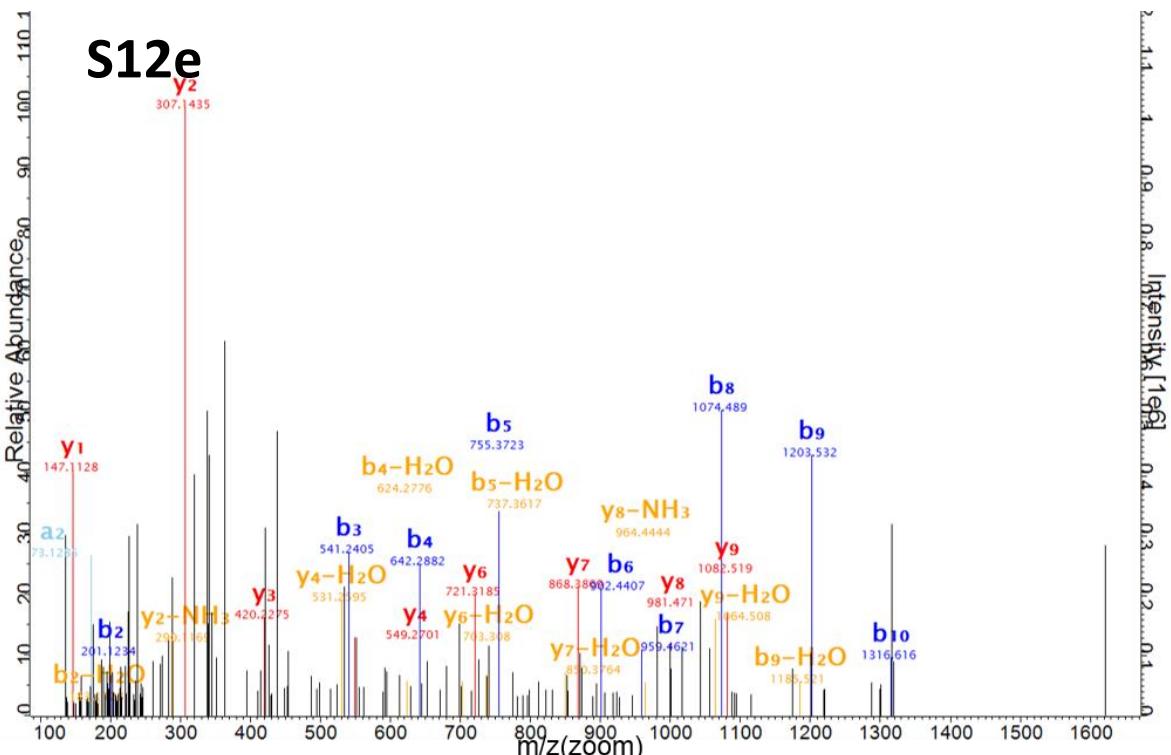


S12c

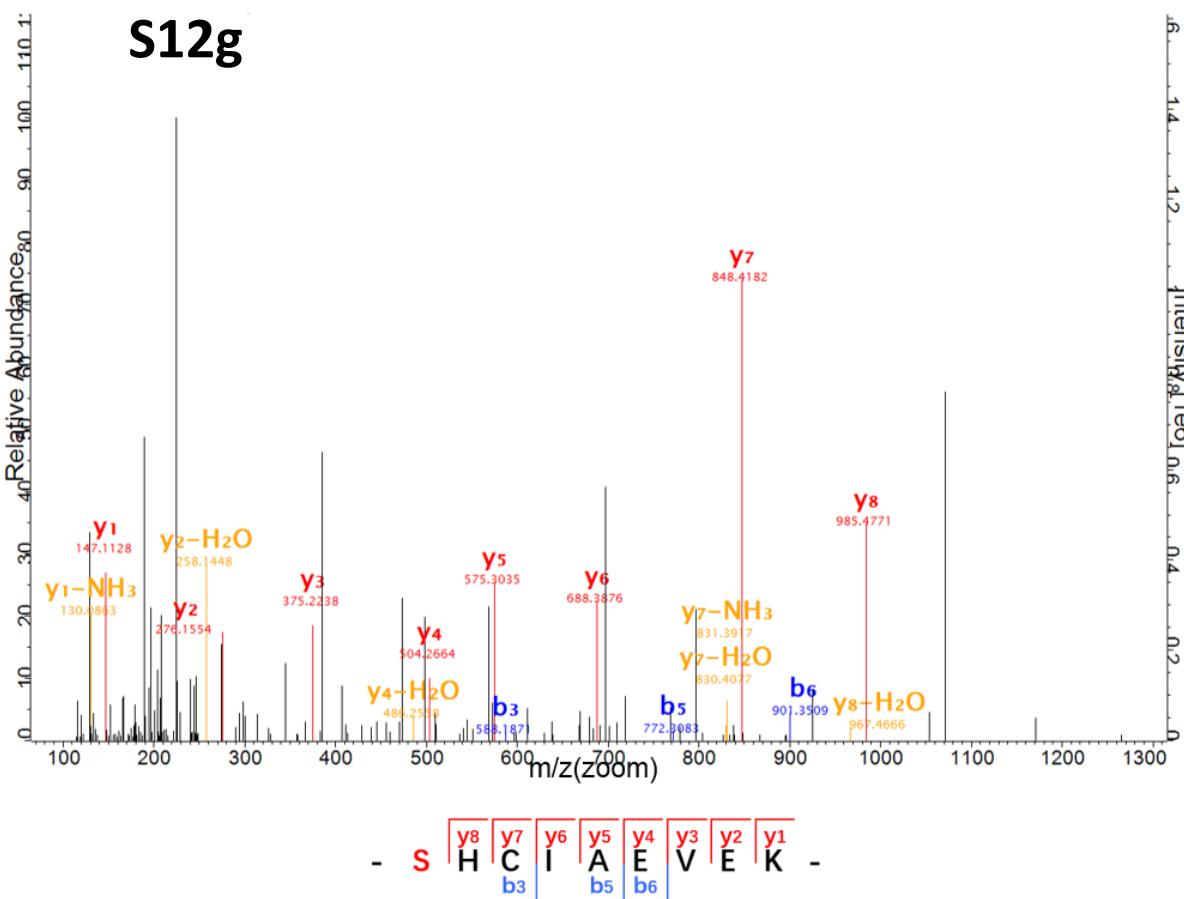


S12d

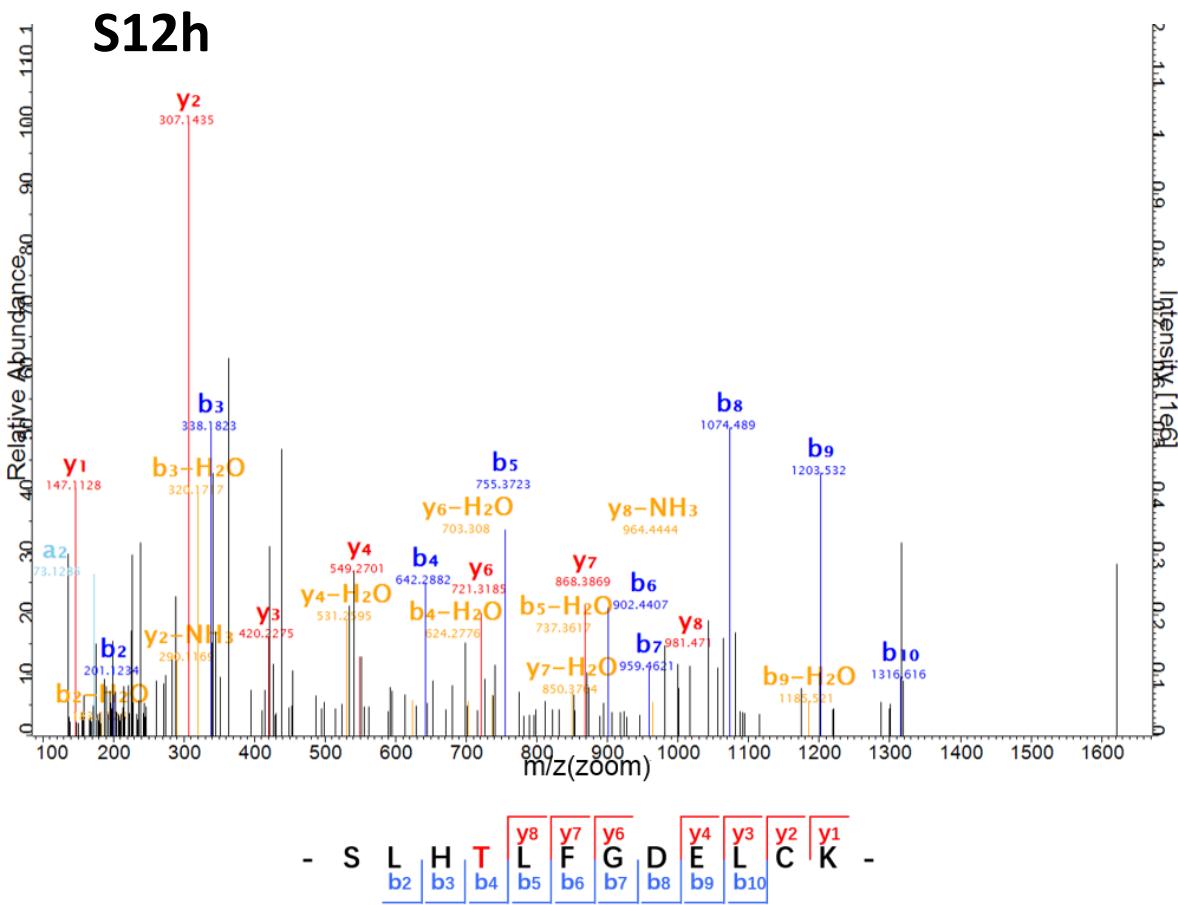




S12g



S12h



S12i

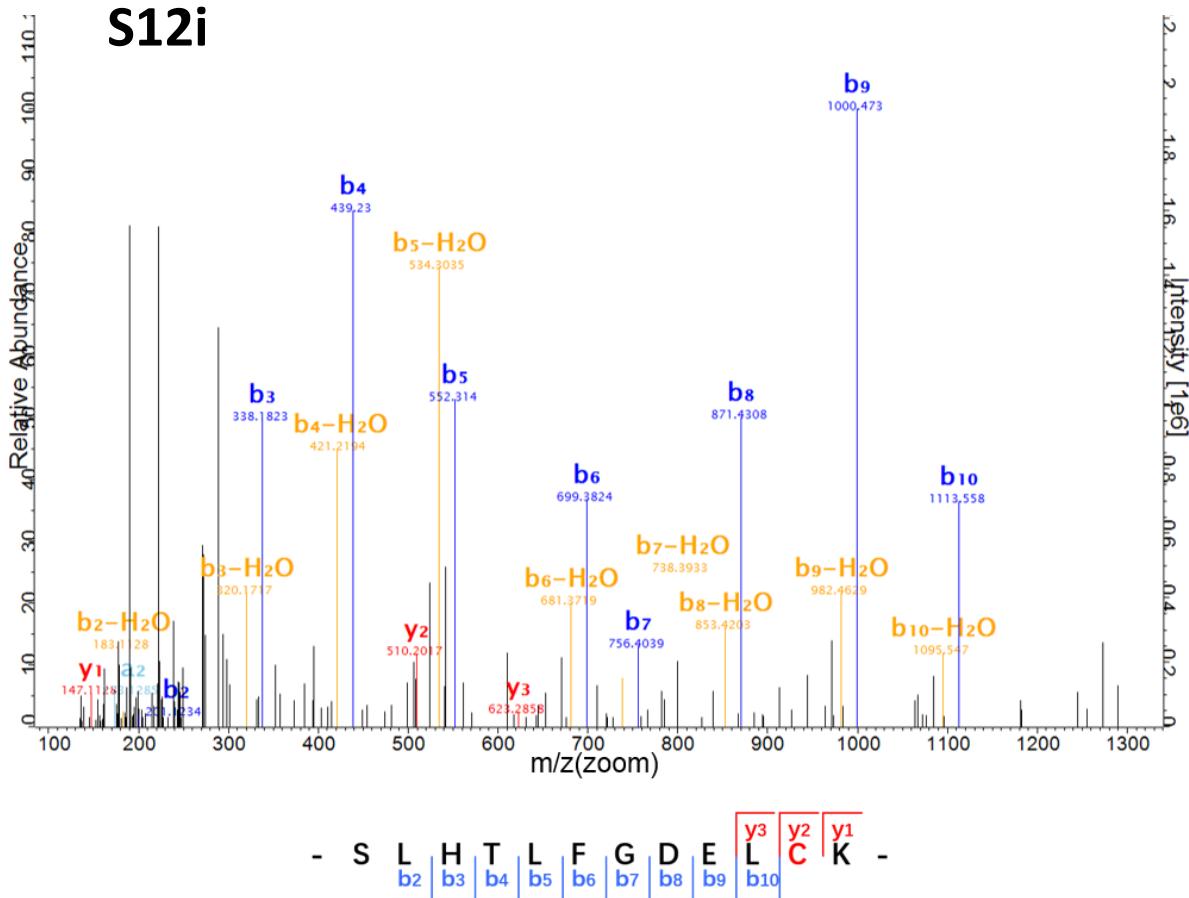
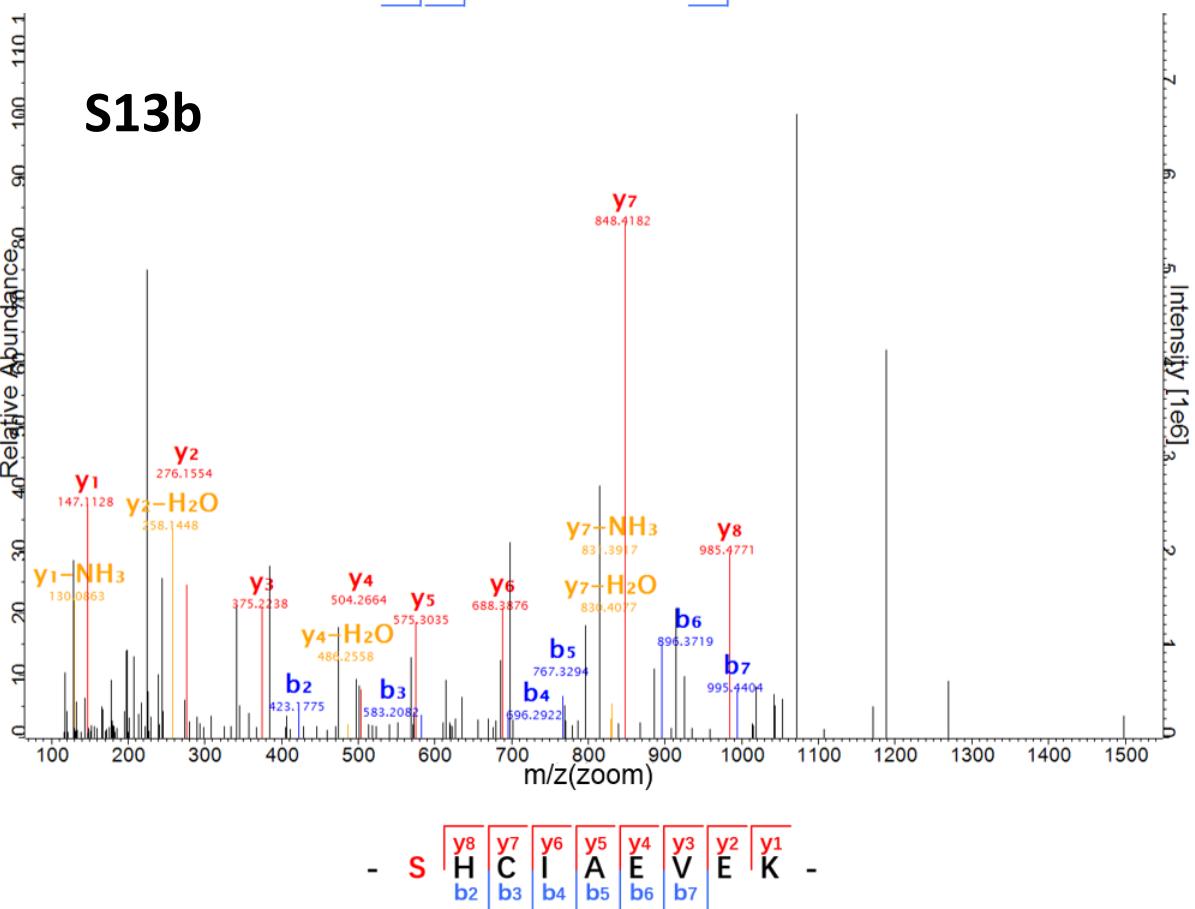
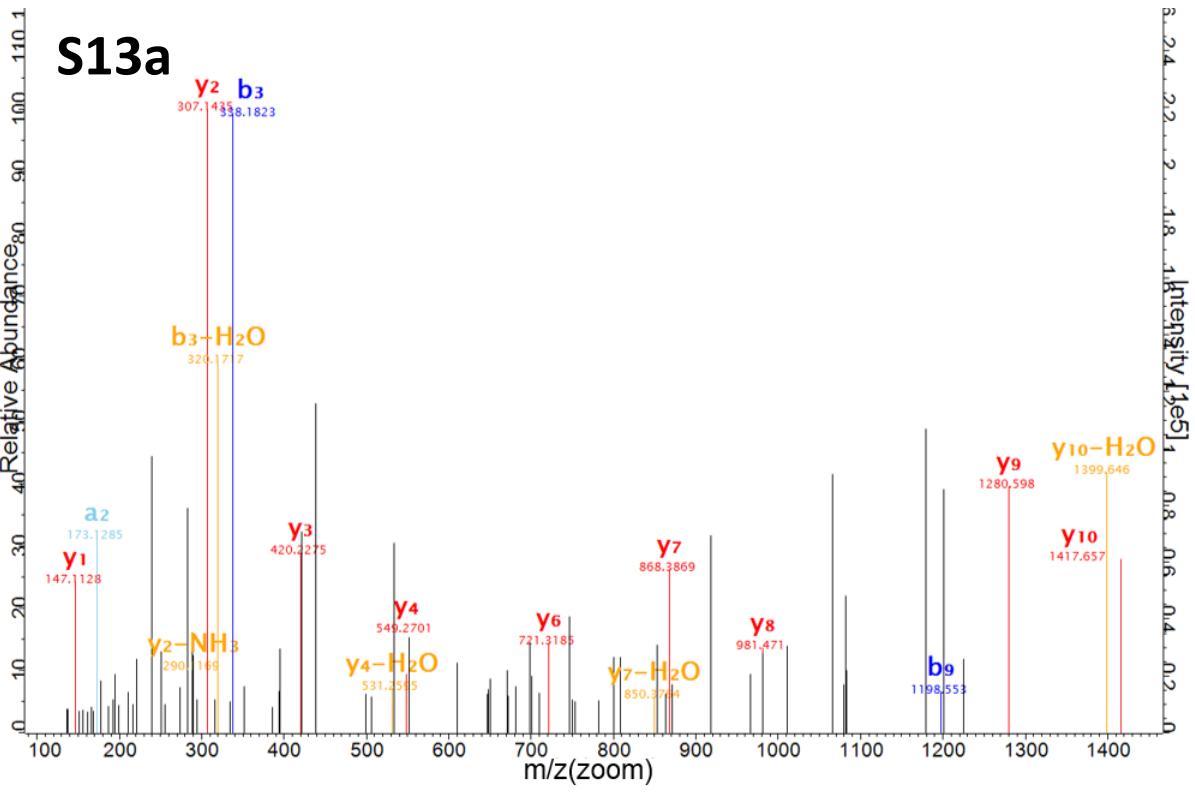
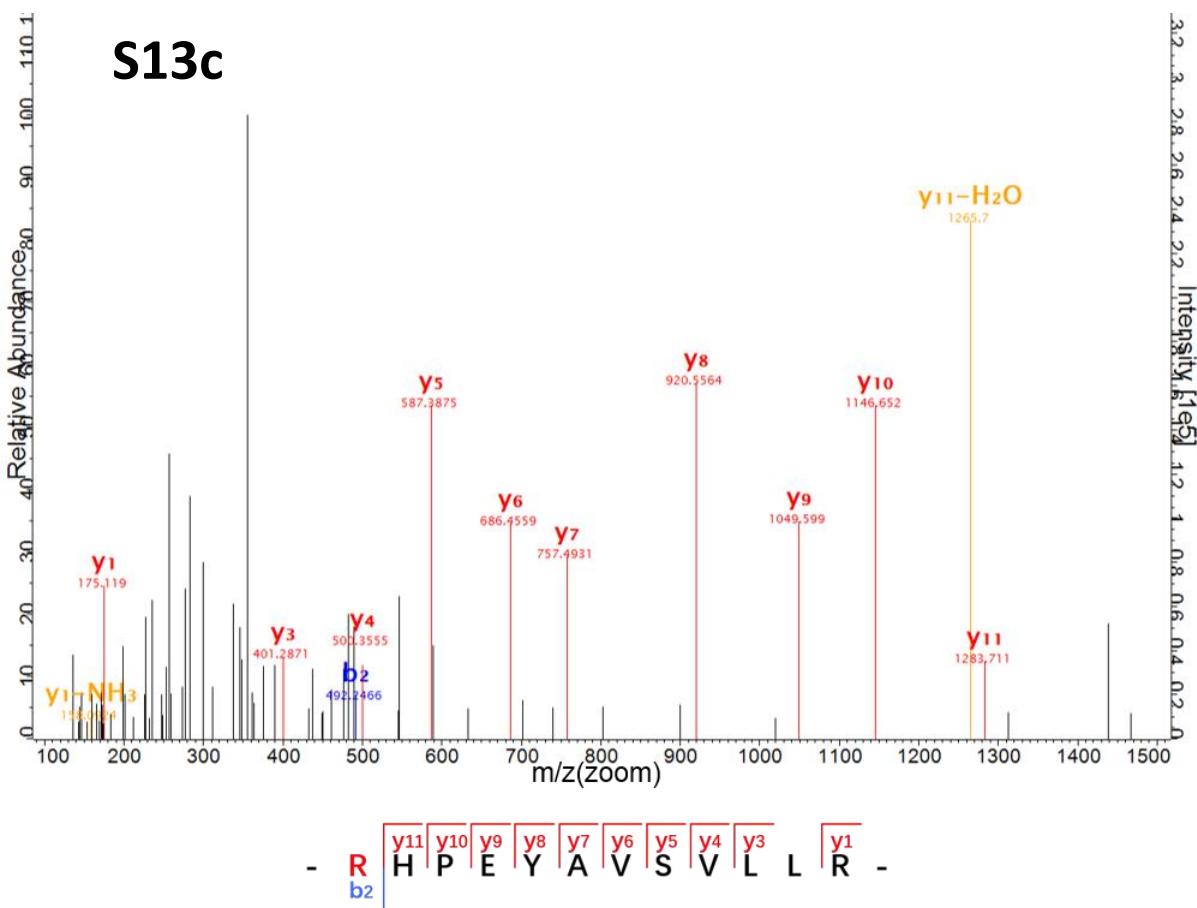


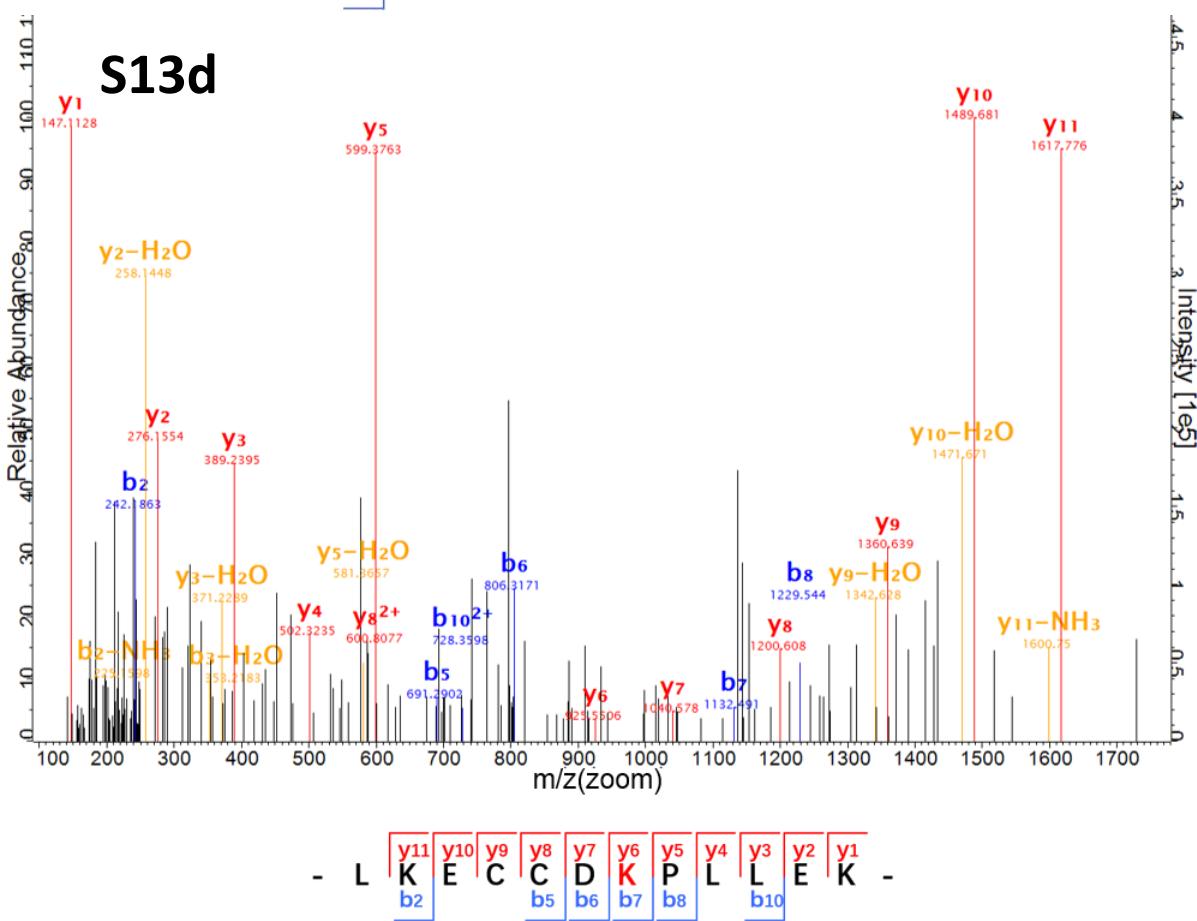
Figure S12a~i. Representative photo-cross-linking sites on BSA by MPISC.



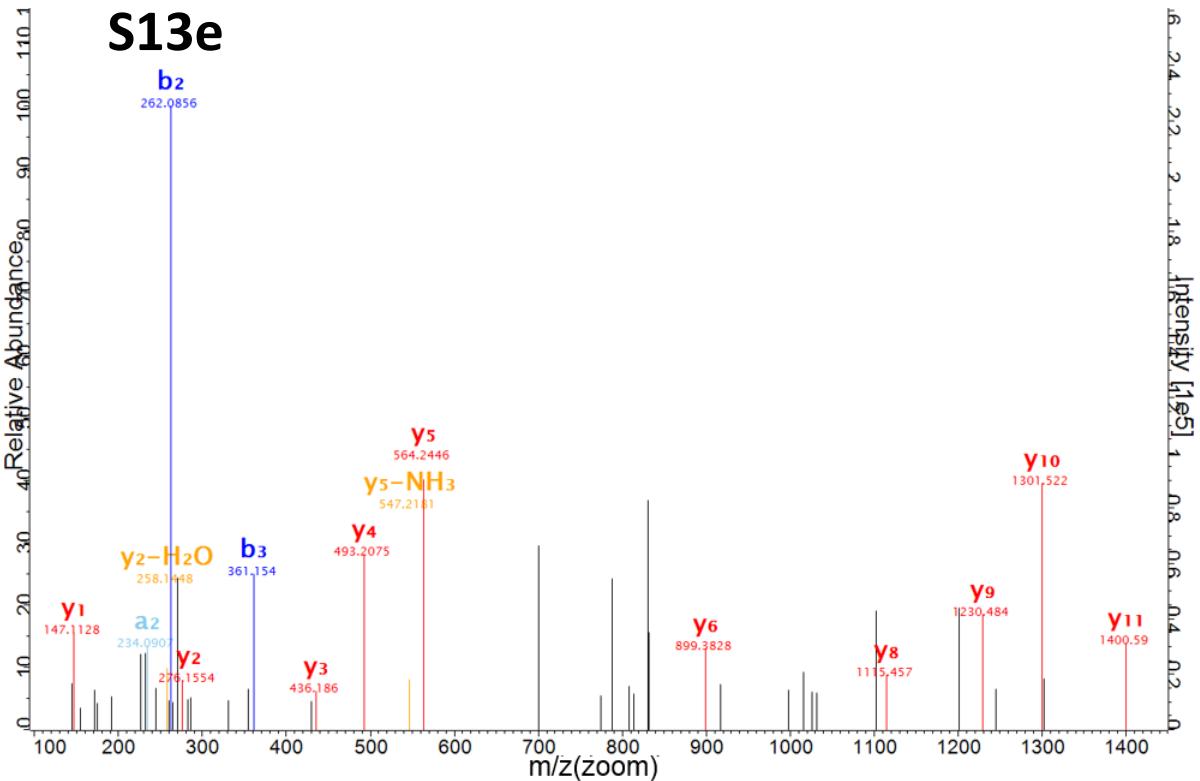
S13c



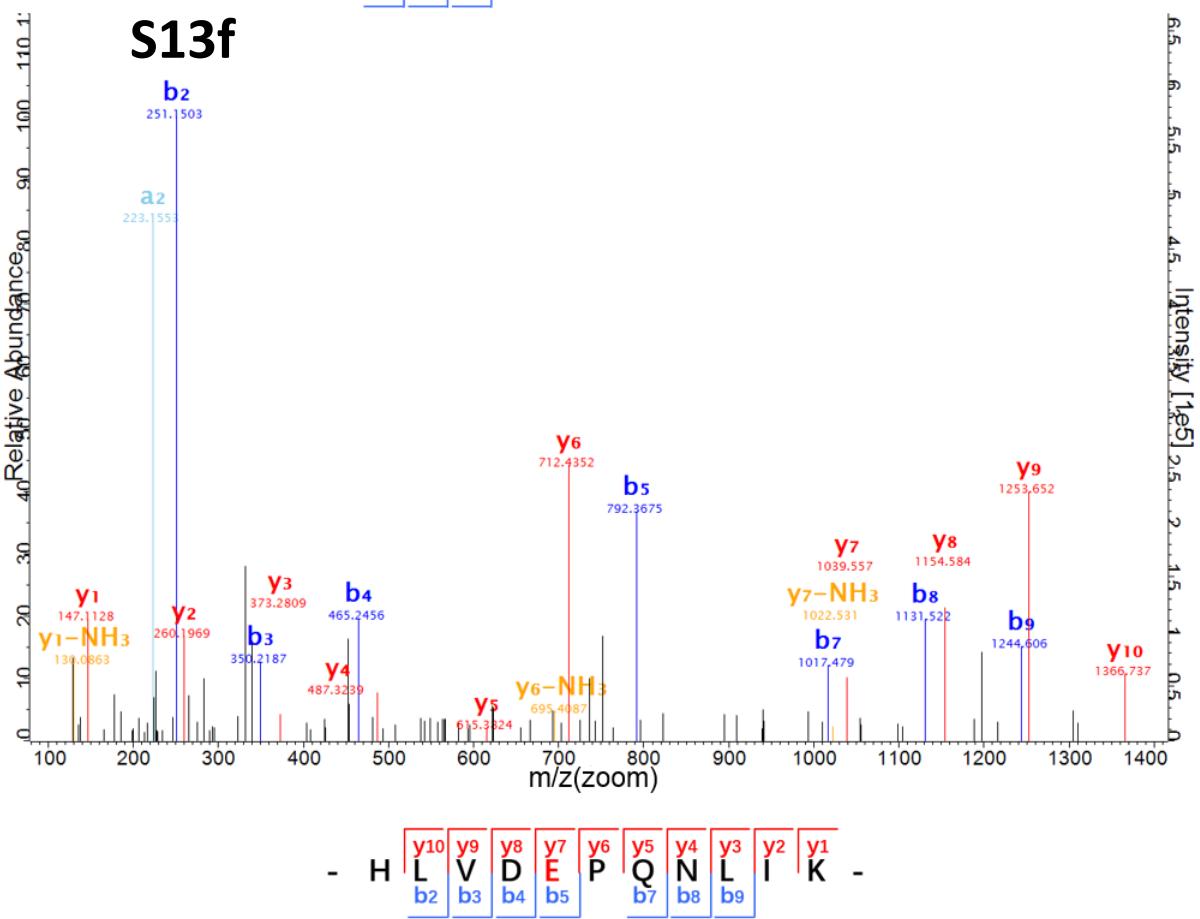
S13d



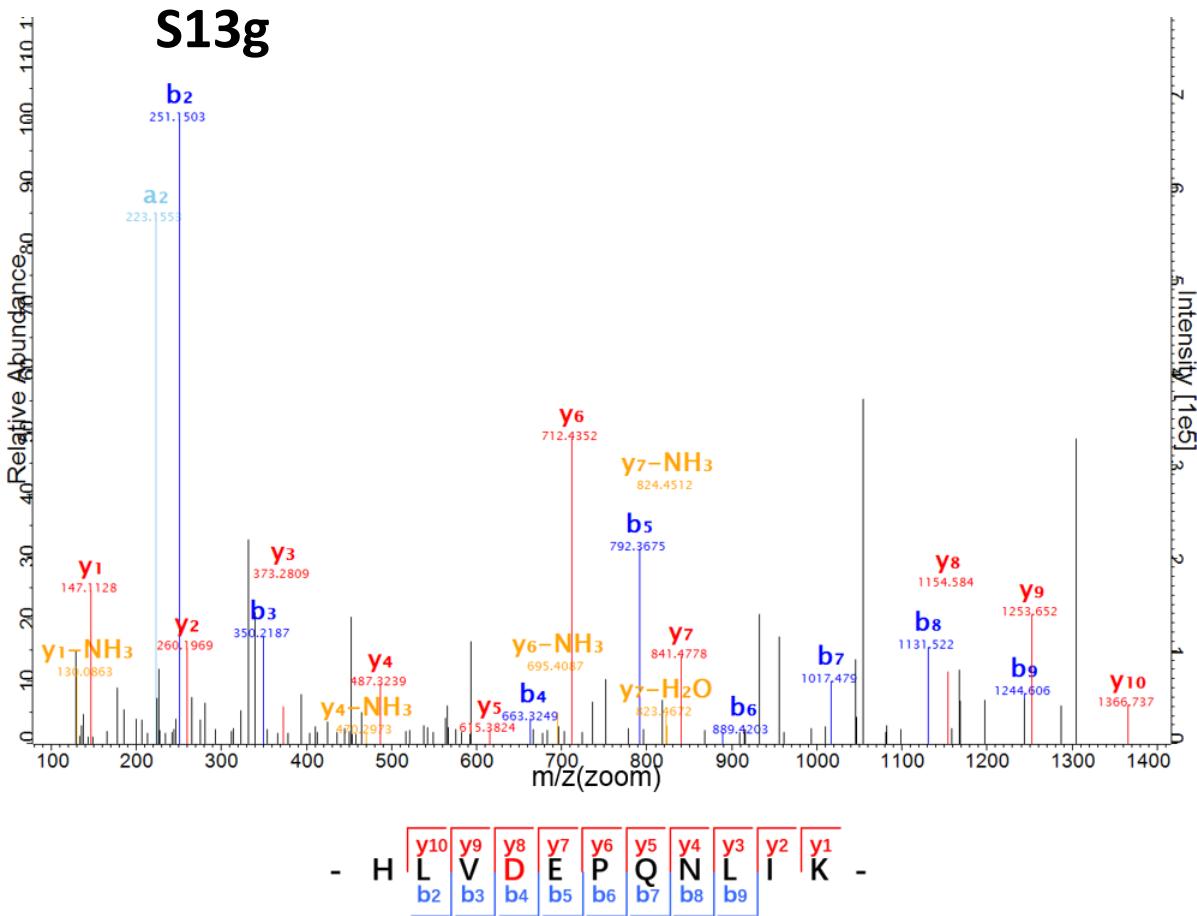
S13e



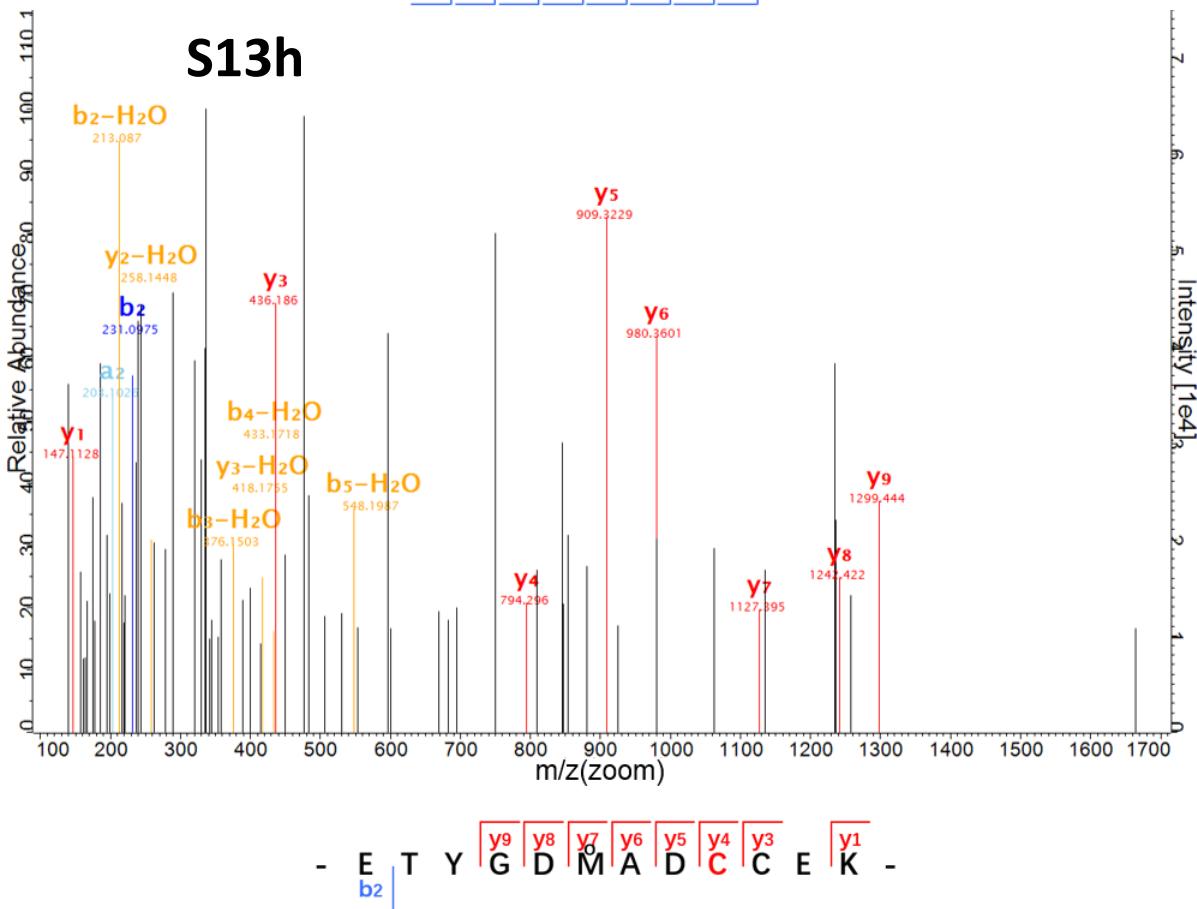
S13f



S13g



S13h



S13i

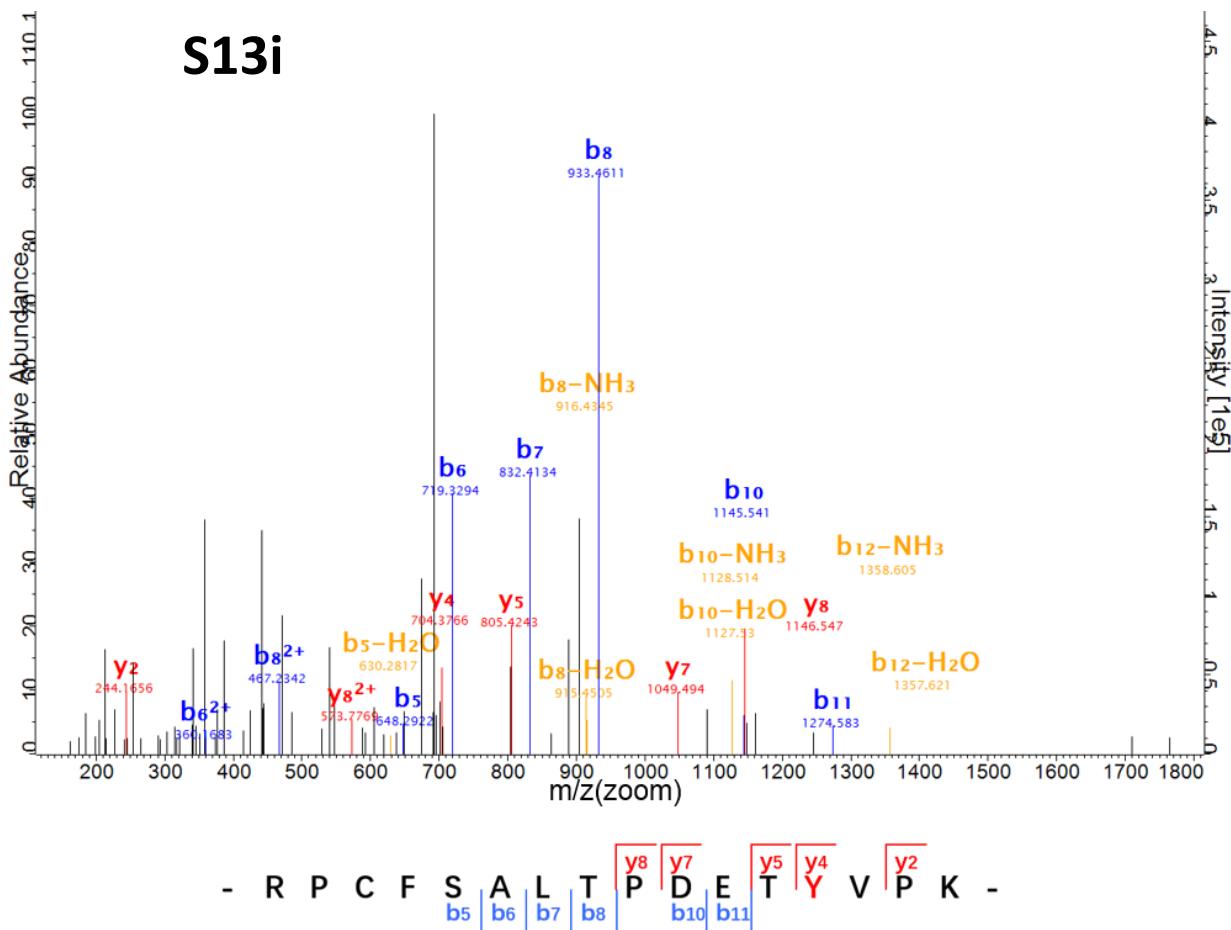


Figure S13a~i. Representative photo-cross-linking sites on BSA by **isx6**.

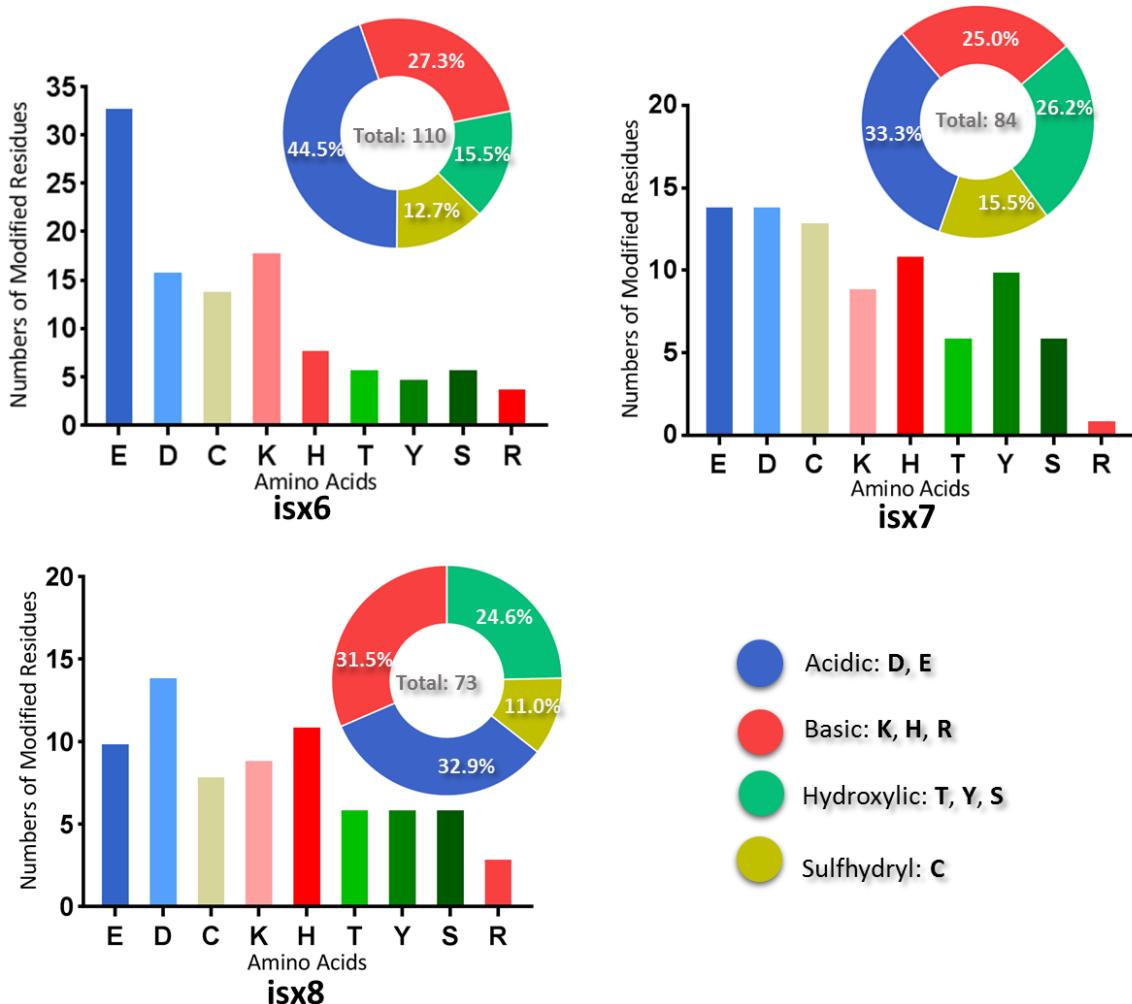


Figure S14. Analysis of photo-cross-linking sites on BSA by isx6~8.

9. Cell Viability Assay

Cell viability assay was performed with HeLa, HEK 293T, A549, and HCT116 cells by Cell Counting Kit-8 (CCK-8, Dojindo). The procedures were based on the previous protocols^[3]. Generally, 3000 cells per well were seeded in 96-well plates and incubated for 12 h in a humidified incubator for adhesion. Isoxazole probes were treated at different final concentrations. After 72 h of incubation, 10 µL of CCK-8 reagent was added to each well. The absorption at 450 nm was measured with the plate reader after another 0.5~1 h incubation. Cell viability was determined as $V_R = (A - A_0)/(A_s - A_0) \times 100\%$, where A is the absorbance of the experimental group, A_s is the absorbance of the control group (DMSO was used as the control), and A_0 is the absorbance of the blank group (no cell). Cell viability and IC₅₀ values were analyzed with GraphPad Prism.

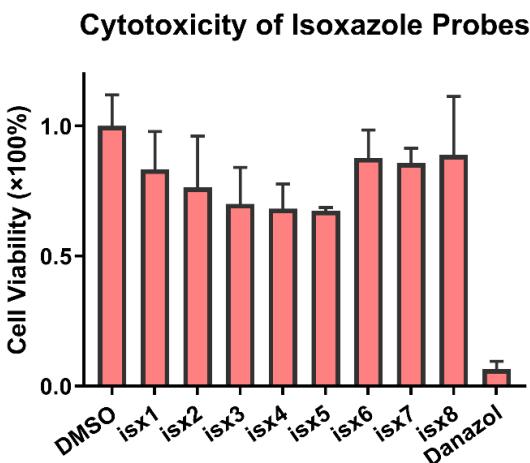


Figure S15. Cell viability of HEK 293T treated with 5 μ M of isoxazole probes. Error bars = standard deviation of the mean, n = 5.

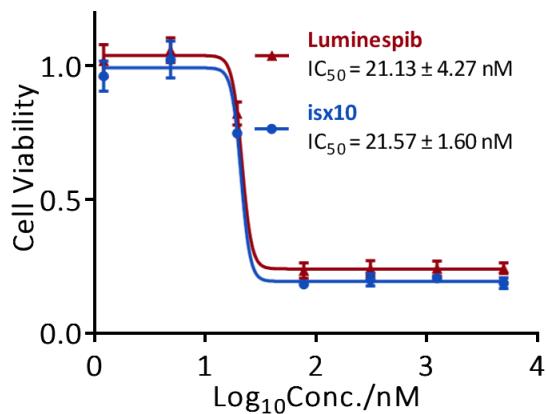


Figure S16. Cell viability of HCT116 treated with **isx10** or Luminespib. Error bars = standard deviation of the mean, n = 5.

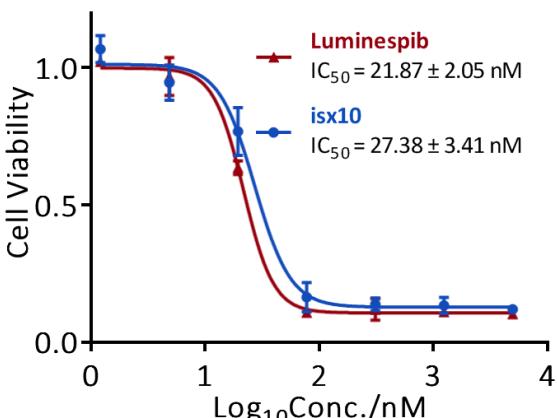


Figure S17. Cell viability of A549 treated with **isx10** or Luminespib. Error bars = standard deviation of the mean, n = 5.

10. UV-triggered Covalent Inhibition of Hsp90 by Luminespib

For cytotoxicity of co-treatment of Luminespib and UV irradiation, HeLa cells (3000 cells per well) were seeded in 96-well plates and incubated overnight for adhesion. The next day, the cell medium was replaced with the Luminespib-containing medium and incubated in the incubator for 4 h. Subsequently, the medium was removed, and cells were washed twice with PBS, followed by UV irradiation for 30 s. For control groups, cells were not treated with **isx10** or UV irradiation. Cells were further incubated in the incubator for 72 h before 10 μ L of CCK-8 reagent was added to each well. After another 0.5~1 h incubation, the absorbance at 450 nm was measured, and the cell viability was calculated.

For WB analysis of Hsp90 client proteins, HeLa cells were seeded in 6-well plates and cultured to 50% confluence. Next, the medium was replaced with the Luminespib-containing medium and incubated in the incubator for 4 h. Subsequently, the medium was removed, and cells were washed twice with PBS, followed by UV irradiation for 30 s. For negative controls, cells were not treated with **isx10** or UV irradiation. Cells were further incubated for 48 h and lysed by the RIPA lysis buffer containing protease inhibitors. The concentration of the resulting lysate was determined by the BCA protein assay kit and adjusted to 1 mg/mL with PBS. Then, WB analysis was performed with primary antibodies of Hsp90 client proteins, including c-Raf (1:1000, #53745, CST), HER2 (1:1000, ab134182, Abcam), Akt (1:1000, #4691, CST).

11. Gel-Based Labeling Experiments

11.1 Labeling of Recombinant Proteins

Gel-based labeling experiments were based on previous protocols^[3]. Briefly, isoxazole probes (**isx1~8**, 5 μ M) were added to a solution of recombinant proteins (BSA, avidin, SIRT5, and esterase) in PBS (1 mg/mL). The mixture was incubated at r.t. for 30 min and then irradiated with 302 nm UV for 5 min on ice. Subsequently, the sample was treated with a click chemistry cocktail (30 μ M TAMRA-N₃ from 30 mM stock solution in DMSO, 100 μ M THPTA from 100 mM freshly prepared stock solution in DMSO, 1 mM TCEP from 1 M freshly prepared stock solution in deionized water, and 1 mM CuSO₄ from 1 M freshly prepared stock solution in deionized water). After 2 h reaction at r.t., prechilled acetone was added to precipitate the protein. The protein was collected by centrifugation at 4°C for 15 min, dissolved in 1× SDS loading buffer, and boiled at 95°C for 10 min before SDS-PAGE analysis. The gel was visualized by in-gel fluorescence scanning and CBB staining.

The labeling of BSA (1 mg/mL) by **isx6** under different pH conditions was performed in the Britton–Robinson buffer, based on above procedures.

For UV time-dependent and dose-dependent labeling of BSA, **isx6** was added to a solution of BSA in PBS (1 mg/mL) in different concentrations. The mixture was divided into 4 groups and incubated at r.t. for 30 min before irradiating with 302 nm UV on ice for different durations (0, 20, 60, 300 s, 500 s). Samples were then clicked with TAMRA-N₃, precipitated by prechilled acetone, resolved in SDS-PAGE gel, and visualized by in-gel fluorescence scanning and CBB staining, based on the procedures mentioned above.

For labeling of recombinant Hsp90, different amounts of human Hsp90 α (2~15 pmol, ab48801, Abcam) were incubated with **isx10** in PBS. Negative control was treated with DMSO. The mixtures were incubated at 37°C for 30 min before UV irradiation for 5 min on ice. Samples were then clicked with TAMRA-N₃, precipitated by prechilled acetone, separated in SDS-PAGE gel, and visualized by in-gel fluorescence scanning and CBB staining, based on the procedures mentioned above. The labeling intensity was quantified by imageJ.

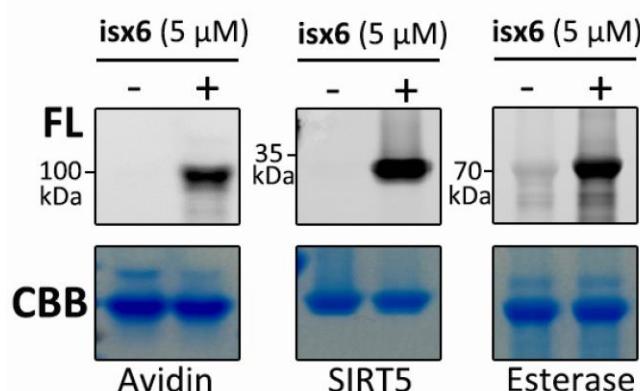


Figure S18. Gel-based labeling of avidin, SIRT5, and esterase with **isx6**.

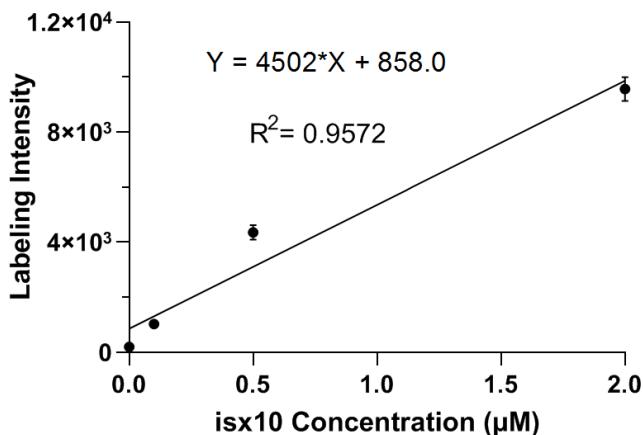


Figure S19. Labeling intensity quantification of **isx10** towards recombinant Hsp90. Error bars = standard deviation of the mean, n = 3.

11.2 In Vitro/Situ Proteome Labeling

For in vitro proteome labeling, cell lysates were first prepared from HeLa cells. Generally, HeLa cells were cultured to 90% confluence. The medium was removed, and cells were washed twice with cold PBS. RIPA lysis buffer (Pierce) with protease inhibitors (Halt) was added, and cells were scraped into a solution. The solution was placed at 0°C for 30 min and then centrifuged to obtain the supernatant as the cell lysate. Protein concentration was determined by the BCA protein assay kit (Pierce) and adjusted to 1 mg/mL with PBS. 2 μM of **isx10** was incubated with 50 μL of the resulting lysate in the presence or absence of Luminespib (20 μM). The control group was treated with DMSO. After incubation at 37°C for 30 minutes, the samples were irradiated with 302 nm UV for 5 min on ice. A freshly premixed click chemistry cocktail was then treated (50 μM TAMRA-N₃ from 30 mM stock solution in DMSO, 100 μM THPTA from 100 mM freshly prepared stock solution in DMSO, 1 mM TCEP from 1 M freshly prepared stock solution in deionized water, and 1 mM CuSO₄ from 1 M freshly prepared stock solution in deionized water). The mixture was incubated at r.t. for 2 h before precipitating with prechilled acetone, followed by centrifugation (14000 rpm, 15 min at 4°C). The resulting pellets were dissolved in 1× SDS loading buffer and boiled at 95°C for 10 min before SDS-PAGE separation. Finally, the gels were visualized by in-gel fluorescence scanning and CBB staining.

For in situ proteome labeling, HeLa or HEK 293T cells were grown to 90% confluence in 6-well plates. Then, the medium was removed, and cells were washed twice with PBS, followed by treatment of isoxazole-containing medium. For **isx10**, Hela cells were treated with 2 μM of **isx10** in the presence or absence of Luminespib (20 μM). For in situ proteome labeling of

isx1~8, **DZP**, and **BZP**, HeLa cells were treated with 5 μ M of each probe. For in situ proteome labeling of Danazol, HEK 293T cells were treated with 5 μ M of Danazol. DMSO was treated as a negative control. After 4 h incubation, the medium was removed, and cells were washed twice with PBS to remove the probes, followed by UV irradiation (302 nm) for 5 min on ice. Subsequently, cells were lysed by RIPA lysis buffer with protease inhibitor. The concentration of the resulting lysate was determined and adjusted to 1 mg/mL with PBS, followed by the click chemistry reaction, SDS-PAGE separation, and visualization procedures described above.

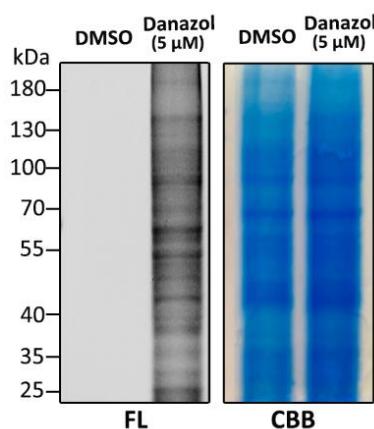


Figure S20. In situ labeling profile of Danazol (5 μ M) with HEK 293T cells.

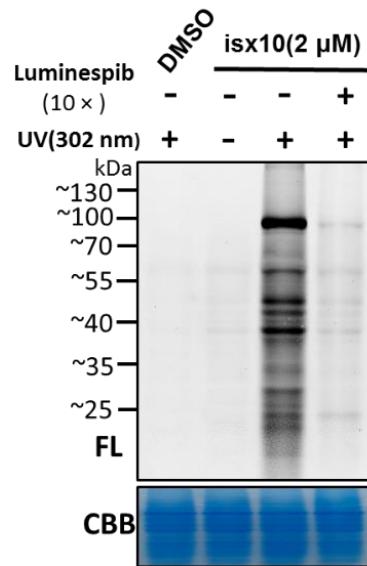


Figure S21. In vitro labeling of HeLa cell lysate by 2 μ M of **isx10**.

12. Cell Imaging

Cell imaging was performed based on previous protocols^[3]. HeLa cells were seeded in glass-bottom dishes and grown to 50% confluence. Next, the cell medium was replaced with an **isx10**-containing medium in the presence or absence of Luminespib (10 \times). Cells treated with DMSO were used as a negative control. After 2 h incubation, the medium was removed, and cells were gently washed twice with PBS, followed by UV irradiation (302 nm) for 2 min on ice. Cells were then fixed with 3.7% formaldehyde for 10 min at r.t. and permeabilized by 0.1% Triton X-100 in PBS for 10 min. Next, cells were incubated with a freshly premixed click chemistry cocktail (50 μ M TAMRA-N₃ from 2.5 mM stock solution in DMSO, 0.1 mM THPTA from 2.5 mM freshly prepared stock solution in deionized water, 1 mM TCEP from 25 mM freshly prepared stock solution in deionized water, and 1 mM CuSO₄ from 25 mM freshly prepared stock solution in deionized water). After shaking at r.t. for 2 h, cells were washed with PBST (0.1% Tween 20 in PBS), blocked with 3% BSA in PBST for 1 h, and treated with anti-Hsp90 (1:1000, CST, #4877) for 1 h at r.t. Subsequently, cells were washed twice with PBST and treated with the secondary antibody (1:1000, ab150077, Abcam) for 1 h and then washed with PBST twice. Finally, cells were imaged with a Leica SP5 confocal microscope.

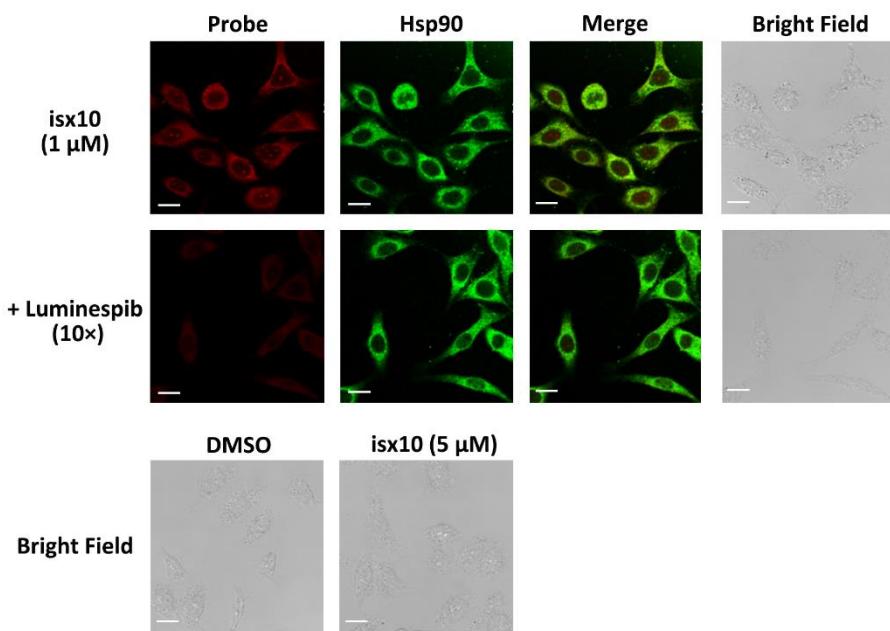


Figure S22. Cellular imaging of **isx10**. Scale bar = 20 μ m.

13. Pull-Down and Chemoproteomic Experiments

The pull-down procedure is based on the previously reported protocols with some optimizations^[3]. For target identification of Danazol, HEK 293T cells were grown to 90% confluence and then treated with 5 μ M of Danazol. For **isx10**, HeLa cells were grown to 90% confluence and then treated with 5 μ M of **isx10** in the presence or absence of Luminespib (50 μ M). Negative controls treated with DMSO were conducted simultaneously. After 4 h of isoxazole probes treatment, the medium was removed, and cells were washed twice with cold PBS to remove the probes. Cells were irradiated by UV (302 nm) for 5 min on ice. Following that, cells were lysed by RIPA lysis buffer containing protease inhibitors. The concentration of the resulting lysate was determined by the BCA protein assay kit and diluted to 1 mg/mL with PBS. A freshly premixed click chemistry cocktail was added to the lysates (50 μ M Biotin-N₃ from 30 mM stock solution in DMSO, 100 μ M THPTA from 100 mM freshly prepared stock solution in DMSO, 1 mM TCEP from 1 M freshly prepared stock solution in deionized water, and 1 mM CuSO₄ from 1 M freshly prepared stock solution in deionized water). The reaction mixture was incubated at r.t. for 2 h and then precipitated by prechilled acetone. The proteins were collected by centrifugation (14000 rpm, 10 min at 4°C) and dissolved in 1% SDS in PBS. Streptavidin beads (Pierce, pre-washed with 1% SDS in PBS) were added and incubated for 2 h at r.t. Then, the supernatant was removed, and the beads were washed with 1% SDS in PBS (thrice), 0.1% SDS in PBS (thrice), and PBS (thrice). The beads were treated with 1× SDS loading buffer and boiled at 95°C for 10 min to release the enriched proteins. The enriched proteins were then separated in SDS-PAGE for the following chemoproteomic or WB analysis. WB analysis were carried out with the corresponding antibodies, including Hsp90 (1:1000, #4877, CST), NASP (1:2000, ab181169, Abcam), ITGB1 (1:1000, ab134179, Abcam), PTGES2 (1:1000, ab229961, Abcam), PDIA1 (1:1000, ab137110, Abcam), and P53 (1:2000, ab32389, Abcam).

For chemoproteomic analysis, the enriched proteins were resolved by SDS-PAGE, followed by CBB staining. The entire gel lanes were cut into small particles, collected, and destained with 25 mM of ammonium bicarbonate in water and 25 mM of ammonium bicarbonate in 50% acetonitrile until the blue color disappeared completely. The gel particles were incubated in 10 mM DTT in 25 mM ammonium bicarbonate buffer for 1 h at 60°C, then treated with 20 mM of IAA in 25 mM ammonium bicarbonate at r.t. for 1 h in dark. Subsequently, the particles were digested with trypsin (Promega) at 37°C overnight. The next day, the supernatants were

collected, and the gel particles were further extracted with 50% acetonitrile (with 1% formic acid). The supernatants were combined and dried before TMT labeling.

For TMT labeling, the peptide concentration of the samples (alkylated, digested) was first quantified using a quantitative colorimetric peptide assay (Pierce). Subsequently, the peptide samples were dried and dissolved in 15 µL of 100 mM TEAB buffer. 0.8 mg of the TMT reagents (TMT10plexTM) were first dissolved in 41 µL anhydrous acetonitrile, then 5 µL of the resulting TMT solution was added to each peptide sample. The mixture was incubated at r.t. for 2 h. Subsequently, 8 µL of 5% hydroxylamine was added to quench the reaction. The labeled peptide samples were mixed equivalently and dried in speedvac. The samples were analyzed with LC-MS/MS after desalting by C18 columns (Waters).

The peptides were detected using an Orbitrap Fusion Lumos mass spectrometer (Thermo, United States). About 1 µg of peptides were separated in a home-made column (75 µm x 15 cm) packed with C18 AQ (5 µm, 300Å, MichromBioResources, Auburn, CA, USA) at a flow rate of 600 nL/min. Mobile phase A (0.1% formic acid in 2% ACN) and mobile phase B (0.1% formic acid in 98% ACN) were used to establish a 90 min gradient comprised of 20 min of 5% B, 40 min of 14-26% B, 19 min of 26-40% B, 1 min of 40-95% B and 10 min of 95% B. Peptides were then ionized by electrospray at 1.9 kV. A full MS spectrum (375-1400 m/z range) was acquired at a resolution of 120,000 at m/z 200 and a maximum ion accumulation time of 20 ms. Dynamic exclusion was set to 30 s. Resolution for HCD MS/MS spectra was set to 30,000 at m/z 200. The AGC setting of MS and MS² were set at 3E6 and 1E5, respectively. The 20 most intense ions above a 1.0E3 counts threshold were selected for fragmentation by HCD with a maximum ion accumulation time of 60 ms. An isolation width of 1.6 m/z units was used for MS². Single and unassigned charged ions were excluded from MS/MS. For HCD, normalized collision energy was set to 25%.

The raw data were processed by using MaxQuant software (1.5.8.3) and processed as per default workflow. MS tolerance is 4.5 ppm, and MS/MS tolerance is 20 ppm. Searches were performed against the UniProtKB human database (taxonomy 9606, version 20200112). Reversed database searches were used to evaluate the false discovery rate (FDR) of site, peptide, and protein identifications. Two missed cleavage sites of trypsin were allowed. Carbamidomethylation (C) was set as a fixed modification, and Acetyl (Protein N-term), Oxidation (M), MPISC (modified by **MPISC**), ISX6 (modified by **isx6**), ISX7 (modified by **isx7**), ISX8 (modified by **isx8**), were set as variable modifications. The FDR of both peptide identification and protein identification is set to be 1%^[4]. The options of “Second peptides”,

“Match between runs”, and “Dependent peptides” were used. Label-free quantification was used to quantify the difference between different samples^[5].

As such, there is no fixed cut-off score threshold, but instead, spectra were accepted until the 1% false discovery rate (FDR) is reached. Only peptides with a minimum length of 7 amino acids were considered for identification and detected in at least one or more of the replicates. All isoxazole-modified peptide spectra were manually validated by applying stringent acceptance criteria: only modification event on amino acid residues with PEP ≤ 0.01 were used for further analysis. Assignments were screened for peptides uniquely labeled on a single amino acid residue in two out of three biological replicates.

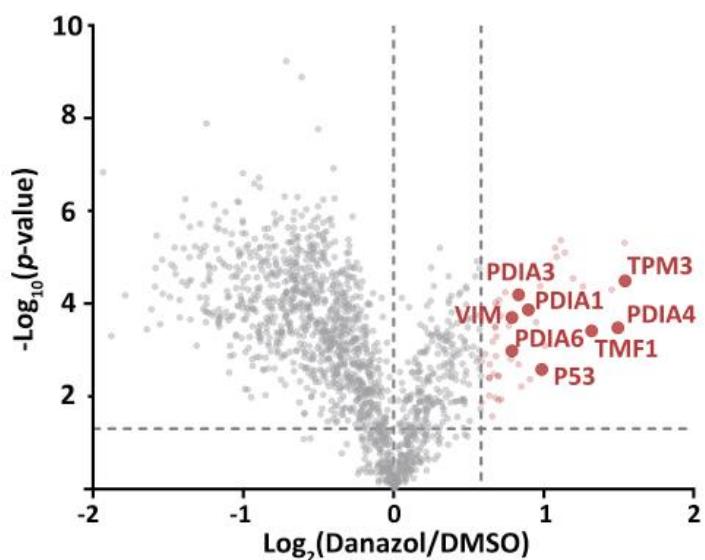


Figure S23. Volcano plot of enriched proteins by Danazol (5 μM) in HEK 293T cells. Quantified criteria: fold enrichment of Danazol/DMSO ≥ 1.5 and $p\text{-value} < 0.05$; Red dots represent qualified protein hits; Chemoproteomic experiments were performed in four replicates.

Table S1. Protein hits qualified in chemoproteomic analysis of Danazol (5 μM) in HEK 293T cells (Danazol/DMSO ratio ≥ 1.5 and $p\text{-value} < 0.05$).

Gene	UniProtKB Entry	UniProtKB Accession	Protein Description	Average Ratio (Danazol/DMSO)	$p\text{-value}$
TPM3	TPM3	P06753	Tropomyosin alpha-3 chain	2.91075	3.23E-05
AKAP8L	AKP8L	Q9ULX6	A-kinase anchor protein 8-like	2.90725	4.79E-06
PDIA4	PDIA4	P13667	Protein disulfide-isomerase A4	2.8165	0.000332
TXLNA	TXLNA	P40222	Alpha-taxilin OS=Homo sapiens	2.74225	4.98E-05
TMF1; ARA160	TMF1	P82094	TATA element modulatory factor	2.49525	0.000382
DNAJC9	DNJC9	Q8WXX5	Dnaj homolog subfamily C member 9	2.398	4.24E-05

YWHAQ	1433T	P27348	14-3-3 protein theta OS=Homo sapiens	2.2945	2.83E-05
DBN1	DREB	Q16643	Drebrin OS=Homo sapiens	2.206	7.89E-06
ANP32A	AN32A	P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A	2.163	4.21E-06
MAP4	MAP4	P27816	Microtubule-associated protein 4	2.12375	9.51E-06
CIAPIN1	CPIN1	Q6FI81	Anamorsin	2.109	6.19E-06
DSG1	DSG1	Q02413	Desmoglein-1	2.01225	0.000812
TP53; P53	P53	P04637	Cellular tumor antigen p53	1.98525	0.002595
MBNL1	MBNL1	Q9NR56	Muscleblind-like protein 1	1.96725	4.11E-05
CCNK	CCNK	O75909	Cyclin-K	1.9305	0.000251
PSMA4	PSA4	P25789	Proteasome subunit alpha type-4	1.87925	0.004292
P4HB; PDIA1	PDIA1	P07237	Protein disulfide-isomerase	1.8665	0.000134
NFS1	NFS1	Q9Y697	Cysteine desulfurase, mitochondrial	1.804	0.006114
SPART	SPART	Q8N0X7	Spartin	1.78425	0.001996
PDIA3	PDIA3	P30101	Protein disulfide-isomerase A3	1.783	6.42E-05
PDIA6	PDIA6	Q15084	Protein disulfide-isomerase A6	1.72775	0.001046
VIM	VIME	P08670	Vimentin	1.7275	0.000199
RAB11FIP4	RFIP4	Q86YS3	Rab11 family-interacting protein 4	1.7215	0.001578
RRBP1	RRBP1	Q9P2E9	Ribosome-binding protein 1	1.70525	0.000297
NARS2	SYNM	Q96I59	Probable asparagine-tRNA ligase, mitochondrial	1.6755	5.67E-05
SLC30A1	ZNT1	Q9Y6M5	Zinc transporter 1	1.64525	0.011541
SCAMP3	SCAM3	O14828	Secretory carrier-associated membrane protein 3	1.6415	0.000182
PAPOLA	PAPOA	P51003	Poly(A) polymerase alpha	1.628	8.25E-05
COQ9	COQ9	O75208	Ubiquinone biosynthesis protein COQ9, mitochondrial	1.623	0.003619
DCTN2	DCTN2	Q13561	Dynactin subunit 2	1.623	0.012117
NUDC	NUDC	Q9Y266	Nuclear migration protein nudC	1.61925	0.003561
SF3A2	SF3A2	Q15428	Splicing factor 3A subunit 2	1.61625	0.000109
FXR1	FXR1	P51114	Fragile X mental retardation syndrome-related protein 1	1.60925	0.000511
LNPK	LNP	Q9C0E8	Endoplasmic reticulum junction formation protein lunapark	1.607	0.001332
CCDC6	CCDC6	Q16204	Coiled-coil domain-containing protein 6	1.6035	9.5E-05
GOLGA3	GOGA3	Q08378	Golgin subfamily A member 3 OS=Homo sapiens	1.60275	0.00033
DPH7	DPH7	Q9BTW6	Diphthine methyltransferase OS=Homo sapiens	1.6015	0.010651
ATP5MC1	AT5G1	P05496	ATP synthase F(0) complex subunit C1, mitochondrial	1.598	0.000303
RP2	XRP2	O75695	Protein XRP2	1.5865	0.003321
UBE2J1	UB2J1	Q9Y385	Ubiquitin-conjugating enzyme E2 J1	1.584	0.000648
EYA3	EYA3	Q99504	Eyes absent homolog 3	1.58075	0.026927
PNISR	PNISR	Q8TF01	Arginine-serine-rich protein PNISR	1.5595	0.00202
MARCKS	MARCS	P29966	Myristoylated alanine-rich C-kinase substrate	1.557	0.00404
MTERF4	MTEF4	Q7Z6M4	Transcription termination factor 4, mitochondrial	1.556	0.003921
CASC3	CASC3	O15234	Protein CASC3	1.55525	0.009573
USP5	UBP5	P45974	Ubiquitin carboxyl-terminal hydrolase 5	1.52725	0.00121
PSMG1	PSMG1	O95456	Proteasome assembly chaperone 1	1.503	0.001731
VPS72	VPS72	Q15906	Vacuolar protein sorting-associated protein 72 homolog	1.50275	0.013451

Table S2. Protein targets identified by chemoproteomic experiments of **isx10** (5 μ M) in HeLa cells (**isx10/DMSO** ratio ≥ 1.5 and p -value < 0.05).

Gene	UniProtKB Entry	UniProtKB accession	Protein Description	Average Ratio (isx10/DMSO)	p -value
HSP90AB1	HS90B	P08238	Heat shock protein HSP 90-beta	4.3910	0.000414015
HSP90AA1	HS90A	P07900	Heat shock protein HSP 90-alpha	1.9058	0.000699223
NASP	NASP	P49321	Nuclear autoantigenic sperm protein, NASP	1.4691	0.000606439
PTGES2	PGES2	Q9H7Z7	Prostaglandin E synthase 2	3.5408	0.003425087
HERPUD1	HERP1	Q15011	Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 1 protein	2.6449	0.019810169
LUC7L	LUC7L	Q9NQ29	Putative RNA-binding protein Luc7-like 1	2.5554	0.012769821
PSMB6	PSB6	P28072	Proteasome subunit beta type-6	2.1178	0.009416685
RALGAPA1	RGPA1	Q6GYQ0	Ral GTPase-activating protein subunit alpha-1	1.4853	0.001715886

Table S3. Protein targets identified by competitive chemoproteomic experiments of **isx10** (5 μ M) in HeLa cells (**isx10/isx10 + Luminespib** ratio ≥ 1.5 and p -value < 0.05).

Gene	UniProtKB Entry	UniProtKB accession	Protein Description	Average Ratio isx10/isx10+Luminespib	p -value
HSP90AB1	HS90B	P08238	Heat shock protein HSP 90-beta	5.1979	0.001172377
NASP	NASP	P49321	Nuclear autoantigenic sperm protein	1.5069	0.02380254
PSMB6	PSB6	P28072	Proteasome subunit beta type-6	2.2269	0.005358568
LUC7L	LUC7L	Q9NQ29	Putative RNA-binding protein Luc7-like 1	2.1915	0.007272105
ITGB1	ITB1	P05556	Integrin beta-1	1.8484	0.027194165
TXN	THIO	P10599	Thioredoxin, Trx	1.5751	0.000278832
RALGAPA1	RGPA1	Q6GYQ0	Ral GTPase-activating protein subunit alpha-1	2.4148	0.00263713

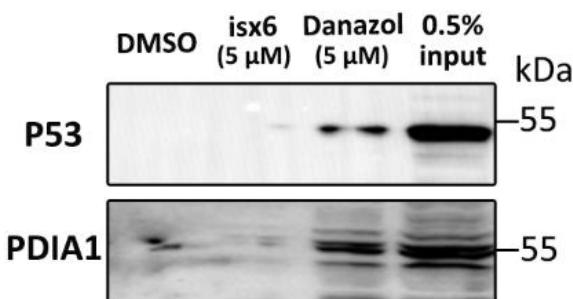


Figure S24. Pull down/WB validation of qualified proteins by Danazol.

14. Protein Disulfide Isomerase (PDI) Activity Assay

The inhibition of Danazol towards protein disulfide isomerase (PDI) was verified by a fluorometric assay kit (Abcam, ab273337). To prepare endogenous protein disulfide isomerases, HEK 293T cells ($\sim 10^7$) were lysed on ice for 10 mins with ice-cold PDI assay buffer (200 μL , supplied in the kit). After centrifugation at 10000 rpm for 5 mins at 4°C, the supernatant lysate was transferred to a fresh tube. Next, 200 μL of saturated ammonium sulfate was added to 100 μL of the resulting lysate and then kept on ice for 20 mins to salt out proteins. After centrifugation at 10000 rpm for 5 mins at 4°C, the supernatant was carefully removed, and the resulting pellet was resuspended with 100 μL of ice-cold PDI assay buffer. Subsequently, 10 μL of the above-reconstituted sample and 0.5 μL of the inhibitors (500 μM of IAA, estrone, 17 β -estradiol, progesterone, and Danazol in DMSO) were added to 39.5 μL of PDI assay buffer in a 96-well plate. Negative control by treating DMSO was performed concurrently. For positive control, 10 μL of exogenous PDI (lyophilized PDI reconstituted with 22 μL of PDI assay buffer, supplied in the kit) was mixed with 40 μL of PDI assay buffer. Next, 1 μL of PDI activator (100 mM in water, supplied in the kit) and 24 μL of PDI assay buffer were mixed and added to each well. After incubating at r.t. for 15 mins, 2 μL of PDI substrate (supplied in the kit) and 23 μL of PDI assay buffer were added to each well for fluorescent detection. The fluorescence (Ex/Em = 490/580 nm) was measured in kinetic mode for 30 mins. Relative PDI activity was calculated as:

$$\text{PDI Activity} = \frac{\mathbf{B}}{(2 \times \Delta t \times V)} = \text{pmol/min}/\mu\text{L} = \mu\text{U}/\mu\text{L}$$

Where **B** is the amount of the sample (pmol) based on the standard fluorescence curve; Δt (5 min) is the reaction duration in the linear range (5-10 min); **V** (10 μL) is the sample volume; **2** stands for the conversion factor, meaning that 1 pmol of the substrate can generate 2 pmol of fluorescence.

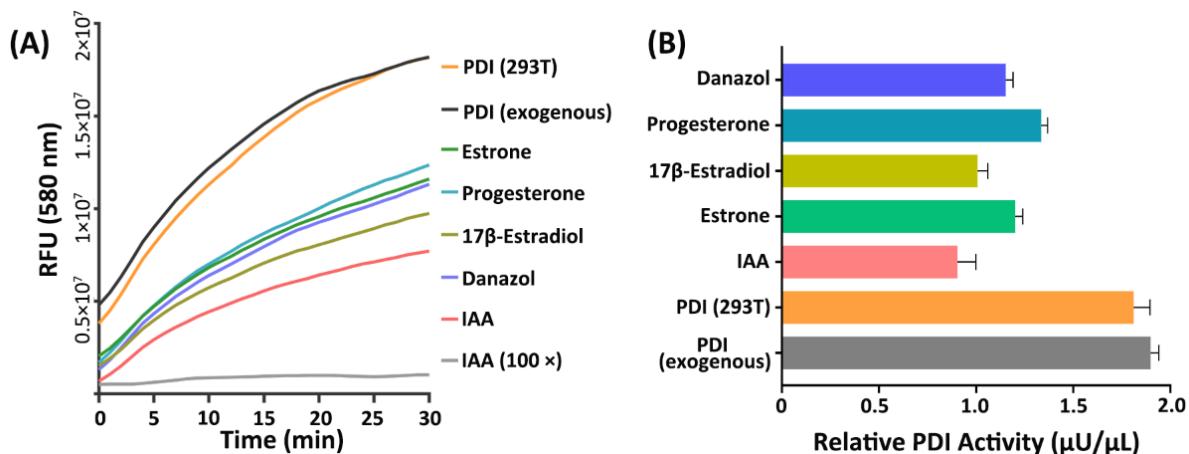


Figure S25. (A) Inhibition of intracellular (HEK 293T cells) PDI activity by iodoacetamide (IAA)/hormones (5 μ M), measured by a fluorescence assay. (B) Relative PDI activity in the presence of IAA/hormones (5 μ M), based on the fluorescence curve in (A) and the standard fluorescence curve; Error bars = standard deviation of the mean, n = 3.

15. Bioinformatic Analysis

Gene expression in normal and tumor tissues was analyzed with the GEPIA^[6], based on the UCSC Xena project (<http://xena.ucsc.edu>). Log₂(TPM + 1) transformation of expression data was applied for long-scale, and the computation was performed with a standard pipeline. TCGA and GTEx normal data were combined and matched with the TCGA tumor data. Protein-protein interaction was analyzed with the STRING database (version: 11.5)^[7]. Gene ontology term analysis of enriched proteins was performed with the DAVID bioinformatics resources^[8].

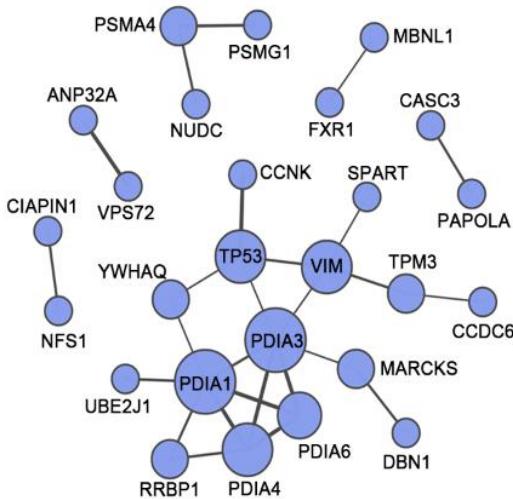


Figure S26. Protein-protein interactions analysis of qualified proteins by danazol. Minimum required interaction score: 0.4; Line thickness indicates the correlation between nodes.

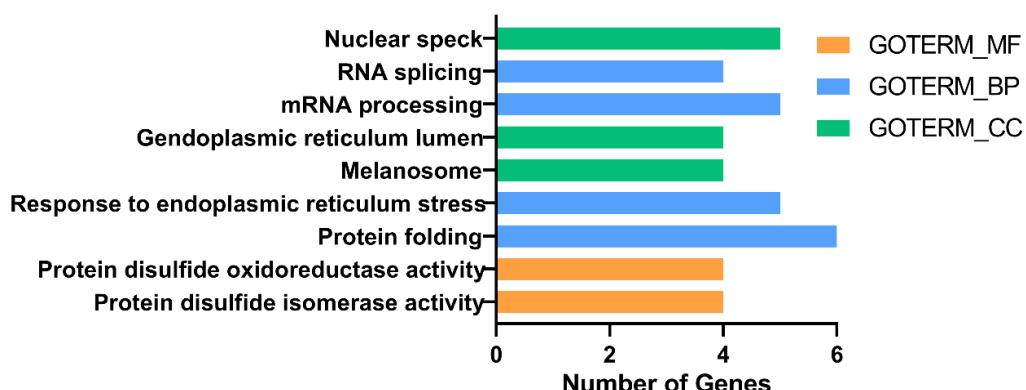


Figure S27. GO-term analysis of protein targets identified by Danazol.

16. Cellular Thermal Shift Assay (CETSA)

Cellular Thermal Shift Assay (CETSA) was based on previous protocols^[9]. HeLa cells were cultured to 90% confluence. The medium was removed, and cells were washed with PBS twice. Next, cells were treated with the medium containing Luminespib (5 μ M) or indomethacin (5 μ M) for 4 h in the incubator. For the negative control, cells were treated with DMSO only. Subsequently, the medium was removed, and cells were washed with PBS twice, trypsinized, and harvested by centrifugation (1000 rpm). The resulting cell pellets were resuspended in PBS and equivalently divided into several groups. Subsequently, these groups were treated with gradient temperatures (43~70°C) in a heater for 3 min. Next, cells were lysed via a liquid nitrogen freeze and thaw cycle three times. The resulting mixture was centrifugated at 14000

rpm for 15 mins at 4°C. Equivalent amounts of the supernatant were transferred to new tubes and mixed with the 5 × SDS-PAGE loading buffer. After boiling at 95°C for 10 min, the mixture was resolved in SDS-PAGE gels and analyzed by WB with corresponding antibodies. SOD1, a thermal-stable protein, was used as a negative control. The blotting intensity was quantified by Image Lab 3.0 (Bio-Rad).

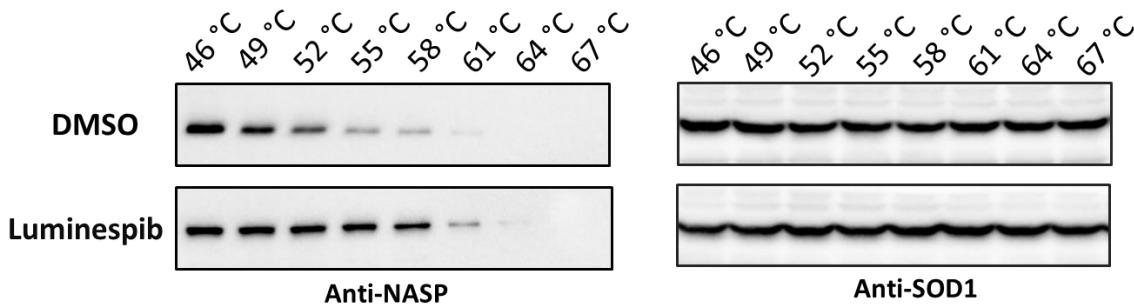


Figure S28. CETSA analysis of the stabilization of NASP by Luminespib (5 μ M) in HeLa cells.

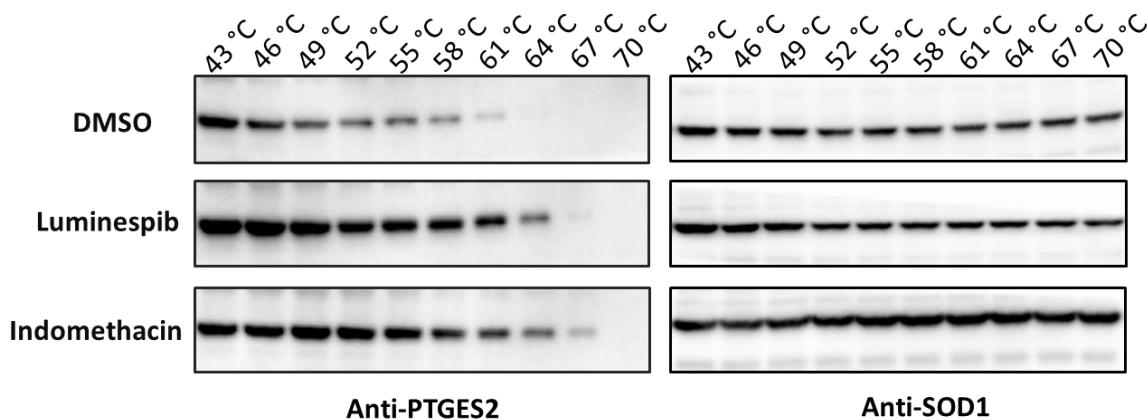


Figure S29. CETSA analysis of the stabilization of PTGES2 by Luminespib (5 μ M) or indomethacin (5 μ M) in HeLa cells.

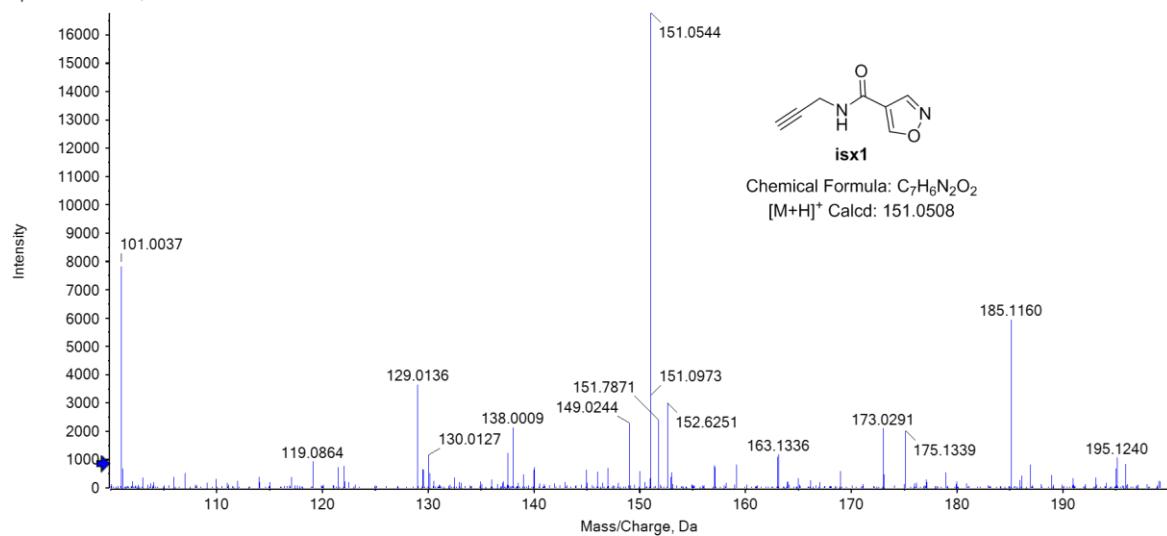
17. References

- [1] a) Z. Li, P. Hao, L. Li, C. Y. Tan, X. Cheng, G. Y. Chen, S. K. Sze, H. M. Shen, S. Q. Yao, *Angew. Chem. Int. Ed.* **2013**, *52*, 8551-8556; b) M. D. Smith, D. Gong, C. G. Sudhahar, J. C. Reno, R. V. Stahelin, M. D. Best, *Bioconjug. Chem.* **2008**, *19*, 1855-1863.
- [2] P. A. Brough, W. Aherne, X. Barril, J. Borgognoni, K. Boxall, J. E. Cansfield, K. M. Cheung, I. Collins, N. G. Davies, M. J. Drysdale, B. Dymock, S. A. Eccles, H. Finch, A. Fink, A. Hayes, R. Howes, R. E. Hubbard, K. James, A. M. Jordan, A. Lockie, V. Martins, A. Massey, T. P. Matthews, E. McDonald, C. J. Northfield, L. H. Pearl, C. Prodromou, S. Ray, F. I. Raynaud, S. D. Roughley, S. Y. Sharp, A. Surgenor, D. L. Walmsley, P. Webb, M. Wood, P. Workman, L. Wright, *J. Med. Chem.* **2008**, *51*, 196-218.

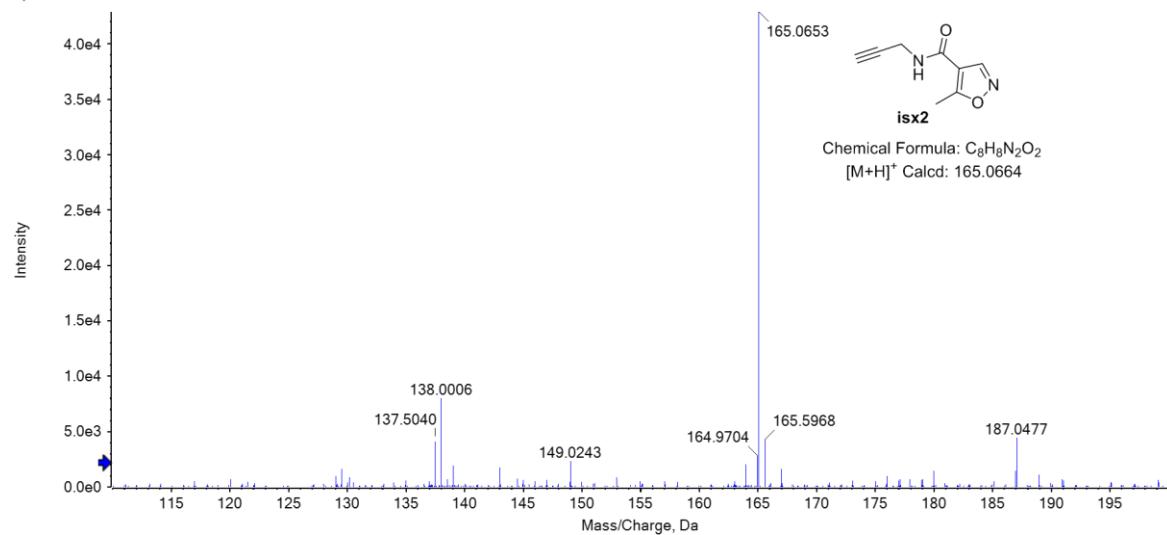
- [3] K. Cheng, J. S. Lee, P. Hao, S. Q. Yao, K. Ding, Z. Li, *Angew. Chem. Int. Ed.* **2017**, *56*, 15044-15048.
- [4] J. E. Elias, S. P. Gygi, *Nat. Methods* **2007**, *4*, 207-214.
- [5] J. Cox, M. Mann, *Nat. Biotechnol.* **2008**, *26*, 1367-1372.
- [6] Z. Tang, C. Li, B. Kang, G. Gao, C. Li, Z. Zhang, *Nucleic Acids Res.* **2017**, *45*, W98-W102.
- [7] D. Szklarczyk, A. L. Gable, K. C. Nastou, D. Lyon, R. Kirsch, S. Pyysalo, N. T. Doncheva, M. Legeay, T. Fang, P. Bork, L. J. Jensen, C. von Mering, *Nucleic Acids Res.* **2021**, *49*, D605-D612.
- [8] B. T. Sherman, M. Hao, J. Qiu, X. Jiao, M. W. Baseler, H. C. Lane, T. Imamichi, W. Chang, *Nucleic Acids Res.* **2022**, *50*, W216-W221.
- [9] a) R. Jafari, H. Almqvist, H. Axelsson, M. Ignatushchenko, T. Lundback, P. Nordlund, D. Martinez Molina, *Nat. Protoc.* **2014**, *9*, 2100-2122; b) D. Martinez Molina, R. Jafari, M. Ignatushchenko, T. Seki, E. A. Larsson, C. Dan, L. Sreekumar, Y. Cao, P. Nordlund, *Science* **2013**, *341*, 84-87.

18. HRMS Spectra

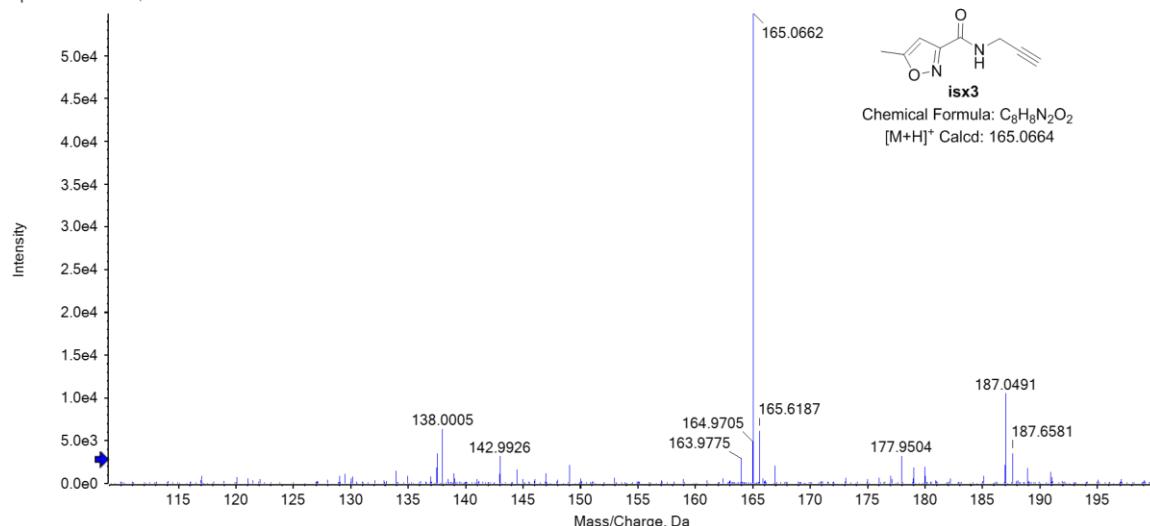
Spectrum from isx1, +MS



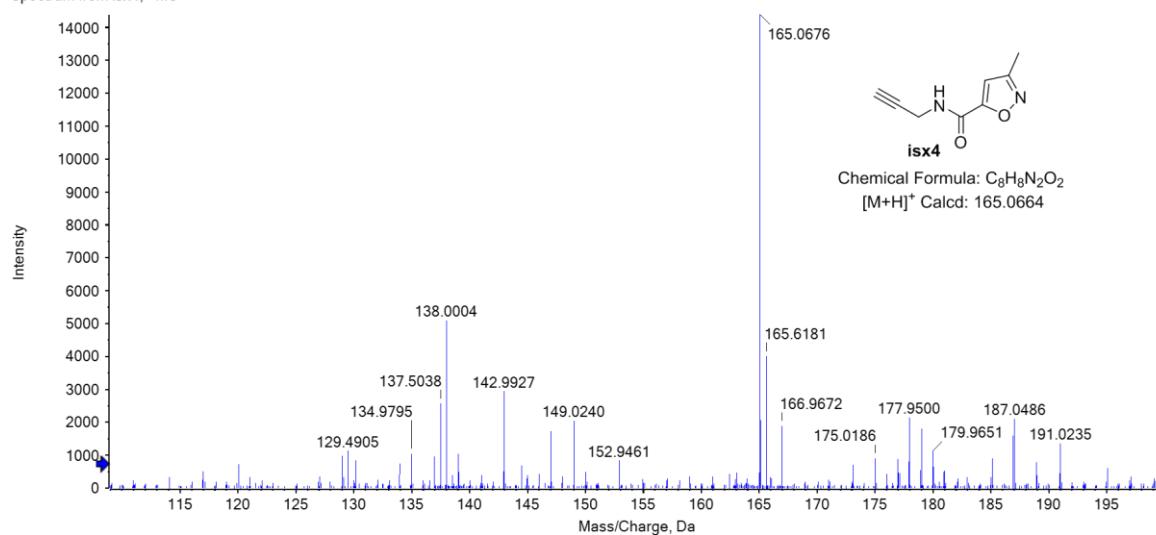
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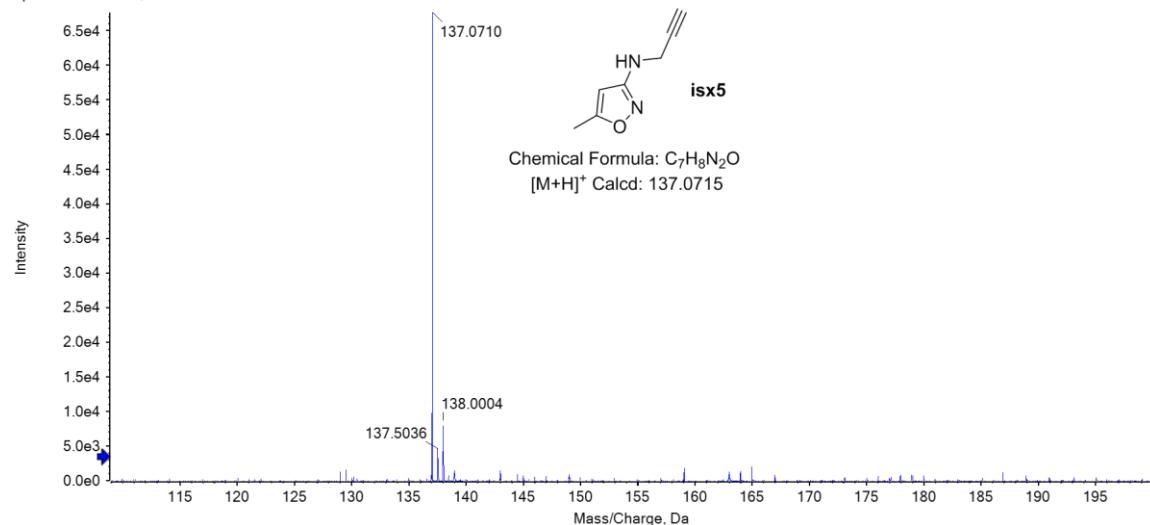
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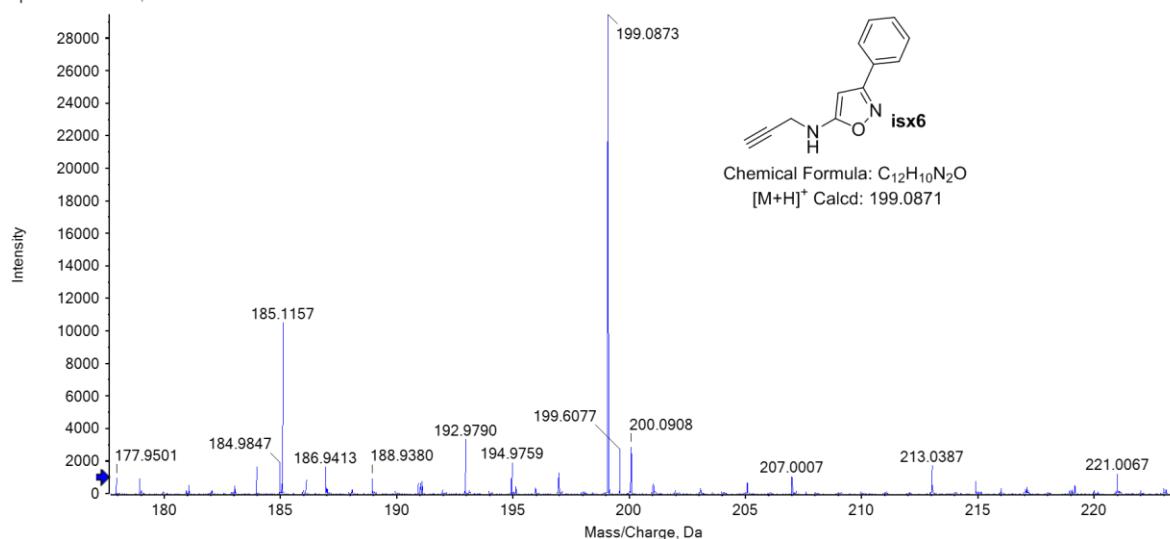
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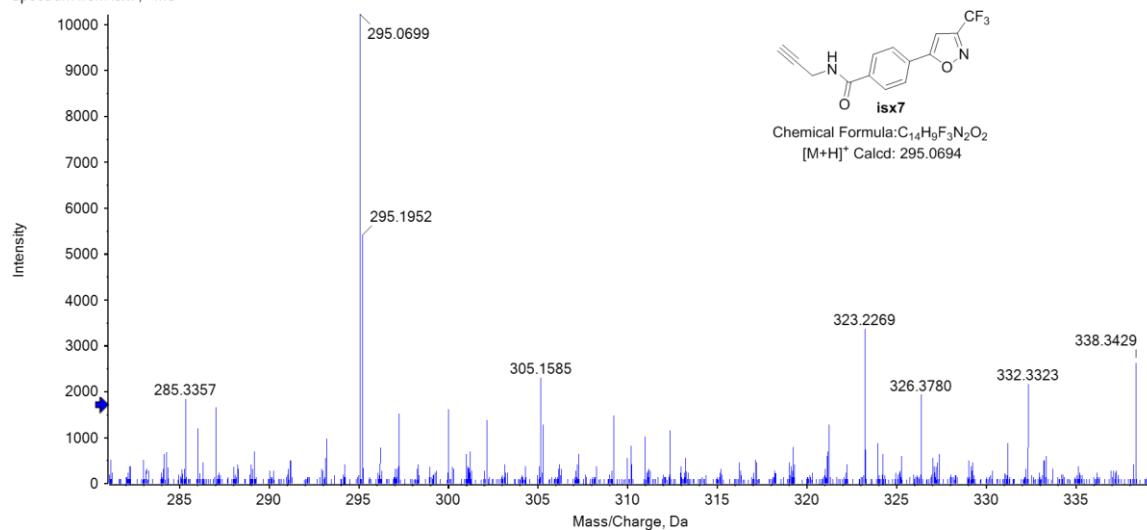
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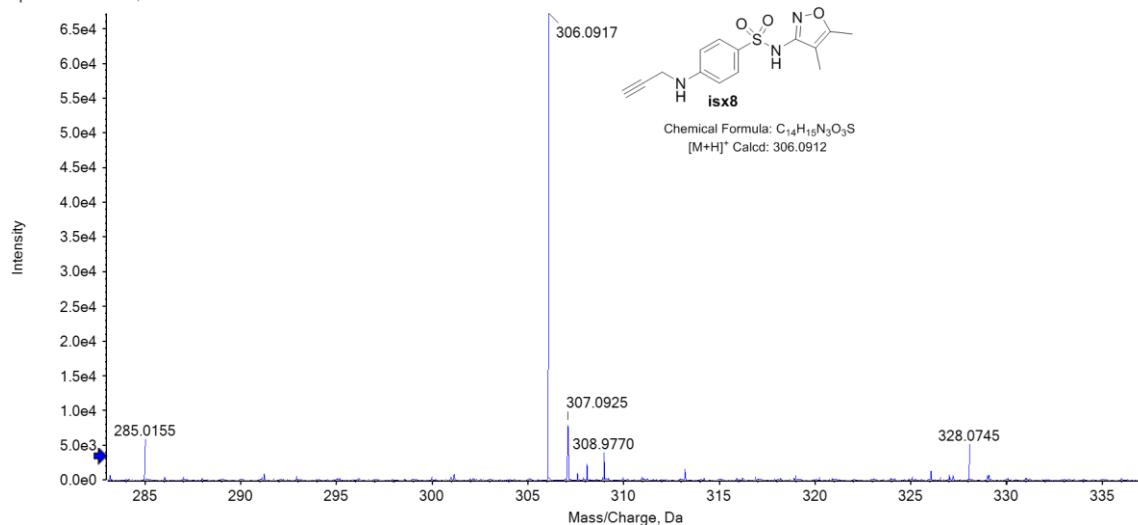
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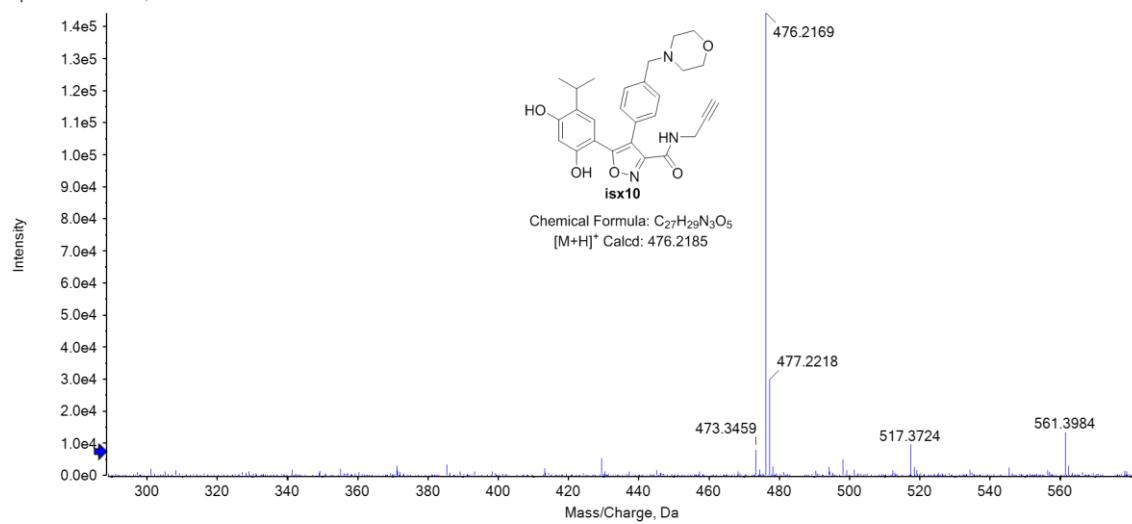
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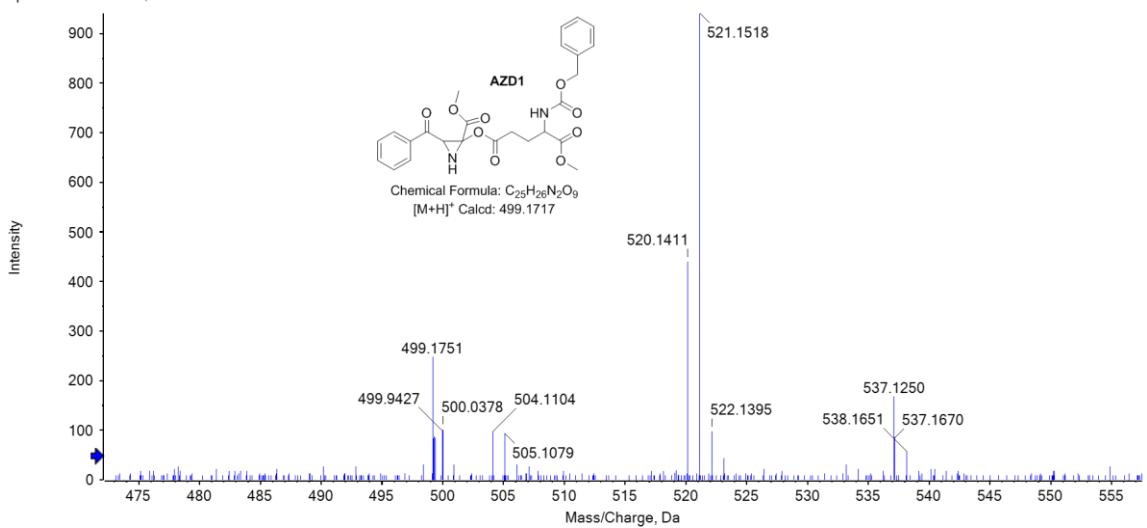
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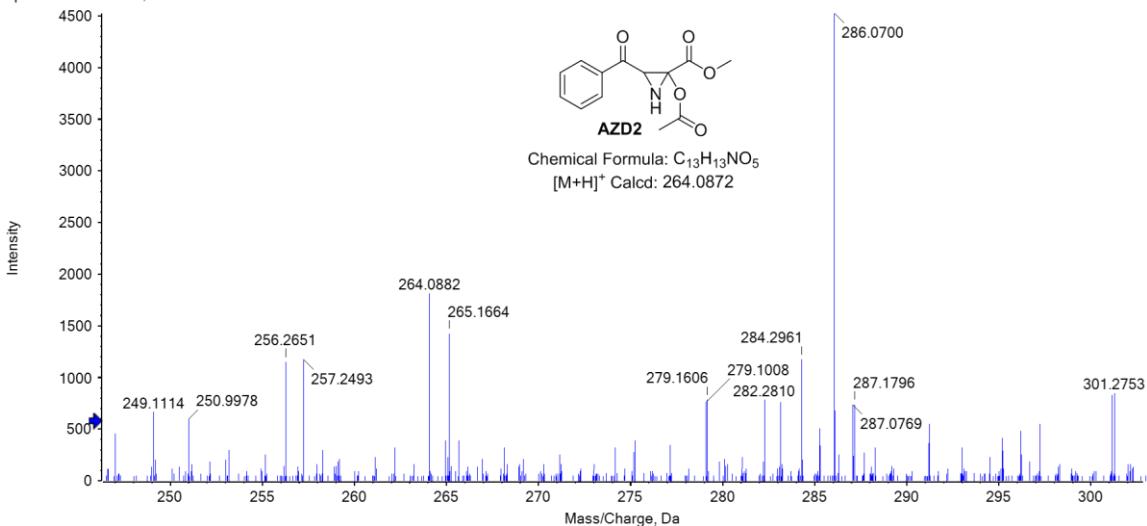
Spectrum from isx10, +MS



Spectrum from AZD1, +MS

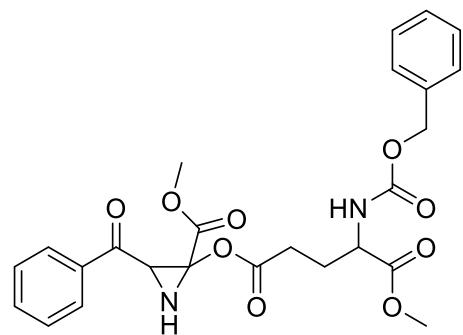


Spectrum from AZD2, +MS

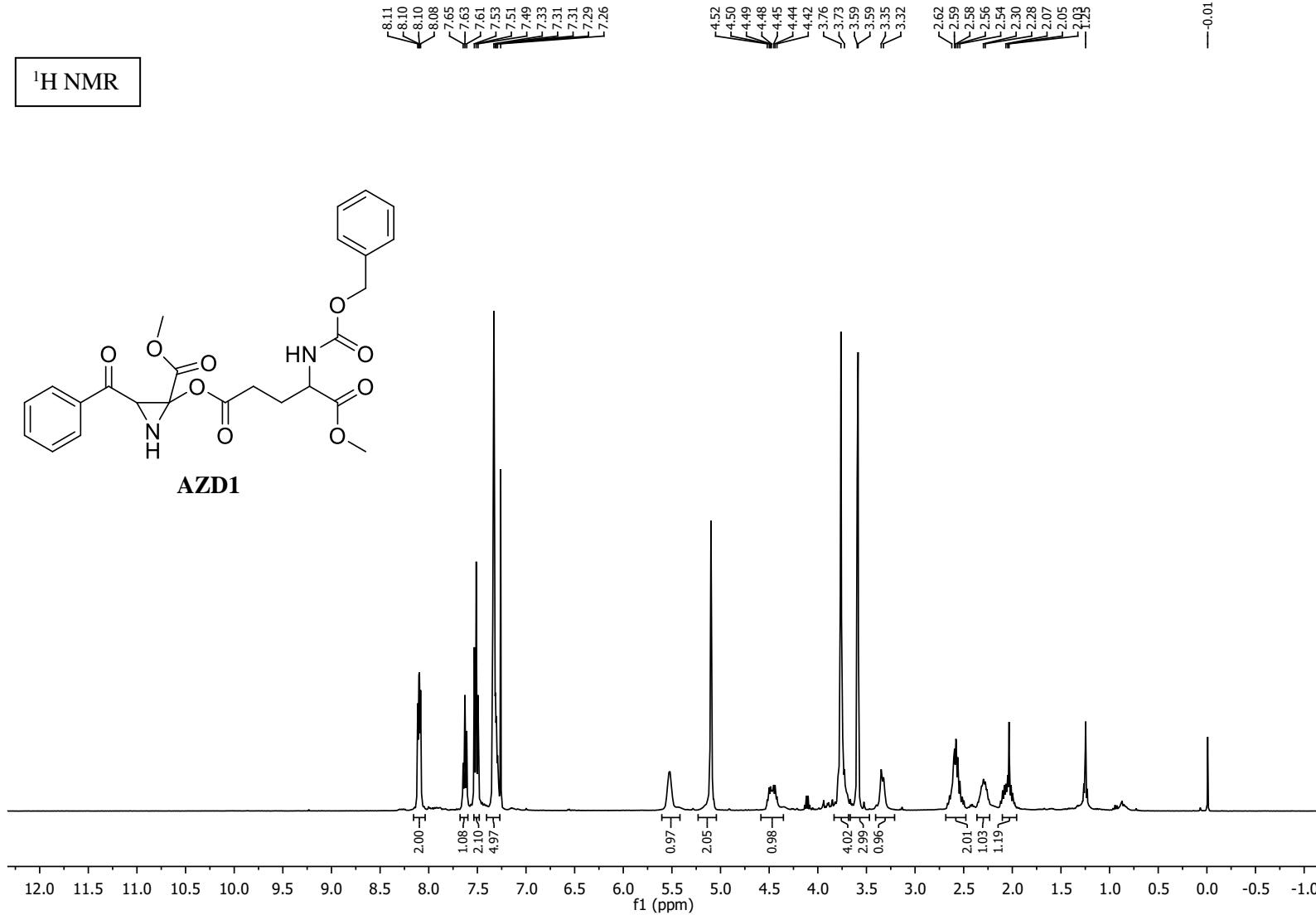


19. NMR Spectra

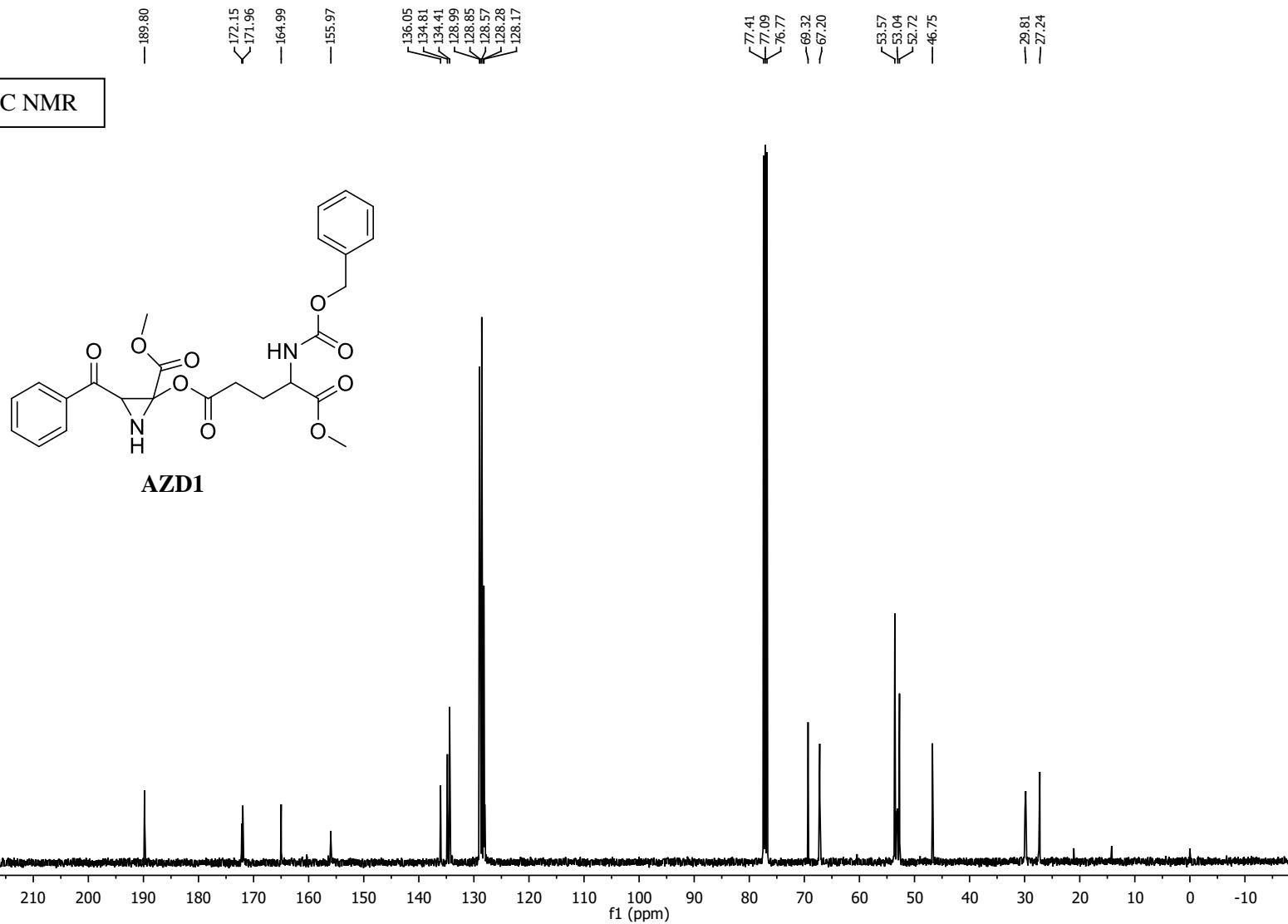
¹H NMR



AZD1

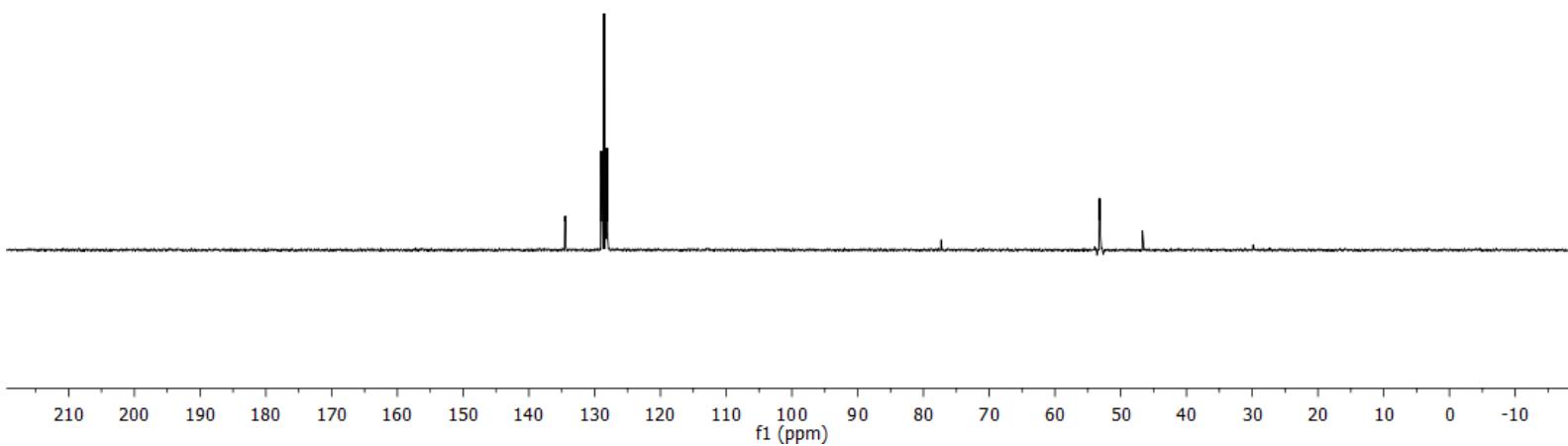
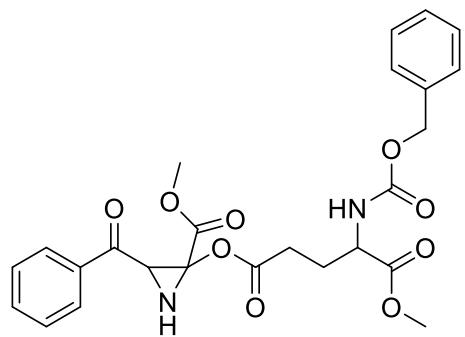


¹³C NMR



SI-53

DEPT90



DEPT135

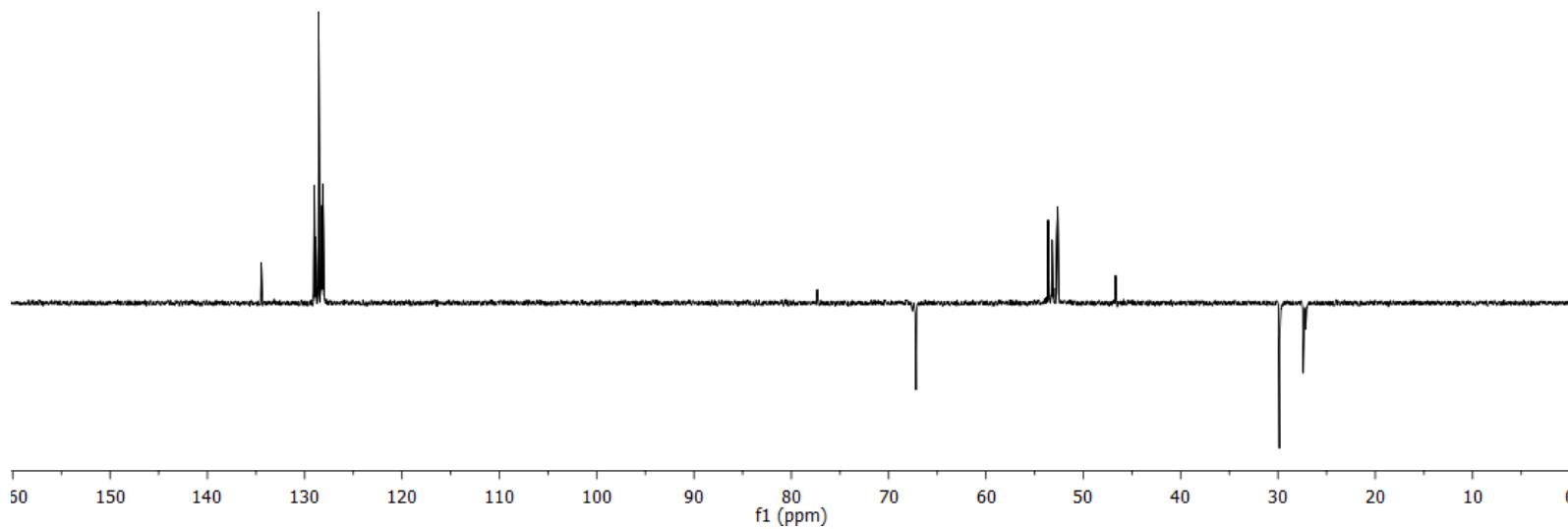
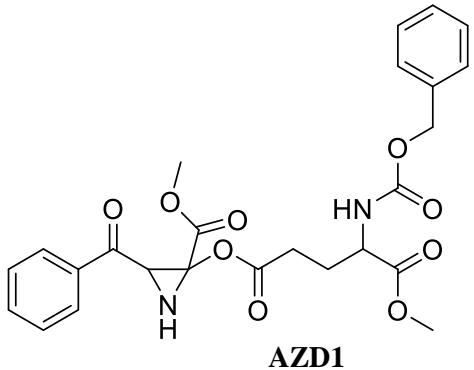
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—128.87
—128.57
—128.26
—128.13

—77.31

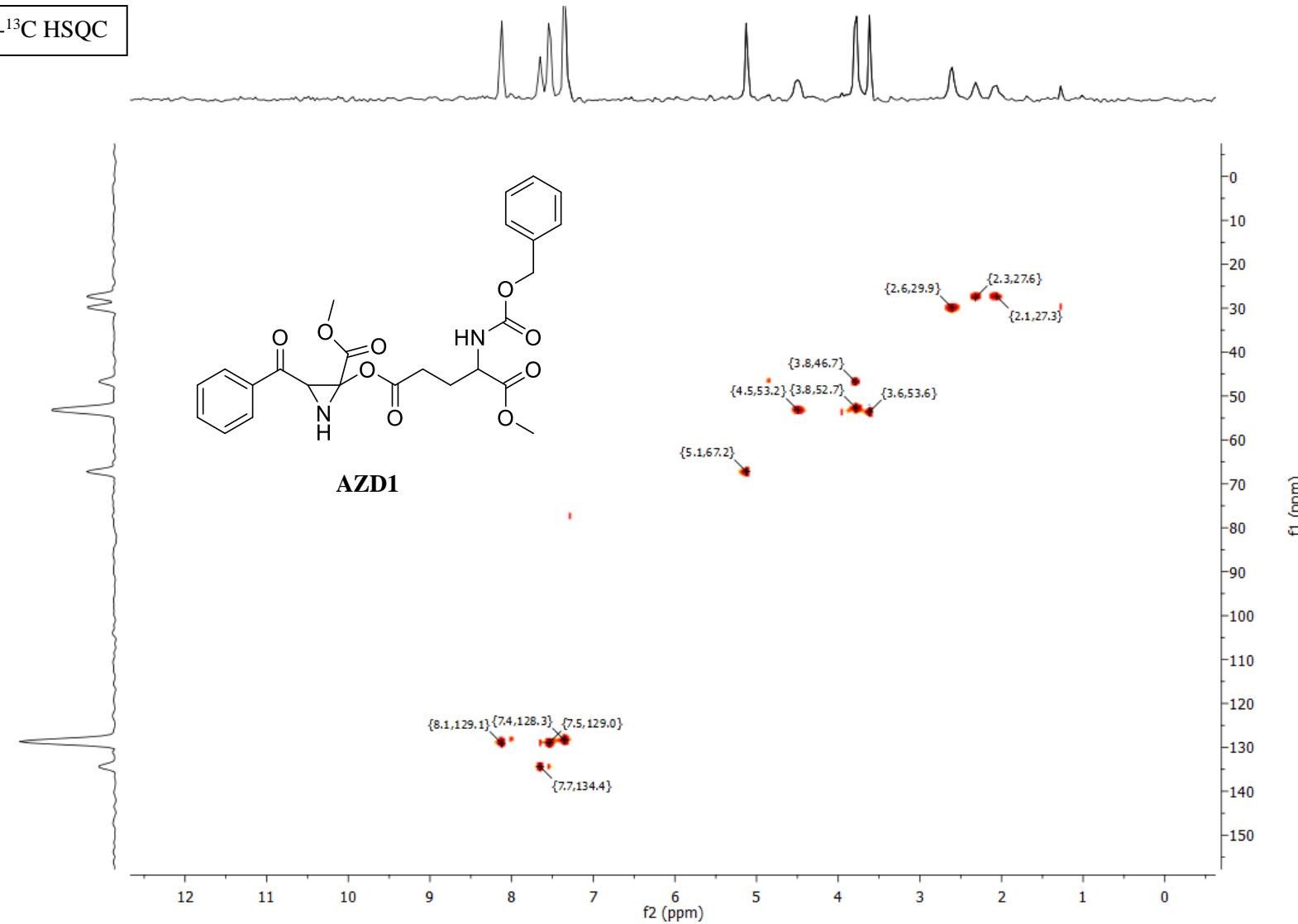
—67.19

—53.61
—53.21
—52.64

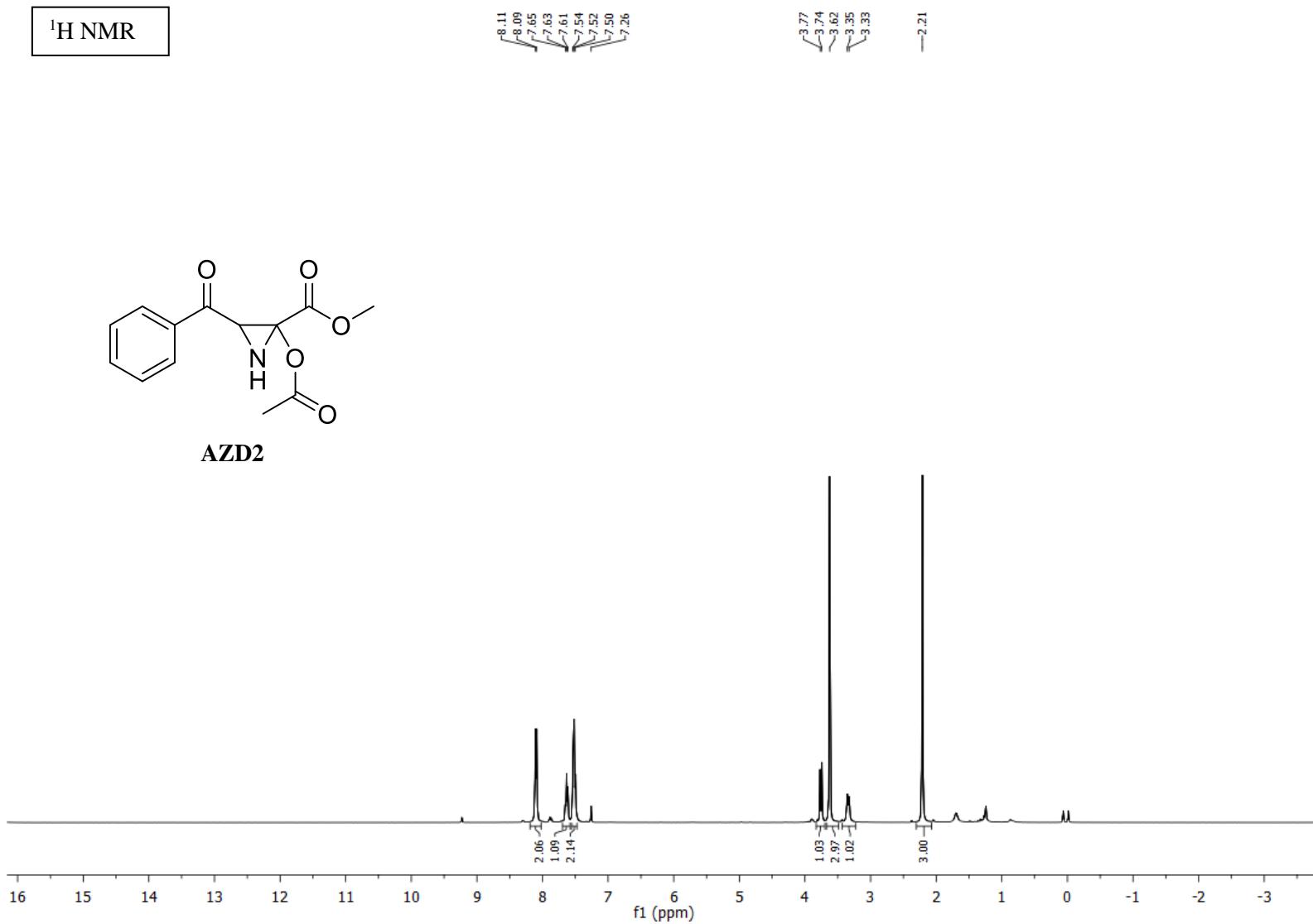
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—29.86
—27.41



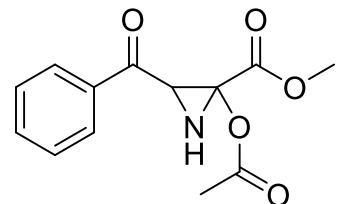
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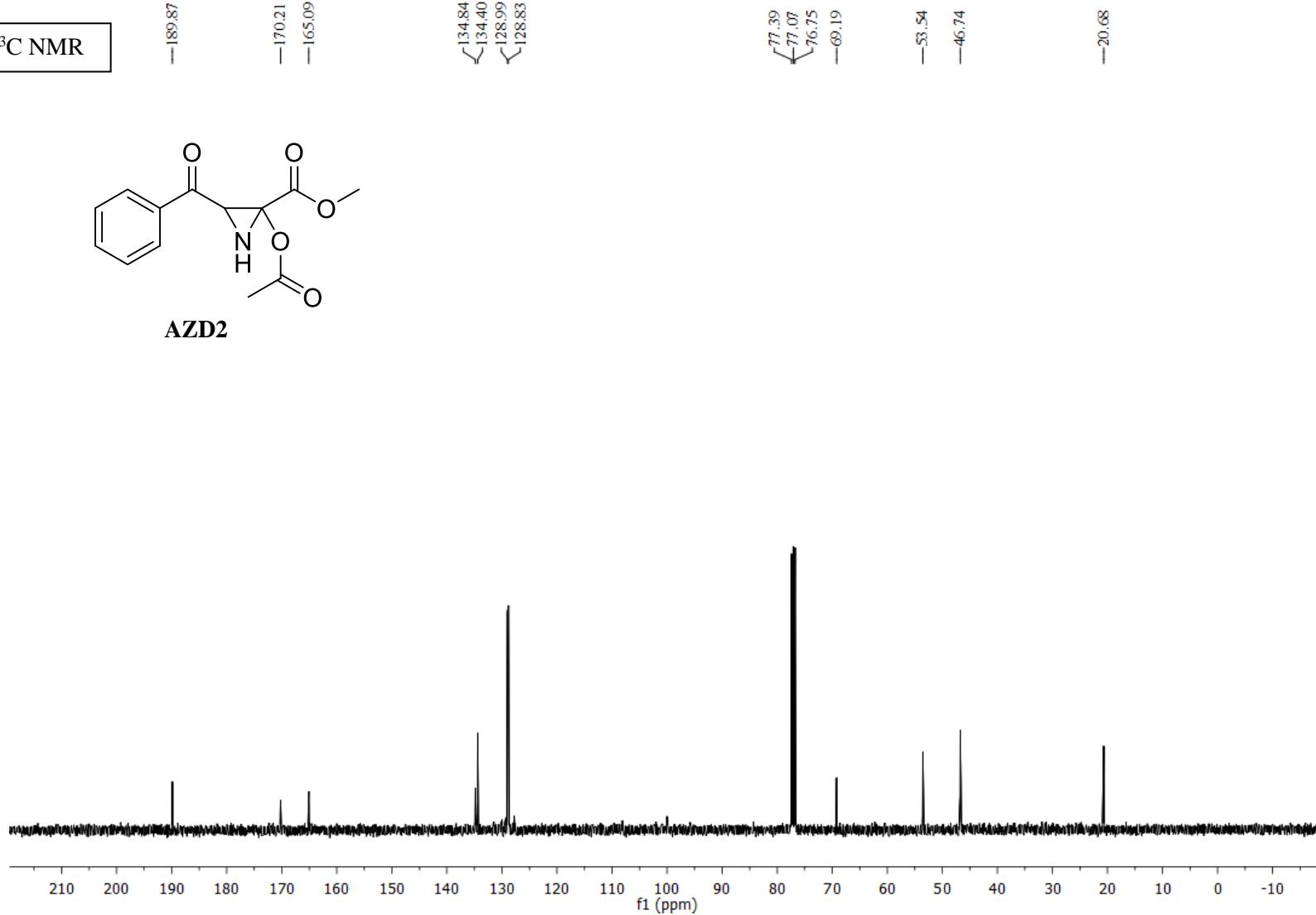
¹H NMR



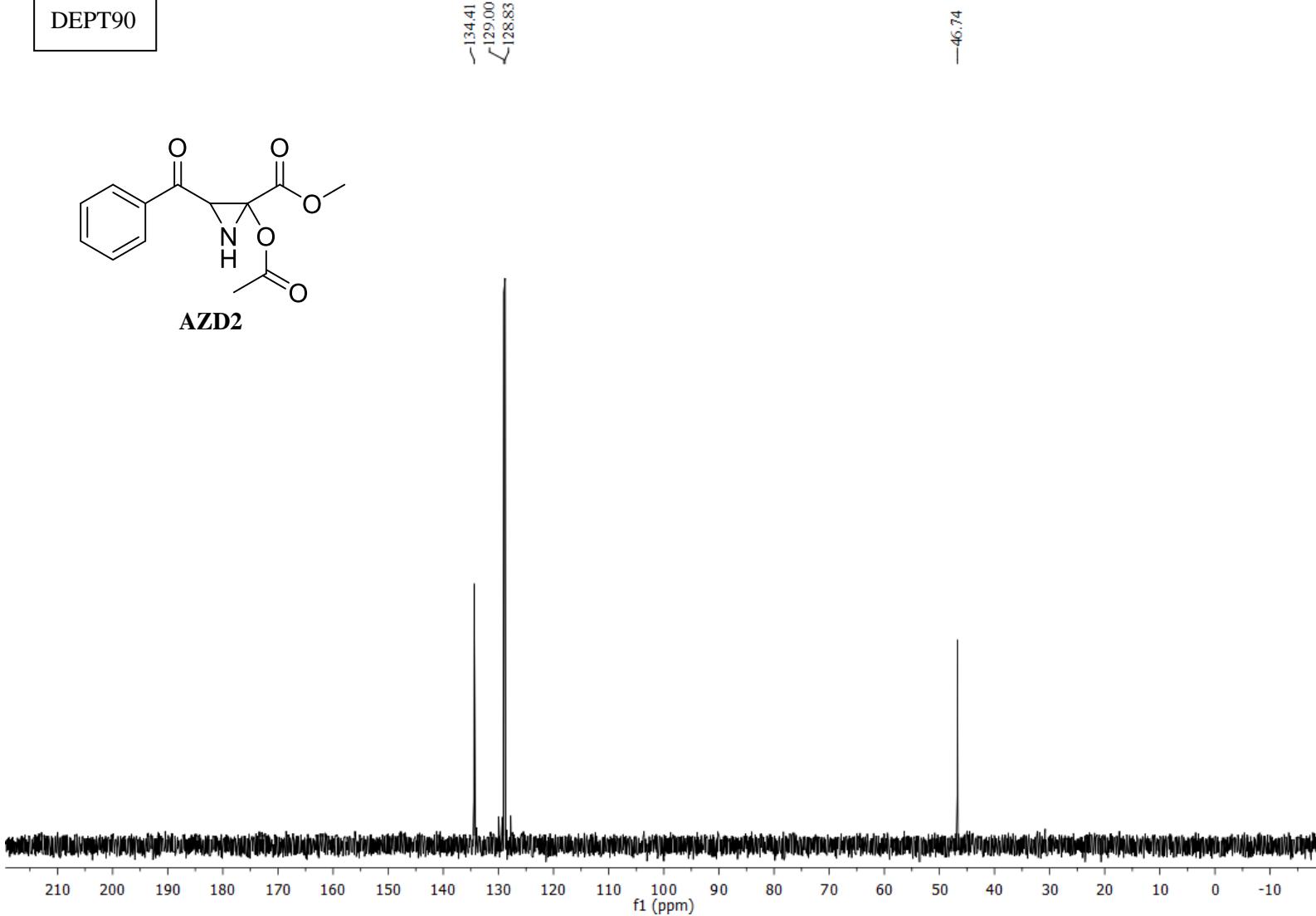
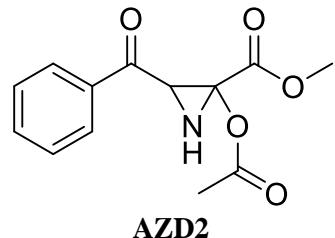
¹³C NMR



AZD2

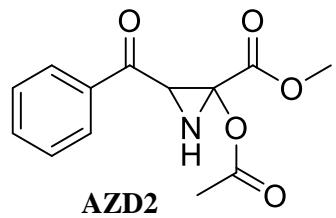


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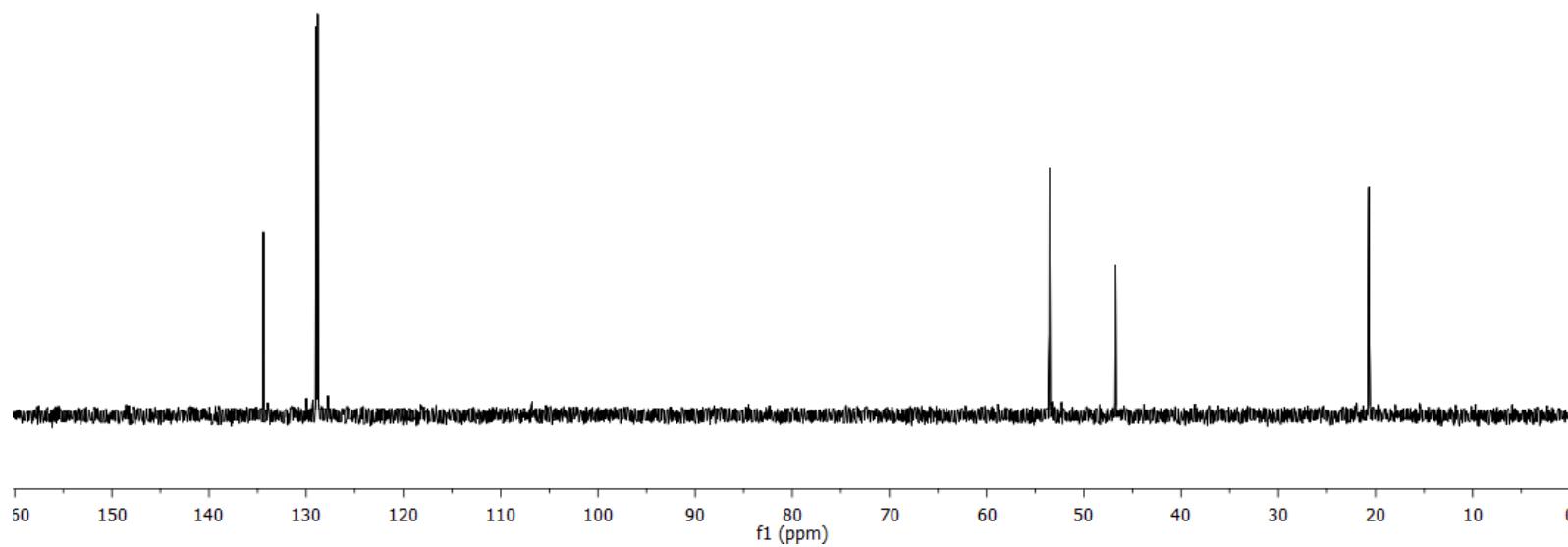
DEPT135

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—128.83

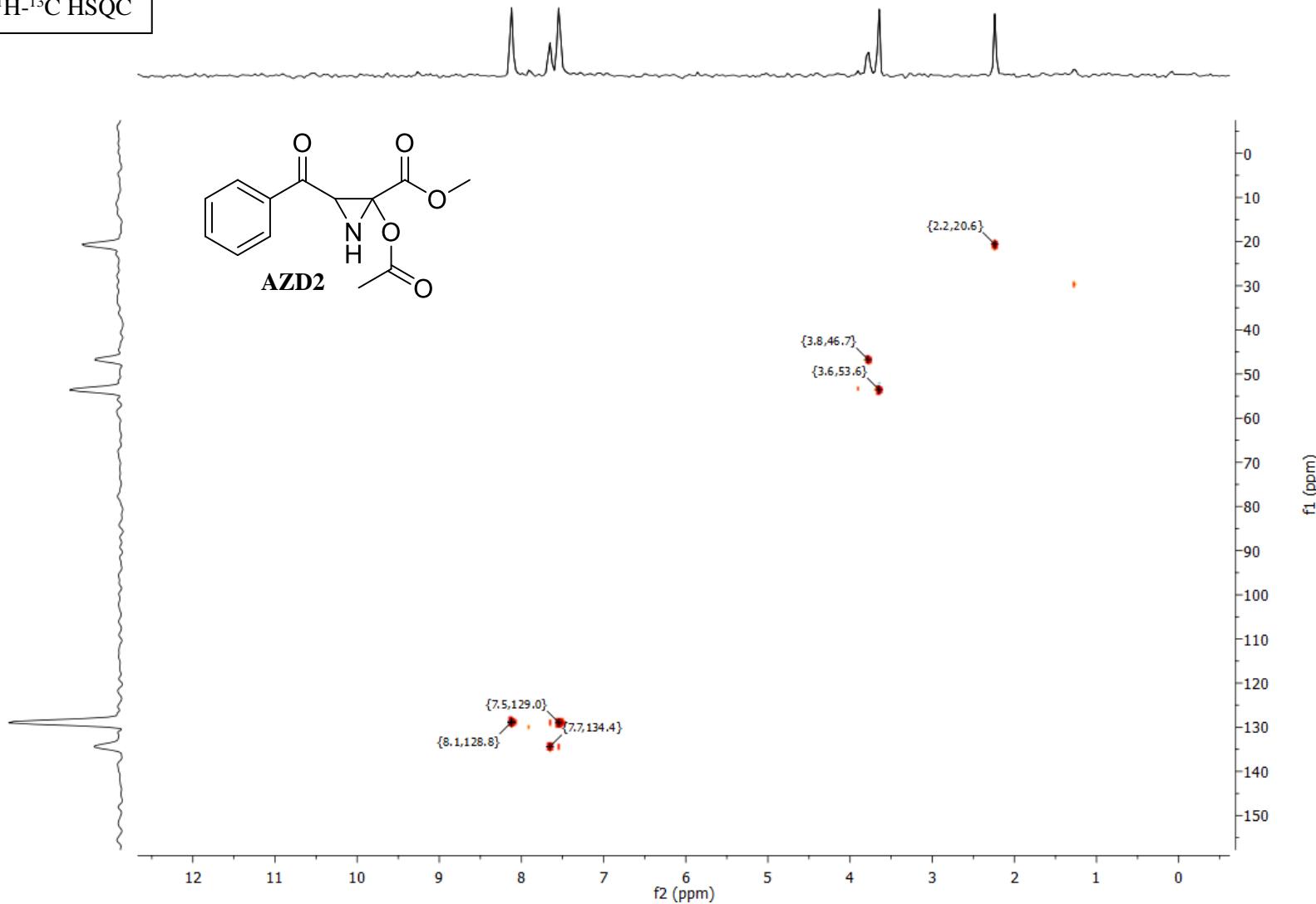


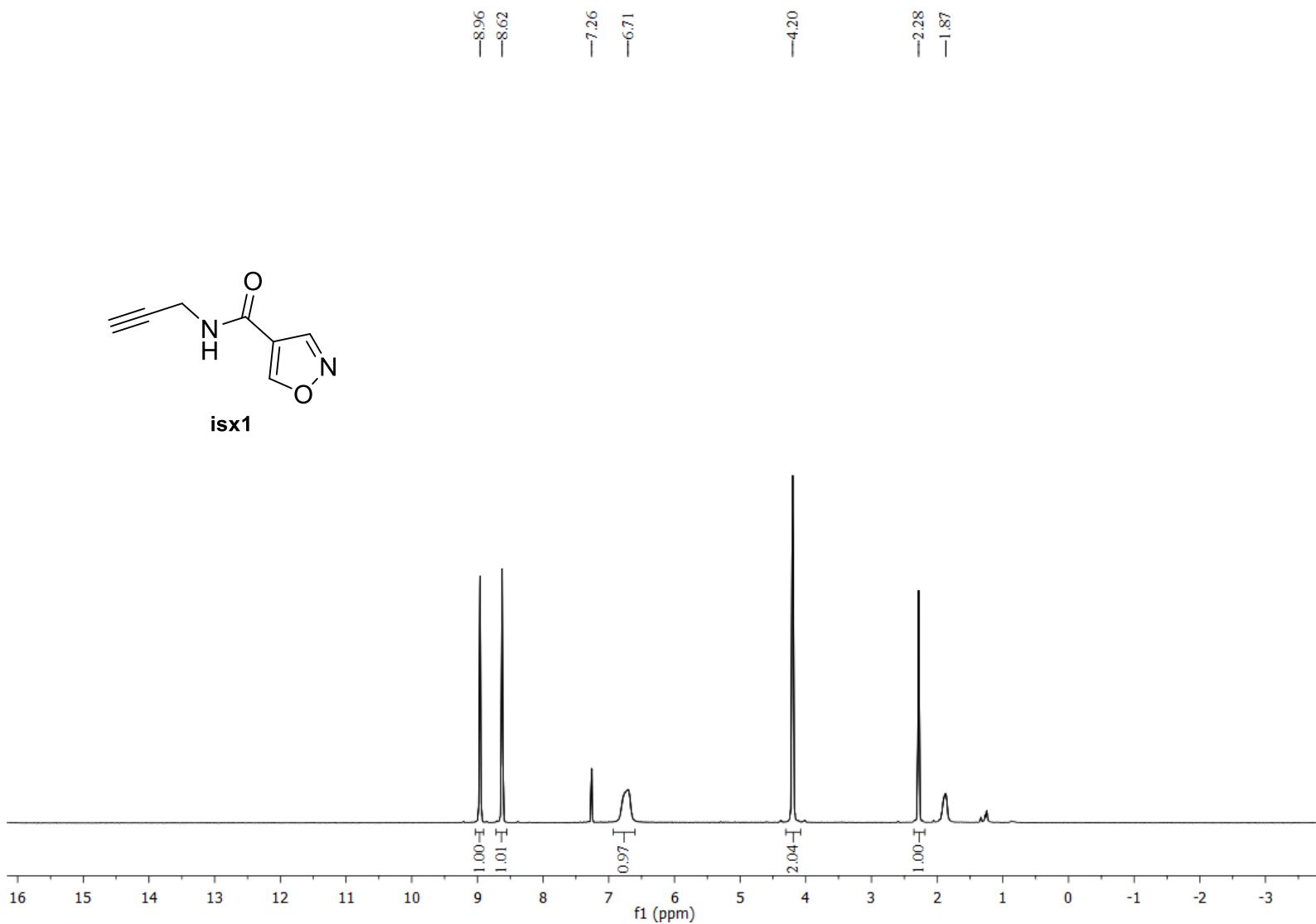
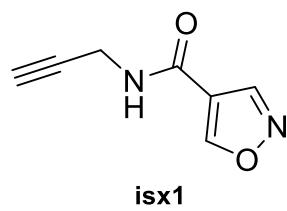
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—20.69

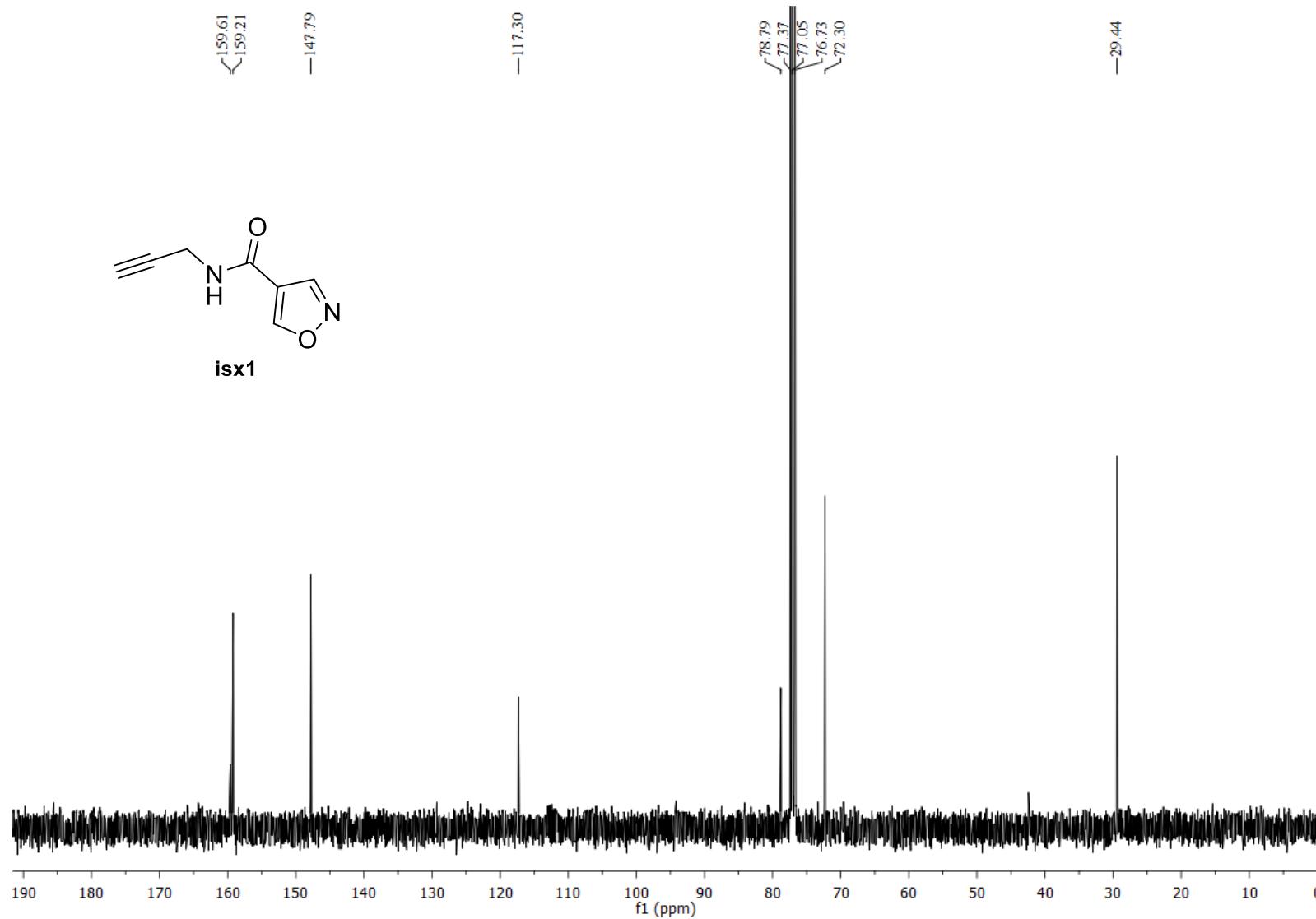
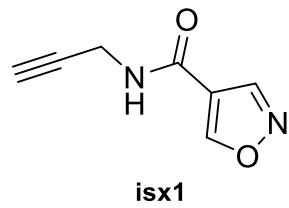


¹H-¹³C HSQC

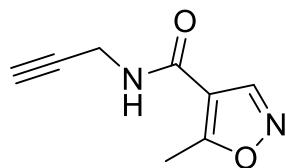




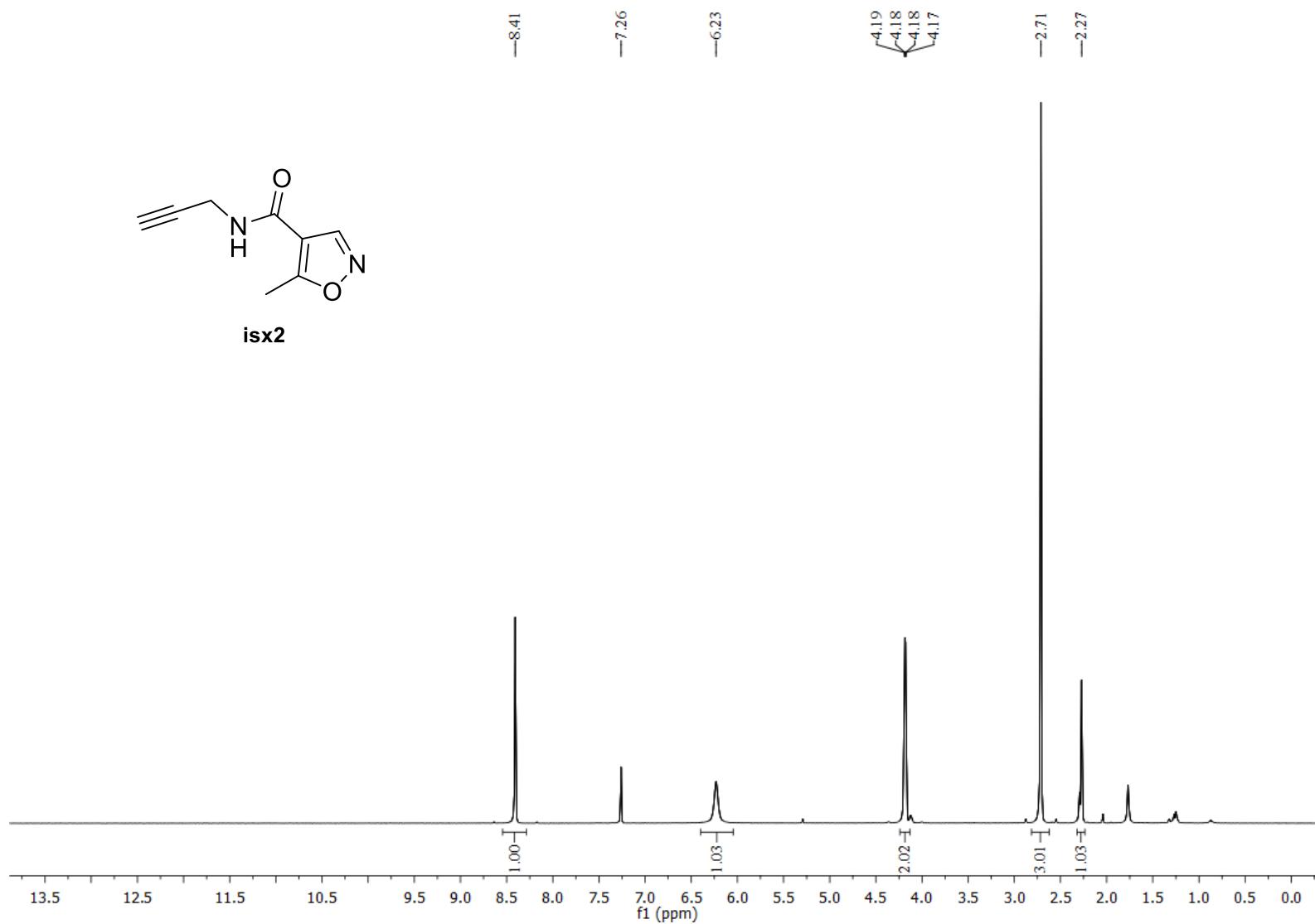
SI-62

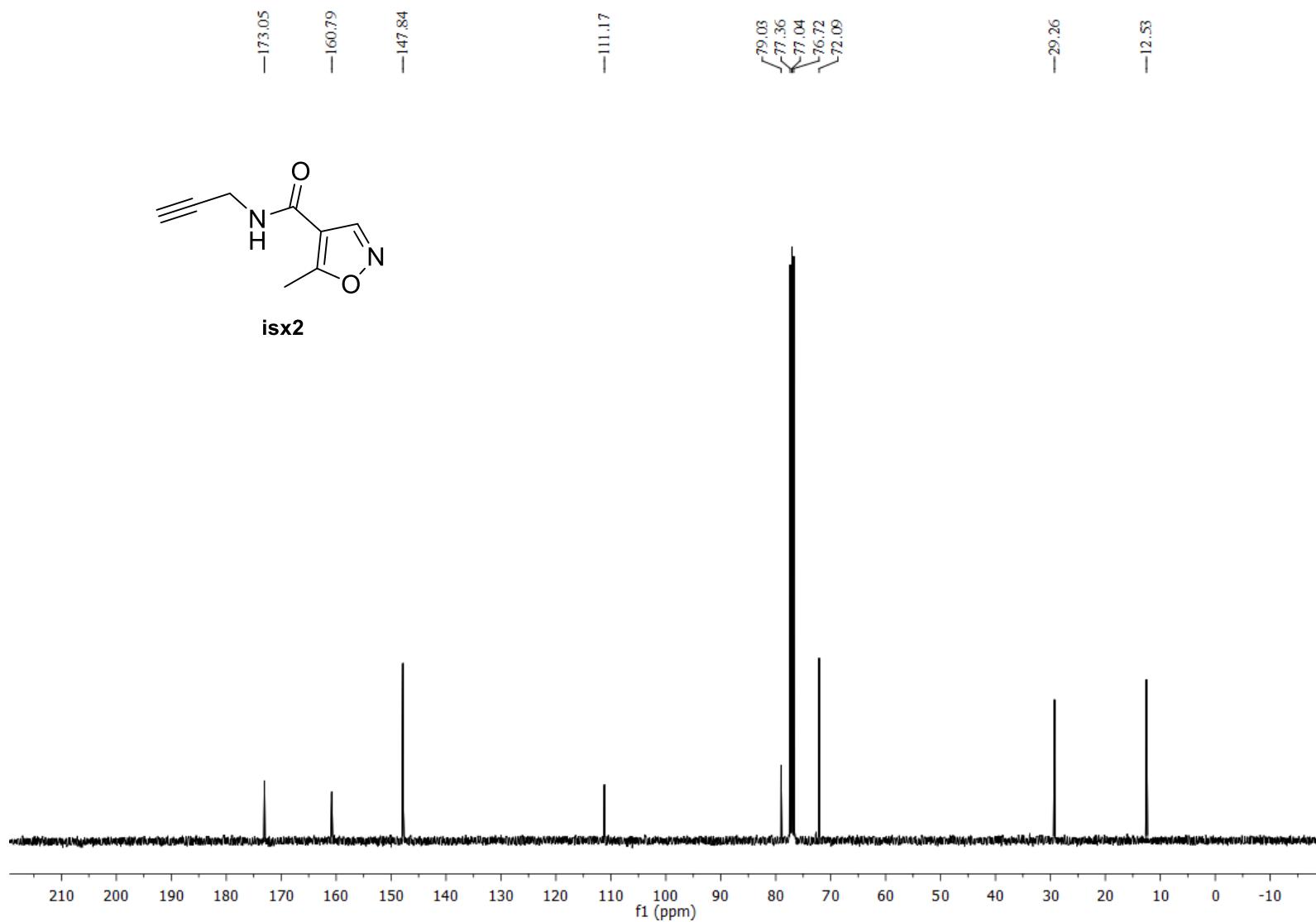


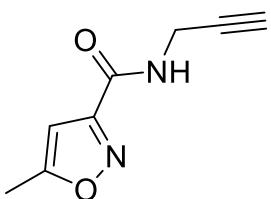
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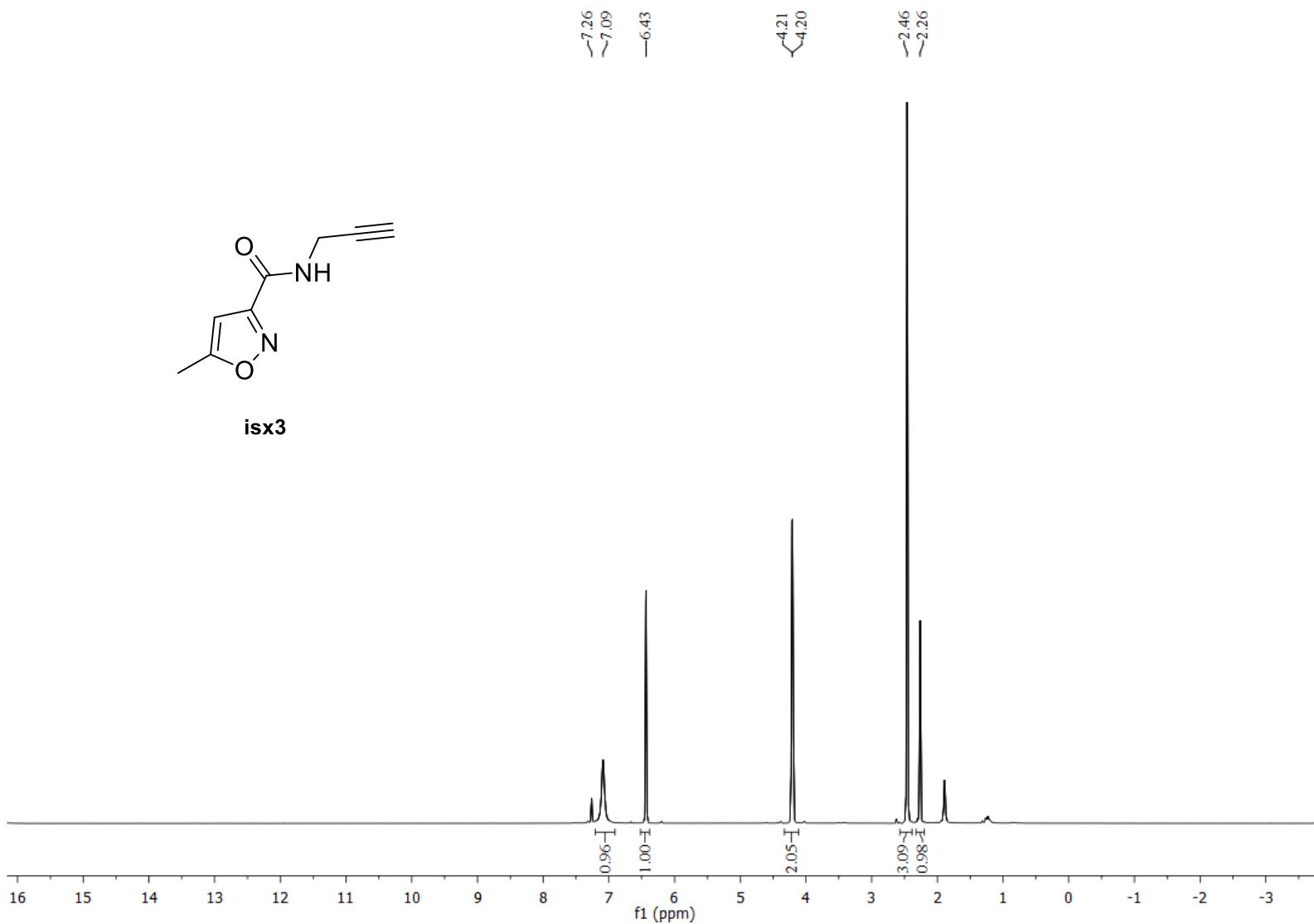
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isx3



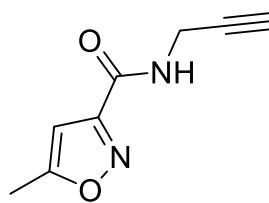
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—158.26

—101.44

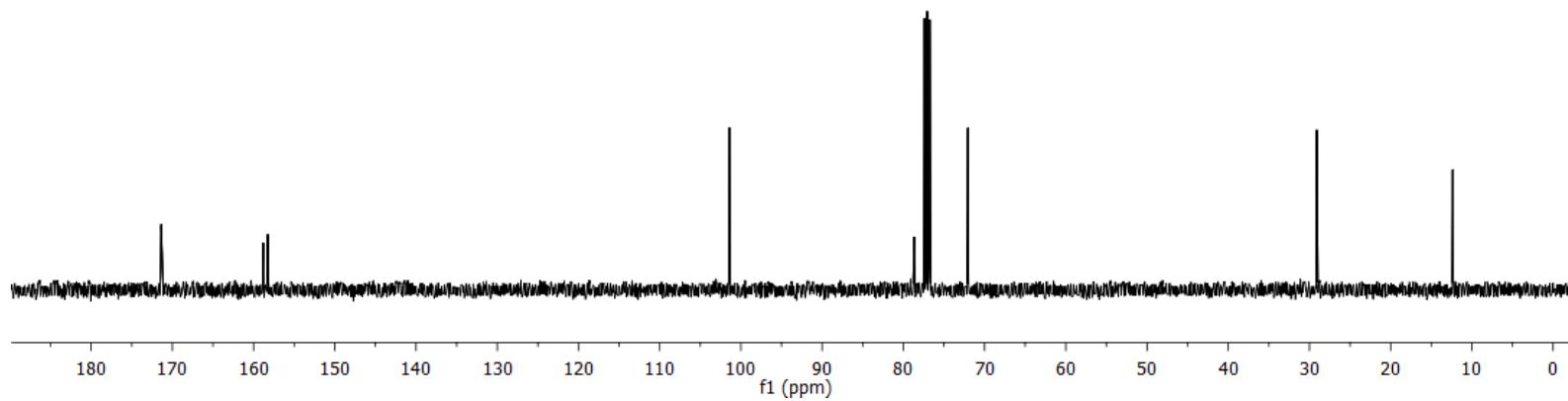
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—72.06

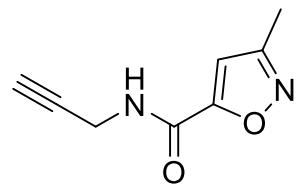
—29.10

—12.35

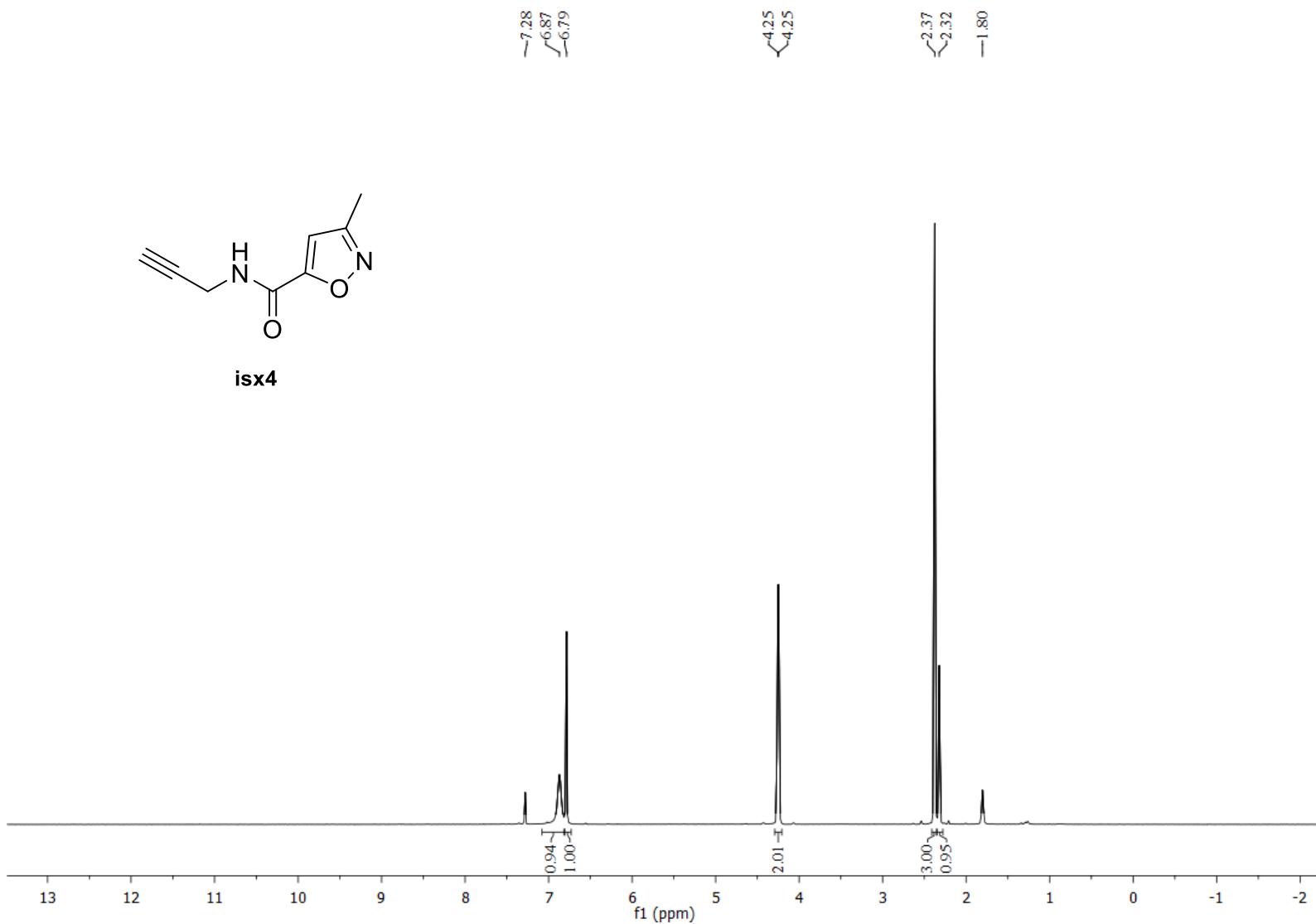


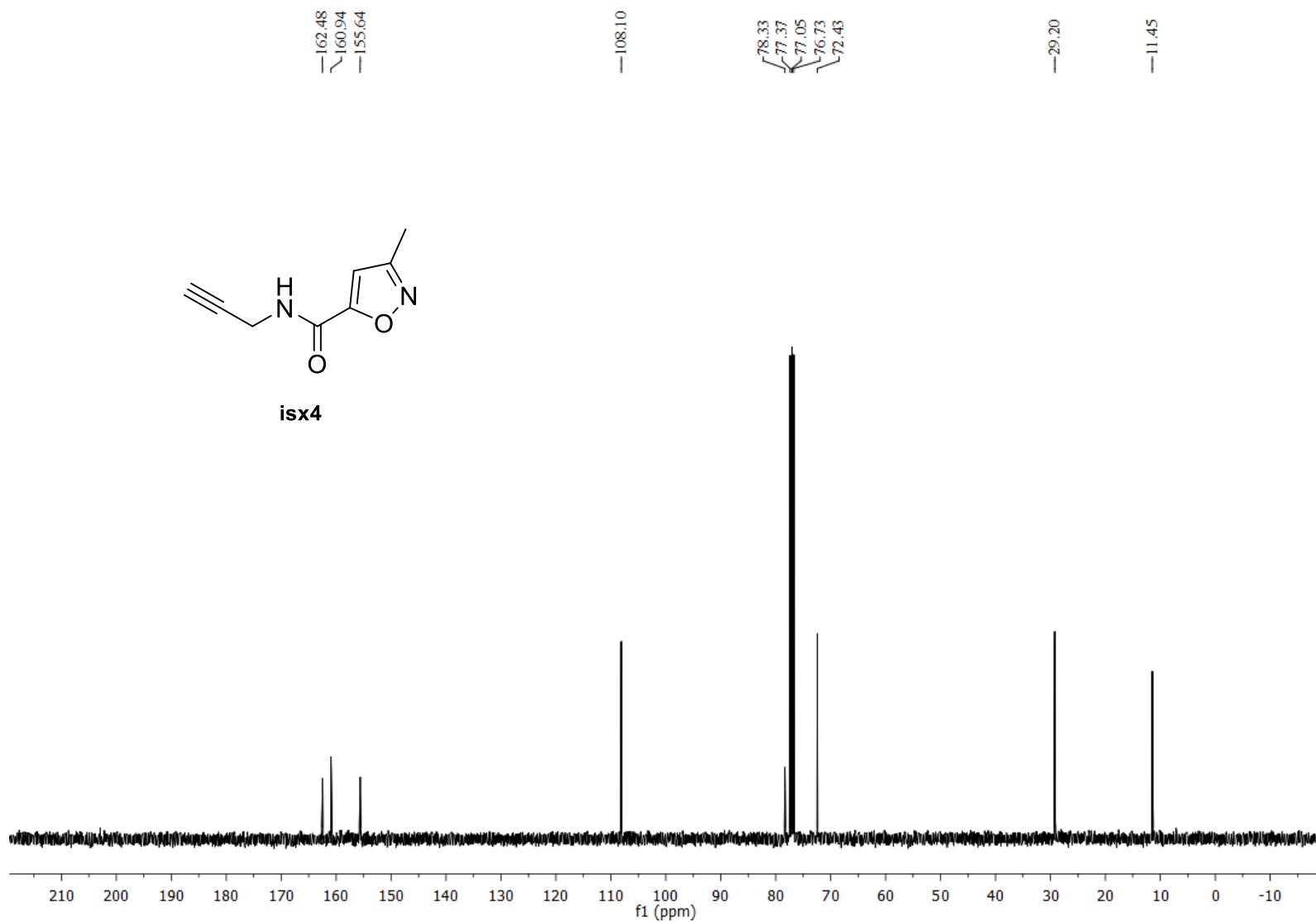
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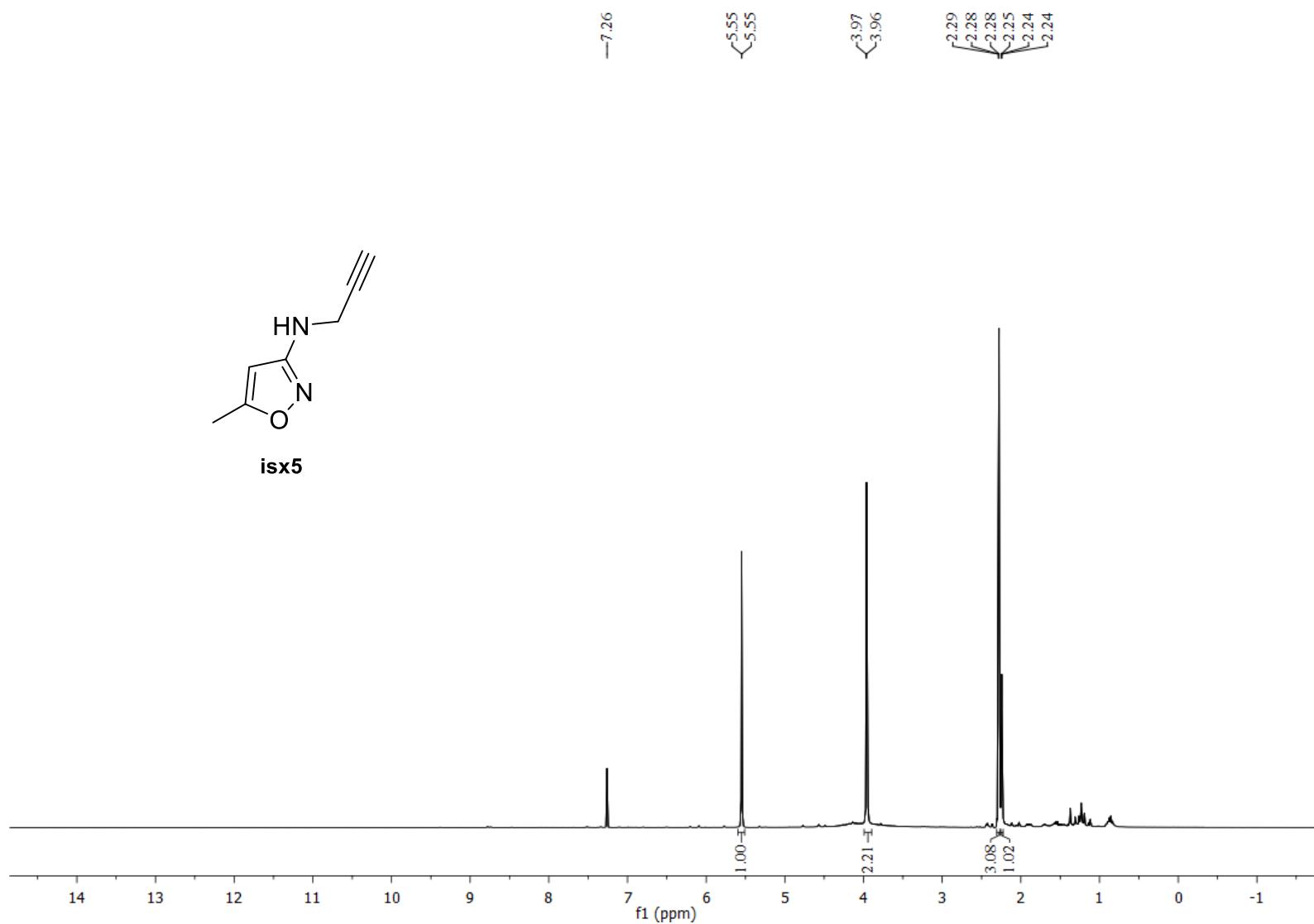


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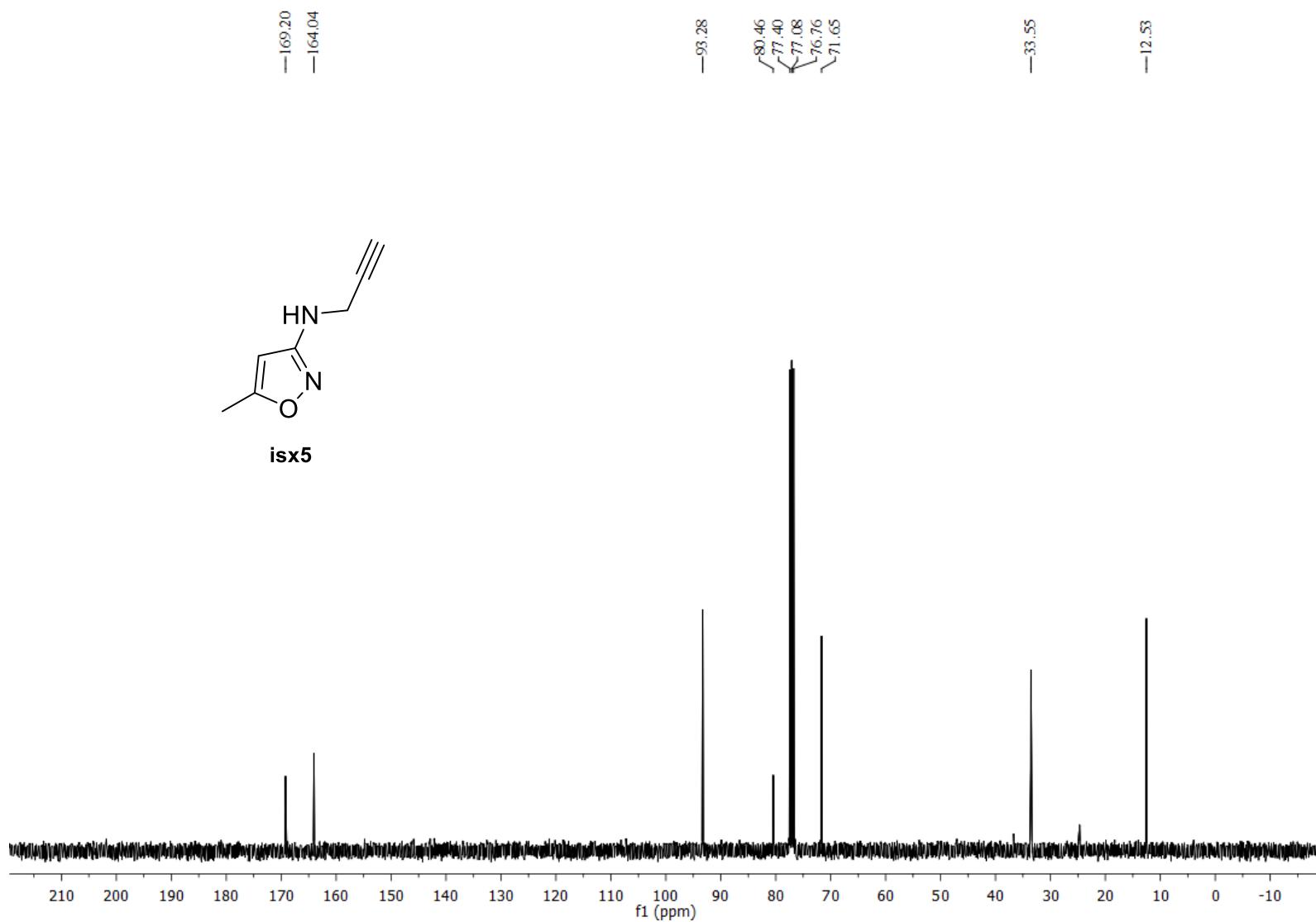


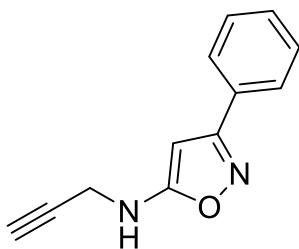


SI-69

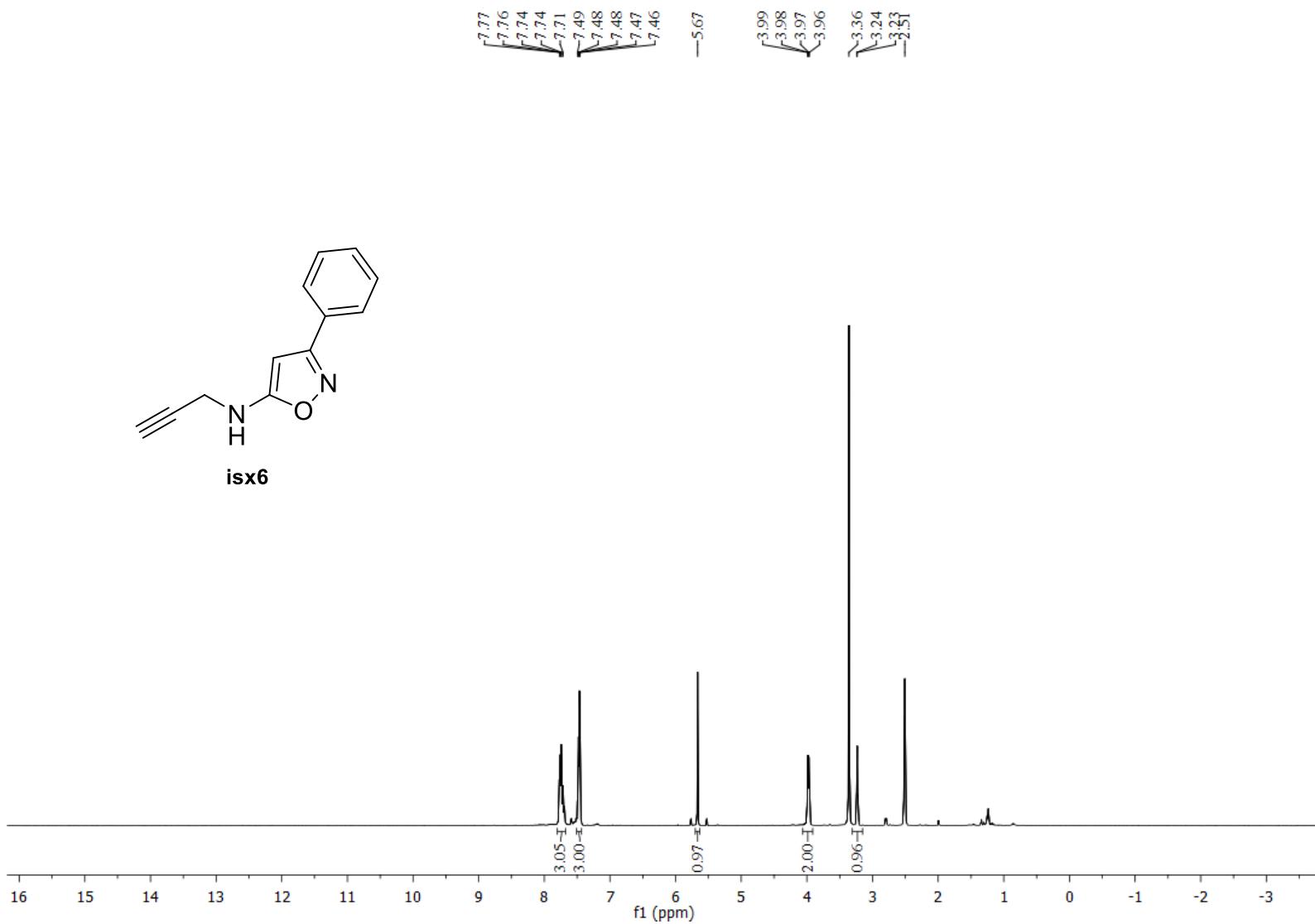


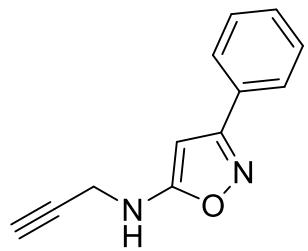
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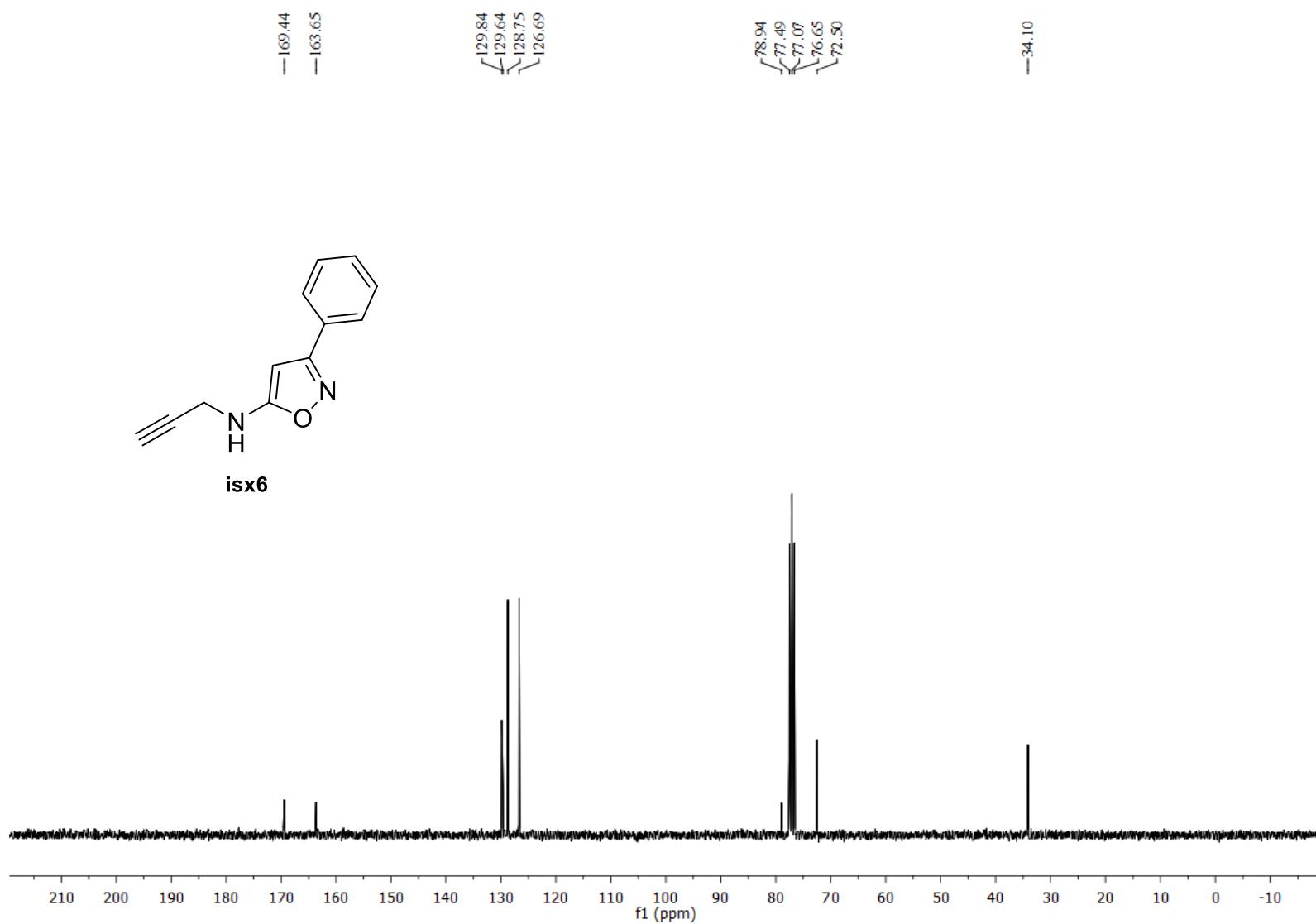


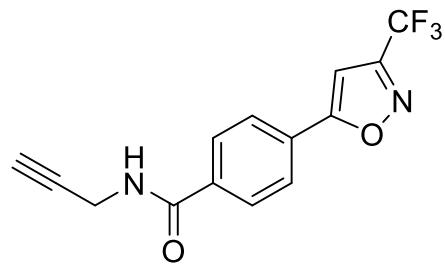
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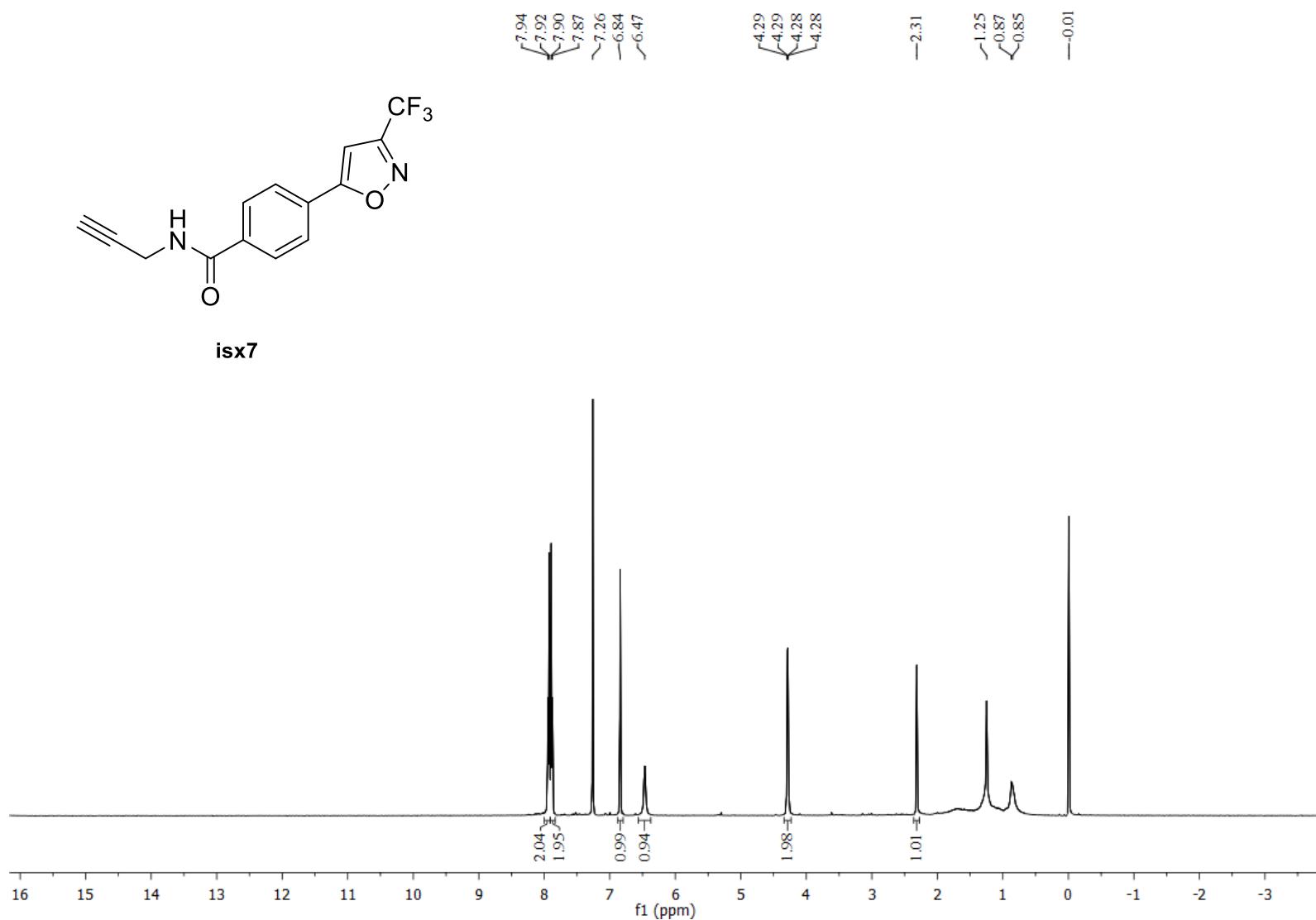


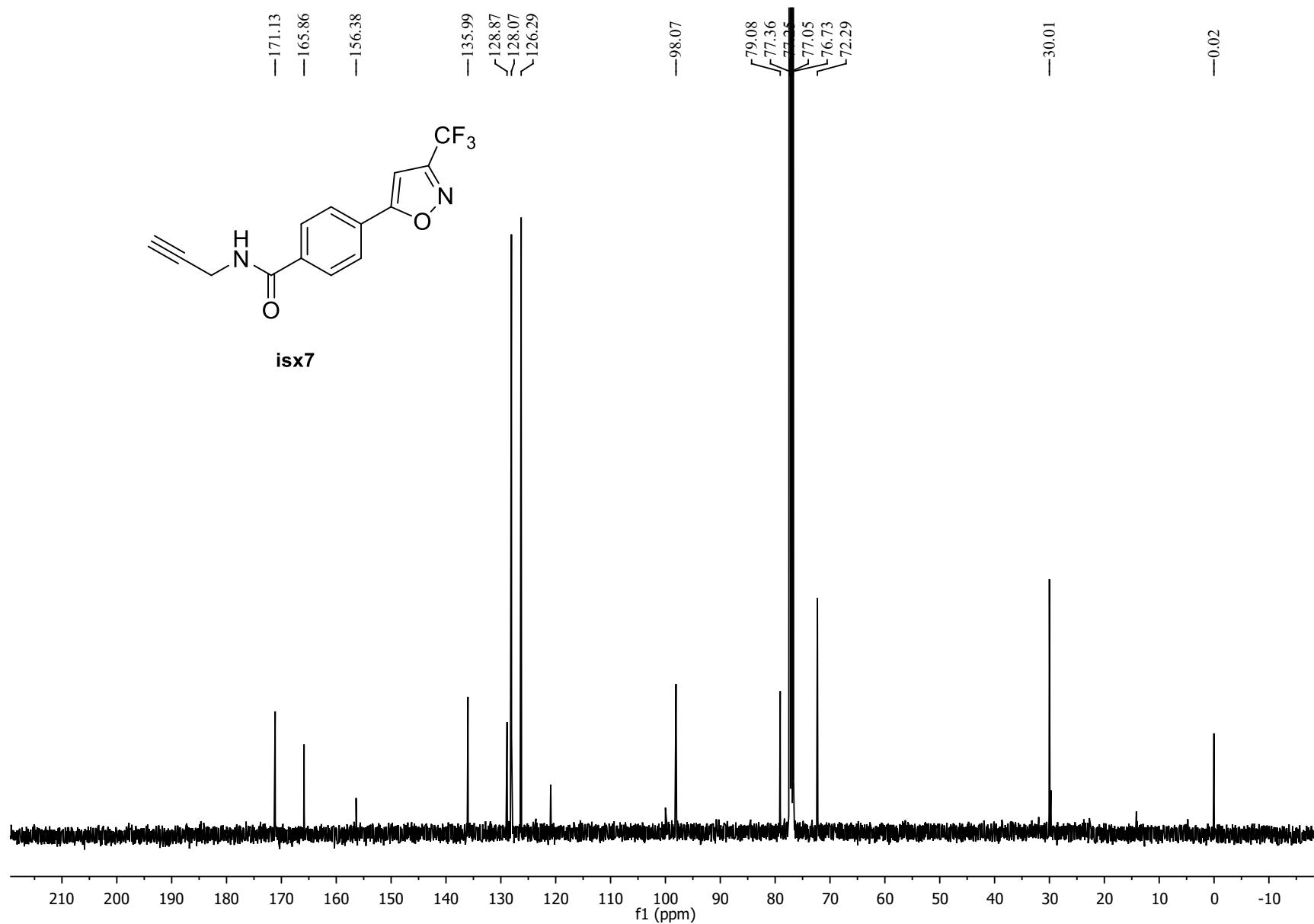
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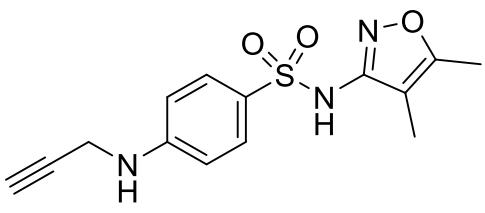




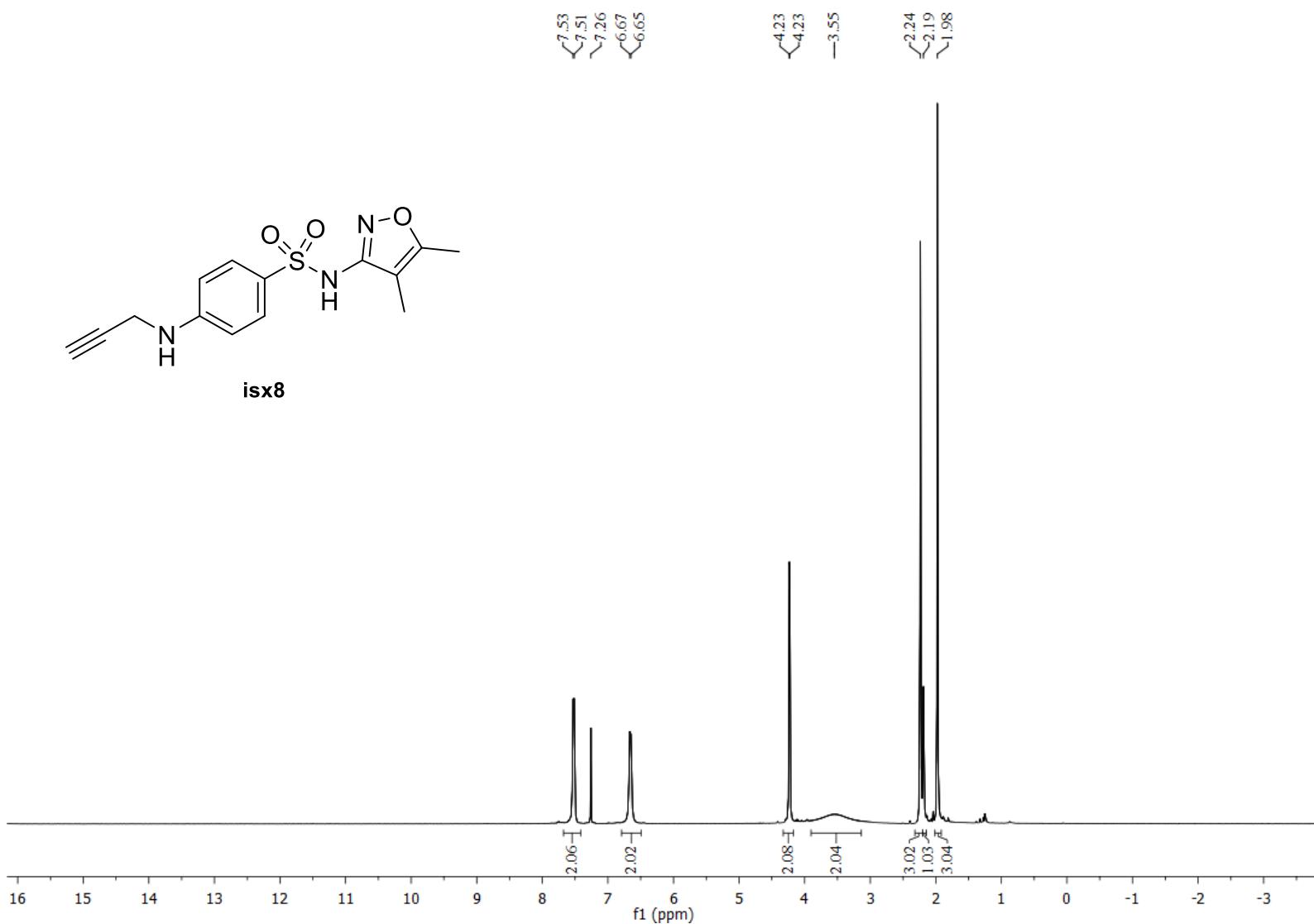
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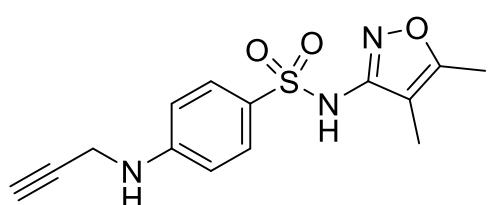




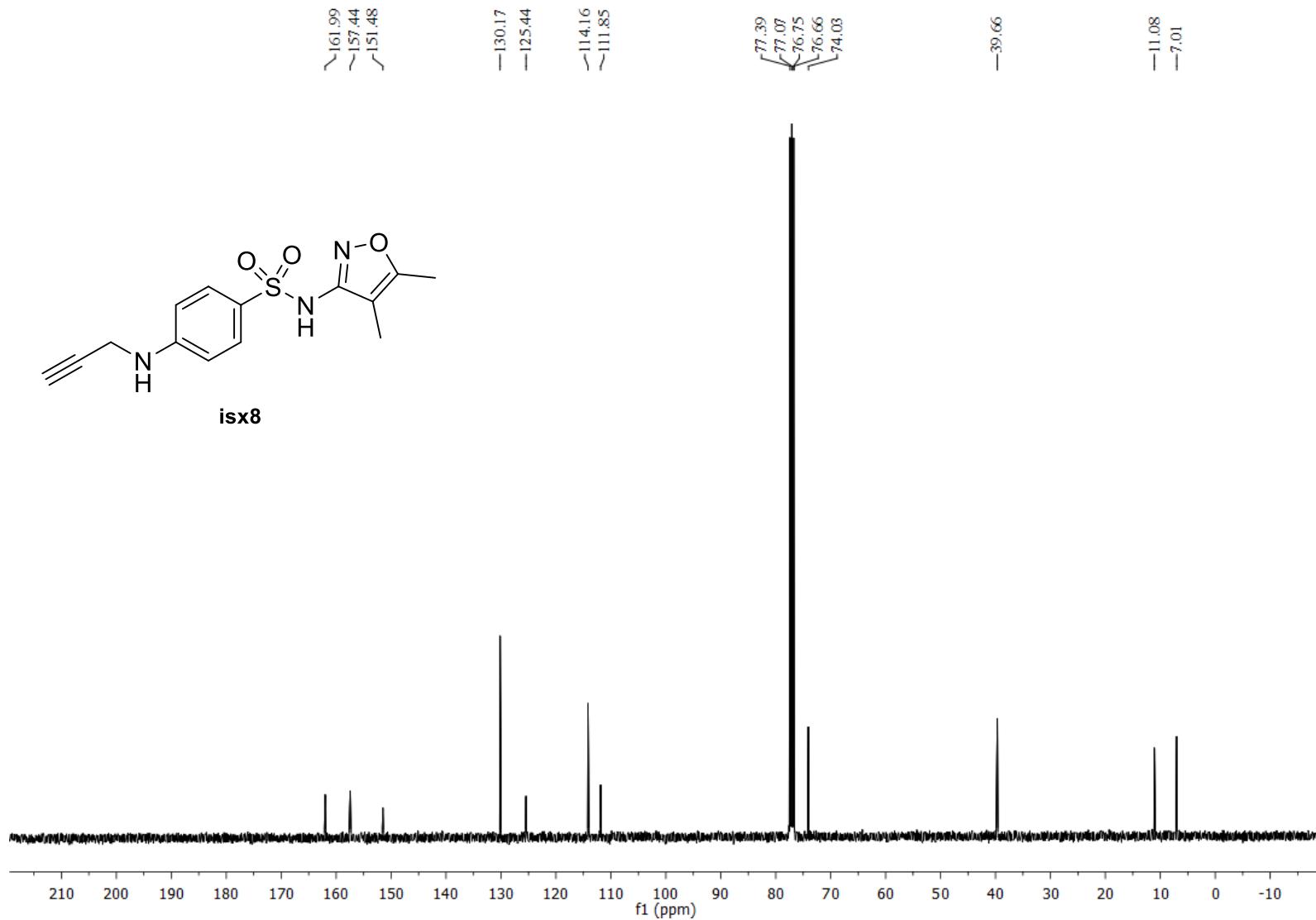


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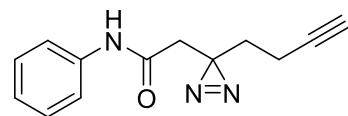


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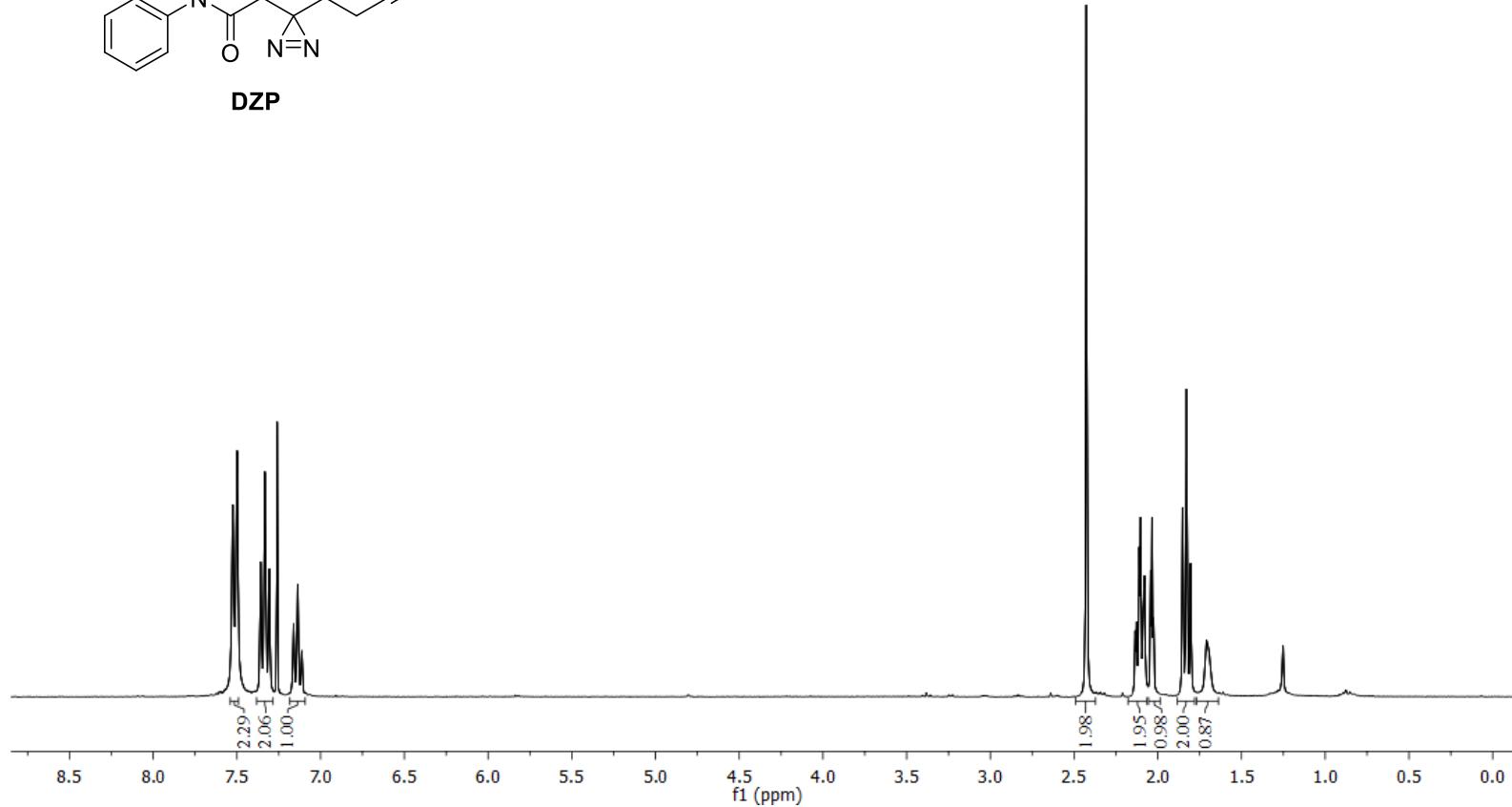


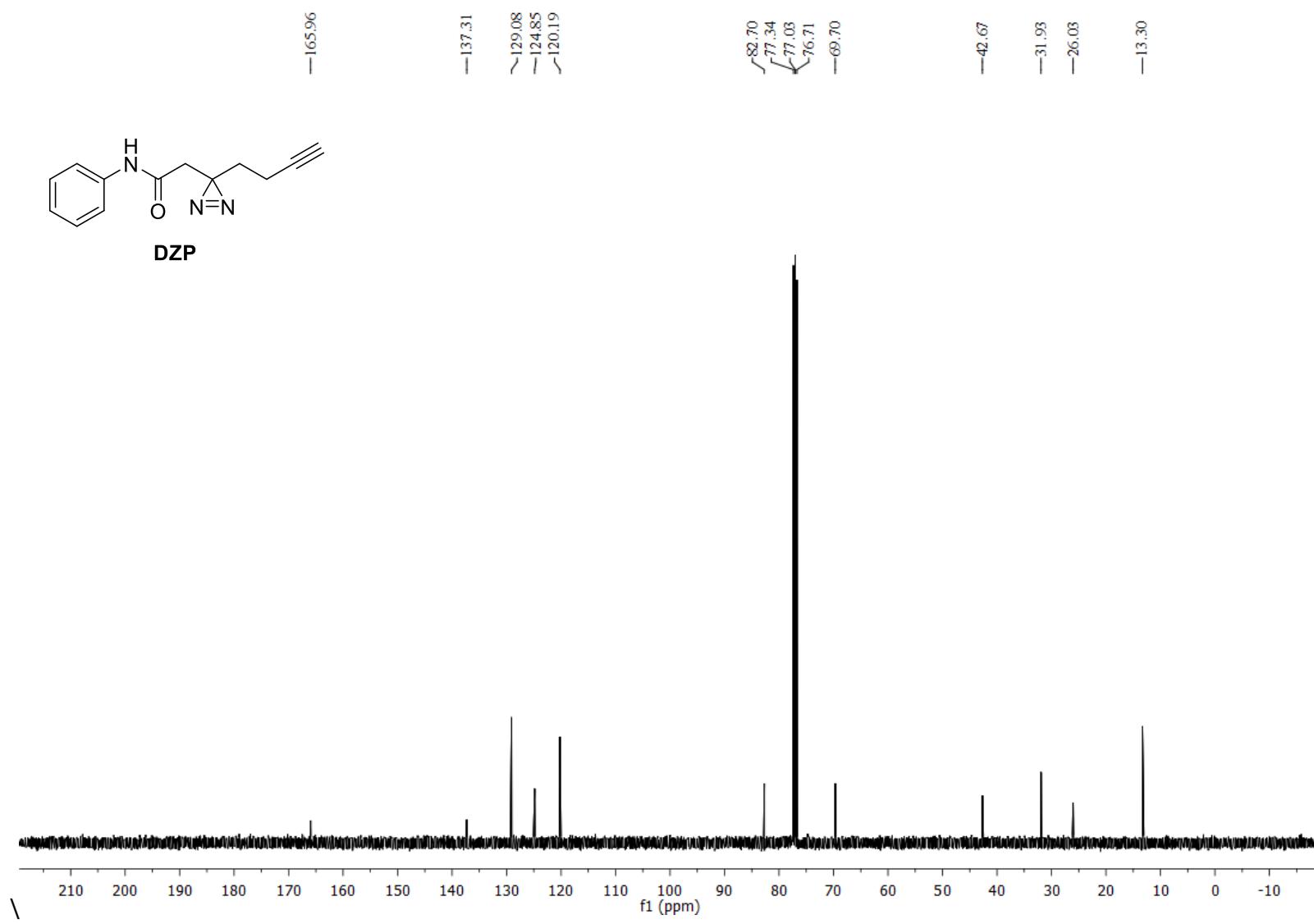
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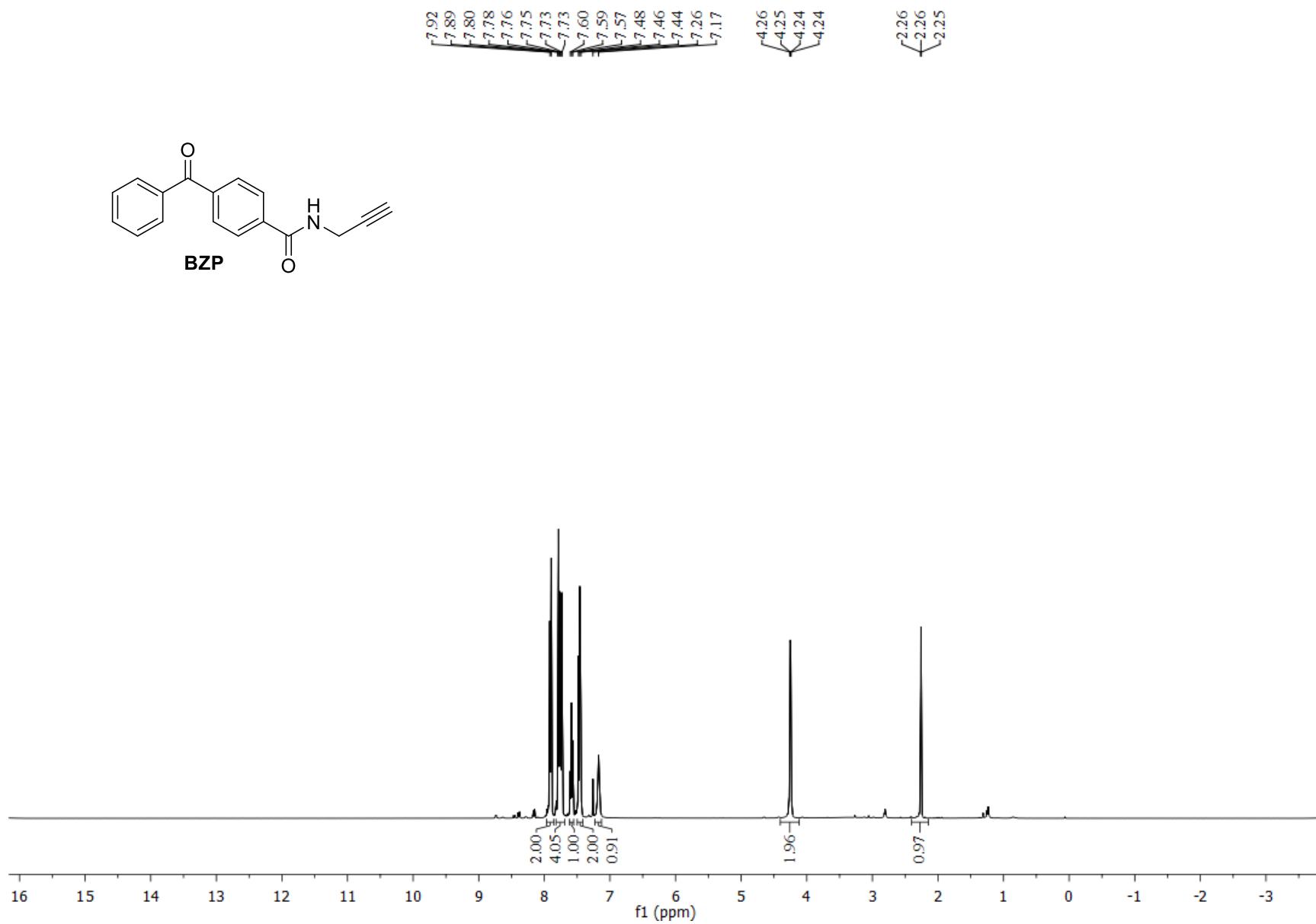
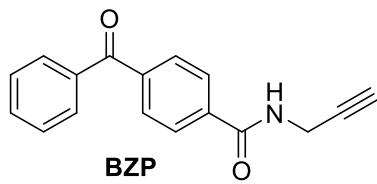
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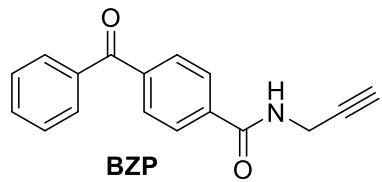


DZP









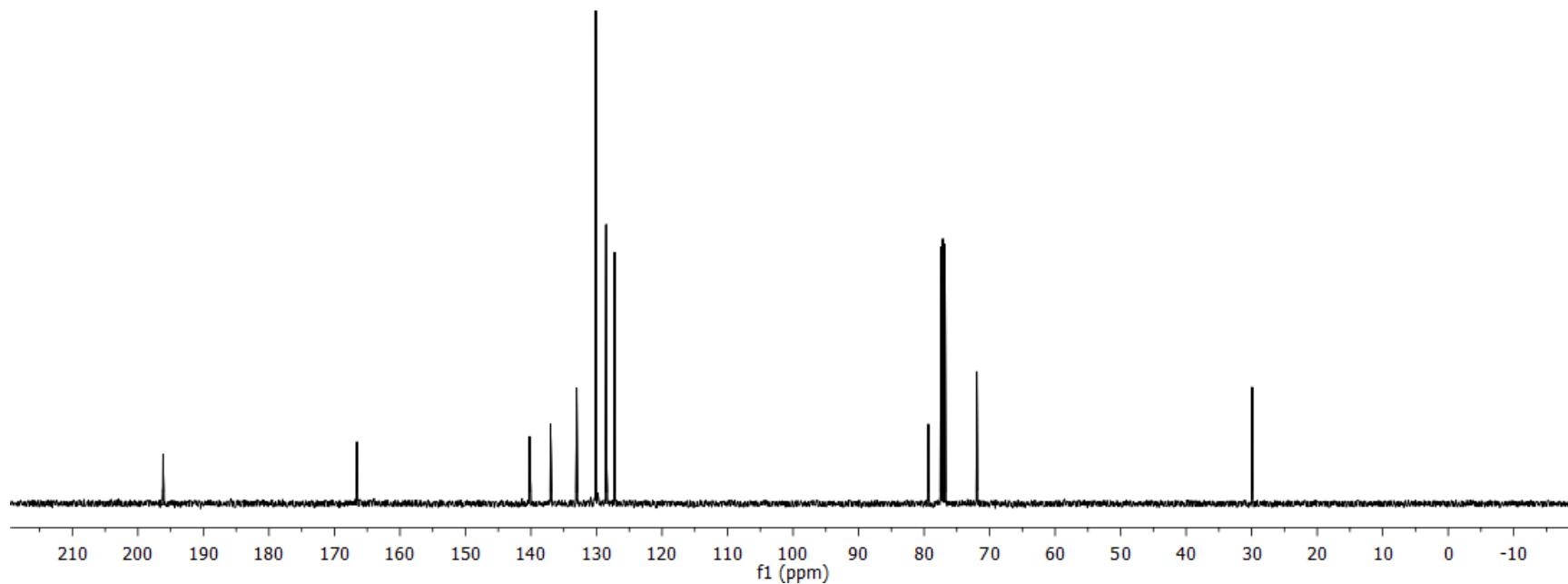
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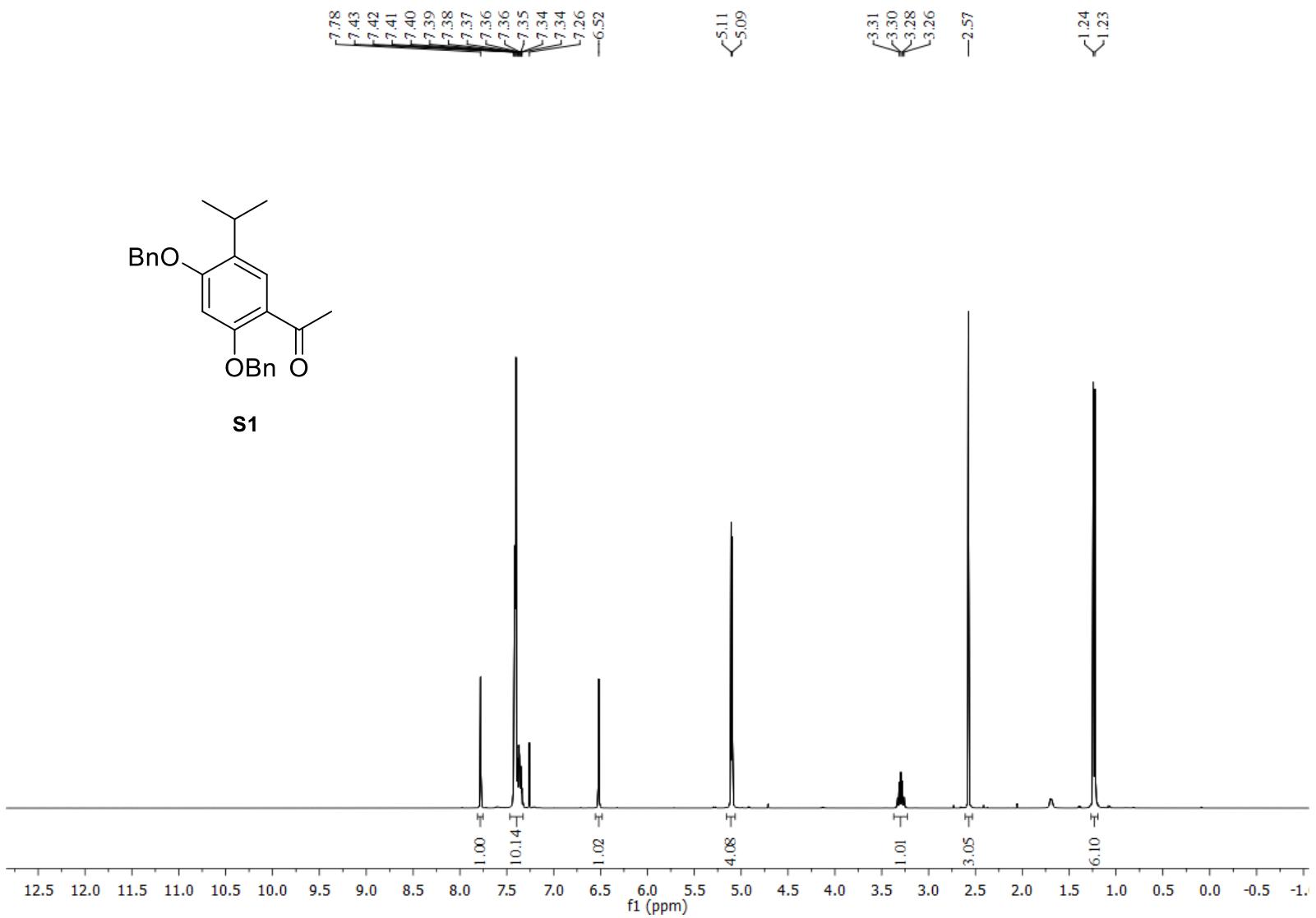
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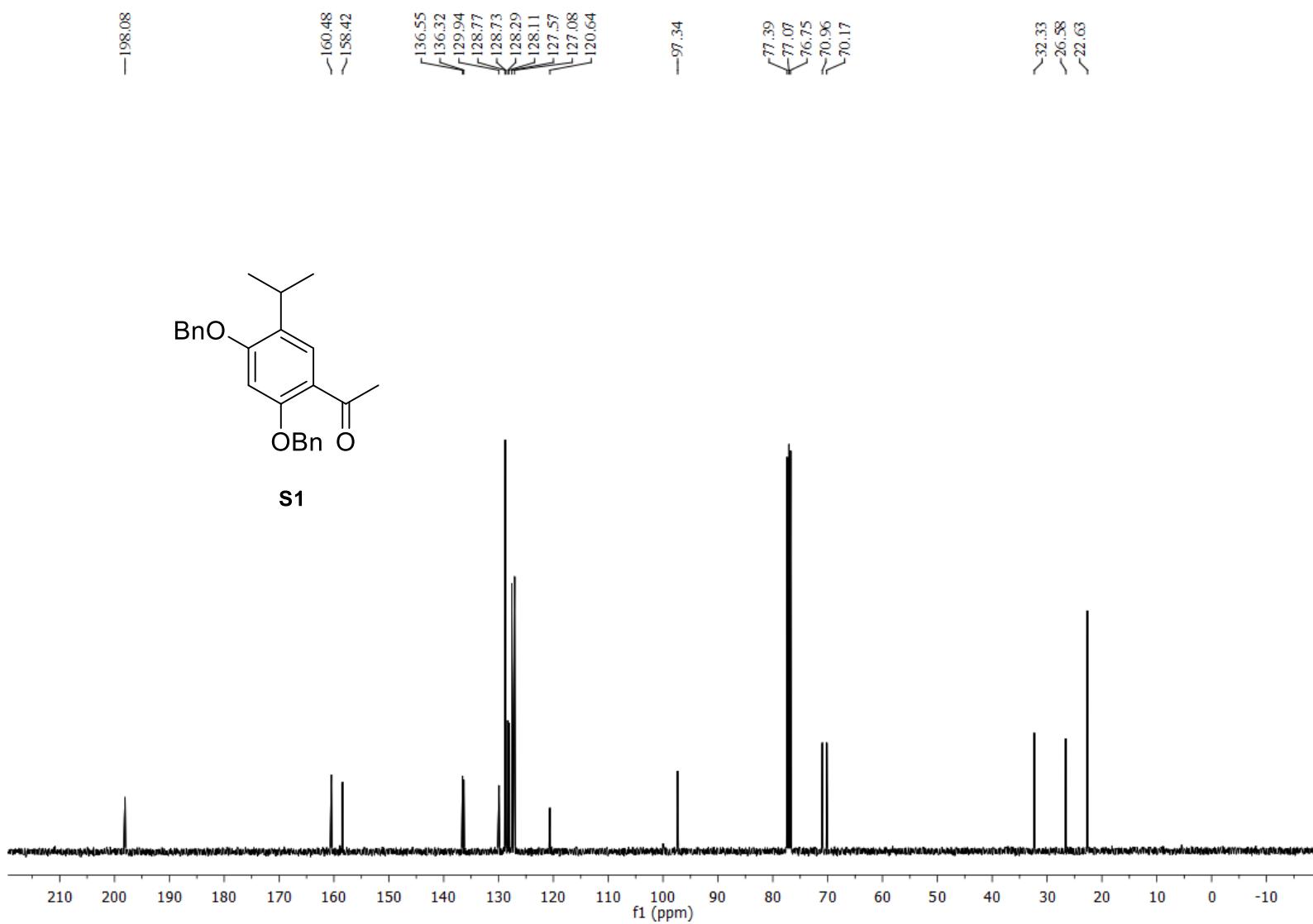
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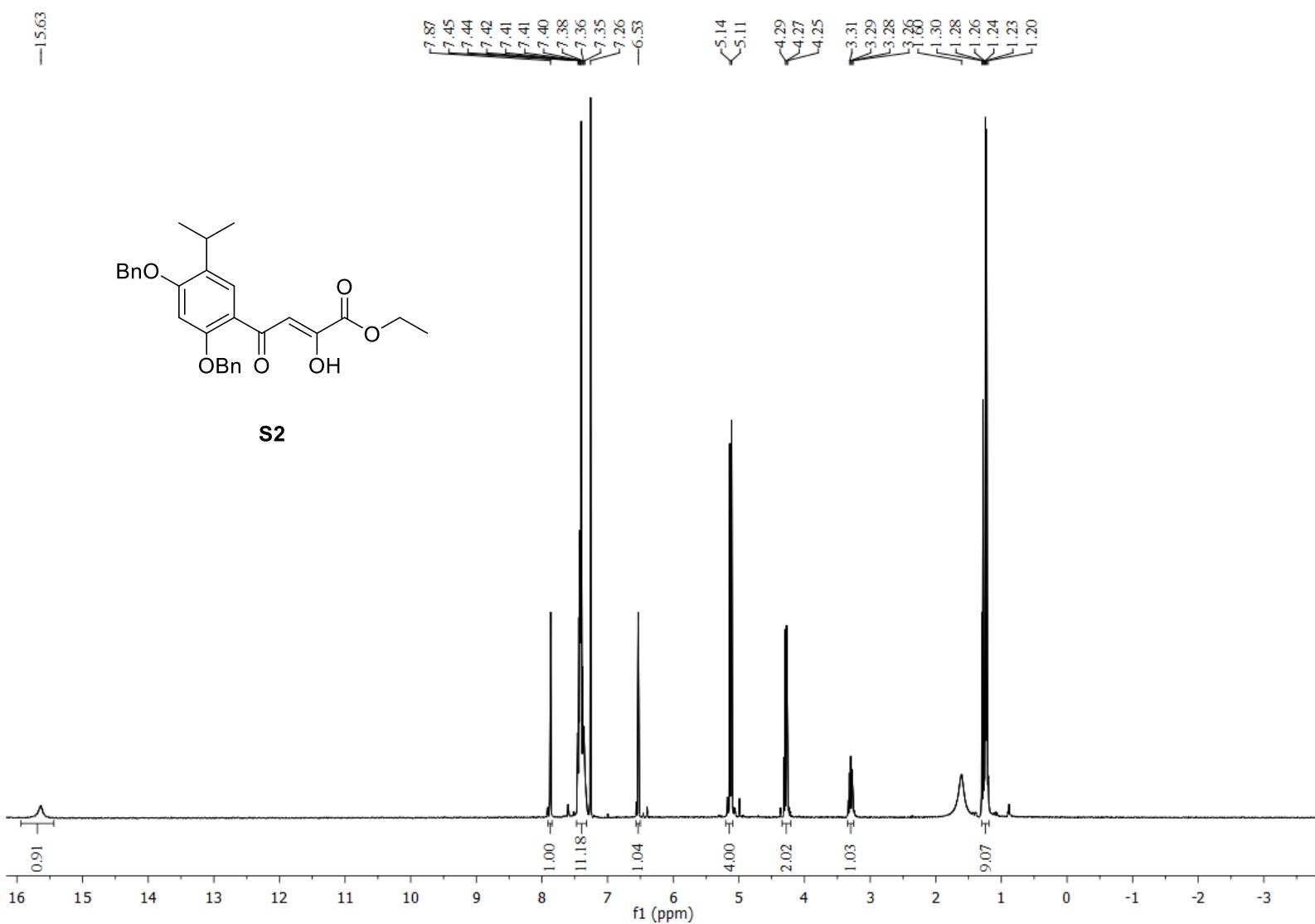
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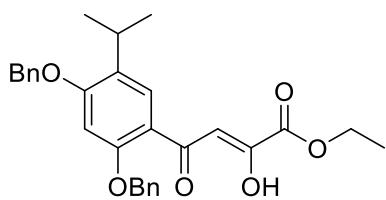
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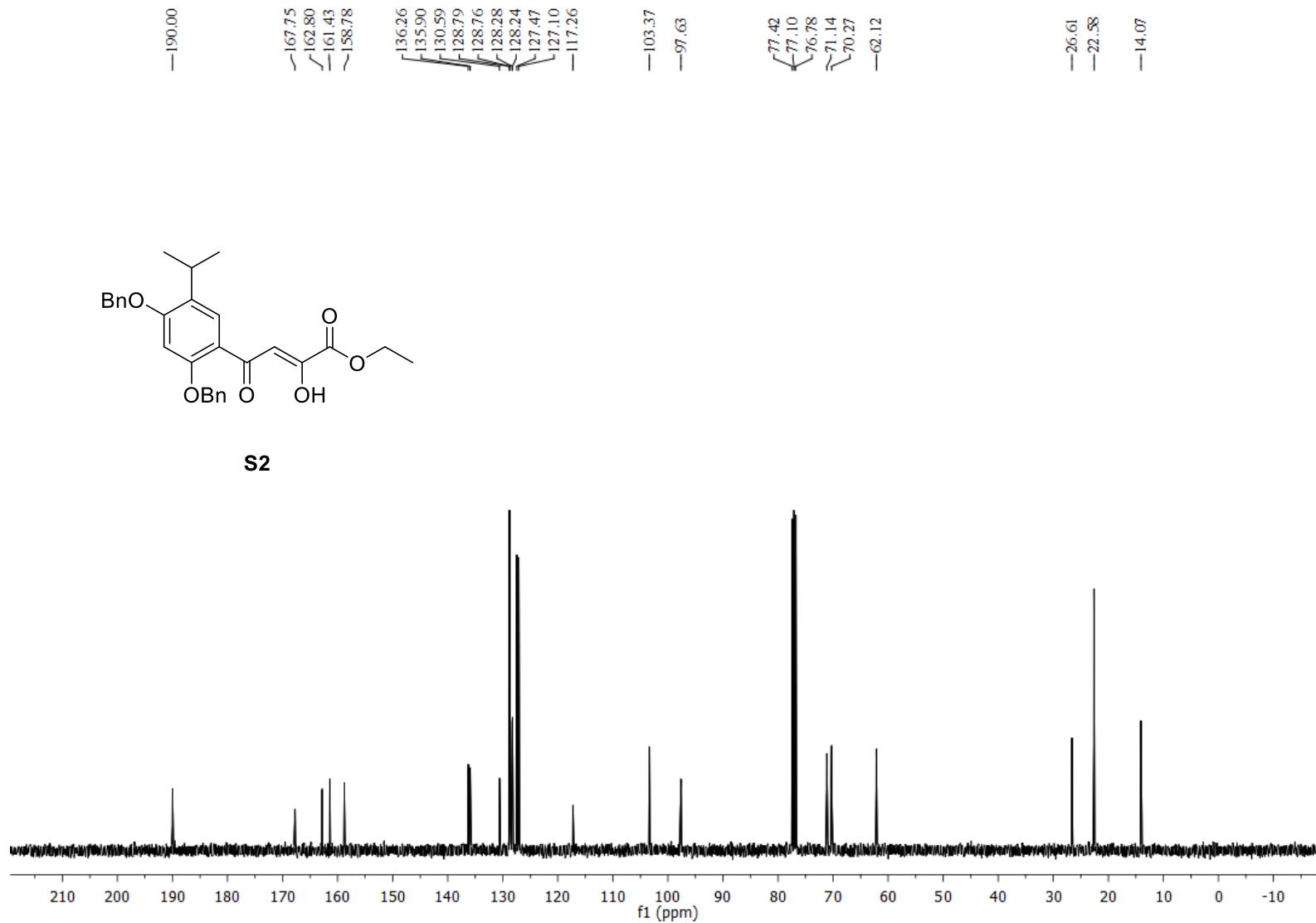


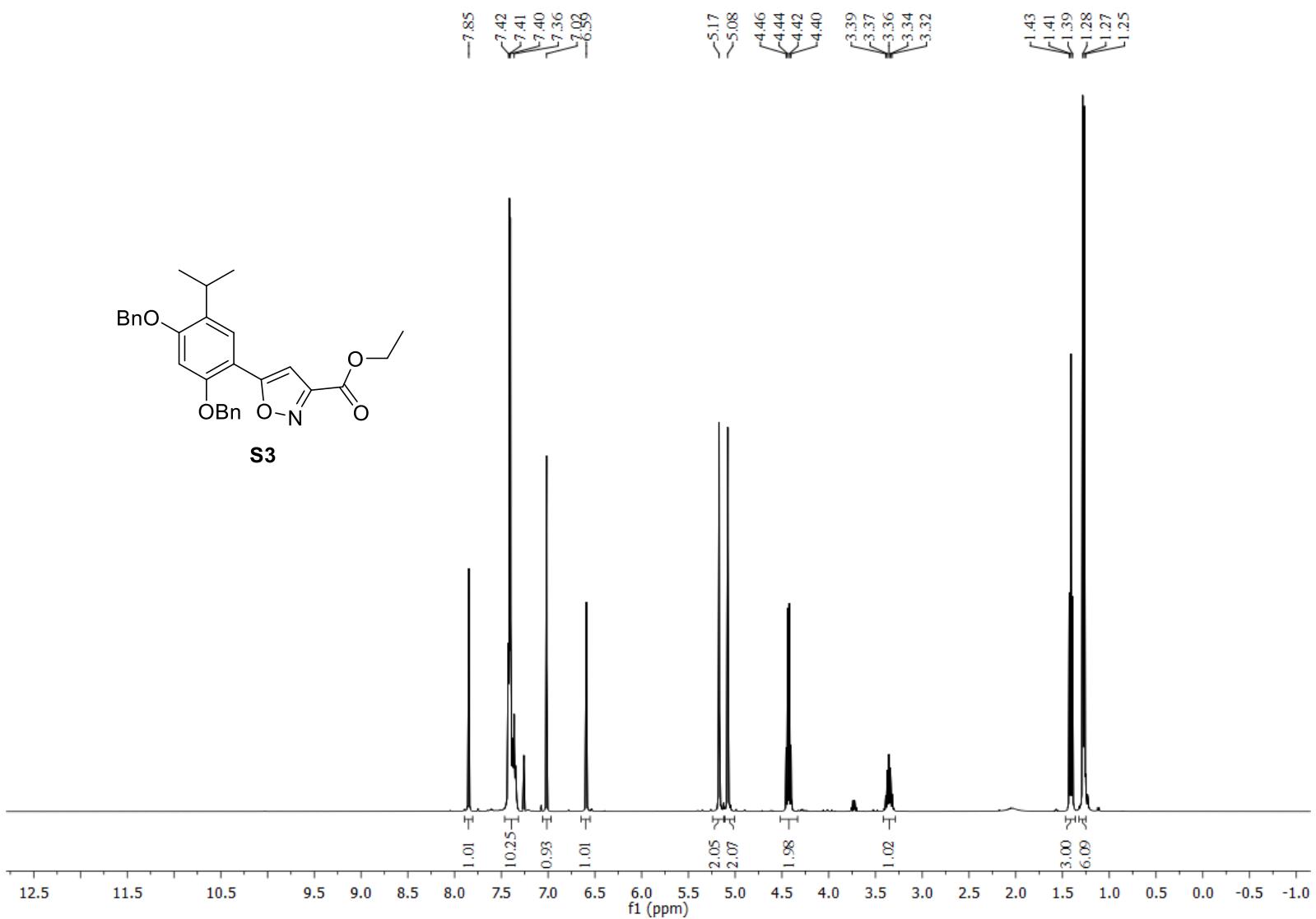


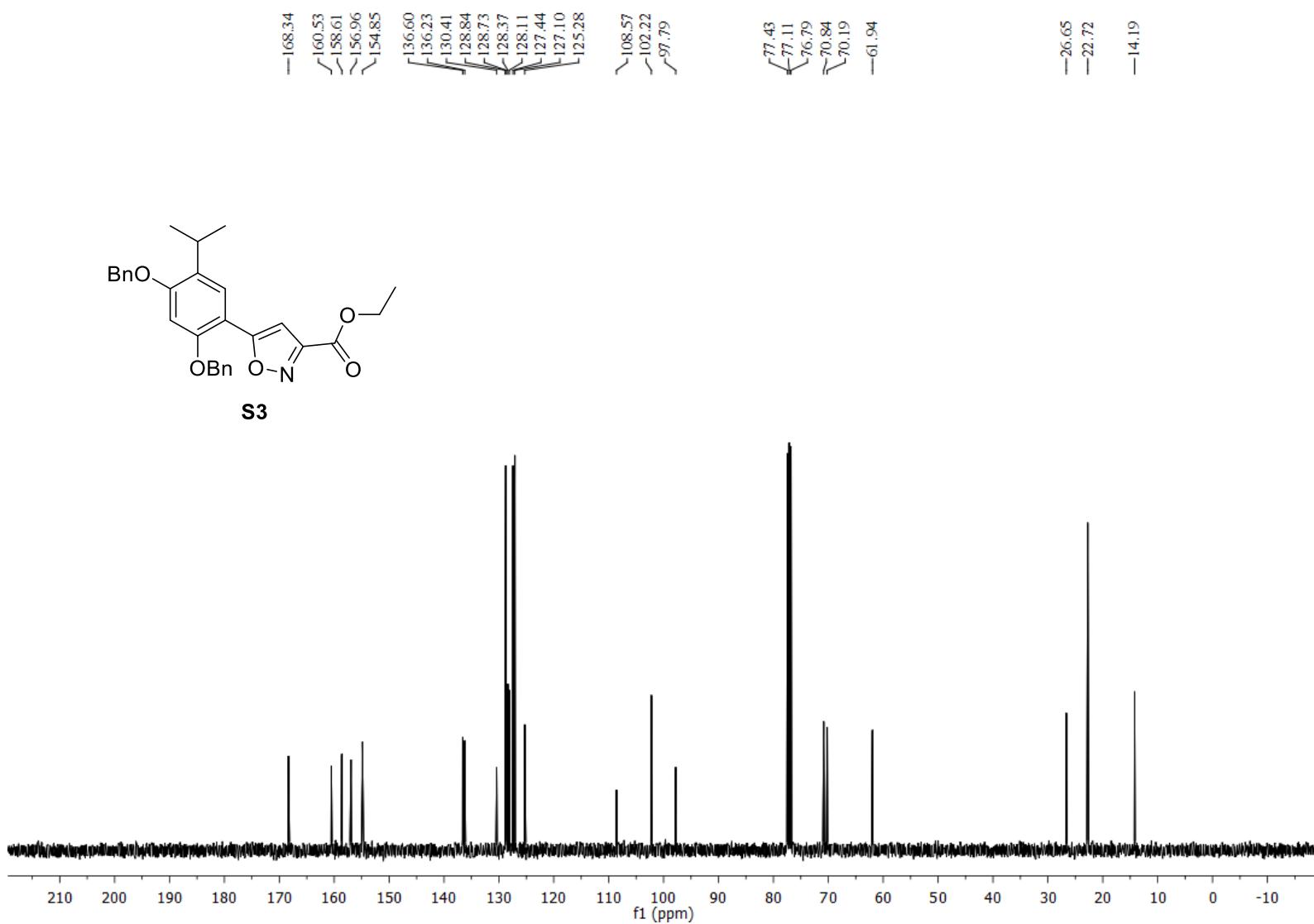
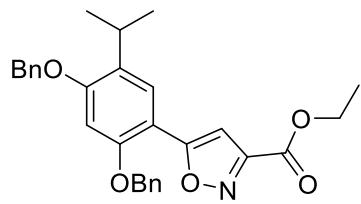


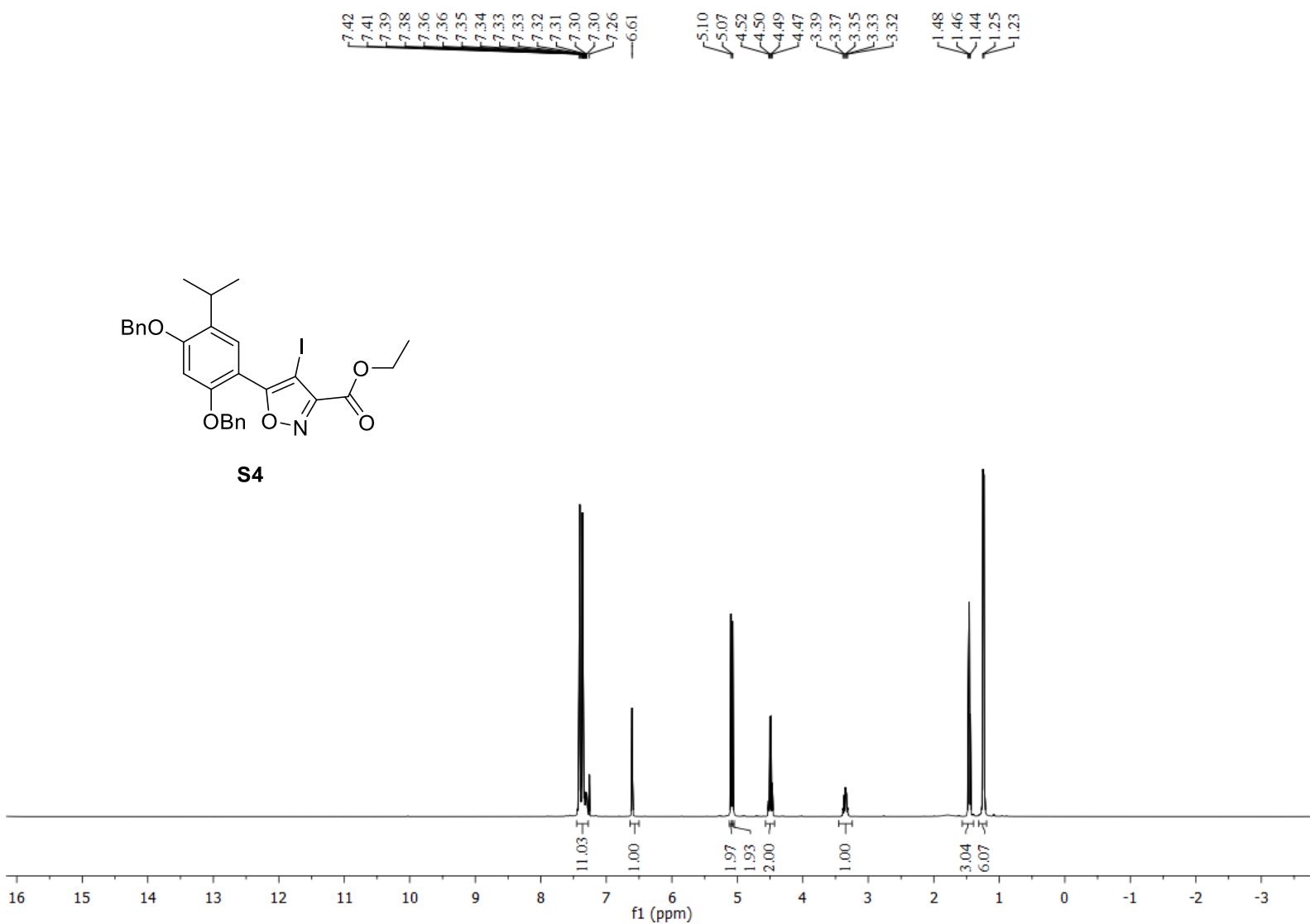
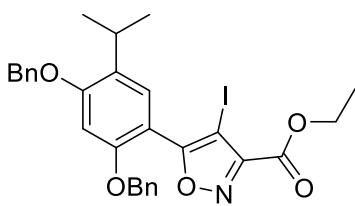


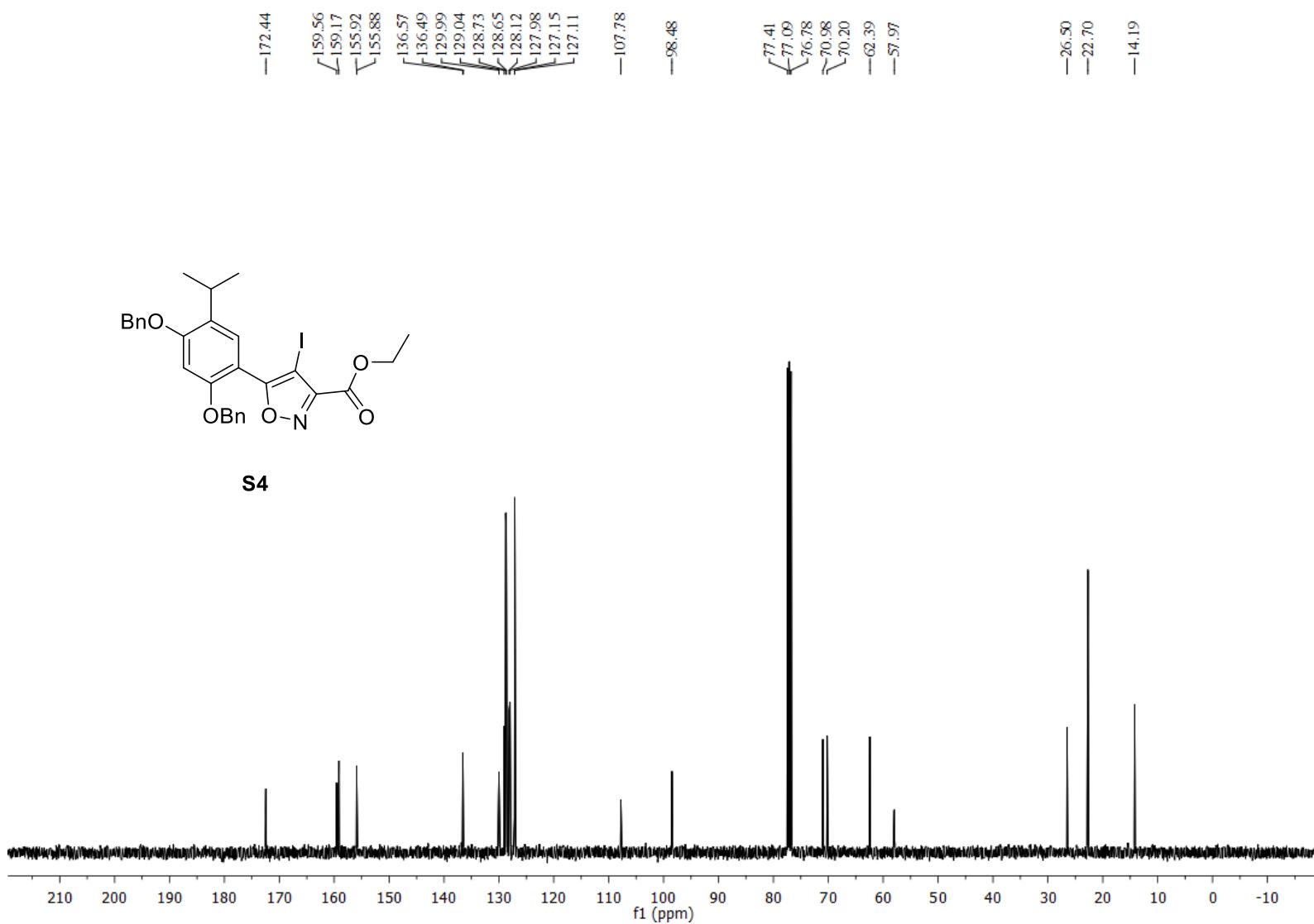
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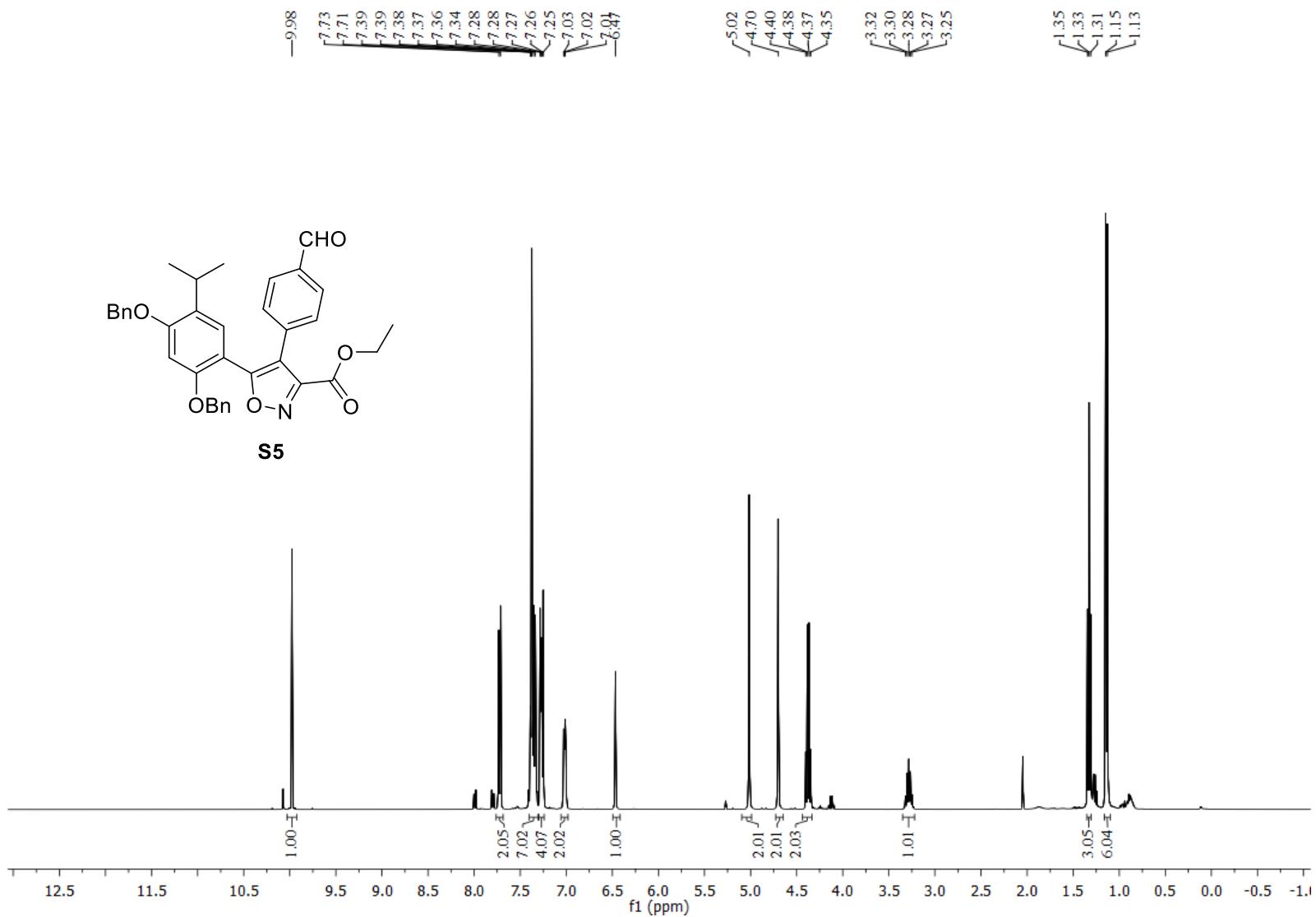


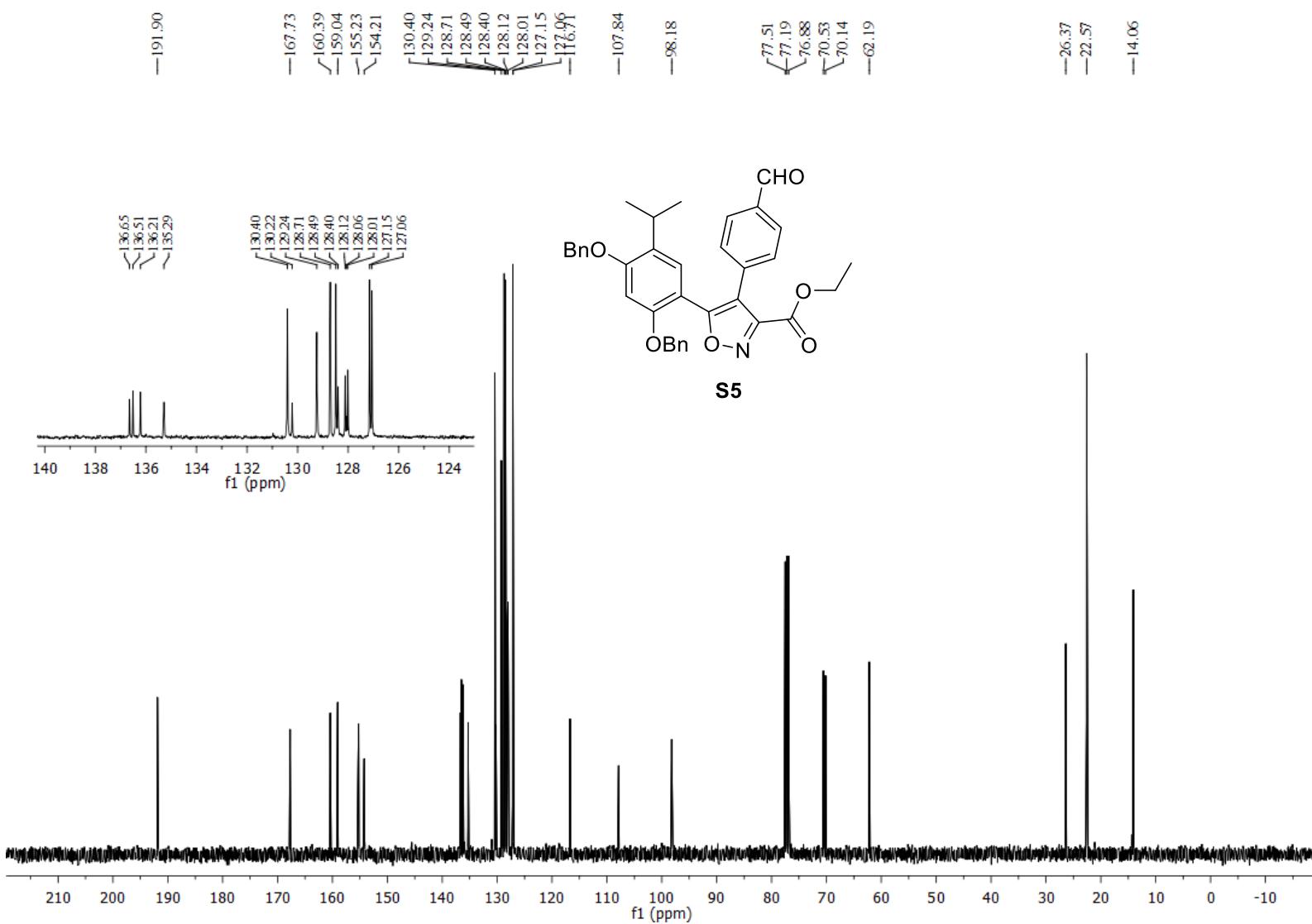


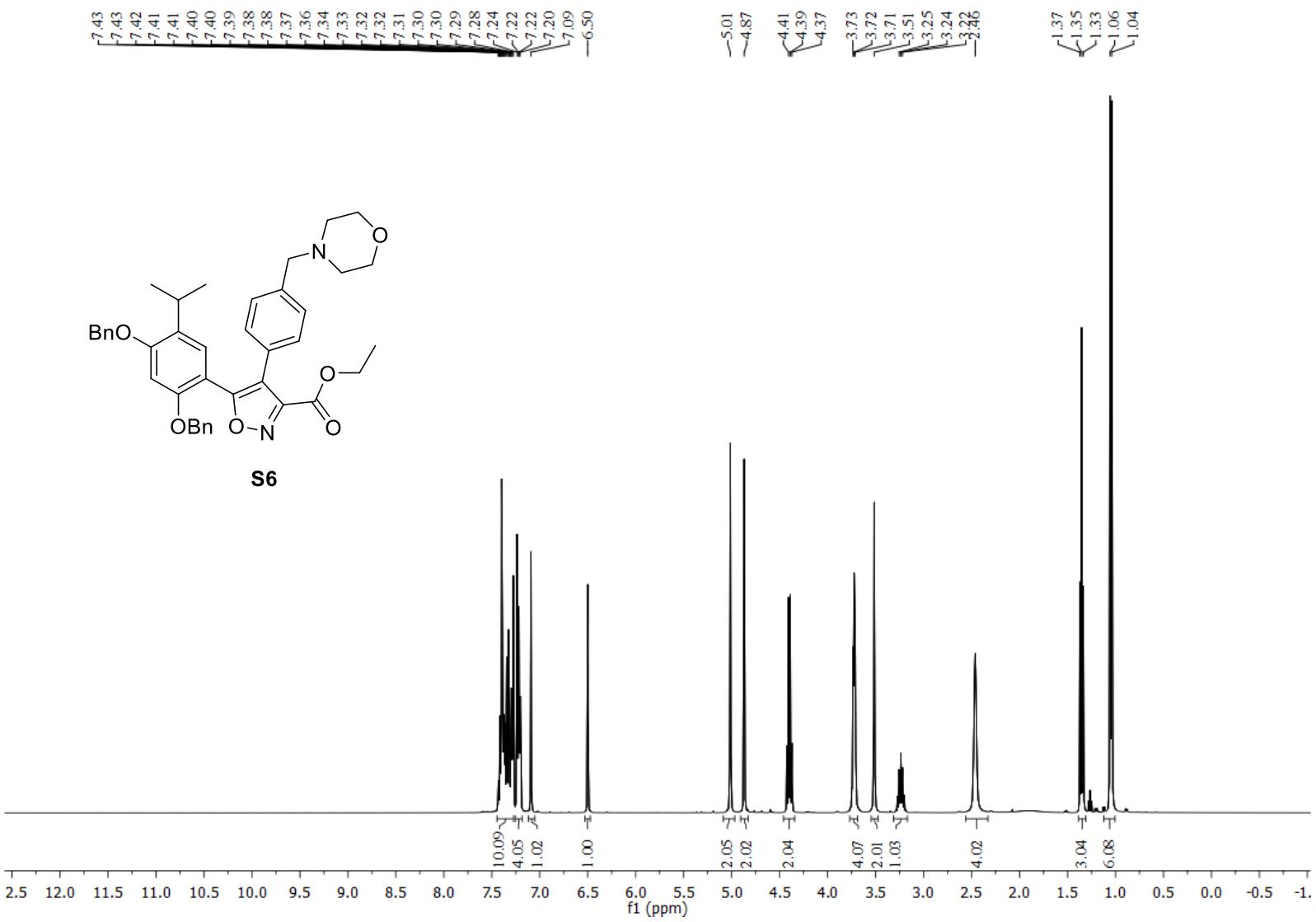


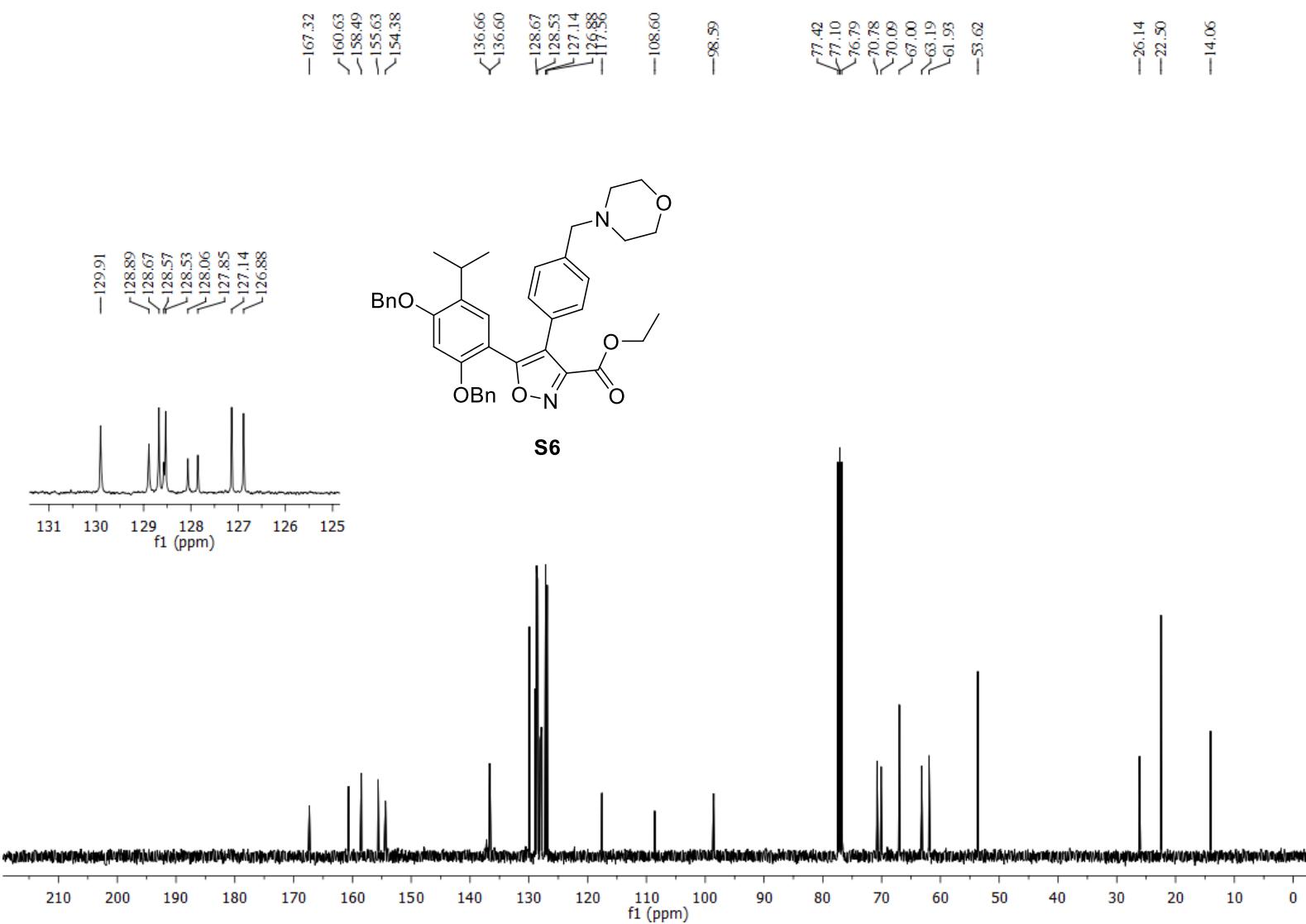


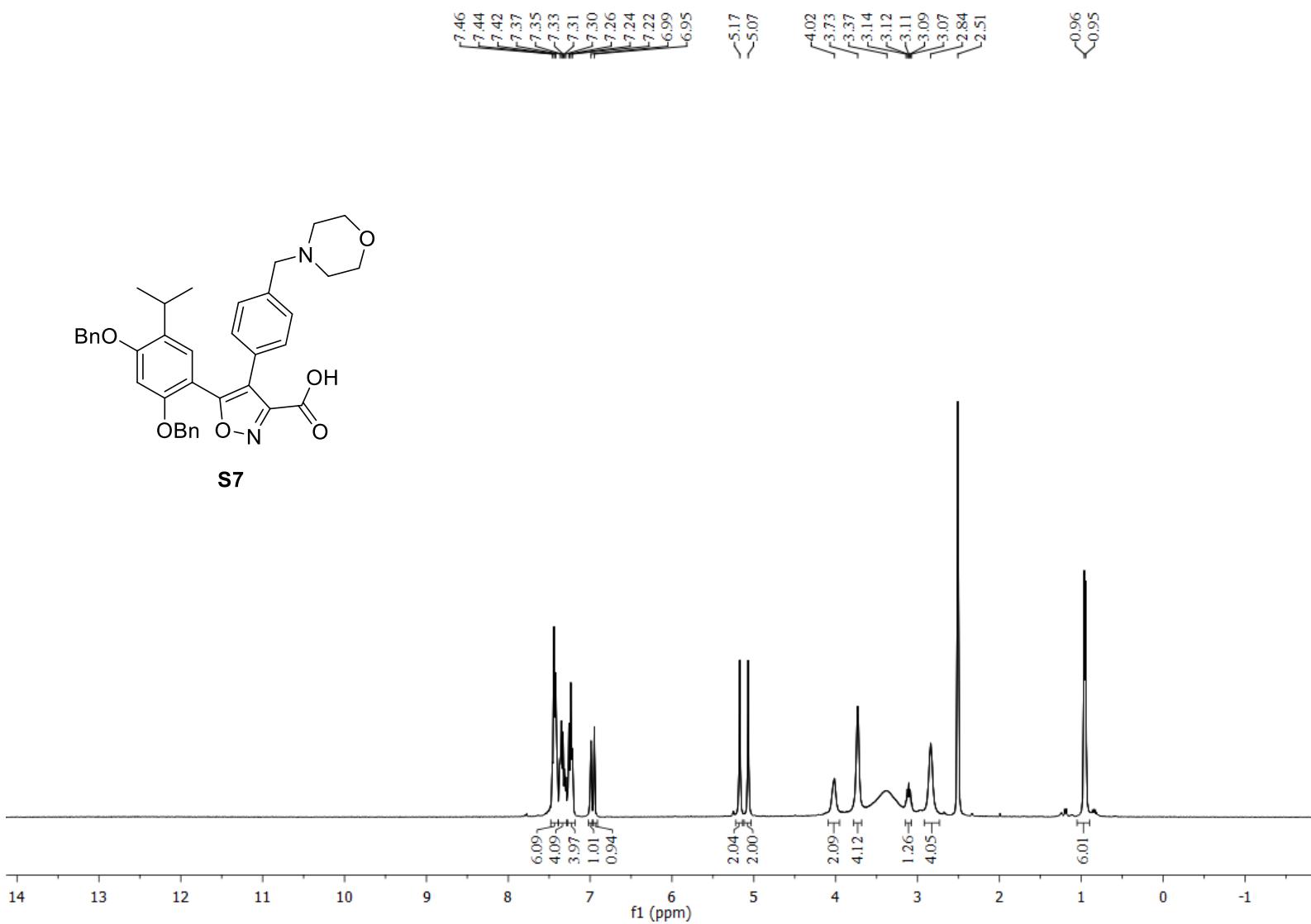


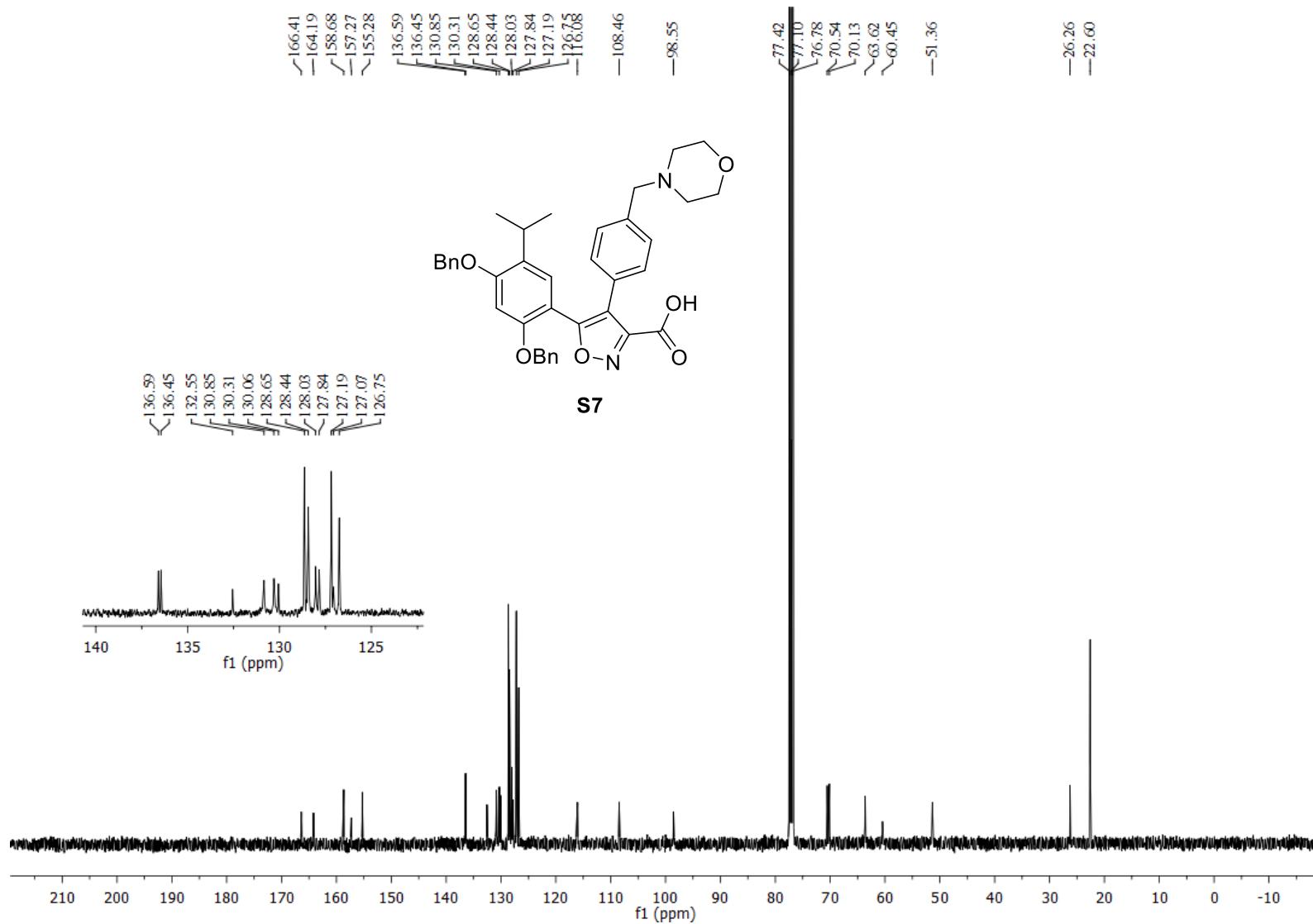


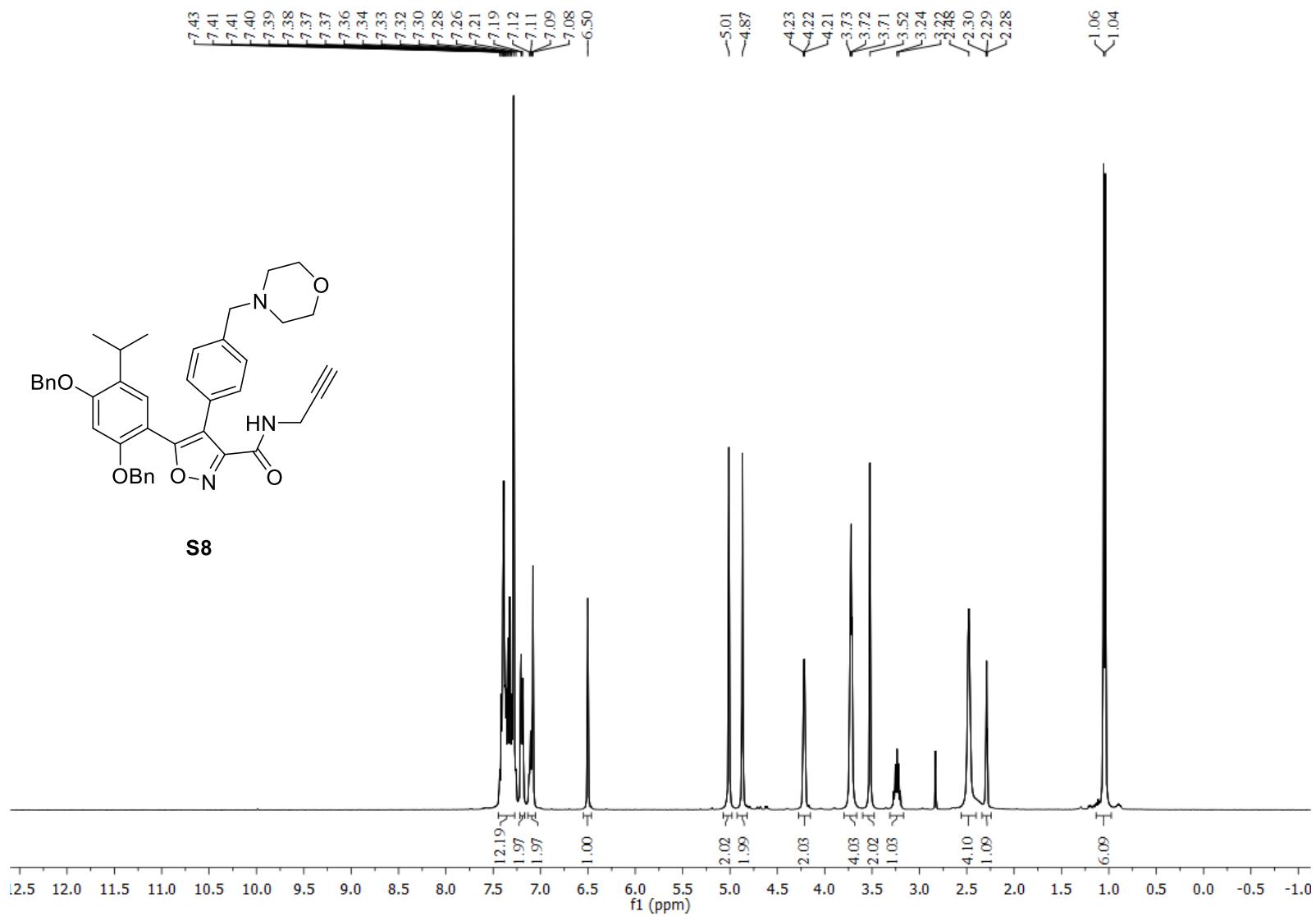


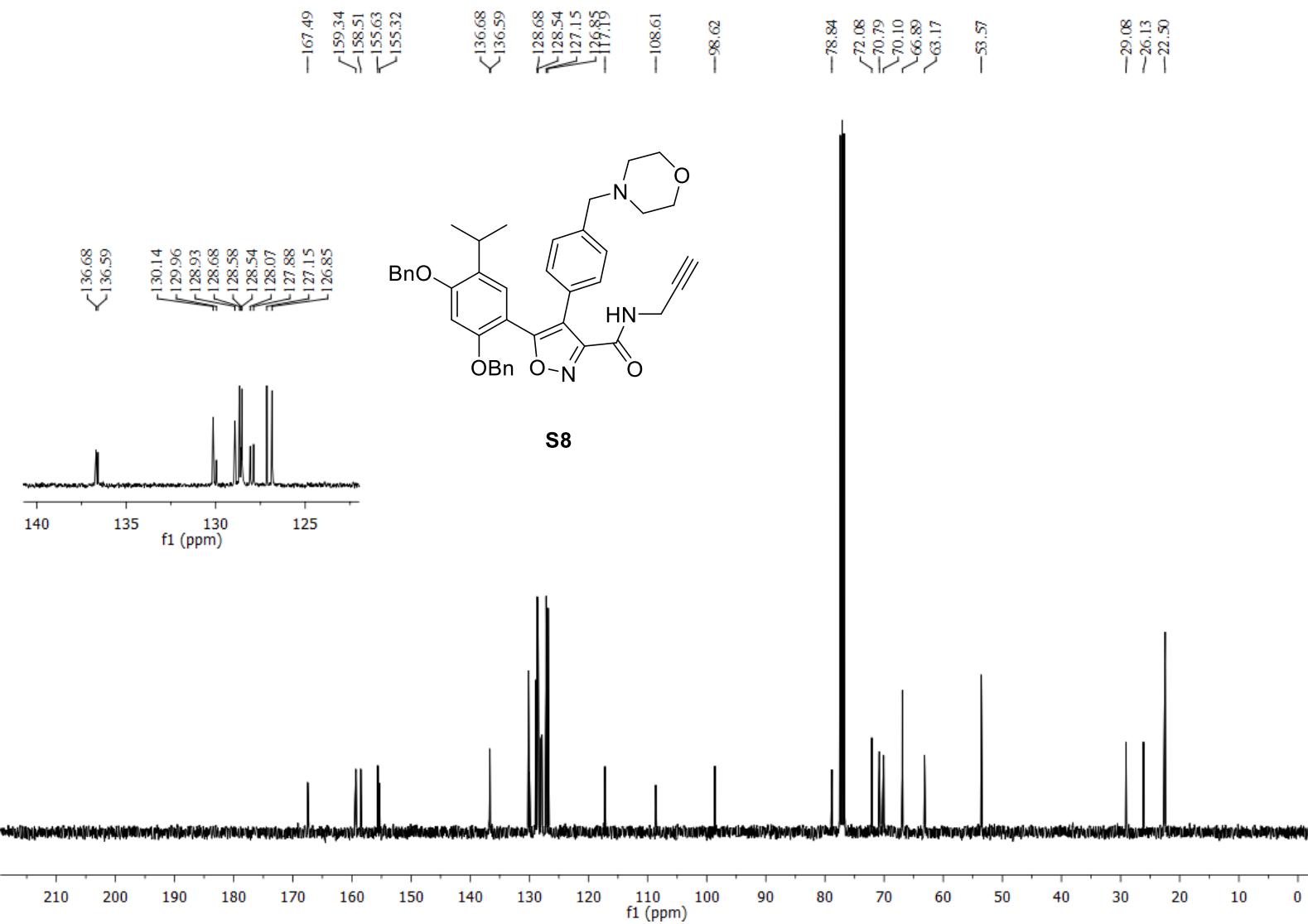


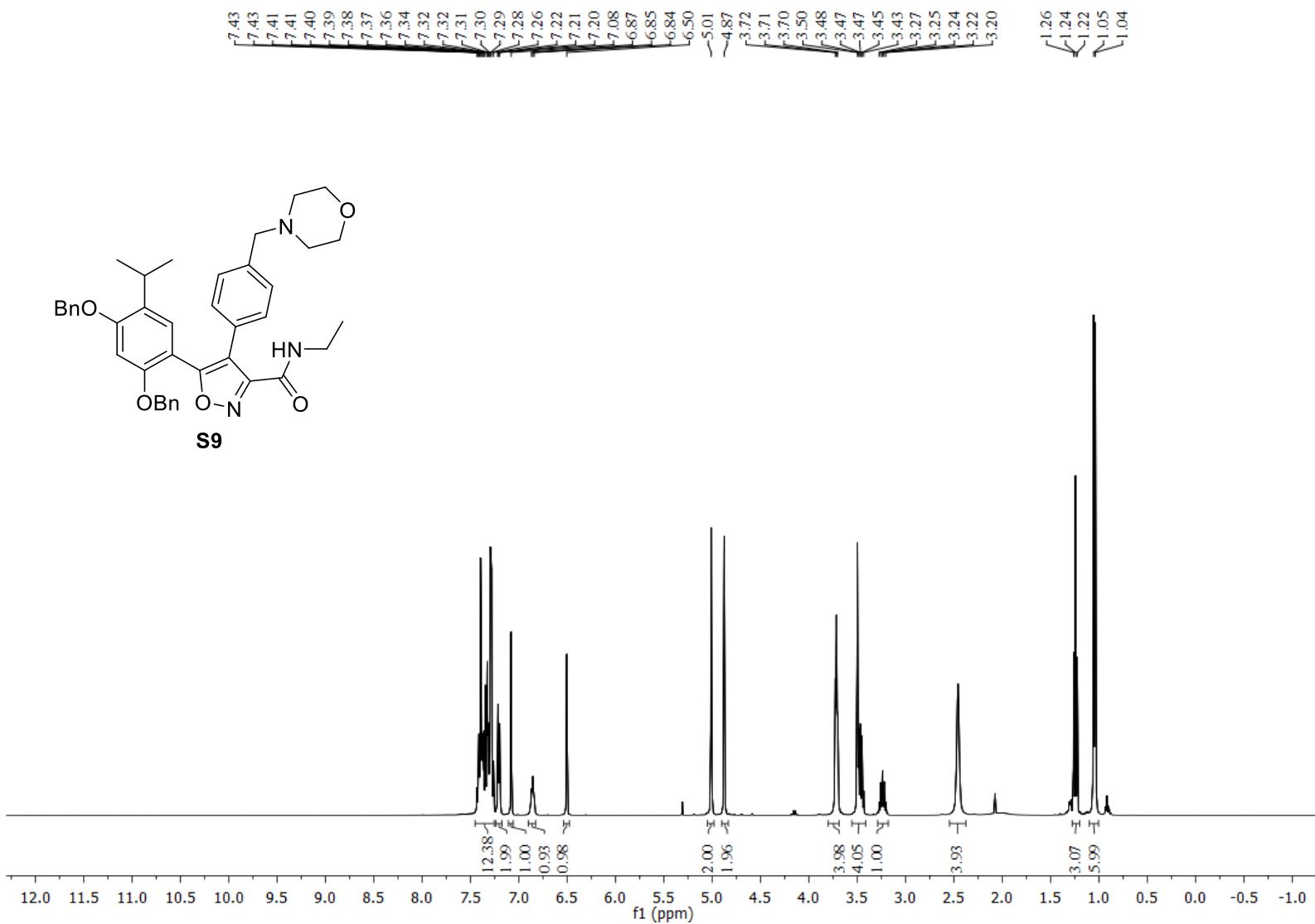




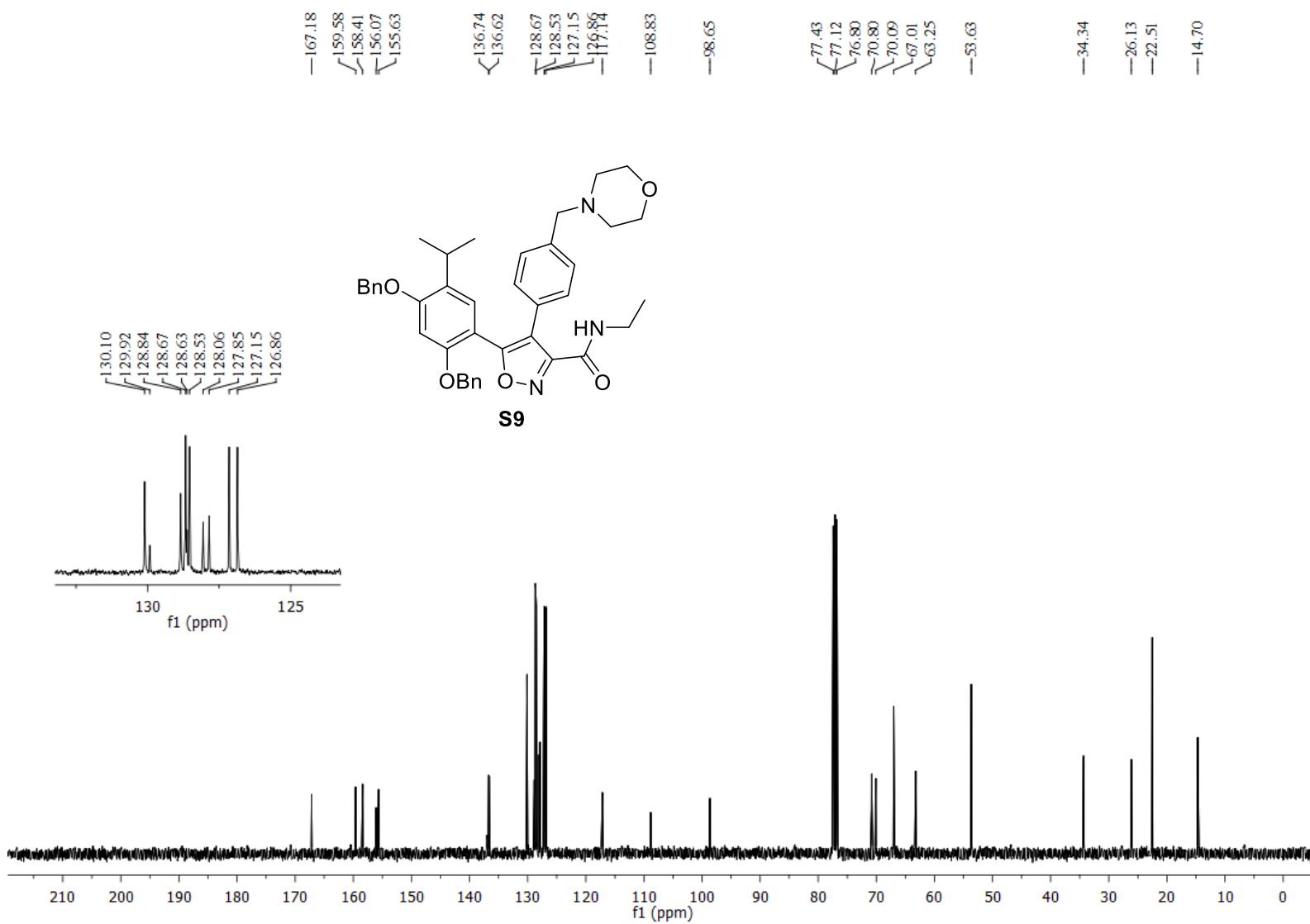


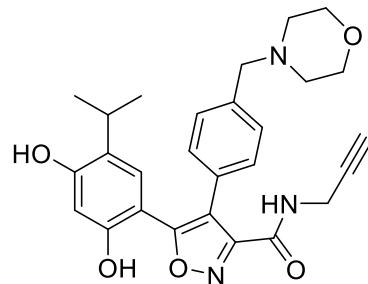




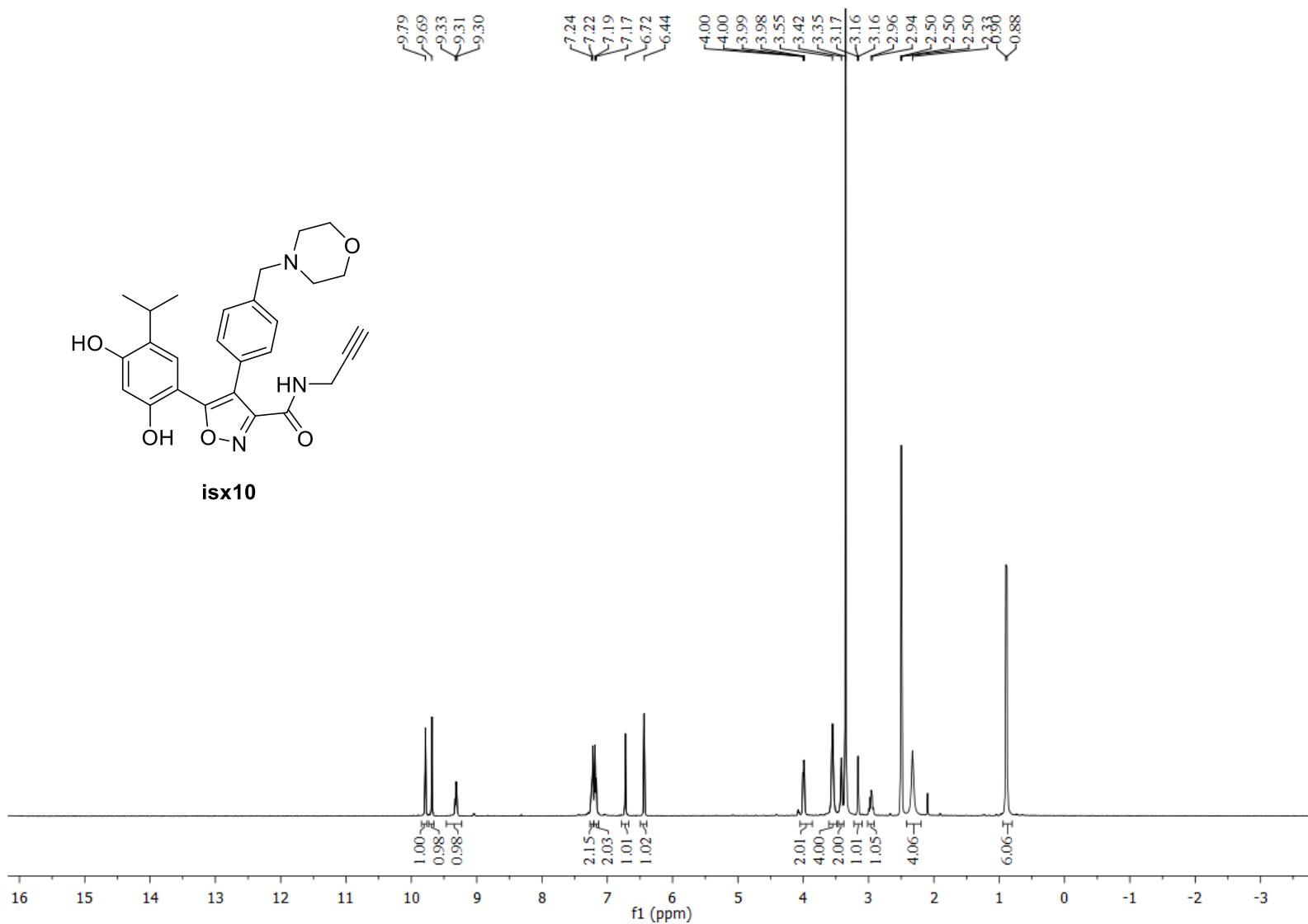


SI-98

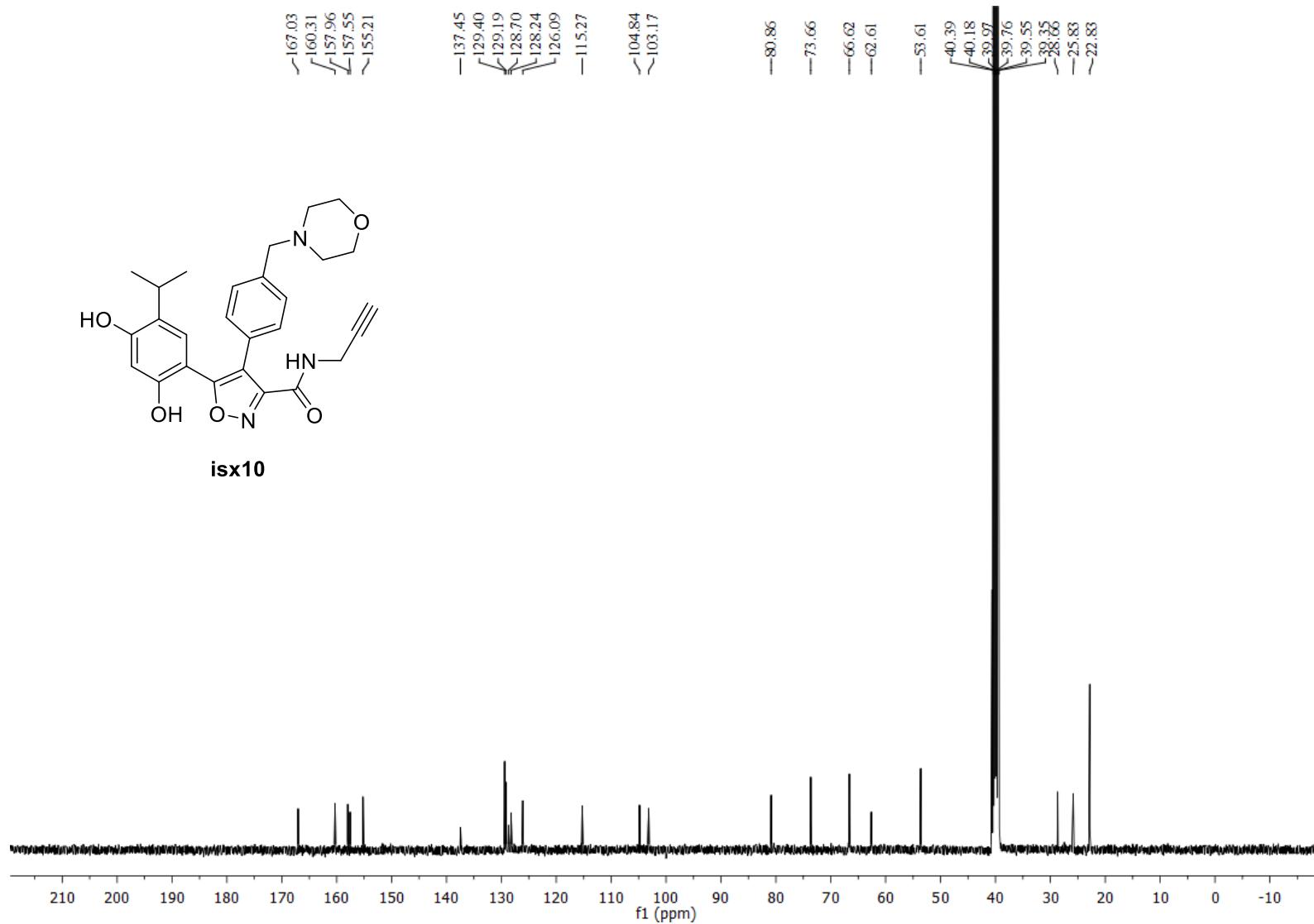
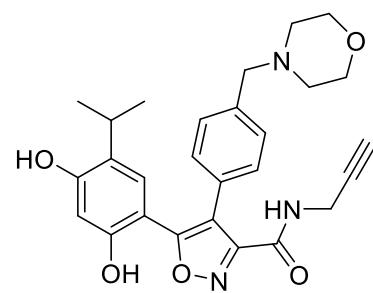


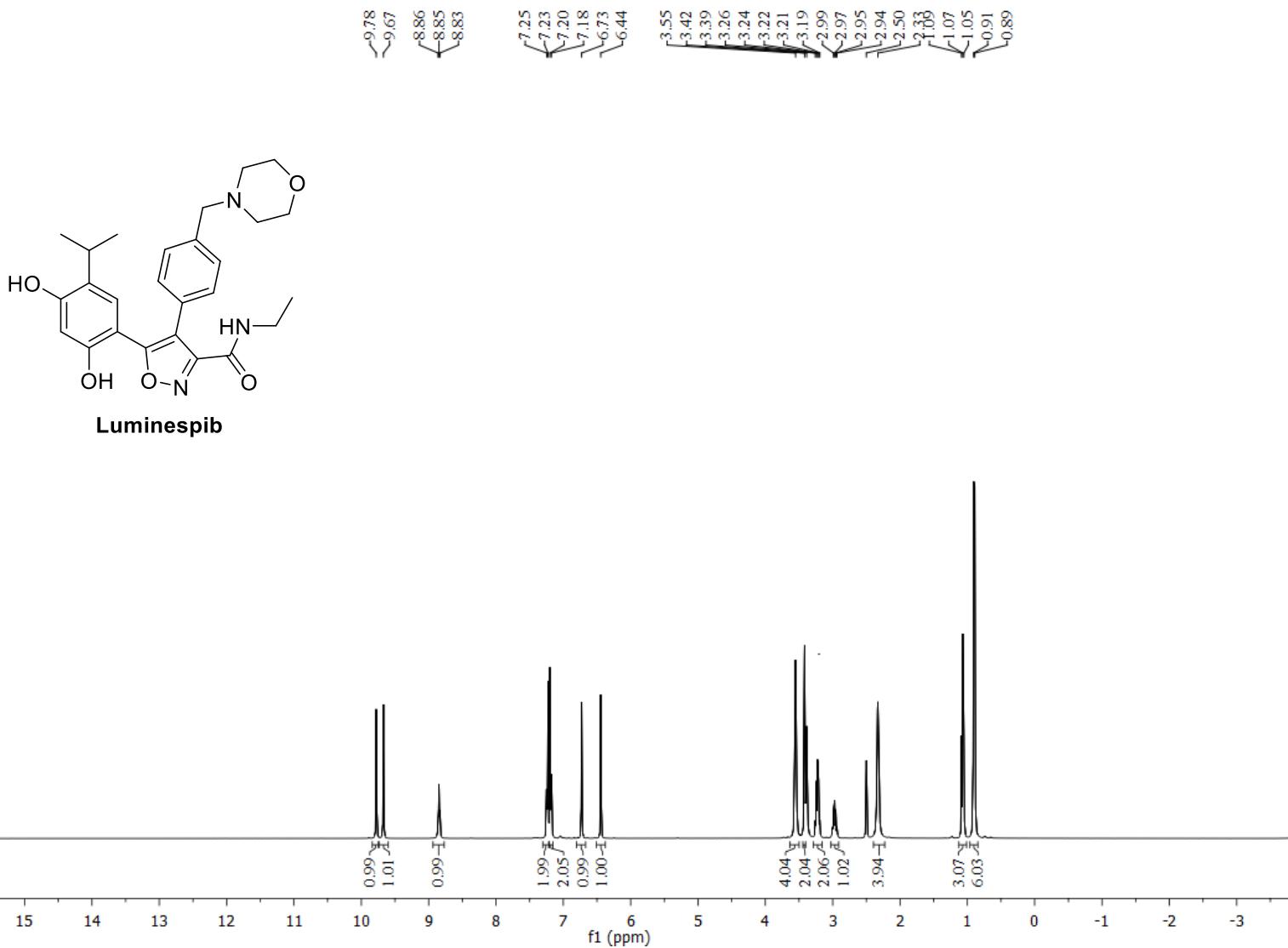


isx10

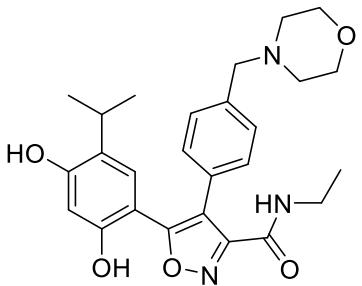


SI-100

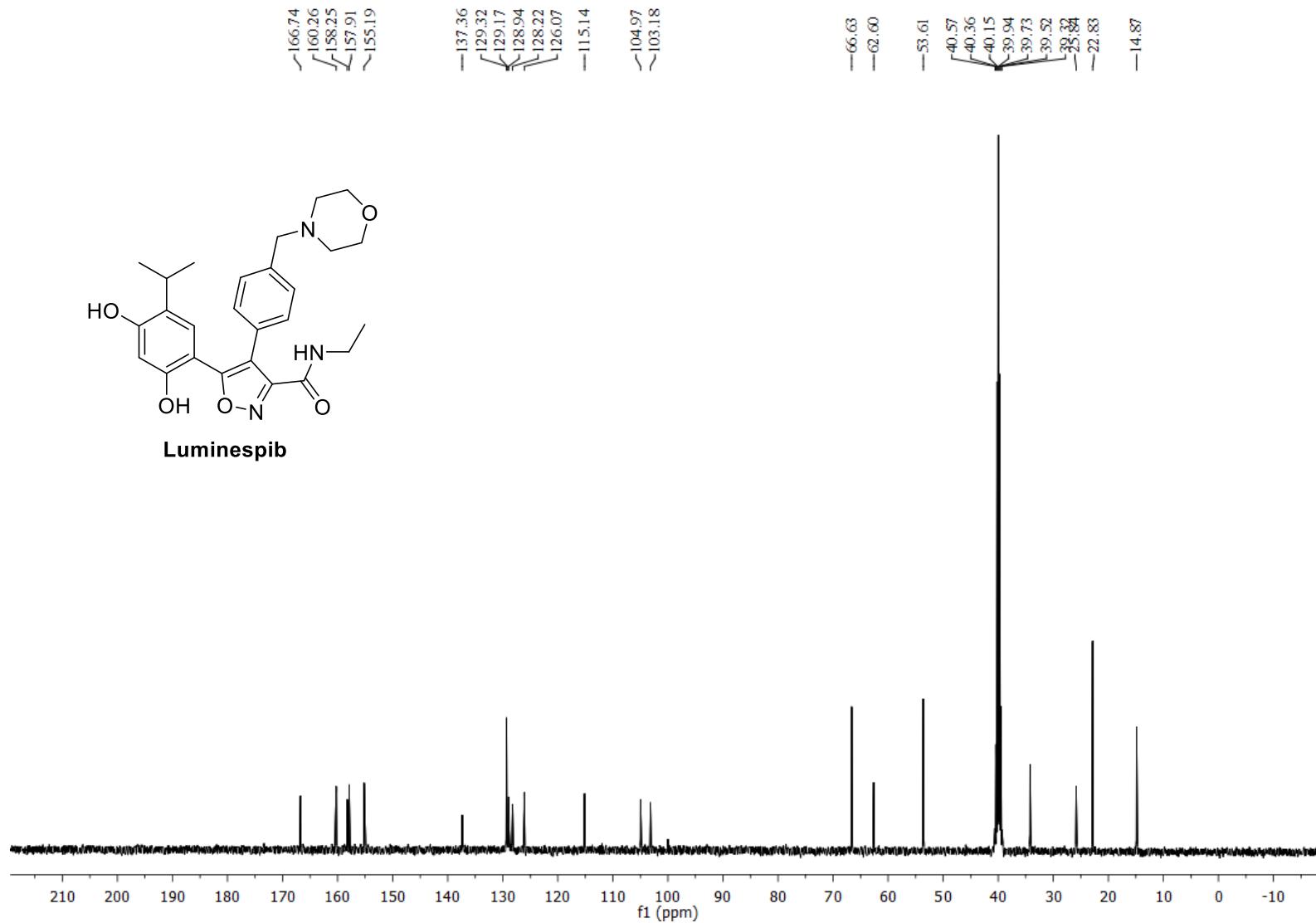




SI-102



Luminespib



20. Full Protein Lists Identified by Chemoproteomic Experiments

20.1 Full Protein Lists Identified by Danazol

UniProt Entry Name	UniProt Accession	Description	Enrichment Ratio (Danazol/DMSO)			
			1st	2nd	3rd	4th
AN32A	P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens OX=9606	2.158	2.198	2.128	2.168
AKP8L	Q9ULX6	A-kinase anchor protein 8-like OS=Homo sapiens OX=9606 GN=AKAP8L PE=1 SV=4	2.909	2.847	2.968	2.905
CPI1	Q6FI81	Anamorsin OS=Homo sapiens OX=9606 GN=CIAPIN1 PE=1 SV=2	2.119	2.072	2.146	2.099
DREB	Q16643	Drebrin OS=Homo sapiens OX=9606 GN=DBN1 PE=1 SV=4	2.247	2.187	2.225	2.165
MAP4	P27816	Microtubule-associated protein 4 OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=3	2.115	2.168	2.08	2.132
I433T	P27348	14-3-3 protein theta OS=Homo sapiens OX=9606 GN=YWHAQ PE=1 SV=1	2.241	2.346	2.243	2.348
TPM3	P06753	Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=2	2.807	2.957	2.863	3.016
MBNL1	Q9NR56	Muscleblind-like protein 1 OS=Homo sapiens OX=9606 GN=MBNL1 PE=1 SV=2	2.021	2	1.934	1.914
DNCJ9	Q8WX55	DnaJ homolog subfamily C member 9 OS=Homo sapiens OX=9606 GN=DNAJC9 PE=1	2.489	2.379	2.415	2.309
TXLNA	P40222	Alpha-taxilin OS=Homo sapiens OX=9606 GN=TXLNA PE=1 SV=3	2.623	2.734	2.748	2.864
SYNM	Q96I59	Probable asparagine-tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=NARS2	1.634	1.65	1.7	1.718
PDIA3	P30101	Protein disulfide-isomerase A3 OS=Homo sapiens OX=9606 GN=PDIA3 PE=1 SV=4	1.75	1.832	1.734	1.816
PAPOA	P51003	Poly(A) polymerase alpha OS=Homo sapiens OX=9606 GN=PAPOA PE=1 SV=4	1.68	1.626	1.629	1.577
CCDC6	Q16204	Coiled-coil domain-containing protein 6 OS=Homo sapiens OX=9606 GN=CCDC6 PE=1	1.557	1.581	1.625	1.651
SF3A2	Q51428	Splicing factor 3A subunit 2 OS=Homo sapiens OX=9606 GN=SFSF3A2 PE=1 SV=2	1.641	1.567	1.666	1.591
PDIA1	P07237	Protein disulfide-isomerase OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=3	1.942	1.829	1.903	1.792
SCAM3	O14828	Secretory carrier-associated membrane protein 3 OS=Homo sapiens OX=9606 GN=SCAMP3	1.689	1.691	1.592	1.594
VIME	P08670	Vimentin OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=4	1.656	1.762	1.692	1.8
CCNK	Q75909	Cyclin-K OS=Homo sapiens OX=9606 GN=CCNK PE=1 SV=2	1.832	1.881	1.978	2.031
RRBPI	Q99P29	Ribosome-binding protein 1 OS=Homo sapiens OX=9606 GN=RRBP1 PE=1 SV=5	1.789	1.673	1.736	1.623
AT5G1	P05496	ATP synthase F(0) complex subunit C1, mitochondrial OS=Homo sapiens OX=9606	1.666	1.632	1.563	1.531
GOGA3	O08378	Golgin subfamily A member 3 OS=Homo sapiens OX=9606 GN=GOLGA3 PE=1 SV=2	1.677	1.63	1.574	1.53
PDIA4	P13667	Protein disulfide-isomerase A4 OS=Homo sapiens OX=9606 GN=PDIA4 PE=1 SV=2	2.618	2.942	2.687	3.019
TMF1	P82094	TATA element modulatory factor OS=Homo sapiens OX=9606 GN=TMF1 PE=1 SV=2	2.295	2.479	2.503	2.704
FXR1	P51114	Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens OX=9606	1.538	1.667	1.551	1.681
UB2J1	Q9Y385	Ubiquitin-conjugating enzyme E2 J1 OS=Homo sapiens OX=9606 GN=UBE2J1 PE=1 SV=2	1.579	1.49	1.681	1.586
DSG1	Q02413	Desmoglein-1 OS=Homo sapiens OX=9606 GN=DSG1 PE=1 SV=2	1.841	2.045	1.972	2.191
PDIA6	Q15084	Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6 PE=1 SV=1	1.641	1.839	1.618	1.813
UBP5	P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens OX=9606 GN=USPS PE=1 SV=2	1.607	1.598	1.456	1.448
LNP	Q9C0E8	Endoplasmic reticulum junction formation protein lunapark OS=Homo sapiens OX=9606	1.538	1.501	1.715	1.674
RFIP4	Q8YGS3	Rab11 family-interacting protein 4 OS=Homo sapiens OX=9606 GN=RAB11FIP4 PE=1 SV=1	1.642	1.584	1.863	1.797
PSMG1	O95456	Proteasome assembly chaperone 1 OS=Homo sapiens OX=9606 GN=PSMG1 PE=1 SV=1	1.408	1.439	1.565	1.6
SPART	Q8NOX7	Spartin OS=Homo sapiens OX=9606 GN=SPART PE=1 SV=1	1.974	1.812	1.747	1.604
PNISR	Q8TF01	Arginine/serine-rich protein PNISR OS=Homo sapiens OX=9606 GN=PNISR PE=1 SV=2	1.685	1.611	1.504	1.438
P53	P04637	Cellular tumor antigen p53 OS=Homo sapiens OX=9606 GN=TP53 PE=1 SV=4	2.245	2.033	1.922	1.741
XRP2	Q75695	Protein XRP2 OS=Homo sapiens OX=9606 GN=RP2 PE=1 SV=4	1.753	1.543	1.622	1.428
NUDC	Q9Y266	Nuclear migration protein nudC OS=Homo sapiens OX=9606 GN=NUDC PE=1 SV=1	1.8	1.656	1.573	1.448
COQ9	Q75208	Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Homo sapiens OX=9606	1.723	1.777	1.473	1.519
MTEF4	Q7Z6M4	Transcription termination factor 4, mitochondrial OS=Homo sapiens OX=9606 GN=MTERF4	1.43	1.445	1.666	1.683
MARCS	P29966	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens OX=9606 GN=MARCKS	1.541	1.392	1.731	1.564
PSA4	P25789	Proteasome subunit alpha type-4 OS=Homo sapiens OX=9606 GN=PSMA4 PE=1 SV=1	2.077	1.689	2.069	1.682
NFS1	Q9Y697	Cysteine desulfurase, mitochondrial OS=Homo sapiens OX=9606 GN=NFS1 PE=1 SV=3	2.098	1.792	1.794	1.532
CASC3	O15234	Protein CASC3 OS=Homo sapiens OX=9606 GN=CASC3 PE=1 SV=2	1.403	1.729	1.384	1.705
DPH7	Q9BTV6	Diphthine methyltransferase OS=Homo sapiens OX=9606 GN=DPH7 PE=1 SV=2	1.722	1.382	1.832	1.47
ZNT1	Q9Y6M5	Zinc transporter 1 OS=Homo sapiens OX=9606 GN=SLC30A1 PE=1 SV=3	1.677	1.938	1.376	1.59
DCTN2	Q13561	Dynactin subunit 2 OS=Homo sapiens OX=9606 GN=DCTN2 PE=1 SV=4	1.914	1.625	1.597	1.356
VPS72	Q15906	Vacuole protein sorting-associated protein 72 homolog OS=Homo sapiens OX=9606	1.746	1.485	1.502	1.278
EYA3	Q99504	Eyes absent homolog 3 OS=Homo sapiens OX=9606 GN=EYA3 PE=1 SV=3	1.409	1.281	1.903	1.73
RL40	P62987	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens OX=9606 GN=UBA52 PE=1 SV=2	1.377	1.577	1.415	1.62
AEDO	Q96SZ5	2-aminoethanethiol dioxygenase OS=Homo sapiens OX=9606 GN=ADO PE=1 SV=2	1.46	1.766	1.246	1.508
TIM44	O43615	Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens	1.375	1.435	1.539	1.606

RADI	P35241	Radixin OS=Homo sapiens OX=9606 GN=RDX PE=1 SV=1	1.458	1.577	1.403	1.517
RED	Q13123	Protein Red OS=Homo sapiens OX=9606 GN=IK PE=1 SV=3	1.535	1.443	1.532	1.44
U2AF2	P26368	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens OX=9606 GN=U2AF2 PE=1 SV=4	1.479	1.509	1.464	1.494
ST134	Q8IZP2	Putative protein FAM104A OS=Homo sapiens OX=9606 GN=ST13P4 PE=5 SV=1	1.5	1.533	1.436	1.467
RFA1	P27694	Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens OX=9606 GN=RPA1	1.392	1.531	1.431	1.574
VAPA	Q9POL0	Vesicle-associated membrane protein-associated protein A OS=Homo sapiens OX=9606	1.49	1.474	1.466	1.45
UBXN1	Q04323	UBX domain-containing protein 1 OS=Homo sapiens OX=9606 GN=UBXN1 PE=1 SV=2	1.47	1.361	1.574	1.458
RANB3	Q9H6Z4	Ran-binding protein 3 OS=Homo sapiens OX=9606 GN=RANBP3 PE=1 SV=1	1.487	1.461	1.462	1.436
COX7C	P15954	Cytochrome c oxidase subunit 7C, mitochondrial OS=Homo sapiens OX=9606 GN=COX7C	1.45	1.368	1.528	1.442
CDC37	Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens OX=9606 GN=CDC37 PE=1 SV=1	1.528	1.429	1.442	1.348
I433S	P31947	14-3-3 protein sigma OS=Homo sapiens OX=9606 GN=SFRN PE=1 SV=1	1.422	1.472	1.378	1.427
LACB2	Q53H82	Endoribonuclease LACTB2 OS=Homo sapiens OX=9606 GN=LACTB2 PE=1 SV=2	1.711	1.374	1.447	1.162
MMTA2	Q9BU76	Multiple myeloma tumor-associated protein 2 OS=Homo sapiens OX=9606 GN=MMTAG2	1.525	1.501	1.326	1.306
UFD1	Q92890	Ubiquitin recycling factor in ER-associated degradation protein 1 OS=Homo sapiens	1.438	1.342	1.481	1.382
ANLN	Q9NQW6	Anillin OS=Homo sapiens OX=9606 GN=ANLN PE=1 SV=2	1.457	1.405	1.415	1.364
SGT1	Q9YY20	Protein SGT1 homolog OS=Homo sapiens OX=9606 GN=SUGT1 PE=1 SV=3	1.456	1.384	1.435	1.363
SYAP1	Q96A49	Synapse-associated protein 1 OS=Homo sapiens OX=9606 GN=SYAP1 PE=1 SV=1	1.15	1.669	1.146	1.663
PSIP1	P75475	PC4 and SFRS1-interacting protein OS=Homo sapiens OX=9606 GN=PSIP1 PE=1 SV=1	1.431	1.404	1.403	1.376
GCP60	Q9H3P7	Golgi resident protein GCP60 OS=Homo sapiens OX=9606 GN=ACBD3 PE=1 SV=4	1.435	1.404	1.395	1.365
ADDA	P35611	Alpha-adducin OS=Homo sapiens OX=9606 GN=ADD1 PE=1 SV=2	1.42	1.296	1.505	1.373
EMD	P50402	Emerin OS=Homo sapiens OX=9606 GN=EMD PE=1 SV=1	1.4	1.423	1.371	1.394
CRLF3	Q8IU18	Cytokine receptor-like factor 3 OS=Homo sapiens OX=9606 GN=CRLF3 PE=1 SV=2	1.289	1.434	1.352	1.503
DSG2	Q14162	Desmoglein-2 OS=Homo sapiens OX=9606 GN=DSG2 PE=1 SV=2	1.71	1.229	1.532	1.101
MKS3	Q5HY8A	Meckelin OS=Homo sapiens OX=9606 GN=TMEM67 PE=1 SV=1	1.568	1.314	1.458	1.222
S39A7	Q92504	Zinc transporter SLC39A7 OS=Homo sapiens OX=9606 GN=SLC39A7 PE=1 SV=2	1.44	1.351	1.429	1.341
MBOA2	Q6ZW7T	Lysophospholipid acyltransferase 2 OS=Homo sapiens OX=9606 GN=MBOAT2 PE=2 SV=2	1.452	1.372	1.404	1.327
BUB1B	O60566	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta OS=Homo sapiens OX=9606	1.281	1.53	1.25	1.493
MA7D1	Q3KQU3	MAP7 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=MAP7D1 PE=1 SV=1	1.557	1.359	1.398	1.22
MAOM	P23368	NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens OX=9606 GN=ME2 PE=1	1.418	1.445	1.322	1.348
CBPD	Q57976	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	1.308	1.117	1.674	1.43
ARI3A	Q99856	AT-rich interactive domain-containing protein 3A OS=Homo sapiens OX=9606 GN=ARID3A	1.362	1.261	1.502	1.39
NDUBB8	Q95169	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial OS=Homo	1.366	1.219	1.548	1.382
S35F6	Q8N357	Solute carrier family 35 member F6 OS=Homo sapiens OX=9606 GN=SLC35F6 PE=1 SV=1	1.464	1.351	1.398	1.291
MRM3	Q9HC36	rRNA methyltransferase 3, mitochondrial OS=Homo sapiens OX=9606 GN=MRM3 PE=1	1.36	1.311	1.422	1.372
ATLA2	Q8NNH9	Atlastin-2 OS=Homo sapiens OX=9606 GN=ATL2 PE=1 SV=2	1.394	1.53	1.21	1.328
ALG9	Q9H6U8	Alpha-1,2-mannosyltransferase ALG9 OS=Homo sapiens OX=9606 GN=ALG9 PE=1 SV=2	1.381	1.38	1.344	1.343
SPAS2	Q86XZ4	Spermatogenesis-associated serine-rich protein 2 OS=Homo sapiens OX=9606 GN=SPATS2	1.202	1.343	1.366	1.526
PURA	Q05777	Transcriptional activator protein Pur-alpha OS=Homo sapiens OX=9606 GN=PURA PE=1	1.402	1.412	1.301	1.311
NFM	P07197	Neurofilament medium polypeptide OS=Homo sapiens OX=9606 GN=NEFM PE=1 SV=3	1.376	1.326	1.384	1.335
RPC1	O14802	DNA-directed RNA polymerase III subunit RPC1 OS=Homo sapiens OX=9606 GN=POLR3A	1.329	1.34	1.365	1.376
CALR	P27797	Calreticulin OS=Homo sapiens OX=9606 GN=CALR PE=1 SV=1	1.323	1.38	1.308	1.364
CALX	P27824	Calnexin OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=2	1.396	1.305	1.381	1.29
MD1L1	Q9Y6D9	Mitotic spindle assembly checkpoint protein MAD1 OS=Homo sapiens OX=9606	1.187	1.204	1.479	1.5
STAU1	Q95793	Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens OX=9606	1.423	1.461	1.211	1.244
IF4G3	O43432	Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens OX=9606 GN=EIF4G3	1.333	1.441	1.231	1.331
TYSY	P04818	Thymidylate synthase OS=Homo sapiens OX=9606 GN=TYMS PE=1 SV=3	1.641	1.237	1.4	1.056
D13L1	Q8TF46	DIS3-like exonuclease 1 OS=Homo sapiens OX=9606 GN=DIS3L PE=1 SV=2	1.417	1.209	1.457	1.243
PDXK	O00764	Pyridoxal kinase OS=Homo sapiens OX=9606 GN=PDXK PE=1 SV=1	1.384	1.254	1.41	1.278
TSN3	O60637	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	1.387	1.368	1.291	1.273
AGK	Q53H12	Acylglycerol kinase, mitochondrial OS=Homo sapiens OX=9606 GN=AGK PE=1 SV=2	1.296	1.267	1.368	1.337
STMFL2	Q9UJ21	Stomatin-like protein 2, mitochondrial OS=Homo sapiens OX=9606 GN=STMFL2 PE=1	1.378	1.306	1.323	1.253
I433E	P62258	14-3-3 protein epsilon OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1	1.265	1.373	1.252	1.359
RINI	P13489	Ribonuclease inhibitor OS=Homo sapiens OX=9606 GN=RNIH PE=1 SV=2	1.372	1.34	1.282	1.251
S29A1	Q99808	Equilibrative nucleoside transporter 1 OS=Homo sapiens OX=9606 GN=SLC29A1 PE=1	1.357	1.311	1.31	1.265
CTNA1	P35221	Catenin alpha-1 OS=Homo sapiens OX=9606 GN=CTNNA1 PE=1 SV=1	1.308	1.392	1.229	1.309
ERLN1	O75477	Erlin 1 OS=Homo sapiens OX=960				

PAIRB	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens OX=9606	1.271	1.364	1.211	1.3
GRP75	P38646	Stress-70 protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=2	1.298	1.255	1.318	1.275
FUBP2	Q92945	Far upstream element-binding protein 2 OS=Homo sapiens OX=9606 GN=HSRPF PE=1	1.254	1.263	1.309	1.318
DLDH	P09622	Dihydrodipolyl dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=DLD PE=1	1.331	1.296	1.275	1.241
HBS1L	Q9Y450	HBS1-like protein OS=Homo sapiens OX=9606 GN=HBS1L PE=1 SV=1	1.467	1.282	1.273	1.112
MIC60	Q16891	MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT PE=1 SV=1	1.311	1.303	1.253	1.246
MA1A1	P33908	Manosyl-oligosaccharide 1,2-alpha-mannosidase IA OS=Homo sapiens OX=9606	1.305	1.229	1.323	1.246
GPT	Q9H3HS	UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminetransferase	1.303	1.376	1.178	1.244
GRSF1	Q12849	G-rich sequence factor 1 OS=Homo sapiens OX=9606 GN=GRSF1 PE=1 SV=3	1.377	1.329	1.218	1.175
PSA3	P25788	Proteasome subunit alpha type-3 OS=Homo sapiens OX=9606 GN=PSMA3 PE=1 SV=2	1.308	1.299	1.249	1.241
ZNF48	Q96MX3	Zinc finger protein 48 OS=Homo sapiens OX=9606 GN=ZNF48 PE=1 SV=2	1.273	1.228	1.317	1.271
TCOF	Q13428	Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 PE=1 SV=3	1.318	1.272	1.261	1.218
SRSF2	Q01130	Serine/arginine-rich splicing factor 2 OS=Homo sapiens OX=9606 GN=SRSF2 PE=1 SV=4	1.208	1.298	1.233	1.324
G3BP1	Q13283	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens OX=9606 GN=G3BP1	1.267	1.203	1.329	1.262
PPM1G	O15355	Protein phosphatase 1G OS=Homo sapiens OX=9606 GN=PPM1G PE=1 SV=1	1.395	1.339	1.182	1.134
PININ	Q9H307	Pinin OS=Homo sapiens OX=9606 GN=PNN PE=1 SV=5	1.334	1.232	1.291	1.192
TOE1	Q96GM8	Target of EGFR protein 1 OS=Homo sapiens OX=9606 GN=TOE1 PE=1 SV=1	1.128	1.241	1.273	1.4
AMPL	P28838	Cytosol aminopeptidase OS=Homo sapiens OX=9606 GN=LAP3 PE=1 SV=3	1.294	1.226	1.292	1.224
NU153	P49790	Nuclear pore complex protein Nurp153 OS=Homo sapiens OX=9606 GN=NUP153 PE=1 SV=2	1.237	1.091	1.436	1.266
ECHI	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens OX=9606	1.382	1.297	1.212	1.137
NUCL	P19338	Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3	1.291	1.237	1.273	1.219
ODPX	Q00330	Pyruvate dehydrogenase protein X component, mitochondrial OS=Homo sapiens OX=9606	1.22	1.271	1.231	1.282
AGO3	Q9H9G7	Protein argonaute-3 OS=Homo sapiens OX=9606 GN=AGO3 PE=1 SV=2	1.14	1.21	1.281	1.36
ZN598	Q86UK7	E3 ubiquitin-protein ligase ZNF598 OS=Homo sapiens OX=9606 GN=ZNF598 PE=1 SV=1	1.478	1.258	1.206	1.027
HNRPK	P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK	1.236	1.232	1.247	1.243
STIM1	Q13586	Stromal interaction molecule 1 OS=Homo sapiens OX=9606 GN=STIM1 PE=1 SV=3	1.423	1.241	1.225	1.068
ENAH	Q8NS87	Protein enabled homolog OS=Homo sapiens OX=9606 GN=ENAH PE=1 SV=2	1.253	1.206	1.272	1.224
SLIT2	Q094813	Slit homolog 2 protein OS=Homo sapiens OX=9606 GN=SLIT2 PE=1 SV=1	1.155	1.275	1.199	1.324
CLIC4	Q9Y696	Chloride intracellular channel protein 4 OS=Homo sapiens OX=9606 GN=CLIC4 PE=1 SV=4	1.49	1.161	1.291	1.006
CPSF6	Q16630	Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens OX=9606	1.236	1.297	1.178	1.236
BOREA	Q53HL2	Borealin OS=Homo sapiens OX=9606 GN=CDCA8 PE=1 SV=2	1.286	1.33	1.142	1.181
RAVR1	Q8YI67	Ribonucleoprotein PTB-binding 1 OS=Homo sapiens OX=9606 GN=RAVER1 PE=1 SV=1	1.21	1.166	1.303	1.255
DC112	Q13409	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1	1.246	1.195	1.272	1.22
IMDH2	P12268	Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens OX=9606 GN=IMPDH2 PE=1	1.198	1.238	1.228	1.269
CERS6	Q6ZMG9	Ceramide synthase 6 OS=Homo sapiens OX=9606 GN=CERS6 PE=1 SV=1	1.2	1.051	1.427	1.25
SEH1	Q96EE3	Nucleoporin SEH1 OS=Homo sapiens OX=9606 GN=SEH1L PE=1 SV=3	1.464	1.216	1.222	1.015
PNPT1	Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial OS=Homo sapiens OX=9606	1.438	1.199	1.243	1.037
ZCH18	Q86VM9	Zinc finger CCHC domain-containing protein 18 OS=Homo sapiens OX=9606 GN=ZC3H18	1.317	1.168	1.288	1.142
UBP10	Q14694	Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens OX=9606 GN=USP10 PE=1	1.268	1.205	1.252	1.189
CDK1	P06493	Cyclin-dependent kinase 1 OS=Homo sapiens OX=9606 GN=CDK1 PE=1 SV=3	1.533	1.069	1.358	0.947
1433Z	P63104	14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1	1.199	1.204	1.244	1.248
TM10C	Q7LY03	tRNA methyltransferase 10 homolog C OS=Homo sapiens OX=9606 GN=TRMT10C PE=1	1.249	1.209	1.238	1.198
SNA4	P54920	Alpha-soluble NSF attachment protein OS=Homo sapiens OX=9606 GN=NAPA PE=1 SV=3	1.166	1.282	1.164	1.28
H10	P07305	Histone H10 OS=Homo sapiens OX=9606 GN=H10 PE=1 SV=3	1.208	1.124	1.311	1.221
PTN1	P18031	Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens OX=9606 GN=PTPN1	1.242	1.227	1.201	1.186
FKBP5	Q13451	Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Homo sapiens OX=9606 GN=FKBP5 PE=1	1.371	1.169	1.248	1.064
NSE3	Q96MG7	Non-structural maintenance of chromosomes element 3 homolog OS=Homo sapiens OX=9606	0.962	1.439	0.979	1.464
LMNB1	P20700	Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=2	1.192	1.208	1.202	1.218
CDS2	Q95674	Phosphatidate cytidyltransferase 2 OS=Homo sapiens OX=9606 GN=CDS2 PE=1 SV=1	1.262	1.125	1.28	1.142
ALG1	Q9BT22	Chitobiosylphosphodolichol beta-mannosyltransferase OS=Homo sapiens OX=9606	1.298	1.212	1.187	1.108
TRM1	Q9NXH9	tRNA (guanine-26(N2))-dimethyltransferase OS=Homo sapiens OX=9606 GN=TRMT1	1.249	1.229	1.172	1.153
SF3A1	Q15459	Splicing factor 3A subunit 1 OS=Homo sapiens OX=9606 GN=SF3A1 PE=1 SV=1	1.219	1.147	1.253	1.179
RS5	P46782	40S ribosomal protein S5 OS=Homo sapiens OX=9606 GN=RP5 PE=1 SV=4	1.096	1.346	1.054	1.294
PSME3	P61289	Proteasome activator complex subunit 3 OS=Homo sapiens OX=9606 GN=PSME3 PE=1	1.227	1.187	1.206	1.166
CTBP2	P56545	C-terminal-binding protein 2 OS=Homo sapiens OX=9606 GN=CTBP2 PE=1 SV=1	1.282	1.154	1.235	1.111
LMP2	Q9BU23	Lipase maturation factor 2 OS=Homo sapiens OX=9606 GN=LMP2 PE=1 SV=2	1.219	1.209	1.18	1.17
CH60	P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPD1 PE=1	1.195	1.2	1.183	1.188
CPSF7	Q8N684	Cleavage and polyadenylation specificity factor subunit 7 OS=Homo sapiens OX=9606	1.17	1.19	1.192	1.213
STIP1	P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens OX=9606 GN=STIP1 PE=1 SV=1	1.255	1.132	1.25	1.128
KINH	P33176	Kinesin-1 heavy chain OS=Homo sapiens OX=9606 GN=KIF5B PE=1 SV=1	1.219	1.186	1.195	1.163
HM13	Q8TCT9	Minor histocompatibility antigen H13 OS=Homo sapiens OX=9606 GN=HM13 PE=1 SV=1	1.175	1.177	1.197	1.199
MCCB	Q9HCC0	Methylcrotonyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606	1.204	1.229	1.142	1.166
TP53B	Q12888	TP53-binding protein 1 OS=Homo sapiens OX=9606 GN=TP53BP1 PE=1 SV=2	1.189	1.26	1.106	1.172
CC038	Q5JP13	Uncharacterized protein C3orf58 OS=Homo sapiens OX=9606 GN=C3orf38 PE=1 SV=1	1.136	1.218	1.144	1.226
DIEFX	Q68CQ4	Digestive organ expansion factor homolog OS=Homo sapiens OX=9606 GN=DIEFX PE=1	1.269	1.158	1.196	1.092
TRM61	Q96FX7	tRNA (adenine-58(N1))-methyltransferase catalytic subunit TRMT61A OS=Homo sapiens	1.474	1.109	1.211	0.912
FLII	Q13045	Protein flightless-1 homolog OS=Homo sapiens OX=9606 GN=FLII PE=1 SV=2	1.134	1.11	1.243	1.217
IMA5	P52294	Importin subunit alpha-5 OS=Homo sapiens OX=9606 GN=KPN1 PE=1 SV=3	1.213	1.14	1.212	1.139
SYAM	Q5J7Z9	Alanine-tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=AARS2 PE=1 SV=1	1.295	1.118	1.228	1.06
PLST	P13797	Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 PE=1 SV=4	1.108	1.205	1.144	1.244

ATX2	Q99700	Ataxin-2 OS=Homo sapiens OX=9606 GN=ATXN2 PE=1 SV=2	1.228	1.159	1.189	1.122
DNL13	P49916	DNA ligase 3 OS=Homo sapiens OX=9606 GN=LIG3 PE=1 SV=2	1.153	1.251	1.097	1.191
SOAT1	P35610	Sterol O-acyltransferase 1 OS=Homo sapiens OX=9606 GN=SOAT1 PE=1 SV=3	1.197	1.179	1.167	1.149
CELF1	Q92879	CUGBP Elavl-like family member 1 OS=Homo sapiens OX=9606 GN=CELF1 PE=1 SV=2	1.163	1.142	1.201	1.18
SYNC	O43776	Asparagine-tRNA ligase, cytosolic OS=Homo sapiens OX=9606 GN=NARS1 PE=1 SV=1	1.211	1.064	1.283	1.127
IMA3	O00629	Importin subunit alpha-3 OS=Homo sapiens OX=9606 GN=KPN4 PE=1 SV=1	1.205	1.132	1.209	1.136
SPG7	Q9UQ90	Paraplegin OS=Homo sapiens OX=9606 GN=SPG7 PE=1 SV=2	1.186	1.082	1.261	1.115
S12A7	Q9Y666	Solute carrier family 12 member 7 OS=Homo sapiens OX=9606 GN=SLC12A7 PE=1 SV=3	1.151	1.012	1.336	1.175
PREP	Q5JRX3	Presequence protease, mitochondrial OS=Homo sapiens OX=9606 GN=PTRM1 PE=1 SV=3	1.183	1.173	1.164	1.154
PTN23	Q9H3S7	Tyrosine-protein phosphatase non-receptor type 23 OS=Homo sapiens OX=9606 GN=PTPN23	1.301	1.198	1.131	1.041
DDX28	Q9NU7L	Probable ATP-dependent RNA helicase DDX28 OS=Homo sapiens OX=9606 GN=DDX28	1.192	1.213	1.121	1.141
GNAQ	P50148	Guanine nucleotide-binding protein G(i) subunit alpha OS=Homo sapiens OX=9606	1.203	1.079	1.257	1.127
BAG3	Q95817	BAG family molecular chaperone regulator 3 OS=Homo sapiens OX=9606 GN=BAG3 PE=1	1.58	1	1.275	0.807
TOM40	O96008	Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens OX=9606	1.195	1.156	1.174	1.135
EBP2	Q99848	Probable rRNA-processing protein EBP2 OS=Homo sapiens OX=9606 GN=EBNA1BP2 PE=1	1.187	1.233	1.098	1.141
TIF1A	O15164	Transcription intermediary factor 1-alpha OS=Homo sapiens OX=9606 GN=TRIM24 PE=1	1.383	1.028	1.289	0.959
GPDM	P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=GPDM	1.237	1.109	1.218	1.092
EFTS	P43897	Elongation factor Ts, mitochondrial OS=Homo sapiens OX=9606 GN=TSFM PE=1 SV=2	1.039	1.218	1.101	1.292
HIP1R	O75146	Huntingtin-interacting protein 1-related protein OS=Homo sapiens OX=9606 GN=HIP1R	0.993	1.035	1.283	1.338
STX5	Q13190	Syntaxin-5 OS=Homo sapiens OX=9606 GN=STX5 PE=1 SV=2	1.171	1.081	1.246	1.149
SYHM	P49590	Probable histidine-tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=HARS2	1.059	1.057	1.265	1.263
G3BP2	Q9UN86	Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens OX=9606 GN=G3BP2	1.253	1.194	1.121	1.068
LETM1	O95202	Mitochondrial proton/calcium exchanger protein OS=Homo sapiens OX=9606 GN=LETM1	1.175	1.171	1.146	1.142
BIP	P11021	Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPAS1 PE=1 SV=2	1.183	1.139	1.177	1.133
SYEM	Q5PH6	Probable glutamate-tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=EARS2	1.223	1.119	1.196	1.093
AC52L	Q9NUB1	Acetyl-coenzyme A synthetase-like 2-like, mitochondrial OS=Homo sapiens OX=9606	1.251	1.113	1.197	1.066
SUCB2	Q96969	Succinate-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens	1.255	1.28	1.062	1.058
PLPR4	Q7Z2D5	Phospholipid phosphatase-related protein type 4 OS=Homo sapiens OX=9606 GN=PLPPR4	1.173	1.106	1.201	1.132
SYVN1	Q86TM6	E3 ubiquitin-protein ligase synovlyn OS=Homo sapiens OX=9606 GN=SYVN1 PE=1 SV=2	1.15	1.182	1.123	1.155
RIPK1	Q13546	Receptor-interacting serine/threonine-protein kinase 1 OS=Homo sapiens OX=9606	1.307	1.129	1.164	1.006
SCMC1	Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens OX=9606	1.264	1.041	1.259	1.036
ZMYM4	Q5VZL5	Zinc finger MYM-type protein 4 OS=Homo sapiens OX=9606 GN=ZMYM4 PE=1 SV=1	1.229	1.136	1.16	1.072
LAT1	Q10150	Large neutral amino acids transporter small subunit 1 OS=Homo sapiens OX=9606	1.088	1.134	1.121	1.212
TX264	Q9Y619	Testis-expressed protein 264 OS=Homo sapiens OX=9606 GN=TEX264 PE=1 SV=1	1.257	1.086	1.203	1.039
ABCBA	Q9RNK6	ATP-binding cassette sub-family B member 10, mitochondrial OS=Homo sapiens OX=9606	1.241	1.11	1.172	1.049
CTDP1	Q9Y5B0	RNA polymerase II subunit A C-terminal domain phosphatase OS=Homo sapiens OX=9606	1.08	1.157	1.127	1.207
IDH3A	P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens OX=9606	1.249	1.119	1.161	1.04
SCFD1	Q8WV8M	Sec1 family domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SCFD1 PE=1	1.079	1.376	0.929	1.184
AHNK	Q96966	Neuroblast differentiation-associated protein AHNK OS=Homo sapiens OX=9606	1.182	1.173	1.107	1.

COASY	Q13057	Bifunctional coenzyme A synthase OS=Homo sapiens OX=9606 GN=COASY PE=1 SV=4	1.087	1.056	1.174	1.14
COX2	P00403	Cytochrome c oxidase subunit 2 OS=Homo sapiens OX=9606 GN=MT-CO2 PE=1 SV=1	1.257	1.018	1.206	0.976
ADAS	O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens OX=9606	1.174	1.136	1.086	1.051
ATX10	Q9UBB4	Ataxin-10 OS=Homo sapiens OX=9606 GN=ATXN10 PE=1 SV=1	1.058	1.088	1.131	1.162
RTCA	O00442	RNA 3'-terminal phosphate cyclase OS=Homo sapiens OX=9606 GN=RTCA PE=1 SV=1	1.164	1.153	1.065	1.055
SYAC	P49588	Alanine--RNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=AARS PE=1 SV=2	1.133	1.087	1.131	1.085
TBCB	Q99426	Tubulin-folding cofactor B OS=Homo sapiens OX=9606 GN=TBCB PE=1 SV=2	1.298	1.287	0.928	0.92
ATD3A	Q9NV17	ATPase family AAA domain-containing protein 3A OS=Homo sapiens OX=9606	1.083	1.101	1.11	1.128
G3P	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1	1.122	1.087	1.122	1.088
SF01	Q15637	Splicing factor 1 OS=Homo sapiens OX=9606 GN=SFI PE=1 SV=4	1.189	1.144	1.062	1.021
NTH	P78549	Endonuclease III-like protein 1 OS=Homo sapiens OX=9606 GN=NTHL1 PE=1 SV=2	1.077	1.058	1.15	1.13
MDN1	Q9NU22	Midasin OS=Homo sapiens OX=9606 GN=MDN1 PE=1 SV=2	1.094	1.018	1.191	1.107
COFI	P23528	Coflin-1 OS=Homo sapiens OX=9606 GN=CF1 PE=1 SV=3	1.191	1.091	1.11	1.016
DAD1	P61803	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo	1.235	0.964	1.241	0.968
DIAP1	O60610	Protein diaphanous homolog 1 OS=Homo sapiens OX=9606 GN=DIAPH1 PE=1 SV=2	1.172	1.095	1.103	1.03
KTN1	Q86U2P	Kinetin OS=Homo sapiens OX=9606 GN=KTN1 PE=1 SV=1	1.129	1.171	1.03	1.069
NUP50	Q9UKX7	Nuclear pore complex Nup50 OS=Homo sapiens OX=9606 GN=NUP50 PE=1 SV=2	1.04	0.962	1.245	1.152
MTX1	Q13505	Metaxin-1 OS=Homo sapiens OX=9606 GN=MTX1 PE=1 SV=3	0.76	1.222	0.926	1.49
PRP18	Q99633	Pre-mRNA-splicing factor 18 OS=Homo sapiens OX=9606 GN=PRP18 PE=1 SV=1	1.208	1.23	0.967	0.985
HTSF1	Q43719	HIV Tat-specific factor 1 OS=Homo sapiens OX=9606 GN=HTATSF1 PE=1 SV=1	1.18	1.112	1.078	1.016
HNRL	Q8WV9	Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens OX=9606 GN=HNRNPLL	1.208	1.118	1.065	0.987
TXNDS	Q8NB89	Thioredoxin domain-containing protein 5 OS=Homo sapiens OX=9606 GN=TXNDC5 PE=1	1.153	1.137	1.05	1.036
UAP1	Q16222	UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens OX=9606 GN=UAP1 PE=1	1.12	1.09	1.097	1.069
LGUL	Q04760	Lactoylglutathione lyase OS=Homo sapiens OX=9606 GN=GLO1 PE=1 SV=4	1.264	1.032	1.144	0.934
CHID1	Q9BWS9	Chitinase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=CHID1 PE=1 SV=1	1.142	1.02	1.164	1.039
IF2P	O60841	Eukaryotic translation initiation factor 5B OS=Homo sapiens OX=9606 GN=EIF5B PE=1	1.051	1.144	1.035	1.126
MIPEP	Q99797	Mitochondrial intermediate peptidase OS=Homo sapiens OX=9606 GN=MIPEP PE=1 SV=2	1.179	0.981	1.199	0.997
RB12B	Q8IXT5	RNA-binding protein 12B OS=Homo sapiens OX=9606 GN=RBMB12 PE=1 SV=2	1.111	1.117	1.06	1.067
TLN2	Q9Y4G6	Talin-2 OS=Homo sapiens OX=9606 GN=TLN2 PE=1 SV=4	1.21	1.094	1.076	0.973
AASS	Q9UDR5	Alpha-aminoacid semialdehyde synthase, mitochondrial OS=Homo sapiens OX=9606	1.3	1.001	1.159	0.893
PHIP	Q8WWQ0	PH-interacting protein OS=Homo sapiens OX=9606 GN=PHIP PE=1 SV=2	1	0.899	1.292	1.161
RPOM	O00411	DNA-directed RNA polymerase, mitochondrial OS=Homo sapiens OX=9606 GN=POLRMT	1.142	0.95	1.235	1.026
HDAC1	Q13547	Histone deacetylase 1 OS=Homo sapiens OX=9606 GN=HDAC1 PE=1 SV=1	1.106	1.022	1.155	1.067
TIPRL	O75663	TIP41-like protein OS=Homo sapiens OX=9606 GN=TIPRL PE=1 SV=2	1.109	1.077	1.096	1.065
PCBP1	Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2	1.126	1.06	1.113	1.047
E12BG	Q9NR50	Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens OX=9606 GN=EIF2B3	1.083	1.151	1.024	1.088
INCE	Q9NQS7	Inner centromere protein OS=Homo sapiens OX=9606 GN=INCENP PE=1 SV=3	1.146	1.04	1.126	1.022
UCRIL	POC7P4	Putative cytochrome b-1 complex subunit Rieske-like protein 1 OS=Homo sapiens OX=9606	1.202	1.034	1.126	0.969
PSD11	O00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens OX=9606	0.915	1.175	0.979	1.257
CSK21	P68400	Casein kinase II subunit alpha OS=Homo sapiens OX=9606 GN=CSNK2A1 PE=1 SV=1	1.076	1.046	1.117	1.086
TPX2	Q9ULW0	Targeting protein for Xklp1 OS=Homo sapiens OX=9606 GN=TPX2 PE=1 SV=2	1.143	1.046	1.115	1.02
KIF1A	Q12756	Kinesin-like protein KIF1A OS=Homo sapiens OX=9606 GN=KIF1A PE=1 SV=2	0.981	1.104	1.052	1.184
DNJC2	Q99543	DnaJ homolog subfamily C member 2 OS=Homo sapiens OX=9606 GN=DNJC2 PE=1	1.164	1.056	1.1	0.998
RRP1	P56182	Ribosomal RNA processing protein 1 homolog A OS=Homo sapiens OX=9606 GN=RRP1	1.109	1.074	1.079	1.045
ZN25	Q9Y2P7	Zinc finger protein 256 OS=Homo sapiens OX=9606 GN=ZNF256 PE=1 SV=2	1.143	1.002	1.152	1.01
ACTZ	P61163	Alpha-actinin-3 OS=Homo sapiens OX=9606 GN=ACTR1A PE=1 SV=1	1.078	1.023	1.13	1.072
BIG1	Q9Y6D6	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens OX=9606	1.22	0.901	1.255	0.926
ACOT1	Q86TX2	Acyl-coenzyme A thioesterase 1 OS=Homo sapiens OX=9606 GN=ACOT1 PE=1 SV=1	1.081	1.072	1.079	1.069
GOGB1	Q14789	Golgin subfamily B member 1 OS=Homo sapiens OX=9606 GN=GOLGB1 PE=1 SV=2	1.053	1.1	1.05	1.097
EZR1	P15311	Ezrin OS=Homo sapiens OX=9606 GN=EZR PE=1 SV=4	1.093	1.137	1.014	1.055
THYN1	Q9P016	Thymocyte nuclear protein 1 OS=Homo sapiens OX=9606 GN=THYN1 PE=1 SV=1	0.901	1.157	0.98	1.259
HS90A	P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9606 GN=HSP90AA1 PE=1 SV=5	1.024	1.097	1.049	1.124
SUN2	Q9UH99	SUN domain-containing protein 2 OS=Homo sapiens OX=9606 GN=SUN2 PE=1 SV=3	1.233	1.041	1.093	0.923
UTP11	Q9Y3A2	Probable U3 small nuclear RNA-associated protein 11 OS=Homo sapiens OX=9606	1.143	1.074	1.065	1.001
HP1B3	Q5SSJ5	Heterochromatin protein 1-binding protein 3 OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1	1.22	1.094	1.037	0.93
MSPD2	Q8NH6P	Motile sperm domain-containing protein 2 OS=Homo sapiens OX=9606 GN=MSPD2 PE=1	1.138	1.036	1.102	1.004
RL8	P62917	60S ribosomal protein L8 OS=Homo sapiens OX=9606 GN=RPL8 PE=1 SV=2	1.079	1.081	1.056	1.059
41	P11171	Protein 4.1 OS=Homo sapiens OX=9606 GN=EPB41 PE=1 SV=4	1.062	0.964	1.179	1.069
RPC5	Q9NVU0	DNA-directed RNA polymerase III subunit RPC5 OS=Homo sapiens OX=9606 GN=POLR3E	1.143	1.056	1.076	0.995
DDX31	Q9H8H2	Probable ATP-dependent RNA helicase DDX31 OS=Homo sapiens OX=9606 GN=DDX31	1.163	1.082	1.049	0.975
LMNA	P02545	Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1	1.115	1.103	1.029	1.017
DNJA1	P31689	DnaJ homolog subfamily A member 1 OS=Homo sapiens OX=9606 GN=DNJA1 PE=1	0.946	1.027	1.098	1.192
MCCA	Q96RQ3	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens OX=9606	1.13	1.032	1.098	1.003
PSCS	P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens OX=9606 GN=ALDH18A1 PE=1	1.112	1.071	1.059	1.019
SCRIB	Q14160	Protein scribble homolog OS=Homo sapiens OX=9606 GN=SCRIB PE=1 SV=4	1.092	1.074	1.055	1.037
MDHM	P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=MDH2 PE=1 SV=3	1.103	1.015	1.114	1.025
RRS1	Q15050	Ribosome biogenesis regulatory protein homolog OS=Homo sapiens OX=9606 GN=RRS1	1.085	1.047	1.081	1.043
THOC5	Q13769	THO complex subunit 5 homolog OS=Homo sapiens OX=9606 GN=THOC5 PE=1 SV=2	1.039	1.222	0.915	1.076
HNRPF	P52597	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens OX=9606 GN=HNRNPFF PE=1	0.941	1.112	1.008	1.191
EMC1	Q8N766	ER membrane protein complex subunit 1 OS=Homo sapiens OX=9606 GN=EMC1 PE=1	1.113	1.096	1.029	1.013

TR150	Q9Y2W1	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens OX=9606 GN=THRAP3	1.101	1.064	1.061	1.025
PUR4	Q15067	Phosphoribosylformylglycinamide synthase OS=Homo sapiens OX=9606 GN=PFAS PE=1	1.343	1.048	1.041	0.812
TGM3	Q90188	Protein-glutamin-glutamate-lysine transcarbamoylase OS=Homo sapiens OX=9606 GN=TGM3	1.096	1.008	1.114	1.024
KAPCA	P17612	cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens OX=9606	1.161	1.089	1.026	0.963
COR1C	Q9ULV4	Coronin-1C OS=Homo sapiens OX=9606 GN=CORO1C PE=1 SV=1	1.14	0.998	1.12	0.98
GPAA1	O43292	Glycosylphosphatidylinositol anchor attachment 1 protein OS=Homo sapiens OX=9606	1.054	1.165	0.958	1.059
EMAL4	Q9HC35	Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens OX=9606 GN=EML4	1.014	0.972	1.149	1.101
AFAD	P55196	Afadin OS=Homo sapiens OX=9606 GN=AFDN PE=1 SV=3	1.067	1.08	1.034	1.046
HSP74	P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens OX=9606 GN=HSPA4 PE=1 SV=4	1.137	1.033	1.078	0.979
ROAA	Q99729	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB	0.772	1.137	0.935	1.379
SKP2	Q13309	S-phase kinase-associated protein 2 OS=Homo sapiens OX=9606 GN=SKP2 PE=1 SV=2	1.275	1.174	0.924	0.85
ZSCA2	Q7Z7L9	Zinc finger and SCAN domain-containing protein 2 OS=Homo sapiens OX=9606	1.115	0.895	1.226	0.985
TAP26	Q9P031	Thyroid transcription factor 1-associated protein 26 OS=Homo sapiens OX=9606	1.047	1.1	1.009	1.059
LC7L3	Q95232	Luc-7-like protein 3 OS=Homo sapiens OX=9606 GN=LUC7L3 PE=1 SV=2	1.095	1.048	1.057	1.012
TFP11	Q9UBB9	Tuftelin-interacting protein 11 OS=Homo sapiens OX=9606 GN=TFP11 PE=1 SV=1	1.117	1.01	1.095	0.99
VPS53	Q5VIR6	Vacuolar protein sorting-associated protein 53 homolog OS=Homo sapiens OX=9606	1.206	1.103	0.994	0.909
NUD12	Q9BQG2	Peroxisomal NADH pyrophosphatase NUDT12 OS=Homo sapiens OX=9606 GN=NUDT12	1.074	1.043	1.029	1.029
HSP7C	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1	1.069	1.023	1.079	1.033
BCCP4	Q9P287	BRCA2 and CDKN1A-interacting protein OS=Homo sapiens OX=9606 GN=BCCP4 PE=1	1.184	1.031	1.06	0.923
FAKDA4	Q96920	FAK-like protein OS=Homo sapiens OX=9606 GN=TRBRG4 PE=1	1.028	1.117	0.97	1.054
MPPB	O75439	Mitochondrial intermembrane protein OS=Homo sapiens OX=9606 GN=MT-CO1 PE=1 SV=2	1.016	1.094	1.066	1.066
TERA	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens OX=9606 GN=VCP PE=1	1.029	1.048	1.034	1.052
SC23A	Q15436	Protein transport protein Sec23A OS=Homo sapiens OX=9606 GN=SEC23A PE=1 SV=2	1.132	1.006	1.072	0.952
CKAP4	Q7065	Cytoskeleton-associated protein 4 OS=Homo sapiens OX=9606 GN=CKAP4 PE=1 SV=2	1.039	1.037	1.043	1.041
CAN2	P17655	Calpain-2 catalytic subunit OS=Homo sapiens OX=9606 GN=CAPN2 PE=1 SV=6	1.138	1.084	0.992	0.944
ADNP	P08621	Activity-dependent neuroprotector homeobox protein OS=Homo sapiens OX=9606	1.068	1.087	0.991	1.008
DX39A	Q00148	ATP-dependent RNA helicase DDX39A OS=Homo sapiens OX=9606 GN=DDX39A PE=1	1.081	1.015	1.054	0.989
WDR33	Q9C0J8	pre-mRNA 3' end processing protein WDR33 OS=Homo sapiens OX=9606 GN=WDR33	1.081	1.046	1.021	0.988
AATM	P00505	Aspartate aminotransferase, mitochondrial OS=Homo sapiens OX=9606 GN=GOT2 PE=1	1.032	1.04	1.023	1.03
SYSC	P49591	Serine--RNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=SARS PE=1 SV=3	1.086	1.036	1.024	0.976
QCR2	P22695	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens OX=9606	1.015	1.059	1	1.043
SMU1	Q2TAY7	WD40 repeat-containing protein SMU1 OS=Homo sapiens OX=9606 GN=SMU1 PE=1 SV=2	1.025	0.976	1.084	1.032
STRAP	Q9Y3F4	Serine-threonine kinase receptor-associated protein OS=Homo sapiens OX=9606 GN=STRAP	0.991	1.068	0.985	1.062
PLCB3	Q01970	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens	1.2	1.057	0.982	0.866
EP300	P09472	Histone acetyltransferase p300 OS=Homo sapiens OX=9606 GN=EP300 PE=1 SV=2	1.177	1.05	0.991	0.884
RD23B	P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens OX=9606 GN=RAD23B	1.009	1.019	1.031	1.042
PSMD7	P51665	26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PSMD7	1.066	1.014	1.035	0.985
SDHA	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens	1.044	1.002	1.047	1.005
JIP4	P060271	C-Jun-aminoterminal kinase-interacting protein 4 OS=Homo sapiens OX=9606 GN=SPAG9	1.088	1.032	1.013	0.961
AP3D1						

SETD3	Q86TU7	Actin-histidine N-methyltransferase OS=Homo sapiens OX=9606 GN=SETD3 PE=1 SV=1	1.18	0.928	1.084	0.852
SNX6	Q9UNH7	Sorting nexin-6 OS=Homo sapiens OX=9606 GN=SNX6 PE=1 SV=1	1.042	0.97	1.051	0.978
CATA	P04040	Catalase OS=Homo sapiens OX=9606 GN=CATPE=1 SV=3	1.064	1.01	1.008	0.956
BAP31	P51572	B-cell receptor-associated protein 31 OS=Homo sapiens OX=9606 GN=BCAP31 PE=1 SV=3	1.088	1.052	0.961	0.929
SET	Q01105	Protein SET OS=Homo sapiens OX=9606 GN=SET PE=1 SV=3	0.923	1.051	0.96	1.094
GARS	P41250	Glycine--tRNA ligase OS=Homo sapiens OX=9606 GN=GARS1 PE=1 SV=3	1.03	1.014	0.999	0.983
HS71B	P0DMV9	Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606 GN=HSPA1B PE=1 SV=1	0.985	0.991	1.021	1.027
ABC B7	Q75027	ATP-binding cassette sub-family B member 7, mitochondrial OS=Homo sapiens OX=9606	1.083	1.004	1.002	0.929
URB2	Q14146	Unhealthy ribosome biogenesis protein 2 homolog OS=Homo sapiens OX=9606 GN=URB2	1.012	1.041	0.968	0.996
MDHC	P40925	Malate dehydrogenase, cytoplasmic OS=Homo sapiens OX=9606 GN=MDH1 PE=1 SV=4	1.016	1	1.008	0.992
XPF	Q92889	DNA repair endonuclease XPF OS=Homo sapiens OX=9606 GN=ERCC4 PE=1 SV=3	1.098	1.108	0.898	0.906
DDX52	Q9Y2R4	Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens OX=9606 GN=DDX52	1.032	0.967	1.038	0.973
PKCB1	Q9ULU4	Protein kinase C-binding protein 1 OS=Homo sapiens OX=9606 GN=ZMYNND8 PE=1 SV=2	0.996	1.004	1	1.008
BR0X	Q5VW32	BR01 domain-containing protein BR0X OS=Homo sapiens OX=9606 GN=BROX PE=1	1.017	1.104	0.904	0.981
BRX1	Q8TDN6	Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens OX=9606 GN=BRIXI PE=1	1.025	0.996	1.005	0.977
RS53A	P61247	40S ribosomal protein S3A OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=2	0.991	1.002	0.997	1.008
PK11P	Q9NWNT1	p21-activated protein kinase-interacting protein 1 OS=Homo sapiens OX=9606 GN=PAK1IP1	1.033	1.012	0.986	0.966
SF3B2	Q13435	Splicing factor 3B subunit 2 OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=2	0.996	0.983	1.014	1.001
ABCD3	P28288	ATP-binding cassette sub-family D member 3 OS=Homo sapiens OX=9606 GN=ABCD3	1.109	0.955	1.036	0.892
NLRX1	Q86UT6	NLR family member X1 OS=Homo sapiens OX=9606 GN=NLRX1 PE=1 SV=1	0.918	0.863	1.14	1.071
PFKAM	P08237	ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens OX=9606 GN=PFKM	1.04	0.975	1.02	0.956
DBB1	Q16531	DNA damage-binding protein 1 OS=Homo sapiens OX=9606 GN=DBB1 PE=1 SV=1	1.038	1.017	0.977	0.957
NU155	T57694	Nuclear pore complex protein Nup155 OS=Homo sapiens OX=9606 GN=NUP155 PE=1 SV=1	1.044	1.011	0.981	0.95
SAM50	Q9YS12	Sorting and assembly machinery component 50 homolog OS=Homo sapiens OX=9606	1.153	1.022	0.96	0.851
HDAC2	Q92769	Histone deacetylase 2 OS=Homo sapiens OX=9606 GN=HDAC2 PE=1 SV=2	1.012	1.036	0.957	0.979
SYLM	Q15031	Probable leucine-tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=LARS2 PE=1	0.989	0.974	1.018	1.002
AAKG1	P54619	5'-AMP-activated protein kinase subunit gamma-1 OS=Homo sapiens OX=9606	1.142	0.958	1.023	0.858
TYY1	P25490	Transcriptional repressor protein YY1 OS=Homo sapiens OX=9606 GN=YY1 PE=1 SV=2	1.002	1.001	0.989	0.988
HSDL2	Q6Y1N6	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens OX=9606 GN=HSDL2 PE=1	0.997	0.987	1.002	0.992
CND2	Q15003	Condensin complex subunit 2 OS=Homo sapiens OX=9606 GN=CAPCH PE=1 SV=3	0.99	0.945	1.043	0.997
RFC3	P40938	Replication factor C subunit 3 OS=Homo sapiens OX=9606 GN=RFC3 PE=1 SV=2	1.398	0.98	0.938	0.658
TRAP1	Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens OX=9606 GN=TRAP1 PE=1	1.009	0.997	0.987	0.975
KS6A1	Q15418	Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens OX=9606 GN=RPS6KA1 PE=1	0.949	1.041	0.943	1.034
NDC1	Q9BTX1	Nucleoporin NDC1 OS=Homo sapiens OX=9606 GN=NDC1 PE=1 SV=2	0.932	1.034	0.948	1.052
IDHC	T58747	Isochoride dehydrogenase [NADPH] cytoplasmic OS=Homo sapiens OX=9606 GN=IDH1 PE=1	1.003	1.002	0.981	0.98
TRFM	P08582	Melanotransferrin OS=Homo sapiens OX=9606 GN=MELTF PE=1 SV=2	1.13	0.946	1.027	0.86
WBP11	Q9Y2W2	WW domain-binding protein 11 OS=Homo sapiens OX=9606 GN=WBP11 PE=1 SV=1	0.978	1.025	0.955	1.001
DDX17	Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17	1.012	0.976	1.003	0.968
EIF3G	Q75821	Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens OX=9606 GN=EIF3G	1.023	1.051	0.929	0.954
KAP2	P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens OX=9606	1.013	1.008	0.969	0.964
WDR12	Q9GZL7	Ribosome biogenesis protein WDR12 OS=Homo sapiens OX=9606 GN=WDR12 PE=1 SV=2	0.924	0.998	0.976	1.054
RPN1	P04843	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 1 OS=Homo sapiens	0.962	0.98	0.994	1.013
TECR	Q9NZ01	Very-long-chain enoyl-CoA reductase OS=Homo sapiens OX=9606 GN=TECR PE=1 SV=1	0.946	1.052	0.923	1.027
RS23	P62266	40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3	0.984	0.992	0.981	0.989
PAX1	P49023	Paxillin OS=Homo sapiens OX=9606 GN=PXN PE=1 SV=3	0.979	0.978	1.101	0.987
NU214	P36568	Nuclear pore complex protein Nup214 OS=Homo sapiens OX=9606 GN=NUP214 PE=1 SV=2	1	0.985	0.984	0.969
PLK1	P53350	Serine/threonine-protein kinase PLK1 OS=Homo sapiens OX=9606 GN=PLK1 PE=1 SV=1	0.891	0.962	1.002	1.082
RS2	P15880	40S ribosomal protein S2 OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=2	0.946	0.995	0.97	1.02
PUF60	Q9UJHX1	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens OX=9606 GN=PUF60 PE=1 SV=1	0.98	0.96	1.005	0.985
PRPS1	P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens OX=9606 GN=PRPS1 PE=1 SV=2	1.023	0.952	1.012	0.941
PRC2C	Q9YS20	Protein PRRC2C OS=Homo sapiens OX=9606 GN=PRRC2C PE=1 SV=4	1.086	0.951	1.008	0.882
GSK3B	P49841	Glycogen synthase kinase-3 beta OS=Homo sapiens OX=9606 GN=GSK3B PE=1 SV=2	1.025	0.982	0.981	0.939
GT252	Q8IYK4	Procollagen galactosyltransferase 2 OS=Homo sapiens OX=9606 GN=COLGALT2 PE=1	0.976	0.981	0.982	0.987
RBM39	Q14498	RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=2	1.091	0.947	1.011	0.877
BMI1	P35226	Polycomb complex protein BMI-1 OS=Homo sapiens OX=9606 GN=BMI1 PE=1 SV=2	1.042	0.947	1.014	0.922
TMM43	Q9BTV4	Transmembrane protein 43 OS=Homo sapiens OX=9606 GN=TMM43 PE=1 SV=1	1.056	0.92	1.042	0.907
PRS6A	P17980	26S proteasome regulatory subunit 6A OS=Homo sapiens OX=9606 GN=PSMC3 PE=1 SV=3	0.991	1.01	0.952	0.971
TKT	P29401	Transtekolase OS=Homo sapiens OX=9606 GN=TKT PE=1 SV=3	0.926	0.994	0.967	1.037
MPPA	P10713	Mitochondrial-processing peptidase subunit alpha OS=Homo sapiens OX=9606 GN=MPMCA	0.992	0.97	0.991	0.969
VATA	P38606	V-type proton ATPase catalytic subunit A OS=Homo sapiens OX=9606 GN=ATP6V1A PE=1	0.983	1.017	0.943	0.975
IRS4	Q14654	Insulin receptor substrate 4 OS=Homo sapiens OX=9606 GN=IRS4 PE=1 SV=1	1.035	0.968	0.989	0.925
KT112	Q96EK9	Protein KT112 homolog OS=Homo sapiens OX=9606 GN=KT112 PE=1 SV=1	0.997	1.02	0.939	0.961
AGM1	Q95394	Phosphoacetylglucosamine mutase OS=Homo sapiens OX=9606 GN=PGM3 PE=1 SV=1	0.998	0.984	0.973	0.959
SRRT	Q9BXPS	Serrate RNA effector molecule homolog OS=Homo sapiens OX=9606 GN=SRRT PE=1 SV=1	0.993	0.967	0.988	0.962
RM03	P09001	39S ribosomal protein L3, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL3 PE=1	0.955	1.068	0.888	0.993
RBGP1	Q9Y3P9	Rab GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RABGAP1 PE=1 SV=3	1.025	0.932	1.019	0.926
NSUN2	Q08J23	RNA cytosine C(5')-methyltransferase NSUN2 OS=Homo sapiens OX=9606 GN=NSUN2	1.002	0.98	0.97	0.948
PYC	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens OX=9606 GN=PC PE=1 SV=2	0.979	0.947	1.002	0.969
DESP	P15924	Desmoplakin OS=Homo sapiens OX=9606 GN=DSP PE=1 SV=3	0.971	0.963	0.983	0.975
AMPB	Q9H4A4	Aminopeptidase B OS=Homo sapiens OX=9606 GN=RNPEP PE=1 SV=2	1.009	0.963	0.982	0.937

RAE1L	P78406	mRNA export factor OS=Homo sapiens OX=9606 GN=RAE1 PE=1 SV=1	0.955	0.917	1.03	0.989
DDX54	Q8TDD1	ATP-dependent RNA helicase DDX54 OS=Homo sapiens OX=9606 GN=DDX54 PE=1 SV=2	0.964	0.96	0.985	0.98
KBP	Q9EK5	KIF-binding protein OS=Homo sapiens OX=9606 GN=KIFBP PE=1 SV=1	1.077	1.041	0.9	0.87
SEPT7	Q16181	Septin 7 OS=Homo sapiens OX=9606 GN=SEPT7 PE=1 SV=2	1.001	0.931	1.011	0.941
GIPC1	O14908	PDZ domain-containing protein GIPC1 OS=Homo sapiens OX=9606 GN=GIPC1 PE=1 SV=2	0.97	0.889	1.054	0.967
MPCP	P00325	Phosphat carrier protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A3 PE=1	0.929	0.981	0.958	1.012
ALD9A1	P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH9A1	0.975	0.97	0.969	0.965
VPS18	Q9P253	Vacuolar protein sorting-associated protein 18 homolog OS=Homo sapiens OX=9606	0.953	1.114	0.834	0.976
SSF1	Q9NQ55	Suppressor of SWI4 1 homolog OS=Homo sapiens OX=9606 GN=PPAN PE=2 SV=1	1.023	0.972	0.965	0.917
NCBP1	Q09161	Nuclear cap-binding protein subunit 1 OS=Homo sapiens OX=9606 GN=NCBP1 PE=1 SV=1	0.962	0.97	0.968	0.976
ARMT1	Q9H993	Damage-control phosphatases ARMT1 OS=Homo sapiens OX=9606 GN=ARMT1 PE=1 SV=1	1.136	0.89	1.037	0.812
RSBNL	Q6PCB5	Lysine-specific demethylase RSBNL OS=Homo sapiens OX=9606 GN=RSBNL PE=1	1.156	0.917	1.005	0.797
THIL	P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens OX=9606 GN=ACAT1 PE=1	0.951	0.977	0.96	0.986
PSMD8	P48556	26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens OX=9606 GN=PSMD8	0.973	0.997	0.936	0.959
ACTB	P60709	Actin, cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1	0.944	0.964	0.968	0.989
KIF4B	Q2VQI3	Chromosome-associated kinesin KIF4B OS=Homo sapiens OX=9606 GN=KIF4B PE=2 SV=2	1.101	0.915	1.01	0.839
TPIS	P60174	Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=TP1 PE=1 SV=3	0.997	0.973	0.958	0.934
WDR46	O15213	WD repeat-containing protein 46 OS=Homo sapiens OX=9606 GN=WDR46 PE=1 SV=3	1.016	0.914	1.017	0.915
NUP98	P52948	Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens OX=9606 GN=NUP98 PE=1	0.995	0.966	0.964	0.936
ELMD2	Q8Z81	ELMO domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ELMOD2 PE=1	0.907	0.903	0.897	1.022
MPRI	P11717	Cation-independent mannose-6-phosphate receptor OS=Homo sapiens OX=9606 GN=IGF2R	1.107	0.969	0.95	0.832
COPG1	Q9Y768	Coatomer subunit gamma-1 OS=Homo sapiens OX=9606 GN=COPG1 PE=1 SV=1	1.05	0.977	0.947	0.881
CHIP	Q9UNE7	E3 ubiquitin-protein ligase CHIP OS=Homo sapiens OX=9606 GN=STUB1 PE=1 SV=2	0.983	0.974	0.953	0.944
FUBP3	Q96124	Far upstream element-binding protein 3 OS=Homo sapiens OX=9606 GN=FUBP3 PE=1 SV=2	0.98	0.97	0.951	0.935
FLOT2	Q14254	Flotillin-2 OS=Homo sapiens OX=9606 GN=FLOT2 PE=1 SV=2	0.975	0.979	0.939	0.943
LAMB2	P55268	Laminin subunit beta-2 OS=Homo sapiens OX=9606 GN=LAMB2 PE=1 SV=2	0.915	0.955	0.962	1.004
PHB2	P55262	Prohibitin-2 OS=Homo sapiens OX=9606 GN=PHB2 PE=1 SV=2	0.941	0.927	0.991	0.977
UBP32	Q8NFA0	Ubiquitin carboxyl-terminal hydrolase 32 OS=Homo sapiens OX=9606 GN=USP32 PE=1	0.917	0.95	0.967	1.001
PRSI0	P62333	26S proteasome regulatory subunit 10B OS=Homo sapiens OX=9606 GN=PSMC6 PE=1	0.89	1.013	0.902	1.027
MITOK	Q9ER9	Mitochondrial potassium channel OS=Homo sapiens OX=9606 GN=CCDC51 PE=1 SV=2	1.005	1.046	0.87	0.905
SYQ	P47897	Glutamine-tRNA ligase OS=Homo sapiens OX=9606 GN=QARS PE=1 SV=1	0.984	0.937	0.972	0.926
SRP54	P61011	Signal recognition particle 54 kDa protein OS=Homo sapiens OX=9606 GN=SRP54 PE=1	0.949	0.882	1.029	0.956
ETFA	P13804	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens OX=9606	1.061	0.925	0.976	0.851
CLAP2	O75122	CLIP-associating protein 2 OS=Homo sapiens OX=9606 GN=CLASP2 PE=1 SV=3	0.941	0.911	0.995	0.964
TADB2	P13148	TAR DNA-binding protein 43 OS=Homo sapiens OX=9606 GN=TARD2B PE=1 SV=1	0.967	0.99	0.91	0.937
PCBP2	Q15366	Poly(C)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1	0.955	0.948	0.957	0.95
RPA2	Q9HY9Y	DNA-directed RNA polymerase I subunit RPA2 OS=Homo sapiens OX=9606 GN=POLR1B	1.037	0.875	1.028	0.867
SDA1	Q9NVU7	Protein SDA1 homolog OS=Homo sapiens OX=9606 GN=SDAD1 PE=1 SV=3	0.925	0.97	0.933	0.978
SEC62	Q94442	Translocation protein SEC62 OS=Homo sapiens OX=				

OGT1	O15294	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	0.938	0.884	0.987	0.93
BMS1	Q14692	Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens OX=9606 GN=BMS1 PE=1	0.955	0.929	0.94	0.915
SRP68	Q9UHB9	Signaling recognition particle subunit SRP68 OS=Homo sapiens OX=9606 GN=SRP68 PE=1	0.971	0.93	0.938	0.898
HCL51	P14317	Hematopoietic lineage cell-specific protein OS=Homo sapiens OX=9606 GN=HCL51 PE=1	1.306	0.716	1.106	0.607
ATPG	P36542	ATP synthase subunit gamma, mitochondrial OS=Homo sapiens OX=9606 GN=ATPSF1C	0.942	0.924	0.943	0.925
CKAP5	Q14008	Cytoskeleton-associated protein 5 OS=Homo sapiens OX=9606 GN=CKAP5 PE=1 SV=3	0.982	0.933	0.933	0.886
RAD50	Q92878	DNA repair protein RAD50 OS=Homo sapiens OX=9606 GN=RAD50 PE=1 SV=1	0.987	0.947	0.919	0.881
OLA1	Q9NTK5	Obg-like ATPase 1 OS=Homo sapiens OX=9606 GN=OLA1 PE=1 SV=2	0.976	0.908	0.958	0.892
DDX6	P26196	Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens OX=9606 GN=DDX6 PE=1	0.981	0.885	0.981	0.885
FSCN1	Q16658	Fascin OS=Homo sapiens OX=9606 GN=FSCN1 PE=1 SV=3	1.055	0.893	0.966	0.818
TBL3	Q12788	Transducin beta-like protein 3 OS=Homo sapiens OX=9606 GN=TBL3 PE=1 SV=2	0.95	0.96	0.906	0.915
ADHX	P11766	Alcohol dehydrogenase class-3 OS=Homo sapiens OX=9606 GN=ADHX PE=1 SV=4	0.978	0.909	0.955	0.887
GSHR	P00390	Glutathione reductase, mitochondrial OS=Homo sapiens OX=9606 GN=GSHR PE=1 SV=2	0.855	0.934	0.927	1.013
PP1A	P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens OX=9606 GN=PP1A PE=1 SV=2	0.992	0.899	0.964	0.873
DSRAD	P55265	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens OX=9606 GN=ADAR	0.949	0.934	0.929	0.914
NNTM	Q13423	NAD(P) hydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=NNT PE=1 SV=3	0.956	0.921	0.941	0.907
TRM6	Q9UIAJ5	tRNA (adenine(58)(N1))-methyltransferase non-catalytic subunit TRM6 OS=Homo sapiens	1.065	0.868	0.987	0.805
PGM1	P36871	Phosphoglucomutase-1 OS=Homo sapiens OX=9606 GN=PGM1 PE=1 SV=3	0.978	0.912	0.946	0.883
NAA10	P41227	N-alpha-acetyltransferase 10 OS=Homo sapiens OX=9606 GN=NA10 PE=1 SV=1	1.083	0.934	0.913	0.788
TMEDA	P49755	Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens OX=9606	0.876	0.925	0.932	0.984
UBP7	Q93009	Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens OX=9606 GN=USP7 PE=1 SV=2	0.952	0.938	0.92	0.906
CAZA1	P52907	F-actin-capping protein subunit alpha-1 OS=Homo sapiens OX=9606 GN=CAPZ1A PE=1	0.939	0.894	0.964	0.918
HIBCH	Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Homo sapiens OX=9606 GN=HIBCH	0.917	0.932	0.925	0.94
C1TM	Q6UB35	Monofunctional C1-tetrahydrolfolate synthase, mitochondrial OS=Homo sapiens OX=9606	0.911	0.924	0.933	0.946
FEN1	P39748	Flap endonuclease 1 OS=Homo sapiens OX=9606 GN=FEN1 PE=1 SV=1	0.951	0.873	0.983	0.903
1433G	P61981	14-3-3 protein gamma OS=Homo sapiens OX=9606 GN=YWHAG PE=1 SV=2	0.746	1.001	0.836	1.122
COPD	P48444	Coatomer subunit delta OS=Homo sapiens OX=9606 GN=ARCN1 PE=1 SV=1	0.955	0.918	0.933	0.896
EHMT2	Q96KQ7	Histone-lysine N-methyltransferase EHMT2 OS=Homo sapiens OX=9606 GN=EHMT2 PE=1	0.927	1	0.852	0.918
PRDX2	P32119	Peroxiredoxin-2 OS=Homo sapiens OX=9606 GN=PRDX2 PE=1 SV=5	0.978	0.904	0.943	0.871
ROCK2	Q75116	Rho-associated protein kinase 2 OS=Homo sapiens OX=9606 GN=ROCK2 PE=1 SV=4	1.002	0.888	0.951	0.843
MINT	Q96T58	Msx2-interacting protein OS=Homo sapiens OX=9606 GN=SPEN PE=1 SV=1	0.949	0.969	0.873	0.892
RL5	P46777	60S ribosomal protein L5 OS=Homo sapiens OX=9606 GN=RPL5 PE=1 SV=3	0.84	0.938	0.897	1.001
TCPD	P50991	T-complex protein 1 subunit delta OS=Homo sapiens OX=9606 GN=CCT4 PE=1 SV=4	0.946	0.919	0.918	0.892
S4A5	Q9BY07	Electrogenic sodium bicarbonate cotransporter 4 OS=Homo sapiens OX=9606 GN=SLC4A5	0.958	0.955	0.882	0.879
NOC3L	Q8WTT2	Nucleolar complex protein 3 homolog OS=Homo sapiens OX=9606 GN=NOC3L PE=1 SV=1	0.958	0.934	0.9	0.877
ROA0	Q13151	Heterogeneous nuclear ribonucleoprotein A OS=Homo sapiens OX=9606 GN=HNRNPA0	0.882	0.936	0.896	0.952
HNRPC	P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC	1.002	0.881	0.948	0.834
RS6	P62753	40S ribosomal protein S6 OS=Homo sapiens OX=9606 GN=RP56 PE=1 SV=1	0.916	0.899	0.932	0.916
RL3	P39023	60S ribosomal protein L3 OS=Homo sapiens OX=9606 GN=RPL3 PE=1 SV=2	0.902	0.909	0.922	0.929
H12	P16403	Histone H1.2 OS=Homo sapiens OX=9606 GN=H1-2 PE=1 SV=2	0.889	0.93	0.899	0.941
NOP14	P78316	Nucleolar protein 14 OS=Homo sapiens OX=9606 GN=NOP14 PE=1 SV=3	0.99	0.881	0.945	0.841
KCRB	P12277	Creative kinase B-type OS=Homo sapiens OX=9606 GN=CKB PE=1 SV=1	0.931	0.926	0.898	0.893
MOES	P26038	Moesin OS=Homo sapiens OX=9606 GN=MSN PE=1 SV=3	0.907	0.898	0.922	0.913
HNRPR	Q43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR PE=1	0.878	0.919	0.9	0.943
EDC4	Q6P291	Enhancer of mRNA-decapping protein 4 OS=Homo sapiens OX=9606 GN=EDC4 PE=1 SV=1	0.911	0.903	0.916	0.908
EXOC4	Q96A65	Exocyst complex component 4 OS=Homo sapiens OX=9606 GN=EXOC4 PE=1 SV=1	0.954	0.896	0.921	0.865
RBMB28	Q9NW13	RNA-binding protein 28 OS=Homo sapiens OX=9606 GN=RBMB28 PE=1 SV=3	0.983	0.895	0.918	0.836
IMB1	Q14974	Importin subunit beta-1 OS=Homo sapiens OX=9606 GN=KPNB1 PE=1 SV=2	0.918	0.89	0.925	0.897
PRPF3	Q44395	U4/U6 small nuclear ribonucleoprotein Prp3 OS=Homo sapiens OX=9606 GN=PRPF3 PE=1	0.942	0.919	0.896	0.873
PRDX4	Q13162	Peroxiredoxin-4 OS=Homo sapiens OX=9606 GN=PRDX4 PE=1 SV=1	0.837	1.142	0.696	0.95
ABR	Q12979	Active breakpoint cluster region-related protein OS=Homo sapiens OX=9606 GN=ABR PE=1	0.93	0.919	0.893	0.882
NT5D1	Q5TF4E	5'-nucleotidase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NT5DC1 PE=1	0.955	0.906	0.903	0.856
CTBP1	Q13363	C-terminal-binding protein 1 OS=Homo sapiens OX=9606 GN=CTBP1 PE=1 SV=2	0.935	0.884	0.926	0.875
PRP4	Q43172	U4/U6 small nuclear ribonucleoprotein Prp4 OS=Homo sapiens OX=9606 GN=PRP4 PE=1	0.923	0.906	0.901	0.884
NOLC1	Q14978	Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens OX=9606 GN=NOLC1 PE=1	0.942	0.879	0.927	0.865
DNMT1	P26358	DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens OX=9606 GN=DNMT1 PE=1 SV=2	0.933	0.908	0.895	0.872
NOMO2	Q5JPE7	Nodal modulator 2 OS=Homo sapiens OX=9606 GN=NOMO2 PE=1 SV=1	0.876	0.878	0.925	0.928
CP51A	Q16850	Lanosterol 14-alpha demethylase OS=Homo sapiens OX=9606 GN=CYP51A1 PE=1 SV=3	0.969	0.955	0.846	0.834
MAGD2	Q9UNF1	Melanoma-associated antigen D2 OS=Homo sapiens OX=9606 GN=MAGED2 PE=1 SV=2	0.864	0.918	0.883	0.939
SMRC2	Q8TAQ2	SWI/SNF complex subunit SMARCC2 OS=Homo sapiens OX=9606 GN=SMARCC2 PE=1	0.972	0.889	0.909	0.831
CSDE1	Q75534	Cold shock domain-containing protein E1 OS=Homo sapiens OX=9606 GN=CSDE1 PE=1	0.924	0.899	0.901	0.876
WDR75	Q8IWA0	WD repeat-containing protein 75 OS=Homo sapiens OX=9606 GN=WDR75 PE=1 SV=1	0.945	0.938	0.862	0.855
ADDG	Q9UEY8	Gamma-adducin OS=Homo sapiens OX=9606 GN=ADD3 PE=1 SV=1	0.931	0.879	0.92	0.868
HEAT3	Q7ZQ42	HEAT repeat-containing protein 3 OS=Homo sapiens OX=9606 GN=HEATR3 PE=1 SV=2	0.891	0.876	0.923	0.907
CAH2	P00918	Carbonic anhydrase 2 OS=Homo sapiens OX=9606 GN=CA2 PE=1 SV=2	0.948	0.83	0.969	0.849
GP143	P51810	G-protein coupled receptor 143 OS=Homo sapiens OX=9606 GN=GPR143 PE=1 SV=2	1.176	0.785	0.98	0.655
MAOX	P48163	NADP-dependent malic enzyme OS=Homo sapiens OX=9606 GN=ME1 PE=1 SV=1	0.92	0.857	0.942	0.877
STX4	Q12846	Syntaxin-4 OS=Homo sapiens OX=9606 GN=STX4 PE=1 SV=2	0.855	0.817	0.984	0.94
AT1A1	P05023	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens OX=9606	0.903	0.891	0.906	0.893
MRE11	P49959	Double-strand break repair protein MRE11 OS=Homo sapiens OX=9606 GN=MRE11 PE=1	0.918	0.91	0.886	0.878

EIF3H	O15372	Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens OX=9606 GN=EIF3H	0.92	0.891	0.905	0.876
OPA1	O60313	Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1	0.922	0.857	0.939	0.873
SYTM	Q9BW92	Threonine--arginine ligase, mitochondrial OS=Homo sapiens OX=9606 GN=TARS2 PE=1 SV=1	0.891	0.868	0.927	0.904
ANXA7	P20073	Annexin A7 OS=Homo sapiens OX=9606 GN=ANXA7 PE=1 SV=3	0.924	0.912	0.882	0.871
RRP1B	Q14684	Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens OX=9606 GN=RRP1B	0.903	0.928	0.867	0.891
TM192	Q8IVY95	Transmembrane protein 192 OS=Homo sapiens OX=9606 GN=TMEM192 PE=1 SV=1	0.952	0.895	0.895	0.841
LYAR	Q9NX58	Cell growth-regulating nucleolar protein OS=Homo sapiens OX=9606 GN=LYAR PE=1 SV=2	0.997	0.936	0.85	0.797
NUP35	Q8NFH5	Nucleoporin NUP35 OS=Homo sapiens OX=9606 GN=NUP35 PE=1 SV=1	0.989	0.804	0.985	0.801
RL18A	Q02543	60S ribosomal protein L18a OS=Homo sapiens OX=9606 GN=RPL18A PE=1 SV=2	1.046	1.02	0.766	0.746
ACOC	P21399	Cytoplasmic aconitase hydratase OS=Homo sapiens OX=9606 GN=ACO1 PE=1 SV=3	0.95	0.868	0.919	0.84
PELP1	Q8IZL8	Proline-, glutamic acid- and leucine-rich protein 1 OS=Homo sapiens OX=9606 GN=PELP1	0.914	0.914	0.871	0.871
HNRQ	O60506	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP	0.834	0.912	0.87	0.951
SRSF6	Q13247	Serine/arginine-rich splicing factor 6 OS=Homo sapiens OX=9606 GN=SRSF6 PE=1 SV=2	0.887	0.862	0.922	0.896
AT2B1	P20200	Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens OX=9606 GN=ATP2B1	0.894	0.883	0.899	0.886
FKB15	Q5T1M5	FK506-binding protein 15 OS=Homo sapiens OX=9606 GN=FKB15 PE=1 SV=2	1.122	0.845	0.909	0.684
CLPX	O76031	ATP-dependent Clp protease ATP-binding subunit clp3-like, mitochondrial OS=Homo sapiens	0.875	0.852	0.928	0.903
WDR43	Q15061	WD repeat-containing protein 43 OS=Homo sapiens OX=9606 GN=WDR43 PE=1 SV=3	0.925	0.916	0.862	0.854
SYMC	P56192	Methionine-tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=MARS PE=1 SV=2	0.903	0.916	0.862	0.874
DHB4	P15169	Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens OX=9606 GN=HSD17B4	0.877	0.86	0.917	0.9
ZNF384	Q8TF68	Zinc finger protein 384 OS=Homo sapiens OX=9606 GN=ZNF384 PE=1 SV=2	0.876	0.846	0.932	0.9
PP5	P53041	Serine/threonine-protein phosphatase 5 OS=Homo sapiens OX=9606 GN=PPP5C PE=1 SV=1	0.868	0.788	0.994	0.903
TDIF2	Q5QEJ6	Deoxyxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens OX=9606	0.9	0.917	0.86	0.876
TMX1	Q9HN1	Thioredoxin-related transmembrane protein 1 OS=Homo sapiens OX=9606 GN=TMX1 PE=1	0.952	0.919	0.856	0.826
ECHA	P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=HADHA	0.86	0.885	0.89	0.916
XRCC5	P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens OX=9606 GN=XRCC5 PE=1	0.897	0.888	0.887	0.877
PEPD	P12955	Xaa-Pro dipeptidase OS=Homo sapiens OX=9606 GN=PEPD PE=1 SV=3	0.851	0.88	0.866	0.924
PCH2	Q15645	Pachytene checkpoint protein 2 homolog OS=Homo sapiens OX=9606 GN=TRIP13 PE=1	0.851	0.907	0.866	0.924
DEK	P35659	Protein DEK OS=Homo sapiens OX=9606 GN=DEK PE=1 SV=1	0.866	0.874	0.898	0.905
USP9X	Q90008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens OX=9606	0.977	0.903	0.864	0.799
LAMC1	P11047	Laminin subunit gamma-1 OS=Homo sapiens OX=9606 GN=LAMC1 PE=1 SV=3	0.916	0.942	0.83	0.853
DRG1	Q9Y295	Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=DRG1	0.929	0.88	0.889	0.842
EKI2	Q9NVF9	Ethanolamine kinase 2 OS=Homo sapiens OX=9606 GN=ETNK2 PE=2 SV=2	0.894	0.894	0.875	0.871
CBSL	P0DN79	Cystathione beta-synthase-like protein OS=Homo sapiens OX=9606 GN=CBSL PE=1 SV=1	0.875	0.897	0.87	0.892
ADT2	P05141	ADP/ATP translocase 2 OS=Homo sapiens OX=9606 GN=SLC2A5 PE=1 SV=7	0.871	0.901	0.865	0.895
GANAB	Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens OX=9606 GN=GANAB PE=1 SV=3	0.877	0.861	0.904	0.887
UBP47	Q96K76	Ubiquitin carboxyl-terminal hydrolase 47 OS=Homo sapiens OX=9606 GN=USP47 PE=1	1.194	0.756	0.966	0.612
CPT1A	P50416	Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens OX=9606 GN=CPT1A	1.035	0.824	0.929	0.739
WDR3	Q9UNX4	WD repeat-containing protein 3 OS=Homo sapiens OX=9606 GN=WDR3 PE=1 SV=1	0.925	0.916	0.847	0.838
CSN1						

HDGR2	Q7Z4V5	Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens OX=9606 GN=HDGFL2	0.988	0.809	0.92	0.753
RU2A	P09661	U2 small nuclear ribonucleoprotein A' OS=Homo sapiens OX=9606 GN=SNRPA1 PE=1	0.818	0.873	0.859	0.917
ARP3	P61158	Actin-related protein 3 OS=Homo sapiens OX=9606 GN=ACTR3 PE=1 SV=3	0.867	0.858	0.874	0.865
LSS	P48449	Lanosterol synthase OS=Homo sapiens OX=9606 GN=LSS PE=1 SV=1	0.94	0.826	0.903	0.794
UBE4A	Q14139	Ubiquitin conjugation factor E4 A OS=Homo sapiens OX=9606 GN=UBE4A PE=1 SV=2	0.991	0.823	0.899	0.746
SPT5H	000267	Transcription elongation factor SPTS OS=Homo sapiens OX=9606 GN=SPT5H PE=1 SV=1	0.906	0.843	0.885	0.823
WDR1	Q75083	WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=WDR1 PE=1 SV=4	0.895	0.85	0.878	0.834
RT30	Q9NP92	39S ribosomal protein S30, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS30 PE=1	0.827	0.84	0.888	0.901
EF1A2	Q05639	Elongation factor 1-alpha 2 OS=Homo sapiens OX=9606 GN=EEF1A2 PE=1 SV=1	0.745	0.865	0.854	0.99
APEX1	P27695	DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens OX=9606 GN=APEX1 PE=1	0.915	0.81	0.916	0.811
SNUT2	Q53GS9	U6/U5 tri-snRNP-associated protein 2 OS=Homo sapiens OX=9606 GN=USP39 PE=1	0.924	0.818	0.907	0.803
RALY	Q9UKM9	RNA-binding protein Raly OS=Homo sapiens OX=9606 GN=RALY PE=1 SV=1	0.91	0.856	0.866	0.815
CMTR1	Q8N1G2	Cap-specific mRNA (nucleoside-2'-O-)methyltransferase 1 OS=Homo sapiens OX=9606	0.797	0.875	0.846	0.928
RL1D1	Q76021	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=RSL1D1 PE=1	0.861	0.848	0.875	0.861
AP1M1	Q9BX55	AP-1 complex subunit mu-1 OS=Homo sapiens OX=9606 GN=AP1M1 PE=1 SV=3	0.907	0.852	0.868	0.816
GUAA	P49915	GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens OX=9606 GN=GMP5 PE=1 SV=1	0.89	0.841	0.879	0.83
EF2	P13639	Elongation factor 2 OS=Homo sapiens OX=9606 GN=EEF2 PE=1 SV=4	0.835	0.859	0.859	0.884
CAN1	P07384	Calpain-1 catalytic subunit OS=Homo sapiens OX=9606 GN=CAPN1 PE=1 SV=1	0.848	0.916	0.804	0.868
H3T1	Q16695	Histone H3.1 OS=Homo sapiens OX=9606 GN=H3T3H3 PE=1 SV=3	0.859	0.848	0.87	0.859
NSDHL	Q15738	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Homo sapiens OX=9606	0.867	0.855	0.861	0.849
BET1L	Q9NYM9	BET1-like protein OS=Homo sapiens OX=9606 GN=BET1L PE=1 SV=1	0.925	0.902	0.812	0.792
SPP45	Q96125	Splicing factor 45 OS=Homo sapiens OX=9606 GN=RBML17 PE=1 SV=1	0.895	0.904	0.812	0.82
SRSF7	Q16629	Serine/arginine-rich splicing factor 7 OS=Homo sapiens OX=9606 GN=SRSF7 PE=1 SV=1	0.838	0.808	0.906	0.875
WIZ	Q95785	Protein Wiz OS=Homo sapiens OX=9606 GN=WIZ PE=1 SV=2	0.898	0.84	0.872	0.815
COPG2	Q9UBF2	Coatomer subunit gamma-2 OS=Homo sapiens OX=9606 GN=COPG2 PE=1 SV=1	0.939	0.814	0.895	0.776
SLA11	Q8N8D3	SLAIN motif-containing protein 1 OS=Homo sapiens OX=9606 GN=SLAIN1 PE=1 SV=3	1.215	0.95	0.706	0.552
SYTC	P26639	Threonine-tRNA ligase 1, cytoplasmic OS=Homo sapiens OX=9606 GN=TARS1 PE=1 SV=3	0.883	0.852	0.859	0.829
CUL1	Q13616	Cullin-1 OS=Homo sapiens OX=9606 GN=CUL1 PE=1 SV=2	0.861	0.851	0.86	0.85
TMUB1	Q9BV87	Transmembrane and ubiquitin-like-domain-containing protein 1 OS=Homo sapiens OX=9606	0.869	0.796	0.917	0.84
PRP31	Q8WWY3	U4/U6 small nuclear ribonucleoprotein PRP31 OS=Homo sapiens OX=9606 GN=PRPF31	0.846	0.838	0.872	0.864
TPR	P12270	Nucleoprotein TPR OS=Homo sapiens OX=9606 GN=TPR PE=1 SV=3	0.892	0.844	0.864	0.818
ROCK1	Q13464	Rho-associated protein kinase 1 OS=Homo sapiens OX=9606 GN=ROCK1 PE=1 SV=1	0.879	0.807	0.903	0.829
AP2A	P05549	Transcription factor AP-2-alpha OS=Homo sapiens OX=9606 GN=TFAP2A PE=1 SV=1	0.841	0.769	0.944	0.863
SRPK1	Q96SB4	SRSF protein kinase 1 OS=Homo sapiens OX=9606 GN=SRPK1 PE=1 SV=2	0.839	0.853	0.855	0.869
NOL6	Q9H6R4	Nucleolar protein 6 OS=Homo sapiens OX=9606 GN=NOL6 PE=1 SV=2	0.911	0.826	0.88	0.798
ACADM	P11310	Medium-chain-specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX=9606	0.917	0.924	0.783	0.789
CKAP2	Q8WWK9	Cytoskeleton-associated protein 2 OS=Homo sapiens OX=9606 GN=CKAP2 PE=1 SV=1	0.838	0.887	0.82	0.867
PCNA	P12004	Proliferating cell nuclear antigen OS=Homo sapiens OX=9606 GN=PCNA PE=1 SV=1	0.819	0.885	0.821	0.887
U3IP2	Q43818	U3 small nucleolar RNA-interacting protein 2 OS=Homo sapiens OX=9606 GN=RRP9 PE=1	0.88	0.89	0.815	0.824
COR1B	Q9BR76	Coronin-1B OS=Homo sapiens OX=9606 GN=CORO1B PE=1 SV=1	0.851	0.875	0.829	0.852
RECO1	P46063	ATP-dependent DNA helicase Q1 OS=Homo sapiens OX=9606 GN=RECOL1 PE=1 SV=3	0.866	0.842	0.86	0.837
EIF3D	Q15371	Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens OX=9606 GN=EIF3D	0.868	0.819	0.884	0.834
CAND1	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens OX=9606 GN=CAND1	0.881	0.867	0.835	0.821
ANXA6	P08133	Annexin A6 OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=3	0.836	0.858	0.843	0.865
GEM1	Q8TEQ6	Gem-associated protein 5 OS=Homo sapiens OX=9606 GN=GEMIN5 PE=1 SV=3	0.903	0.887	0.813	0.798
CHRDL1	Q9UJHD1	Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens OX=9606	0.843	0.823	0.877	0.856
BRE1B	Q75150	E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens OX=9606 GN=RNF40 PE=1 SV=5	1.249	1.032	0.612	0.505
MDC1	Q14676	Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens OX=9606 GN=MDC1	0.856	0.82	0.879	0.842
DHRS7	Q9Y394	Dehydrogenase/reductase SDH family member 7 OS=Homo sapiens OX=9606 GN=DHRS7	0.741	0.816	0.875	0.964
ARGI2	P78540	Arginase-2, mitochondrial OS=Homo sapiens OX=9606 GN=ARG2 PE=1 SV=1	0.85	0.813	0.884	0.845
MOGS	Q13724	Mannosyl-oligosaccharide glucosidase OS=Homo sapiens OX=9606 GN=MOGS PE=1 SV=5	0.845	0.819	0.875	0.849
AL1B1	P30837	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH1B1	0.815	0.896	0.794	0.874
PRP17	O60508	Pre-mRNA-processing factor 17 OS=Homo sapiens OX=9606 GN=CDC40 PE=1 SV=1	0.934	0.856	0.828	0.759
IF2B1	Q9NZ8B	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens OX=9606	0.856	0.837	0.851	0.831
MTA1	Q13330	Metastasis-associated protein MTA1 OS=Homo sapiens OX=9606 GN=MTA1 PE=1 SV=2	0.862	0.86	0.827	0.826
CLPB	Q9H078	Caseinolytic peptidase B protein homolog OS=Homo sapiens OX=9606 GN=CLPB PE=1	0.841	0.837	0.85	0.846
IPO5	Q00410	Importin-5 OS=Homo sapiens OX=9606 GN=IPO5 PE=1 SV=4	0.835	0.838	0.849	0.852
SMCA1	P28370	Probable global transcription activator SNF2L1 OS=Homo sapiens OX=9606 GN=SMARCA1	0.884	0.806	0.88	0.803
PAXII	Q6ZW49	PAX-interacting protein 1 OS=Homo sapiens OX=9606 GN=PAXPI1 PE=1 SV=2	0.822	0.798	0.889	0.863
AFG32	Q9Y4W6	AFG3-like protein 2 OS=Homo sapiens OX=9606 GN=AFG3L2 PE=1 SV=2	0.914	0.829	0.854	0.775
RL19	P84098	60S ribosomal protein L19 OS=Homo sapiens OX=9606 GN=RPL19 PE=1 SV=1	0.819	0.866	0.82	0.866
ERP44	Q9BS26	Endoplasmic reticulum resident protein 44 OS=Homo sapiens OX=9606 GN=ERP44 PE=1	0.839	0.854	0.831	0.847
ACL6A	O96019	Actin-like protein 6A OS=Homo sapiens OX=9606 GN=ACTL6A PE=1 SV=1	0.852	0.841	0.844	0.833
WDR82	Q6UXN9	WD repeat-containing protein 82 OS=Homo sapiens OX=9606 GN=WDR82 PE=1 SV=1	0.913	0.822	0.86	0.775
BAG6	P46379	Large proline-rich protein BAG6 OS=Homo sapiens OX=9606 GN=BAG6 PE=1 SV=2	0.804	0.835	0.849	0.881
PUR8	P30566	Adenylosuccinate lyase OS=Homo sapiens OX=9606 GN=ADSL PE=1 SV=2	0.826	0.836	0.847	0.857
TIM50	Q3ZCQ8	Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens	0.899	0.862	0.818	0.785
MTNA	Q9BV20	Methylthioribose-1-phosphate isomerase OS=Homo sapiens OX=9606 GN=MR1 PE=1 SV=1	0.948	0.797	0.876	0.736
CISY	Q75390	Citrate synthase, mitochondrial OS=Homo sapiens OX=9606 GN=CS PE=1 SV=2	0.88	0.815	0.862	0.799
STT3A	P46977	Dolichyl-diphospholigosaccharide-protein glycosyltransferase subunit STT3A OS=Homo	0.868	0.846	0.831	0.81

UTP20	Q75691	Small subunit processome component 20 homolog OS=Homo sapiens OX=9606 GN=UTP20	0.871	0.887	0.79	0.805
NPM	P06748	Nucleophosmin OS=Homo sapiens OX=9606 GN=NPM1 PE=1 SV=2	0.83	0.814	0.862	0.846
STRN	O43815	Striatin OS=Homo sapiens OX=9606 GN=STRN PE=1 SV=4	0.814	0.85	0.824	0.861
HCF1C1	P51610	Host cell factor 1 OS=Homo sapiens OX=9606 GN=HCF1C1 PE=1 SV=2	0.823	0.825	0.849	0.851
SAFB1	Q15424	Scaffold attachment factor B1 OS=Homo sapiens OX=9606 GN=SAFB PE=1 SV=4	0.854	0.836	0.836	0.818
DHE3	P00367	Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens OX=9606 GN=GLUD1 PE=1	0.824	0.859	0.812	0.847
FUMH	P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens OX=9606 GN=FHE PE=1 SV=3	0.806	0.82	0.849	0.863
P5CR2	Q96C36	Pyroline-5-carboxylate reductase 2 OS=Homo sapiens OX=9606 GN=PYCR2 PE=1 SV=1	0.834	0.809	0.86	0.834
EIF3C	Q99613	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens OX=9606 GN=EIF3C	0.842	0.834	0.834	0.826
DDX18	Q9NVP1	ATP-dependent RNA helicase DDX18 OS=Homo sapiens OX=9606 GN=DDX18 PE=1 SV=2	0.841	0.852	0.815	0.825
ILF2	P12905	Interleukin enhancer-binding factor 2 OS=Homo sapiens OX=9606 GN=ILF2 PE=1 SV=2	0.76	0.875	0.788	0.908
TNP01	Q92973	Transportin-1 OS=Homo sapiens OX=9606 GN=TNP01 PE=1 SV=2	0.846	0.796	0.87	0.818
SCAF4	P95104	SR-related and CTD-associated factor 4 OS=Homo sapiens OX=9606 GN=SCAF4 PE=1	0.832	0.822	0.841	0.832
PGAM5	Q96HS1	Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens OX=9606	0.875	0.811	0.85	0.787
EFTU	P49411	Elongation factor Tu, mitochondrial OS=Homo sapiens OX=9606 GN=TUFM PE=1 SV=2	0.851	0.82	0.841	0.811
SUMO4	Q6EEV6	Small ubiquitin-related modifier 4 OS=Homo sapiens OX=9606 GN=SUMO4 PE=1 SV=2	0.884	0.816	0.843	0.778
PUR2	P22102	Trifunctional purine biosynthetic protein adenosine-3'-OS=Homo sapiens OX=9606	0.824	0.836	0.825	0.836
EIF3E	P60228	Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens OX=9606 GN=EIF3E	0.887	0.839	0.819	0.775
NSF	P46459	Vesicle-fusing ATPase OS=Homo sapiens OX=9606 GN=NSF PE=1 SV=3	0.845	0.824	0.836	0.815
ACLY	P53396	ATP-citrate lyase OS=Homo sapiens OX=9606 GN=ACLY PE=1 SV=3	0.841	0.819	0.841	0.818
QSER1	Q2KHR3	Glutamine and serine-rich protein 1 OS=Homo sapiens OX=9606 GN=QSER1 PE=1 SV=3	0.863	0.853	0.806	0.796
FKBP4	P02790	Peptidyl-prolyl cis-trans isomerase FKB4 OS=Homo sapiens OX=9606 GN=FKBP4 PE=1	0.85	0.811	0.846	0.808
NT5D2	Q9H857	5'-nucleotidase domain-containing protein 2 OS=Homo sapiens OX=9606 GN=NT5D2C PE=1	0.826	0.831	0.826	0.831
PSA1	P25786	Proteasome subunit alpha-1 OS=Homo sapiens OX=9606 GN=PSMA1 PE=1 SV=1	0.79	0.842	0.813	0.867
XP01200	P55060	Exportin-2 OS=Homo sapiens OX=9606 GN=CE1L PE=1 SV=3	0.849	0.808	0.845	0.805
PSMD2	Q13200	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PSMD2	0.838	0.819	0.833	0.814
RENT1	Q92900	Regulator of nonsense transcripts 1 OS=Homo sapiens OX=9606 GN=UPF1 PE=1 SV=2	0.843	0.791	0.861	0.808
EHD1	Q9H4M9	EH domain-containing protein 1 OS=Homo sapiens OX=9606 GN=EHD1 PE=1 SV=2	0.83	0.772	0.88	0.819
ABCFL1	Q8NE71	ATP-binding cassette sub-family 1 OS=Homo sapiens OX=9606 GN=ABCFL1 PE=1	0.849	0.838	0.808	0.797
TFR1	P02786	Transferin receptor protein 1 OS=Homo sapiens OX=9606 GN=TFR1 PE=1 SV=2	0.816	0.83	0.816	0.83
PCCA	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens OX=9606	0.742	0.867	0.774	0.906
PP2AB	P62714	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens	0.731	0.849	0.789	0.917
FACE1	Q75844	CAAX prenyl protein 1 OS=Homo sapiens OX=9606 GN=ZMPSTE24 PE=1 SV=2	0.773	0.844	0.798	0.871
KPRB	O60256	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Homo sapiens OX=9606	0.883	0.792	0.847	0.76
CNOT1	Q5YK6	CCR4-NOT transcription complex subunit 1 OS=Homo sapiens OX=9606 GN=CNOT1 PE=1	0.826	0.817	0.823	0.812
SYFB	Q9NSD9	Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens OX=9606 GN=FARSB PE=1	0.844	0.82	0.816	0.793
DCTN1	Q14203	Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 PE=1 SV=3	0.909	0.787	0.844	0.73
HARS1	P12081	Histidine-tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=HARS PE=1 SV=2	0.861	0.847	0.787	0.767
KDM2A	Q9Y2K7	Lysine-specific demethylase 2A OS=Homo sapiens OX=96				

DFFA	O00273	DNA fragmentation factor subunit alpha OS=Homo sapiens OX=9606 GN=DFFA PE=1 SV=1	0.771	0.806	0.802	0.838
HUWE1	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens OX=9606 GN=HUWE1 PE=1 SV=3	0.82	0.797	0.811	0.788
RL4	P36578	60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=5	0.843	0.764	0.842	0.764
LBR	Q14739	Delta(14)-sterol reductase LBR OS=Homo sapiens OX=9606 GN=LBR PE=1 SV=2	0.792	0.839	0.768	0.813
HNRPH1	P31943	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens OX=9606 GN=HNRNPH1	0.81	0.788	0.818	0.796
DD19B	Q9UMR2	ATP-dependent RNA helicase DDX19B OS=Homo sapiens OX=9606 GN=DDX19B PE=1	0.809	0.815	0.788	0.794
LPPRC	P42704	Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens OX=9606	0.787	0.802	0.8	0.816
PP6K3	Q5I9H7	Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606	0.782	0.785	0.817	0.82
IPO8	Q15397	Importin-8 OS=Homo sapiens OX=9606 GN=IPO8 PE=1 SV=2	0.783	0.744	0.859	0.817
DDX47	Q9HOS4	Probable ATP-dependent RNA helicase DDX47 OS=Homo sapiens OX=9606 GN=DDX47	0.811	0.818	0.784	0.79
TCPQ	P50990	T-complex protein 1 subunit theta OS=Homo sapiens OX=9606 GN=CCT8 PE=1 SV=4	0.778	0.798	0.802	0.823
SF3B3	Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens OX=9606 GN=SF3B3 PE=1 SV=4	0.84	0.772	0.827	0.761
MTA2	Q04776	Metastasis-associated protein MTA2 OS=Homo sapiens OX=9606 GN=MTA2 PE=1 SV=1	0.815	0.793	0.806	0.784
AP2A1	O95782	AP-2 complex subunit alpha 1 OS=Homo sapiens OX=9606 GN=AP2A1 PE=1 SV=3	0.844	0.784	0.812	0.754
HEM6	P36551	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens	0.699	0.807	0.783	0.904
MCM6	Q14566	DNA replication licensing factor MCM6 OS=Homo sapiens OX=9606 GN=MCM6 PE=1	0.815	0.764	0.832	0.781
OST48	P39656	Dolichyl-diphospholigosaccharide-protein glycosyltransferase 48 kDa subunit OS=Homo	0.809	0.783	0.813	0.787
RCC1	P18754	Regulator of chromosome condensation OS=Homo sapiens OX=9606 GN=RCC1 PE=1 SV=1	0.808	0.794	0.802	0.788
HNRPM	P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM	0.819	0.784	0.811	0.777
DAAF5	Q86Y56	Dynein assembly factor 5, axonemal OS=Homo sapiens OX=9606 GN=DAAF5 PE=1 SV=4	0.893	0.747	0.844	0.706
SYRC	P54136	Arginine- <i>t</i> RNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=RARS PE=1 SV=2	0.824	0.793	0.798	0.768
PLRG1	Q43660	Pleiotropic regulator 1 OS=Homo sapiens OX=9606 GN=PLRG1 PE=1 SV=1	0.779	0.795	0.795	0.811
SERPH	P05454	Serpin H1 OS=Homo sapiens OX=9606 GN=SERP1H1 PE=1 SV=2	0.842	0.813	0.775	0.748
NONO	Q15233	Non-POU domain-containing octamer-binding protein OS=Homo sapiens OX=9606	0.81	0.773	0.815	0.778
SYVC	P26640	Valine- <i>t</i> RNA ligase OS=Homo sapiens OX=9606 GN=VARS PE=1 SV=4	0.829	0.796	0.791	0.76
SAC1	Q9NTJ5	Phosphatidylinositol phosphatase SAC1 OS=Homo sapiens OX=9606 GN=SACM1L PE=1	0.88	0.808	0.774	0.711
RER1	Q15258	Protein RER1 OS=Homo sapiens OX=9606 GN=RER1 PE=1 SV=1	0.85	0.748	0.837	0.737
IF4G2	P78344	Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens OX=9606 GN=EIF4G2	0.76	0.826	0.758	0.823
GPI8	Q92643	GPI-anchor transamidase OS=Homo sapiens OX=9606 GN=PIKG PE=1 SV=2	0.805	0.772	0.811	0.779
PDC6I	Q8WUM4	Programmed cell death 6-interacting protein OS=Homo sapiens OX=9606 GN=PDCD6IP	0.803	0.801	0.782	0.78
VDAC1	P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens OX=9606	0.683	0.843	0.733	0.905
ASSY	P00966	Argininosuccinate synthase OS=Homo sapiens OX=9606 GN=ASS1 PE=1 SV=2	0.83	0.796	0.784	0.752
RUVB2	Q9Y230	RubB-like 2 OS=Homo sapiens OX=9606 GN=RUVBL2 PE=1 SV=3	0.822	0.792	0.788	0.759
SYYC	P54577	Tyrosine- <i>t</i> RNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=YARS PE=1 SV=4	0.808	0.771	0.809	0.772
TCPG	P49368	T-complex protein 1 subunit gamma OS=Homo sapiens OX=9606 GN=CCT3 PE=1 SV=4	0.802	0.776	0.804	0.777
XPO6	Q96QUB	Exportin-6 OS=Homo sapiens OX=9606 GN=XPO6 PE=1 SV=1	0.904	0.741	0.832	0.682
COPB2	P35060	Coatomer subunit beta' OS=Homo sapiens OX=9606 GN=COPB2 PE=1 SV=2	0.78	0.785	0.794	0.799
EIF3L	Q9Y262	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens OX=9606 GN=EIF3L	0.776	0.798	0.778	0.8
RL10	P27635	60S ribosomal protein L10 OS=Homo sapiens OX=9606 GN=RPL10 PE=1 SV=4	0.811	0.751	0.824	0.764
METK2	P31153	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens OX=9606 GN=MAT2A	0.761	0.801	0.774	0.814
ROA1	P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens OX=9606 GN=HNRNPA1	0.575	0.973	0.594	1.007
SAHH	P32526	Adenosylhomocysteinase OS=Homo sapiens OX=9606 GN=AHCY PE=1 SV=4	0.798	0.788	0.786	0.776
FHL1	Q13642	Four and a half LIM domains protein 1 OS=Homo sapiens OX=9606 GN=FHL1 PE=1 SV=4	0.678	0.782	0.784	0.904
PYGB	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens OX=9606 GN=PYGB PE=1 SV=5	0.749	0.772	0.799	0.823
CHER8	Q8IWX8	Calretinin homeostasis endoplasmic reticulum protein OS=Homo sapiens OX=9606	0.799	0.766	0.804	0.77
GTPB3	Q969Y2	tRNA modification GTPase GTPBP3, mitochondrial OS=Homo sapiens OX=9606	0.741	0.873	0.7	0.824
UBA6	A0AVT1	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens OX=9606 GN=UBA6 PE=1	0.86	0.758	0.807	0.712
HLTF	Q14527	Helicase-like transcription factor OS=Homo sapiens OX=9606 GN=HLTF PE=1 SV=2	0.781	0.734	0.836	0.785
GT251	Q8BNB5	Procollagen I proline/lysine/proline 4 OS=Homo sapiens OX=9606 GN=COLGALT1 PE=1	0.8	0.761	0.807	0.768
DHC24	Q15392	Delta(24)-sterol reductase OS=Homo sapiens OX=9606 GN=DHCR24 PE=1 SV=2	0.817	0.753	0.815	0.75
TCPB	P78371	T-complex protein 1 subunit beta OS=Homo sapiens OX=9606 GN=CCT2 PE=1 SV=4	0.804	0.761	0.806	0.763
HS90B	P08238	Heat shock protein HSP 90-beta OS=Homo sapiens OX=9606 GN=HSP90AB1 PE=1 SV=4	0.718	0.803	0.761	0.851
PDSSA	Q29RF7	Sister chromatid cohesion protein PDSS homolog 1 OS=Homo sapiens OX=9606 GN=PDSS5A	0.825	0.751	0.815	0.742
ZW10	Q43264	Centromere/kinetochore protein zw10 homolog OS=Homo sapiens OX=9606 GN=ZW10	0.829	0.777	0.787	0.738
DMAP1	Q9NPFS	DNA methyltransferase 1-associated protein 1 OS=Homo sapiens OX=9606 GN=DMAP1	0.81	0.799	0.764	0.755
KHDR1	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo	0.736	0.775	0.788	0.829
PRP6	P094906	Pre-mRNA-processing factor 6 OS=Homo sapiens OX=9606 GN=PRPF6 PE=1 SV=1	0.796	0.78	0.784	0.768
SUCB1	Q9P2R7	Succinate-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens	0.746	0.777	0.786	0.818
NU133	Q8WUM0	Nuclear pore complex protein Nup133 OS=Homo sapiens OX=9606 GN=NUP133 PE=1 SV=2	0.839	0.727	0.835	0.724
ABCE1	P61221	ATP-binding cassette sub-family E member 1 OS=Homo sapiens OX=9606 GN=ABCE1 PE=1	0.821	0.778	0.783	0.742
PSD13	Q9UNM6	26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens OX=9606	0.741	0.807	0.754	0.821
THOC3	Q96J01	THO complex subunit 3 OS=Homo sapiens OX=9606 GN=THOC3 PE=1 SV=1	0.779	0.736	0.826	0.781
ANXA5	P08758	Annexin A5 OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=2	0.758	0.771	0.789	0.803
SMC1A	Q14683	Structural maintenance of chromosomes protein 1A OS=Homo sapiens OX=9606 GN=SMC1A	0.795	0.789	0.771	0.766
ZFR	Q96KR1	Zinc finger RNA-binding protein OS=Homo sapiens OX=9606 GN=ZFR PE=1 SV=2	0.779	0.79	0.767	0.779
CND1	Q15021	Condensin complex subunit 1 OS=Homo sapiens OX=9606 GN=NCAPD2 PE=1 SV=3	0.831	0.712	0.845	0.724
SRSF5	Q13243	Serine/arginine-rich splicing factor 5 OS=Homo sapiens OX=9606 GN=SRSF5 PE=1 SV=1	0.808	0.791	0.764	0.748
TTL12	Q14166	Tubulin-tyrosine ligase-like protein 12 OS=Homo sapiens OX=9606 GN=TTLL12 PE=1	0.834	0.809	0.744	0.722
RL6	Q02878	60S ribosomal protein L6 OS=Homo sapiens OX=9606 GN=RPL6 PE=1 SV=3	0.795	0.781	0.772	0.759
CLU	Q75153	Clustered mitochondria protein homolog OS=Homo sapiens OX=9606 GN=CLUH PE=1	0.791	0.755	0.798	0.761

HNRL2	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens OX=9606	0.754	0.744	0.807	0.797
EGLN1	Q9GZT9	Egl nine homolog 1 OS=Homo sapiens OX=9606 GN=EGLN1 PE=1 SV=1	0.778	0.797	0.753	0.772
RM37	Q9BZE1	39S ribosomal protein L37, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL37 PE=1	0.779	0.761	0.788	0.771
HDHD5	Q9BXW7	Halocid acid dehalogenase-like hydrolase domain-containing 5 OS=Homo sapiens OX=9606	0.818	0.765	0.782	0.732
ANXA2	P07355	Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=2	0.743	0.799	0.749	0.806
HD	P42858	Huntingtin OS=Homo sapiens OX=9606 GN=HTT PE=1 SV=2	0.799	0.721	0.829	0.749
NOL10	Q9BSC4	Nuclear protein 10 OS=Homo sapiens OX=9606 GN=NOL10 PE=1 SV=1	0.817	0.726	0.819	0.728
CLH1	Q00610	Clathrin heavy chain 1 OS=Homo sapiens OX=9606 GN=CLTC PE=1 SV=5	0.754	0.782	0.761	0.79
AATC	P17174	Aspartate aminotransferase, cytoplasmic OS=Homo sapiens OX=9606 GN=GOT1 PE=1 SV=3	0.837	0.862	0.684	0.704
LMA2L	Q9H0V9	VIP36-like protein OS=Homo sapiens OX=9606 GN=LMAN2L PE=1 SV=1	0.631	0.731	0.798	0.925
TF3C5	Q9Y5Q8	General transcription factor 3C polypeptide 5 OS=Homo sapiens OX=9606 GN=GTF3C5	0.766	0.828	0.716	0.775
PTBP1	P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=1	0.755	0.763	0.778	0.786
CAF1A	Q13111	Chromatin assembly factor 1 subunit A OS=Homo sapiens OX=9606 GN=CHAF1A PE=1	0.817	0.732	0.808	0.724
MOT1	P53985	Monocarboxylate transporter 1 OS=Homo sapiens OX=9606 GN=SLC16A1 PE=1 SV=3	0.727	0.808	0.732	0.814
RFC5	P40937	Replication factor C subunit 5 OS=Homo sapiens OX=9606 GN=RFC5 PE=1 SV=1	0.841	0.737	0.801	0.702
PRAF3	O75915	PRA1 family protein 3 OS=Homo sapiens OX=9606 GN=ARL6IP5 PE=1 SV=1	0.747	0.776	0.763	0.793
S61A1	P61619	Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens OX=9606	0.708	0.785	0.752	0.834
ZCCHV	Q7Z2W4	Zinc finger CCHC-type antiviral protein 1 OS=Homo sapiens OX=9606 GN=ZC3HAV1 PE=1	0.757	0.769	0.769	0.782
SFPQ	P23246	Splicing factor, pre-mRNA, proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1	0.751	0.761	0.776	0.786
BZW2	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens OX=9606	0.79	0.759	0.777	0.747
FACD2	Q9BXW9	Fanconi anemia group D2 protein OS=Homo sapiens OX=9606 GN=FANCD2 PE=1 SV=2	0.876	0.654	0.882	0.658
RBMX	P38159	RNA-binding motif protein, X chromosome OS=Homo sapiens OX=9606 GN=RBMX PE=1	0.75	0.792	0.742	0.785
PARP1	P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens OX=9606 GN=PARP1 PE=1 SV=4	0.755	0.751	0.783	0.778
SPTB2	P01082	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTB1 PE=1	0.782	0.76	0.773	0.752
MYO6	Q9UM54	Unconventional myosin-VI OS=Homo sapiens OX=9606 GN=MYO6 PE=1 SV=4	0.753	0.788	0.744	0.779
MTCH2	Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens OX=9606 GN=MTCH2 PE=1 SV=1	0.728	0.901	0.64	0.792
SRPRA	P08240	Signal recognition particle receptor subunit alpha OS=Homo sapiens OX=9606 GN=SRPRA	0.738	0.726	0.804	0.791
TCPE	P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens OX=9606 GN=CTC5 PE=1 SV=1	0.761	0.771	0.758	0.768
PCKGM	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens OX=9606	0.817	0.805	0.723	0.712
OAT	P04181	Ornithine aminotransferase, mitochondrial OS=Homo sapiens OX=9606 GN=OAT PE=1	0.767	0.777	0.75	0.76
VDAC2	P45880	Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens OX=9606	0.683	0.747	0.776	0.848
HNRL1	Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens OX=9606	0.886	0.753	0.764	0.65
PSMD6	P50108	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens OX=9606 GN=PSMD6	0.788	0.743	0.783	0.738
AL7A1	P49419	Alpha-aminoacidic semialdehyde dehydrogenase OS=Homo sapiens OX=9606	0.773	0.789	0.737	0.753
NBSR1	Q9UH09	NADH-cytochrome b5 reductase 1 OS=Homo sapiens OX=9606 GN=CYB5R1 PE=1 SV=1	0.79	0.737	0.788	0.735
PSA	P55786	Putumycin-sensitive aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=2	0.755	0.768	0.756	0.77
QCR1	P31930	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens OX=9606	0.735	0.733	0.791	0.789
HKX1	P19367	Hexokinase-1 OS=Homo sapiens OX=9606 GN=HK1 PE=1 SV=3	0.762	0.758	0.765	0.76
ACSL3	Q95573	Long-chain-fatty-acid-CoA ligase 3 OS=Homo sapiens OX=9606 GN=ACSL3 PE=1 SV=3	0.84</			

UTP15	Q8TED0	U3 small nucleolar RNA-associated protein 15 homolog OS=Homo sapiens OX=9606	0.774	0.719	0.779	0.723
SYDC	P14868	Aspartate-tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=DARS PE=1 SV=2	0.776	0.743	0.754	0.721
SR140	O15042	U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens OX=9606	0.761	0.728	0.769	0.735
ACON	Q99798	Aconitase hydratase, mitochondrial OS=Homo sapiens OX=9606 GN=ACO2 PE=1 SV=2	0.787	0.742	0.753	0.71
OSBL9	Q96SU4	Oxysterol-binding protein-related protein 9 OS=Homo sapiens OX=9606 GN=OSBPL9 PE=1	0.754	0.764	0.732	0.741
GLPK3	Q14409	Glycerol kinase 3 OS=Homo sapiens OX=9606 GN=GK3P PE=2 SV=2	0.764	0.712	0.782	0.729
KCTD8	Q62WB6	BTB/POZ domain-containing protein KCTD8 OS=Homo sapiens OX=9606 GN=KCTD8	0.793	0.758	0.733	0.7
CLPT1	O96005	Cleft lip and palate transmembrane protein 1 OS=Homo sapiens OX=9606 GN=CLPTM1	0.764	0.704	0.789	0.727
PRS4	P62191	26S proteasome regulatory subunit 4 OS=Homo sapiens OX=9606 GN=PSMC1 PE=1 SV=1	0.741	0.739	0.753	0.75
ARP2	P61160	Actin-related protein 2 OS=Homo sapiens OX=9606 GN=ACTR2 PE=1 SV=1	0.76	0.691	0.798	0.725
RDH11	Q8TC12	Retinol dehydrogenase 11 OS=Homo sapiens OX=9606 GN=RDH11 PE=1 SV=2	0.695	0.714	0.771	0.791
EIF3B	P55884	Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens OX=9606 GN=EIF3B	0.819	0.691	0.79	0.667
H2AW	Q90PM6	Core histone macro-H2A.2 OS=Homo sapiens OX=9606 GN=H2AFY2 PE=1 SV=3	0.737	0.737	0.745	0.745
YTDC2	Q9HGS0	3'-5' RNA helicase YTHDC2 OS=Homo sapiens OX=9606 GN=YTHDC2 PE=1 SV=2	0.76	0.72	0.761	0.722
RS11	P62280	40S ribosomal protein S11 OS=Homo sapiens OX=9606 GN=RPSS11 PE=1 SV=3	0.717	0.676	0.807	0.76
DHX15	O43143	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens	0.748	0.705	0.775	0.731
MK01	P23482	Mitogen-activated protein kinase 1 OS=Homo sapiens OX=9606 GN=MAPK1 PE=1 SV=3	0.751	0.742	0.737	0.728
HNRPL	P14866	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens OX=9606 GN=HNRNPL PE=1	0.703	0.739	0.738	0.776
IL36B	Q9NZH7	Interleukin-1 beta OS=Homo sapiens OX=9606 GN=IL36B PE=2 SV=1	0.856	0.612	0.867	0.62
DKC1	O60832	H/ACA ribonucleoprotein complex subunit DKC1 OS=Homo sapiens OX=9606 GN=DKC1	0.743	0.691	0.788	0.732
PUM3	Q15397	Pumilio homolog 3 OS=Homo sapiens OX=9606 GN=PUM3 PE=1 SV=3	0.774	0.728	0.748	0.704
RL13	P26373	60S ribosomal protein L13 OS=Homo sapiens OX=9606 GN=RLPL13 PE=1 SV=4	0.776	0.721	0.755	0.701
ZN512	Q96ME7	Zinc finger protein 512 OS=Homo sapiens OX=9606 GN=ZNFX12 PE=1 SV=2	0.685	0.717	0.757	0.793
RBM34	P42696	RNA-binding protein 34 OS=Homo sapiens OX=9606 GN=RBMS4 PE=1 SV=2	0.761	0.701	0.774	0.712
PSB5	P28074	Proteasome subunit beta type-5 OS=Homo sapiens OX=9606 GN=PSMB5 PE=1 SV=3	0.657	0.706	0.762	0.819
PCYO9	Q9UHG3	Premylosteine oxidase 1 OS=Homo sapiens OX=9606 GN=PCYO1 PE=1 SV=3	0.76	0.692	0.779	0.709
COPB	P53618	Coatomer subunit beta OS=Homo sapiens OX=9606 GN=COPB1 PE=1 SV=3	0.73	0.742	0.726	0.739
ARC1A	Q92747	Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens OX=9606 GN=ARPC1A	0.734	0.727	0.741	0.734
EIF3A	Q14152	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens OX=9606 GN=EIF3A	0.722	0.744	0.724	0.746
HNRH3	P31942	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNPH3	0.713	0.71	0.758	0.755
DC1L1	Q9Y6G9	Cyttoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens OX=9606	0.772	0.755	0.709	0.693
ERMP1	Q7ZK26	Endoplasmic reticulum metallopeptidase 1 OS=Homo sapiens OX=9606 GN=ERMP1 PE=1	0.765	0.708	0.755	0.699
NPL4	Q8TAT6	Nuclear protein localization protein 4 homolog OS=Homo sapiens OX=9606 GN=NPLQC4	0.698	0.681	0.782	0.762
MCM7	P33993	DNA replication licensing factor MCM7 OS=Homo sapiens OX=9606 GN=MCM7 PE=1	0.752	0.698	0.763	0.708
RRP12	Q5JTH9	RRP12-like protein OS=Homo sapiens OX=9606 GN=RRP12 PE=1 SV=2	0.732	0.696	0.764	0.728
SYMPK	Q92797	Sympkin OS=Homo sapiens OX=9606 GN=SYMPK PE=1 SV=2	0.739	0.709	0.75	0.721
XRCC6	P12956	X-ray repair cross-complementing protein 6 OS=Homo sapiens OX=9606 GN=XRCC6 PE=1	0.689	0.744	0.714	0.771
SMAP2	Q8WU79	Stromal membrane-associated protein 2 OS=Homo sapiens OX=9606 GN=SMAP2 PE=1	0.686	0.799	0.661	0.77
PRDX3	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens OX=9606	0.693	0.728	0.729	0.766
GWL	Q96GX5	Serine/threonine-protein kinase greatwall OS=Homo sapiens OX=9606 GN=MASTL PE=1	0.716	0.729	0.727	0.739
IPO7	O95373	Importin-7 OS=Homo sapiens OX=9606 GN=IPO7 PE=1 SV=1	0.734	0.731	0.724	0.721
UFL1	Q94874	E3 UFM1-protein ligase 1 OS=Homo sapiens OX=9606 GN=UFL1 PE=1 SV=2	0.734	0.722	0.732	0.72
ACACA	Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens OX=9606 GN=ACACA PE=1 SV=2	0.749	0.73	0.723	0.705
BAZ1B	Q9UIG0	Tyrosine-protein kinase BAZ1B OS=Homo sapiens OX=9606 GN=BAZ1B PE=1 SV=2	0.744	0.743	0.71	0.71
TCRG1	O14776	Transcription elongation regulator 1 OS=Homo sapiens OX=9606 GN=TCERG1 PE=1 SV=2	0.789	0.682	0.769	0.664
MK671	Q9BYG3	MKH7 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens OX=9606	0.73	0.735	0.716	0.721
SYEP	P07814	Bifunctional glutamate/proline-tRNA ligase OS=Homo sapiens OX=9606 GN=EPRS PE=1	0.761	0.714	0.736	0.689
DHX9	Q98211	ATP-dependent RNA helicase A OS=Homo sapiens OX=9606 GN=DHX9 PE=1 SV=4	0.692	0.728	0.721	0.759
CSK	P41240	Tyrosine-protein kinase CSK OS=Homo sapiens OX=9606 GN=CSK PE=1 SV=1	0.722	0.714	0.736	0.727
RBMI4	Q96PK6	RNA-binding protein 14 OS=Homo sapiens OX=9606 GN=RBMI4 PE=1 SV=2	0.719	0.718	0.73	0.73
PPM1F	P49593	Protein phosphatase 1F OS=Homo sapiens OX=9606 GN=PPM1F PE=1 SV=3	0.804	0.701	0.743	0.648
DHCR7	Q9UBM7	7-dehydrocholesterol reductase OS=Homo sapiens OX=9606 GN=DHCR7 PE=1 SV=1	0.84	0.711	0.728	0.616
AL3A2	P51648	Aldehyde dehydrogenase family 3 member A2 OS=Homo sapiens OX=9606 GN=ALDH3A2	0.716	0.762	0.686	0.731
SERA	Q43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=4	0.729	0.727	0.721	0.718
KS6A3	P51812	Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens OX=9606 GN=RPS6KA3 PE=1	0.72	0.68	0.768	0.726
TRAK2	O60296	Trafficking kinesin-binding protein 2 OS=Homo sapiens OX=9606 GN=TRAK2 PE=1 SV=2	0.733	0.726	0.72	0.713
CHD4	Q14839	Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens OX=9606 GN=CHD4	0.73	0.718	0.727	0.716
NUMA1	Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUMA1 PE=1 SV=2	0.726	0.72	0.725	0.719
PESC	O00541	Pescadillo homolog OS=Homo sapiens OX=9606 GN=PES1 PE=1 SV=1	0.726	0.707	0.737	0.719
RL15	P61313	60S ribosomal protein L15 OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=2	0.731	0.668	0.778	0.71
IPYR	Q15181	Inorganic pyrophosphatase OS=Homo sapiens OX=9606 GN=PPA1 PE=1 SV=2	0.727	0.69	0.754	0.715
LIS1	P43034	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens OX=9606	0.691	0.743	0.699	0.751
NEUA	Q8NF8W	N-acetylneuraminate cytidylyltransferase OS=Homo sapiens OX=9606 GN=CMAS PE=1 SV=2	0.85	0.644	0.79	0.598
MARE3	Q9UPY8	Microtubule-associated protein RP/EB family member 3 OS=Homo sapiens OX=9606	0.732	0.734	0.704	0.706
TF3C1	Q12789	General transcription factor 3C polypeptide 1 OS=Homo sapiens OX=9606 GN=GTF3C1	0.786	0.681	0.754	0.653
RPB3	P19387	DNA-directed RNA polymerase II subunit RPB3 OS=Homo sapiens OX=9606 GN=POLR2C	0.687	0.749	0.688	0.75
U520	Q75643	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens OX=9606	0.725	0.709	0.728	0.712
FACR1	Q8WWV9	Fatty acyl-CoA reductase 1 OS=Homo sapiens OX=9606 GN=FAR1 PE=1 SV=1	0.678	0.715	0.72	0.758
RL17	P18621	60S ribosomal protein L17 OS=Homo sapiens OX=9606 GN=RPL17 PE=1 SV=3	0.725	0.701	0.734	0.71
PREB	Q9HCU5	Prolactin regulatory element-binding protein OS=Homo sapiens OX=9606 GN=PREB PE=1	0.7	0.769	0.666	0.731

G6PI	P06744	Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=4	0.728	0.703	0.729	0.704
RBBP5	Q15291	Retinoblastoma-binding protein 5 OS=Homo sapiens OX=9606 GN=RBBP5 PE=1 SV=2	0.674	0.675	0.756	0.758
STRN3	Q10330	Striatin-3 OS=Homo sapiens OX=9606 GN=STRN3 PE=1 SV=3	0.75	0.712	0.718	0.677
UTP18	Q9Y511	U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens OX=9606	0.726	0.715	0.716	0.705
H2B3B	Q8N257	Histone H2B type 3-B OS=Homo sapiens OX=9606 GN=HIST3H2B PE=1 SV=3	0.575	0.791	0.628	0.864
LKHA4	P09960	Leukotriene A 4 hydrolase OS=Homo sapiens OX=9606 GN=LTA4H PE=1 SV=2	0.766	0.672	0.755	0.663
CEBPZ	Q03701	CCAAT/enhancer-binding protein zeta OS=Homo sapiens OX=9606 GN=CEBPZ PE=1 SV=3	0.73	0.702	0.724	0.696
TBA1A	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens OX=9606 GN=TUBA1A PE=1 SV=1	0.64	0.723	0.698	0.789
MBB1A	Q9BQGO	Myb-binding protein 1A OS=Homo sapiens OX=9606 GN=MYBPIA PE=1 SV=2	0.723	0.699	0.726	0.702
CAPI	Q01518	Adenyl cyclase-associated protein 1 OS=Homo sapiens OX=9606 GN=CAPI PE=1 SV=5	0.742	0.698	0.726	0.683
HNRPU	P00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU	0.693	0.713	0.709	0.73
HYEP	P07099	Epoxide hydrolase 1 OS=Homo sapiens OX=9606 GN=EPHX1 PE=1 SV=1	0.703	0.711	0.711	0.719
TBB2A	Q13885	Tubulin beta-2 chain OS=Homo sapiens OX=9606 GN=TUBB2A PE=1 SV=1	0.702	0.619	0.807	0.711
ALDH2	P05091	Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH2 PE=1	0.76	0.697	0.72	0.661
DIDO1	Q9BT0C0	Death-inducer obliterator 1 OS=Homo sapiens OX=9606 GN=DIDO1 PE=1 SV=5	0.672	0.71	0.704	0.743
BIEA	P53004	Biliverdin reductase A OS=Homo sapiens OX=9606 GN=BLVRA PE=1 SV=2	0.684	0.716	0.697	0.729
DDX21	Q9NR30	Nucleolar RNA helicase 2 OS=Homo sapiens OX=9606 GN=DDX21 PE=1 SV=5	0.684	0.704	0.708	0.73
CMS1	Q9BQ75	Protein CMS1 OS=Homo sapiens OX=9606 GN=CMSS1 PE=1 SV=2	0.709	0.693	0.72	0.704
PYGL	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens OX=9606 GN=PYGL PE=1 SV=4	0.701	0.713	0.7	0.711
MATR3	P43243	Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=2	0.707	0.711	0.701	0.705
SMC4	Q9NTJ3	Structural maintenance of chromosomes protein 4 OS=Homo sapiens OX=9606 GN=SMC4	0.705	0.705	0.707	0.707
RLA0	P05388	60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1	0.709	0.701	0.711	0.702
FLNB	Q75369	Filamin-B OS=Homo sapiens OX=9606 GN=FLNB PE=1 SV=2	0.76	0.705	0.701	0.651
ARI1B	Q8NFD5	AT-rich interactive domain-containing protein 1B OS=Homo sapiens OX=9606 GN=ARID1B	0.73	0.728	0.68	0.678
DPOD1	P28340	DNA polymerase delta catalytic subunit OS=Homo sapiens OX=9606 GN=POLD1 PE=1	0.684	0.716	0.692	0.724
SC31A	P04979	Protein transport protein Sec31A OS=Homo sapiens OX=9606 GN=SEC31A PE=1 SV=3	0.715	0.698	0.71	0.693
PLAK	P14923	Junction plakophilin OS=Homo sapiens OX=9606 GN=JUP PE=1 SV=3	0.678	0.702	0.704	0.729
SMRC1	Q92922	SWI/SNF complex subunit SMARCC1 OS=Homo sapiens OX=9606 GN=SMARCC1 PE=1	0.665	0.709	0.696	0.742
DDX51	Q8N8A6	ATP-dependent RNA helicase DDX51 OS=Homo sapiens OX=9606 GN=DDX51 PE=1 SV=3	0.737	0.712	0.691	0.668
MOV10	Q9HCE1	Helicase MOV10 OS=Homo sapiens OX=9606 GN=MOV10 PE=1 SV=2	0.712	0.693	0.711	0.692
EIF2A	Q9BY44	Eukaryotic translation initiation factor 2A OS=Homo sapiens OX=9606 GN=EIF2A PE=1	0.708	0.698	0.705	0.695
NOC2L	Q9YT39	Nucleolar complex protein 2 homolog OS=Homo sapiens OX=9606 GN=NOC2L PE=1 SV=4	0.691	0.698	0.704	0.71
DYHC1	Q14204	Cyttoplasmic dynein 1 heavy chain 1 OS=Homo sapiens OX=9606 GN=DYNCH1 PE=1	0.719	0.689	0.71	0.68
FHOD1	Q9Y613	FH1/FH2 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=FHOD1 PE=1 SV=3	0.73	0.67	0.728	0.669
TMIM33	P57088	Transmembrane protein 33 OS=Homo sapiens OX=9606 GN=TMEM33 PE=1 SV=2	0.663	0.692	0.706	0.736
FTO	Q9CB01	Alpha-ketoglutarate-dependent dioxygenase FTO OS=Homo sapiens OX=9606 GN=FTO	0.76	0.623	0.773	0.633
GDI8	P50395	Rab GDP dissociation inhibitor beta OS=Homo sapiens OX=9606 GN=GDI2 PE=1 SV=2	0.62	0.746	0.646	0.777
WDR36	Q8N136	WD repeat-containing protein 36 OS=Homo sapiens OX=9606 GN=WDR36 PE=1 SV=1	0.683	0.685	0.709	0.711
MCM3	P25205	DNA replication licensing factor MCM3 OS=Homo sapiens OX=				

TCPZ	P40227	T-complex protein 1 subunit zeta OS=Homo sapiens OX=9606 GN=CCT6A PE=1 SV=3	0.692	0.677	0.691	0.676
TOP2B	Q02880	DNA topoisomerase 2-beta OS=Homo sapiens OX=9606 GN=TOP2B PE=1 SV=3	0.692	0.684	0.682	0.674
ABCF2	Q9UG63	ATP-binding cassette subfamily F member 2 OS=Homo sapiens OX=9606 GN=ABCF2 PE=1	0.684	0.675	0.69	0.681
MP2K1	Q02750	Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens OX=9606	0.714	0.665	0.699	0.651
ACTH	P63267	Actin, gamma-enteric smooth muscle OS=Homo sapiens OX=9606 GN=ACTG2 PE=1 SV=1	0.419	0.665	0.635	1.008
NOG2	Q13823	Nucleolar GTP-binding protein 2 OS=Homo sapiens OX=9606 GN=GNL2 PE=1 SV=1	0.712	0.69	0.672	0.651
CTR9	Q6PD62	RNA polymerase-associated protein CTR9 homolog OS=Homo sapiens OX=9606 GN=CTR9	0.68	0.691	0.67	0.681
CA167	Q55NV9	Uncharacterized protein C1orf167 OS=Homo sapiens OX=9606 GN=C1orf167 PE=2 SV=2	0.676	0.669	0.691	0.683
GLRX3	Q76003	Glutaredoxin-3 OS=Homo sapiens OX=9606 GN=GLRX3 PE=1 SV=2	0.667	0.698	0.661	0.692
NU205	Q92621	Nuclear pore complex protein Nup205 OS=Homo sapiens OX=9606 GN=NUP205 PE=1 SV=3	0.661	0.689	0.67	0.698
RL7A	F62424	60S ribosomal protein L7a OS=Homo sapiens OX=9606 GN=RPL7A PE=1 SV=2	0.713	0.688	0.669	0.645
RBBP7	Q16576	Histone-binding protein RBBP7 OS=Homo sapiens OX=9606 GN=RBBP7 PE=1 SV=1	0.628	0.703	0.653	0.731
SLTM	Q9NH19	SAPF-like transcription modulator OS=Homo sapiens OX=9606 GN=SLTM PE=1 SV=2	0.736	0.636	0.72	0.623
CDC5L	Q99459	Cell division cycle 5-like protein OS=Homo sapiens OX=9606 GN=CDCL5 PE=1 SV=2	0.663	0.68	0.675	0.693
NAA15	Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens OX=9606	0.645	0.689	0.665	0.711
NMT1	P30419	Glycopeptidyl N-tetradecanoxytransferase 1 OS=Homo sapiens OX=9606 GN=NMT1 PE=1	0.691	0.704	0.651	0.663
CDC27	P30260	Cell division cycle protein 27 homolog OS=Homo sapiens OX=9606 GN=CDC27 PE=1 SV=2	0.667	0.684	0.669	0.687
RL34	P49207	60S ribosomal protein L34 OS=Homo sapiens OX=9606 GN=RPL34 PE=1 SV=3	0.665	0.704	0.649	0.687
SRS1	Q75494	Serine/arginine-rich splicing factor 10 OS=Homo sapiens OX=9606 GN=SRSF10 PE=1 SV=1	0.762	0.639	0.709	0.595
CARM1	Q86X55	Histone-arginine methyltransferase CARM1 OS=Homo sapiens OX=9606 GN=CARM1 PE=1	0.668	0.648	0.704	0.682
IQGQA1	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens OX=9606 GN=IQGAP1 PE=1	0.705	0.647	0.704	0.646
RBM5	P52756	RNA-binding protein 5 OS=Homo sapiens OX=9606 GN=RBMS5 PE=1 SV=2	0.696	0.677	0.671	0.653
DDX56	Q9NY93	Probable ATP-dependent RNA helicase DDX56 OS=Homo sapiens OX=9606 GN=DDX56	0.672	0.664	0.683	0.675
TOR1B	O14657	Torsin-1B OS=Homo sapiens OX=9606 GN=TOR1B PE=1 SV=2	0.68	0.636	0.712	0.666
CPNE1	Q9829	Copine-1 OS=Homo sapiens OX=9606 GN=CPNE1 PE=1 SV=1	0.737	0.577	0.772	0.604
SYFA	Q9Y285	Phenylalanine-tRNA ligase alpha subunit OS=Homo sapiens OX=9606 GN=FARS1A PE=1	0.655	0.677	0.668	0.69
TBB4B	P68371	Tubulin beta-4B chain OS=Homo sapiens OX=9606 GN=TUBB4B PE=1 SV=1	0.667	0.65	0.695	0.678
H2AY	O75367	Core histone macro-H2A.1 OS=Homo sapiens OX=9606 GN=H2AFY PE=1 SV=4	0.695	0.651	0.693	0.649
EF1G	P26641	Elongation factor 1-gamma OS=Homo sapiens OX=9606 GN=EEF1G PE=1 SV=3	0.686	0.645	0.699	0.657
PB1	Q8U86	Protein polybromo-1 OS=Homo sapiens OX=9606 GN=PB1 PE=1 SV=1	0.744	0.627	0.713	0.601
RM44	Q9H9J2	39S ribosomal protein L44, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL44 PE=1	0.67	0.658	0.683	0.671
NOP56	O00567	Nucleolar protein 56 OS=Homo sapiens OX=9606 GN=NOP56 PE=1 SV=4	0.672	0.675	0.664	0.667
API1B1	Q10567	AP-1 complex subunit beta-1 OS=Homo sapiens OX=9606 GN=API1B1 PE=1 SV=2	0.683	0.677	0.659	0.653
ROA3	P51991	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens OX=9606 GN=HNRNPA3	0.668	0.654	0.682	0.668
KDM1A	O60341	Lysine-specific histone demethylase 1A OS=Homo sapiens OX=9606 GN=KDM1A PE=1	0.732	0.647	0.686	0.606
LDHB	P07195	1-lactate dehydrogenase B chain OS=Homo sapiens OX=9606 GN=LDHB PE=1 SV=2	0.623	0.677	0.655	0.711
RBBP4	Q09028	Histone-binding protein RBBP4 OS=Homo sapiens OX=9606 GN=RBBP4 PE=1 SV=3	0.627	0.645	0.687	0.706
PHF6	Q9JWS0	PHD finger protein 6 OS=Homo sapiens OX=9606 GN=PHF6 PE=1 SV=1	0.691	0.66	0.672	0.642
RBGPR	Q9H2M9	Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens OX=9606	0.648	0.657	0.675	0.684
MCMBP	Q9TB3	Mini-chromosome maintenance complex-binding protein OS=Homo sapiens OX=9606	0.69	0.669	0.661	0.642
SMAP1	Q9YIB5	Stromal membrane-associated protein 1 OS=Homo sapiens OX=9606 GN=SMAP1 PE=1	0.745	0.63	0.696	0.589
TM9S3	Q9HD45	Transmembrane 9 superfamily member 3 OS=Homo sapiens OX=9606 GN=TM9SF3 PE=1	0.603	0.726	0.604	0.727
UN45A	Q9H3U1	Protein unc-45 homolog A OS=Homo sapiens OX=9606 GN=UNC45A PE=1 SV=1	0.649	0.662	0.667	0.681
EXOSX	Q01780	Exosome component 10 OS=Homo sapiens OX=9606 GN=EXOSC10 PE=1 SV=2	0.726	0.638	0.688	0.605
EFGM	Q96R9P	Elongation factor G, mitochondrial OS=Homo sapiens OX=9606 GN=EFGM PE=1 SV=2	0.671	0.64	0.688	0.657
RPF2	Q9HTB2	Ribosome production factor 2 homolog OS=Homo sapiens OX=9606 GN=RPF2 PE=1 SV=2	0.49	0.69	0.613	0.863
EF1D	P29692	Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=5	0.677	0.704	0.623	0.648
SRSF1	Q9T7955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=2	0.647	0.678	0.648	0.679
VWDAC3	Q9Y277	Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens OX=9606	0.484	0.656	0.642	0.87
S10A8	P05109	Protein S100-A8 OS=Homo sapiens OX=9606 GN=S100A8 PE=1 SV=1	0.628	0.641	0.683	0.697
RBML9	Q9Y4C8	Probable RNA-binding protein 19 OS=Homo sapiens OX=9606 GN=RBML9 PE=1 SV=3	0.716	0.638	0.684	0.61
TRM1L	Q7ZT25	TRMT1-like protein OS=Homo sapiens OX=9606 GN=TRMT1L PE=1 SV=2	0.735	0.651	0.669	0.593
ALDR	P15121	Aldehyde reductase family 1 member B1 OS=Homo sapiens OX=9606 GN=AKR1B1 PE=1	0.686	0.618	0.706	0.636
H2B2F	Q5QNW6	Histone H2B type 2-F OS=Homo sapiens OX=9606 GN=H2B2F PE=1 SV=3	0.383	0.686	0.564	1.009
ELAV1	Q15717	ELAV-like protein 1 OS=Homo sapiens OX=9606 GN=ELAV1 PE=1 SV=2	0.643	0.648	0.671	0.677
SIN3A	Q96ST3	Paired amphipathic helix protein Sin3a OS=Homo sapiens OX=9606 GN=SIN3A PE=1 SV=2	0.632	0.649	0.67	0.687
SPT6H	Q7KZ85	Transcription elongation factor SPT6 OS=Homo sapiens OX=9606 GN=SPT6H PE=1 SV=2	0.667	0.656	0.662	0.651
SMCA5	O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A	0.674	0.646	0.671	0.644
UCHL5	Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase L5 OS=Homo sapiens OX=9606 GN=UCHL5	0.66	0.634	0.683	0.656
AT2A2	P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens OX=9606	0.674	0.628	0.687	0.64
EWS	Q01844	RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 PE=1 SV=1	0.623	0.672	0.64	0.691
RL29	P47914	60S ribosomal protein L29 OS=Homo sapiens OX=9606 GN=RPL29 PE=1 SV=2	0.684	0.601	0.713	0.626
HACD3	Q9P035	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens OX=9606	0.625	0.651	0.659	0.687
FAS	P49327	Fatty acid synthase OS=Homo sapiens OX=9606 GN=FASN PE=1 SV=3	0.662	0.655	0.655	0.648
IPO4	Q8TEX9	Importin-4 OS=Homo sapiens OX=9606 GN=IPO4 PE=1 SV=2	0.637	0.637	0.672	0.673
NDKA	P15531	Nucleoside diphosphate kinase A OS=Homo sapiens OX=9606 GN=NME1 PE=1 SV=1	0.698	0.639	0.669	0.613
KDM3B	Q7LBC6	Lysine-specific demethylase 3B OS=Homo sapiens OX=9606 GN=KDM3B PE=1 SV=2	0.654	0.655	0.654	0.655
PSMD3	O43422	26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PSMD3	0.666	0.649	0.659	0.643
RS8	F62241	40S ribosomal protein S8 OS=Homo sapiens OX=9606 GN=RPSS8 PE=1 SV=2	0.65	0.637	0.67	0.657
GFPT1	Q06210	Glutamine-fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens	0.692	0.579	0.729	0.61

VP33A	Q96AX1	Vacuolar protein sorting-associated protein 33A OS=Homo sapiens OX=9606 GN=VPS33A	0.738	0.578	0.721	0.565
THIM	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens OX=9606 GN=ACAA2 PE=1	0.66	0.622	0.679	0.64
ACTN2	P35609	Alpha-actinin-2 OS=Homo sapiens OX=9606 GN=ACTN2 PE=1 SV=1	0.695	0.611	0.689	0.606
DCA13	Q9NV06	DDB1- and CUL4-associated factor 13 OS=Homo sapiens OX=9606 GN=DCAF13 PE=1	0.672	0.638	0.662	0.628
EX3L4	Q17RC7	Exocyst complex component 3-like protein 4 OS=Homo sapiens OX=9606 GN=EXOC3L4	0.822	0.635	0.641	0.496
PHB	P35232	Prohibitin OS=Homo sapiens OX=9606 GN=PHB PE=1 SV=1	0.601	0.67	0.624	0.695
MYH9	P35579	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4	0.677	0.633	0.66	0.616
RRP5	Q14690	Protein RRP5 homolog OS=Homo sapiens OX=9606 GN=PDCD11 PE=1 SV=3	0.634	0.649	0.642	0.658
PSPC1	Q8WXF1	Paraspeckle component 1 OS=Homo sapiens OX=9606 GN=PSPC1 PE=1 SV=1	0.625	0.646	0.643	0.664
COPA	P53621	Coatomer subunit alpha OS=Homo sapiens OX=9606 GN=COPA PE=1 SV=2	0.638	0.652	0.635	0.649
ACTN4	O43707	Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=2	0.652	0.637	0.649	0.634
NOP2	P46087	Probable 28S rRNA (cytosine(4447-C5))-methyltransferase OS=Homo sapiens OX=9606	0.659	0.628	0.658	0.627
TCPA	P17987	T-complex protein 1 subunit alpha OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1	0.651	0.634	0.652	0.635
SMCA4	P51532	Transcription activator BRG1 OS=Homo sapiens OX=9606 GN=SMARCA4 PE=1 SV=2	0.646	0.639	0.647	0.639
HEAT1	Q9H583	HEAT repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=HEATR1 PE=1 SV=3	0.666	0.637	0.645	0.617
RIF1	Q5UIPO	Telomere-associated protein RIF1 OS=Homo sapiens OX=9606 GN=RIF1 PE=1 SV=2	0.635	0.628	0.654	0.647
ASNS	P08243	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens OX=9606 GN=ASNS	0.628	0.646	0.635	0.653
KPYM	P14618	Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=4	0.624	0.643	0.637	0.657
RACK1	P63244	Receptor of activated protein kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1	0.592	0.649	0.629	0.69
6PGD	P52209	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens OX=9606 GN=6PGD	0.664	0.636	0.643	0.616
API1G1	O43747	AP-1 complex subunit gamma-1 OS=Homo sapiens OX=9606 GN=API1G1 PE=1 SV=5	0.662	0.635	0.644	0.618
SYCC	P49589	Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=CARPS1 PE=1 SV=3	0.690	0.602	0.674	0.582
DDX1	Q92499	ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 PE=1 SV=2	0.631	0.622	0.656	0.646
CRTAP	O75718	Cartilage-associated protein OS=Homo sapiens OX=9606 GN=CRTAP PE=1 SV=1	0.613	0.619	0.658	0.665
P66B	Q8WXI9	Transcriptional repressor p66-beta OS=Homo sapiens OX=9606 GN=GATA2B PE=1 SV=1	0.652	0.572	0.709	0.622
DDX5	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=5	0.622	0.637	0.638	0.654
PUR6	P22234	Multifunctional protein ADE2 OS=Homo sapiens OX=9606 GN=PAICS PE=1 SV=3	0.623	0.631	0.644	0.652
GTF2I	P78347	General transcription factor II-I OS=Homo sapiens OX=9606 GN=GTF2I PE=1 SV=2	0.63	0.645	0.63	0.645
RBML15	Q96T37	RNA-binding protein 15 OS=Homo sapiens OX=9606 GN=RBML15 PE=1 SV=2	0.647	0.605	0.668	0.625
AP2M1	P2M1	AP-2 complex subunit mu OS=Homo sapiens OX=9606 GN=AP2M1 PE=1 SV=2	0.652	0.622	0.648	0.618
PGRC1	O00264	Membrane-associated progesterone receptor component 1 OS=Homo sapiens OX=9606	0.612	0.65	0.619	0.657
VIGILN	Q100341	Vigilin OS=Homo sapiens OX=9606 GN=HDLBP PE=1 SV=2	0.65	0.621	0.647	0.619
WDR5	P61964	WD repeat-containing protein 5 OS=Homo sapiens OX=9606 GN=WDR5 PE=1 SV=1	0.66	0.635	0.633	0.609
ACTN1	P12814	Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=2	0.652	0.603	0.665	0.615
DX39B	Q13838	Spliceosome RNA helicase DX39B OS=Homo sapiens OX=9606 GN=DX39B PE=1 SV=1	0.646	0.617	0.621	0.621
NCKP1	Q9Y2A7	Nck-associated protein 1 OS=Homo sapiens OX=9606 GN=NCKAP1 PE=1 SV=1	0.619	0.625	0.641	0.648
NACA2	Q9H009	Nascent polypeptide-associated complex subunit alpha-2 OS=Homo sapiens OX=9606	0.64	0.633	0.632	0.626
SYK	Q15046	Lysine-tRNA ligase OS=Homo sapiens OX=9606 GN=KARS1 PE=1 SV=3	0.600	0.624	0.64	

ACAD9	Q9H845	Complex I assembly factor ACAD9, mitochondrial OS=Homo sapiens OX=9606 GN=ACAD9	0.633	0.611	0.624	0.602
CROCC	Q5TZA2	Rootletin OS=Homo sapiens OX=9606 GN=CROCC PE=1 SV=1	0.622	0.664	0.571	0.61
ARI1A	O14497	AT-rich interactive domain-containing protein 1A OS=Homo sapiens OX=9606 GN=ARID1A	0.621	0.627	0.605	0.611
PWP2	Q15269	Periodic tryptophan protein 2 homolog OS=Homo sapiens OX=9606 GN=PWP2 PE=2 SV=2	0.615	0.625	0.606	0.615
FAF2	Q96CS3	FAS-associated factor 2 OS=Homo sapiens OX=9606 GN=FAF2 PE=1 SV=2	0.635	0.659	0.573	0.594
PABP1	P11940	Polyadenylate-binding protein 1 OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=2	0.604	0.587	0.643	0.625
SGPL1	Q95470	Sphingosine-1-phosphate lyase 1 OS=Homo sapiens OX=9606 GN=SGPL1 PE=1 SV=3	0.594	0.604	0.624	0.635
NOP58	Q9Y2X3	Nucleolar protein 58 OS=Homo sapiens OX=9606 GN=NOP58 PE=1 SV=1	0.57	0.614	0.612	0.659
MP2K4	P45985	Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens OX=9606	0.592	0.59	0.631	0.629
STAG2	Q8N3U4	Cohesin subunit SA-2 OS=Homo sapiens OX=9606 GN=STAG2 PE=1 SV=3	0.61	0.61	0.61	0.611
GCS3	P23378	Glycine dehydrogenase (decarboxylating), mitochondrial OS=Homo sapiens OX=9606	0.605	0.583	0.638	0.615
DHX30	Q7L2E3	ATP-dependent RNA helicase DHX30 OS=Homo sapiens OX=9606 GN=DHX30 PE=1 SV=1	0.638	0.604	0.615	0.582
SSRP1	Q89845	FACT complex subunit SSRP1 OS=Homo sapiens OX=9606 GN=SSRP1 PE=1 SV=1	0.569	0.599	0.618	0.65
MK15	Q8T0D8	Mitogen-activated protein kinase 15 OS=Homo sapiens OX=9606 GN=MAPK15 PE=1 SV=1	0.608	0.638	0.58	0.609
ANM5	O14744	Protein arginine N-methyltransferase 5 OS=Homo sapiens OX=9606 GN=PRMT5 PE=1 SV=4	0.648	0.608	0.608	0.57
PABP4	Q13310	Polyadenylate-binding protein 4 OS=Homo sapiens OX=9606 GN=PABPC4 PE=1 SV=1	0.588	0.61	0.606	0.628
IDE	P14735	Insulin-degrading enzyme OS=Homo sapiens OX=9606 GN=IDE PE=1 SV=4	0.643	0.63	0.585	0.573
GDIA	P31150	Rab GDP dissociation inhibitor alpha OS=Homo sapiens OX=9606 GN=GDII PE=1 SV=2	0.594	0.597	0.618	0.622
RS16	P62249	40S ribosomal protein S16 OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=2	0.673	0.559	0.653	0.542
PSDE	Q00487	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens OX=9606	0.586	0.618	0.595	0.628
CCD22	O60826	Coiled-coil domain-containing protein 22 OS=Homo sapiens OX=9606 GN=CCDC22 PE=1	0.65	0.612	0.599	0.564
FDFT	P37268	Squalene synthase OS=Homo sapiens OX=9606 GN=FDFT1 PE=1 SV=1	0.49	0.543	0.66	0.732
PIGT	Q96N92	GPI transamidase component PIG-T OS=Homo sapiens OX=9606 GN=PIGT PE=1 SV=1	0.591	0.636	0.576	0.621
SAE2	Q9UBT2	SUMO-activating enzyme subunit 2 OS=Homo sapiens OX=9606 GN=UBA2 PE=1 SV=2	0.603	0.611	0.601	0.609
SYDM	Q6P148	Aspartate-tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=DARS2 PE=1 SV=1	0.589	0.61	0.597	0.619
CD11A	Q9UQ88	Cyclin-dependent kinase 11A OS=Homo sapiens OX=9606 GN=CDK11A PE=1 SV=4	0.615	0.525	0.686	0.586
CDC73	Q6P1J9	Parafibromin OS=Homo sapiens OX=9606 GN=CDC73 PE=1 SV=1	0.595	0.59	0.615	0.61
P4HA1	P13674	Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens OX=9606 GN=P4HA1 PE=1 SV=2	0.61	0.574	0.631	0.594
UGGG1	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens OX=9606 GN=UGGT1	0.639	0.61	0.593	0.566
RL21	P46778	60S ribosomal protein L21 OS=Homo sapiens OX=9606 GN=RPL21 PE=1 SV=2	0.631	0.591	0.612	0.573
OTUB1	Q96FW1	Ubiquitin thioesterase OTUB1 OS=Homo sapiens OX=9606 GN=OTUB1 PE=1 SV=2	0.659	0.586	0.612	0.544
METH	Q97070	Methionine synthase OS=Homo sapiens OX=9606 GN=MTR PE=1 SV=2	0.596	0.632	0.566	0.599
HECD1	Q9ULT8	E3 ubiquitin-protein ligase HECD1 OS=Homo sapiens OX=9606 GN=HECTD1 PE=1 SV=3	0.654	0.594	0.599	0.545
PIPNB	P48739	Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens OX=9606 GN=PITPNB	0.641	0.561	0.633	0.554
PDSSB	Q9NT15	Sister chromatid cohesion protein PDSS5 homolog B OS=Homo sapiens OX=9606 GN=PDSS5	0.668	0.545	0.647	0.529
NOL11	Q9RH80	Nucleolar protein 11 OS=Homo sapiens OX=9606 GN=NOL11 PE=1 SV=1	0.555	0.559	0.635	0.639
ESTD	P10768	S-formylglutathione hydrolase OS=Homo sapiens OX=9606 GN=ESD PE=1 SV=2	0.543	0.612	0.579	0.652
MLEC	Q14165	Malectin OS=Homo sapiens OX=9606 GN=MLEC PE=1 SV=1	0.59	0.632	0.561	0.602
DDX42	Q86XP3	ATP-dependent RNA helicase DDX42 OS=Homo sapiens OX=9606 GN=DDX42 PE=1 SV=1	0.56	0.586	0.605	0.633
PCAT2	Q7L5N7	Lysophosphatidylcholine acyltransferase 2 OS=Homo sapiens OX=9606 GN=LPCAT2 PE=1	0.59	0.589	0.602	0.601
PYRG1	P17812	CTP synthase 1 OS=Homo sapiens OX=9606 GN=CTPS1 PE=1 SV=2	0.688	0.681	0.509	0.503
SRCAP	Q6ZRS2	Helicase SRCAP OS=Homo sapiens OX=9606 GN=SRCAP PE=1 SV=3	0.643	0.574	0.614	0.548
HAUS3	Q6CZ6	HAUS augmin-like complex subunit 3 OS=Homo sapiens OX=9606 GN=HAUS3 PE=1 SV=1	0.653	0.568	0.616	0.536
S12A2	P55011	Solute carrier family 12 member 2 OS=Homo sapiens OX=9606 GN=SLC12A2 PE=1 SV=1	0.613	0.588	0.596	0.572
SAHH2	Q43865	S-adenosylhomocysteine hydrolase-like protein 1 OS=Homo sapiens OX=9606 GN=AHCYL1	0.545	0.643	0.54	0.637
AP3B1	Q00203	AP-3 complex subunit beta-1 OS=Homo sapiens OX=9606 GN=AP3B1 PE=1 SV=3	0.621	0.574	0.606	0.56
RAN	P62826	GTP-binding nuclear protein Ran OS=Homo sapiens OX=9606 GN=RAN PE=1 SV=3	0.593	0.57	0.61	0.587
STRP2	Q9LULQ0	Striatin-interacting protein 2 OS=Homo sapiens OX=9606 GN=STRP2 PE=1 SV=2	0.543	0.549	0.626	0.632
BPN1	Q95861	3'(2',5'-bisphosphate nucleotidase 1 OS=Homo sapiens OX=9606 GN=BPN1 PE=1 SV=1	0.588	0.668	0.51	0.58
CDK9	P50750	Cyclin-dependent kinase 9 OS=Homo sapiens OX=9606 GN=CDK9 PE=1 SV=3	0.57	0.564	0.607	0.601
SBDS	Q9Y3A5	Ribosome maturation protein SBDS OS=Homo sapiens OX=9606 GN=SBDS PE=1 SV=4	0.579	0.564	0.607	0.592
HAT1	O14929	Histone acetyltransferase type B catalytic subunit OS=Homo sapiens OX=9606 GN=HAT1	0.645	0.642	0.528	0.526
SEP11	Q9NV2A	Septin-11 OS=Homo sapiens OX=9606 GN=SEPTIN11 PE=1 SV=3	0.623	0.643	0.528	0.545
RFC2	P35250	Replication factor C subunit 2 OS=Homo sapiens OX=9606 GN=RFC2 PE=1 SV=3	0.538	0.632	0.536	0.629
SUCA	P53597	Succinate-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens	0.64	0.562	0.603	0.53
MCM2	P49736	DNA replication licensing factor MCM2 OS=Homo sapiens OX=9606 GN=MCM2 PE=1	0.573	0.585	0.578	0.59
IF4A2	O14240	Eukaryotic initiation factor 4A-II OS=Homo sapiens OX=9606 GN=EIF4A2 PE=1 SV=2	0.648	0.545	0.615	0.517
IF4A1	P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens OX=9606 GN=EIF4A1 PE=1 SV=1	0.562	0.578	0.584	0.6
RCC2	Q9PF28	Protein RCC2 OS=Homo sapiens OX=9606 GN=RCC2 PE=1 SV=2	0.566	0.57	0.592	0.596
FBRL	P22087	rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens OX=9606 GN=FBL PE=1 SV=2	0.584	0.567	0.594	0.576
IMA1	P52292	Importin subunit alpha-1 OS=Homo sapiens OX=9606 GN=KPNA2 PE=1 SV=1	0.589	0.576	0.584	0.571
CLAP1	Q7Z460	CLIP-associating protein 1 OS=Homo sapiens OX=9606 GN=CLASP1 PE=1 SV=1	0.603	0.576	0.583	0.557
VPS35	Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens OX=9606 GN=VPS35 PE=1	0.596	0.574	0.585	0.563
LSG1	Q9H089	Large subunit GTPase 1 homolog OS=Homo sapiens OX=9606 GN=LSG1 PE=1 SV=2	0.622	0.562	0.593	0.536
EMAL2	Q95834	Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2	0.691	0.576	0.568	0.474
AMOT	Q4VC55	Angiomotin OS=Homo sapiens OX=9606 GN=AMOT PE=1 SV=1	0.579	0.569	0.585	0.575
CSTF3	Q12996	Cleavage stimulation factor subunit 3 OS=Homo sapiens OX=9606 GN=CSTF3 PE=1 SV=1	0.572	0.61	0.543	0.579
RT29	P51398	28S ribosomal protein S29, mitochondrial OS=Homo sapiens OX=9606 GN=DAP3 PE=1	0.616	0.544	0.605	0.535
ZN629	Q9UEG4	Zinc finger protein 629 OS=Homo sapiens OX=9606 GN=ZN629 PE=1 SV=2	0.609	0.584	0.563	0.54
NU160	Q12769	Nuclear pore complex protein Nup160 OS=Homo sapiens OX=9606 GN=NUP160 PE=1 SV=3	0.572	0.558	0.587	0.573

AOR	O60306	RNA helicase aquarius OS=Homo sapiens OX=9606 GN=AQR PE=1 SV=4	0.594	0.567	0.578	0.551
SNX2	Q60749	Sorting nexin-2 OS=Homo sapiens OX=9606 GN=SNX2 PE=1 SV=2	0.533	0.58	0.563	0.613
IF2A	P05198	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens OX=9606 GN=EIF2S1	0.594	0.575	0.567	0.549
U5S1	Q15029	116 kDa US small nuclear ribonucleoprotein component OS=Homo sapiens OX=9606	0.584	0.552	0.587	0.555
KIF2A	O00139	Kinesin-like protein KIF2A OS=Homo sapiens OX=9606 GN=KIF2A PE=1 SV=3	0.582	0.545	0.594	0.557
RAGP1	P46060	Ran GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RANGAP1 PE=1 SV=1	0.558	0.575	0.564	0.581
IMPA3	Q9NX62	Golgi-resident adenosine 3',5'-bisphosphate 3'-phosphatase OS=Homo sapiens OX=9606	0.587	0.534	0.604	0.555
VATB2	P21281	V-type proton ATPase subunit B, brain isoform OS=Homo sapiens OX=9606 GN=ATP6V1B2	0.586	0.611	0.526	0.549
GYS1	P13807	Glycogen [starch] synthase, muscle OS=Homo sapiens OX=9606 GN=GYS1 PE=1 SV=2	0.654	0.567	0.562	0.487
EXOS9	Q02625	Exosome complex component RRP45 OS=Homo sapiens OX=9606 GN=EXOSC9 PE=1 SV=1	0.622	0.528	0.6	0.51
RCL1	Q9Y2P8	RNA 3'-terminal phosphate cyclase-like protein OS=Homo sapiens OX=9606 GN=RCL1	0.534	0.522	0.607	0.593
PRDX6	P30041	Peroxiredoxin-6 OS=Homo sapiens OX=9606 GN=PRDX6 PE=1 SV=3	0.579	0.569	0.558	0.548
CUL2	Q13617	Cullin-2 OS=Homo sapiens OX=9606 GN=CUL2 PE=1 SV=2	0.594	0.602	0.525	0.532
ERF1	P62495	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens OX=9606 GN=ETF1	0.56	0.543	0.583	0.565
ODPB	P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens	0.537	0.587	0.538	0.588
UBR4	Q5T457	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens OX=9606 GN=UBR4 PE=1 SV=1	0.488	0.562	0.557	0.642
TSPY4	P0CV99	Testis-specific Y-encoded protein 4 OS=Homo sapiens OX=9606 GN=TSPY4 PE=3 SV=1	0.523	0.554	0.569	0.602
DDX49	Q9Y6V7	Probable ATP-dependent RNA helicase DDX49 OS=Homo sapiens OX=9606 GN=DDX49	0.493	0.534	0.584	0.632
EF1A1	P68104	Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1	0.56	0.55	0.572	0.561
M20M	P02978	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens OX=9606	0.453	0.556	0.554	0.679
SCPDL	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens OX=9606 GN=SCCPDH	0.584	0.589	0.532	0.537
UTP4	Q96X6	U3 small nucleolar RNA-associated protein 4 homolog OS=Homo sapiens OX=9606	0.543	0.579	0.54	0.576
NXF1	Q9UBU9	Nuclear RNA export factor 1 OS=Homo sapiens OX=9606 GN=NXF1 PE=1 SV=1	0.547	0.545	0.573	0.571
PUR1	P06203	Amidophosphoribosyltransferase OS=Homo sapiens OX=9606 GN=PPAT PE=1 SV=1	0.547	0.548	0.568	0.569
RL10A	P62906	60S ribosomal protein L10a OS=Homo sapiens OX=9606 GN=RPL10A PE=1 SV=2	0.573	0.512	0.604	0.54
RM39	Q9NYK5	39S ribosomal protein L13, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL39 PE=1	0.505	0.59	0.523	0.61
RL18	P07020	60S ribosomal protein L18 OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=2	0.502	0.542	0.569	0.615
NIPB1	Q6K79	Nipped B-like protein OS=Homo sapiens OX=9606 GN=NIPB1 PE=1 SV=2	0.546	0.564	0.547	0.565
ESYT1	Q9BSJ8	Extended synaptotagmin-1 OS=Homo sapiens OX=9606 GN=ESYT1 PE=1 SV=1	0.58	0.554	0.556	0.531
GAPD1	Q14C86	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens	0.558	0.574	0.536	0.552
PDIP2	Q9Y257	Polymerase delta-interacting protein 2 OS=Homo sapiens OX=9606 GN=POLDIP2 PE=1	0.389	0.517	0.563	0.749
BAZ1A	Q9NLR2	Bromodomain adjacent to zinc finger domain protein 1A OS=Homo sapiens OX=9606	0.596	0.471	0.642	0.508
SON	P18583	Protein SON OS=Homo sapiens OX=9606 GN=SON PE=1 SV=4	0.548	0.609	0.502	0.558
IF5	P55010	Eukaryotic translation initiation factor 5 OS=Homo sapiens OX=9606 GN=EIF5 PE=1 SV=2	0.576	0.523	0.583	0.53
HMC51	Q1581	Hydroxyethylglutaryl-CoA synthase, cytoplasmic OS=Homo sapiens OX=9606	0.549	0.563	0.541	0.554
TM209	Q96SK2	Transmembrane protein 209 OS=Homo sapiens OX=9606 GN=TMEM209 PE=1 SV=1	0.642	0.473	0.627	0.462
SPTC2	Q15270	Serine palmitoyltransferase 2 OS=Homo sapiens OX=9606 GN=SPTLC2 PE=1 SV=1	0.655	0.487	0.601	0.447
RTF1	Q92541	RNA polymerase-associated protein RTF1 homolog OS=Homo sapiens OX=9606 GN=RTF1	0.563	0.535	0.556	0.529
VPP1	Q93050</td					

G6PD	P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens OX=9606 GN=G6PD PE=1 SV=4	0.514	0.568	0.48	0.531
ZBTB11	O95625	Zinc finger and BTB domain-containing protein 11 OS=Homo sapiens OX=9606	0.579	0.424	0.628	0.459
TCAF1	Q9Y4C2	TRPM8 channel-associated factor 1 OS=Homo sapiens OX=9606 GN=TCAF1 PE=1 SV=3	0.554	0.472	0.574	0.489
NCDN	Q9JB66	Neurochondrin OS=Homo sapiens OX=9606 GN=NCDN PE=1 SV=1	0.56	0.428	0.622	0.476
MUTA	P22033	Methylmalonyl-CoA mutase, mitochondrial OS=Homo sapiens OX=9606 GN=MMUT PE=1	0.508	0.565	0.477	0.53
BRD4	O60885	Bromodomain-containing protein 4 OS=Homo sapiens OX=9606 GN=BRD4 PE=1 SV=2	0.491	0.547	0.492	0.547
TBB5	P07437	Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=2	0.347	0.589	0.422	0.717
MCM4	P33991	DNA replication licensing factor MCM4 OS=Homo sapiens OX=9606 GN=MCM4 PE=1	0.499	0.511	0.523	0.536
RL27A	P46776	60S ribosomal protein L27a OS=Homo sapiens OX=9606 GN=RPL27A PE=1 SV=2	0.559	0.517	0.515	0.477
FXRD1	Q96CU9	FAD-dependent oxidoreductase domain-containing protein 1 OS=Homo sapiens OX=9606	0.537	0.448	0.587	0.49
XPP1	Q9NWQ7	Xaa-Pro aminopeptidase 1 OS=Homo sapiens OX=9606 GN=XPNPEP1 PE=1 SV=3	0.53	0.505	0.526	0.501
ANX11	P50995	Annexin A11 OS=Homo sapiens OX=9606 GN=ANXA11 PE=1 SV=1	0.468	0.507	0.516	0.56
CPSF2	Q9P210	Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens OX=9606	0.502	0.481	0.545	0.523
TM9S2	Q99805	Transmembrane 9 superfamily member 2 OS=Homo sapiens OX=9606 GN=TM9SF2 PE=1	0.579	0.452	0.572	0.447
VA0D1	P61421	V-type proton ATPase subunit d 1 OS=Homo sapiens OX=9606 GN=ATPV6V0D1 PE=1 SV=1	0.496	0.517	0.505	0.526
TTC28	Q96AY4	Tetratricopeptide repeat protein 28 OS=Homo sapiens OX=9606 GN=ITC28 PE=1 SV=4	0.468	0.348	0.703	0.523
RBM33	Q96EV2	RNA-binding protein 33 OS=Homo sapiens OX=9606 GN=RBMB32 PE=1 SV=3	0.502	0.484	0.537	0.518
APT	P07741	Adenine phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=APRT PE=1 SV=2	0.47	0.487	0.531	0.55
Z280C	Q98ND2	Zinc finger protein 280C OS=Homo sapiens OX=9606 GN=ZNF280C PE=1 SV=1	0.459	0.511	0.503	0.561
PRP19	Q9UJMS4	Pre-mRNA-processing factor 19 OS=Homo sapiens OX=9606 GN=PRPF19 PE=1 SV=1	0.518	0.494	0.519	0.495
DDX20	Q9UH16	Probable ATP-dependent RNA helicase DDX20 OS=Homo sapiens OX=9606 GN=DDX20	0.604	0.479	0.524	0.416
SAE1	Q9UBE0	SUMO-activating enzyme subunit 1 OS=Homo sapiens OX=9606 GN=SAE1 PE=1 SV=1	0.472	0.551	0.461	0.538
RL13A	P40429	60S ribosomal protein L13a OS=Homo sapiens OX=9606 GN=RPL13A PE=1 SV=2	0.492	0.505	0.505	0.519
POGZ	Q7ZK3	Pogo transposable element with ZNF domains OS=Homo sapiens OX=9606 GN=POGZ PE=1	0.354	0.587	0.405	0.67
TEX10	Q9NXF1	Testis-expressed protein 10 OS=Homo sapiens OX=9606 GN=TEX10 PE=1 SV=2	0.523	0.494	0.508	0.48
SEPT2	Q15019	Septin-2 OS=Homo sapiens OX=9606 GN=SEPTIN2 PE=1 SV=1	0.491	0.473	0.529	0.511
PDPK1	Q15530	3-phosphoinositide-dependent protein kinase 1 OS=Homo sapiens OX=9606 GN=PDPK1	0.446	0.503	0.495	0.559
PLD3	Q8IV08	5'-3' exonuclease PLD3 OS=Homo sapiens OX=9606 GN=PLD3 PE=1 SV=1	0.505	0.499	0.5	0.495
FERM2	Q96AC1	Fermitin family homolog 2 OS=Homo sapiens OX=9606 GN=FERMT2 PE=1 SV=1	0.536	0.475	0.524	0.464
HELLS	Q9NRZ9	Lymphoid-specific helicase OS=Homo sapiens OX=9606 GN=HELLS PE=1 SV=1	0.485	0.53	0.47	0.514
LRC47	Q8NIG4	Leucine-rich repeat-containing protein 47 OS=Homo sapiens OX=9606 GN=LRRC47 PE=1	0.548	0.497	0.5	0.454
RB3GP	Q15042	Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens OX=9606	0.489	0.495	0.504	0.51
VPS4B	Q75351	Vacuolar protein sorting-associated protein 4B OS=Homo sapiens OX=9606 GN=VPS4B	0.494	0.511	0.485	0.502
IF2G	P41091	Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens OX=9606 GN=EIF2S3	0.504	0.489	0.507	0.491
DNJB1	P25685	DnaJ homolog subfamily B member 1 OS=Homo sapiens OX=9606 GN=DNAJB1 PE=1	0.455	0.491	0.499	0.539
UTP6	Q9NYH9	U3 small nuclear RNA-associated protein 6 homolog OS=Homo sapiens OX=9606	0.576	0.505	0.481	0.422
AP2B1	P63010	AP-2 complex subunit beta OS=Homo sapiens OX=9606 GN=AP2B1 PE=1 SV=1	0.515	0.496	0.495	0.477
VP26A	Q75436	Vacuolar protein sorting-associated protein 26A OS=Homo sapiens OX=9606 GN=VPS26A	0.488	0.537	0.456	0.501
PPME1	Q9Y570	Protein phosphatase methylesterase 1 OS=Homo sapiens OX=9606 GN=PPME1 PE=1 SV=3	0.48	0.458	0.531	0.507
PR40A	Q75400	Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens OX=9606 GN=PRPF40A	0.476	0.473	0.512	0.509
OGFD1	Q8NS43	Prolyl 3-hydroxyproline OGFD1 OS=Homo sapiens OX=9606 GN=OGFD1 PE=1 SV=1	0.472	0.489	0.494	0.512
DHX29	Q7Z478	ATP-dependent RNA helicase DHX29 OS=Homo sapiens OX=9606 GN=DHX29 PE=1 SV=2	0.501	0.508	0.474	0.482
IF4A3	P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens OX=9606 GN=EIF4A3 PE=1 SV=4	0.493	0.482	0.497	0.486
TF3C4	Q9UKN8	General transcription factor 3C polypeptide 4 OS=Homo sapiens OX=9606 GN=GTTF3C4	0.445	0.474	0.502	0.534
MRPP3	O15091	Mitochondrial ribonuclease P catalytic subunit OS=Homo sapiens OX=9606 GN=PRORP	0.476	0.475	0.502	0.501
EF1B	P24534	Elongation factor 1-beta OS=Homo sapiens OX=9606 GN=EEF1B2 PE=1 SV=3	0.445	0.501	0.474	0.533
TASOR	Q9UK61	Protein TASOR OS=Homo sapiens OX=9606 GN=TASOR PE=1 SV=3	0.495	0.489	0.485	0.479
GDN	P07093	Glia-derived nexin OS=Homo sapiens OX=9606 GN=SERPINE2 PE=1 SV=1	0.475	0.508	0.464	0.496
MRP7	Q5T3U5	Multidrug resistance-associated protein 7 OS=Homo sapiens OX=9606 GN=ABCC10 PE=1	0.492	0.514	0.458	0.479
SMHD1	A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo	0.439	0.546	0.425	0.528
NU107	P57740	Nuclear pore complex protein Nup107 OS=Homo sapiens OX=9606 GN=NUP107 PE=1 SV=1	0.461	0.458	0.51	0.507
XPOT	O43592	Exportin-T OS=Homo sapiens OX=9606 GN=XPOT PE=1 SV=2	0.548	0.438	0.526	0.421
RM15	Q9P015	39S ribosomal protein L15, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL15 PE=1	0.475	0.51	0.456	0.49
SEC63	Q9UGP8	Translocation protein SEC63 homolog OS=Homo sapiens OX=9606 GN=SEC63 PE=1 SV=2	0.394	0.542	0.409	0.563
DAPLE	Q9P219	Protein Daple OS=Homo sapiens OX=9606 GN=CCDC88C PE=1 SV=3	0.481	0.423	0.533	0.469
RPP38	P78345	Ribonuclease P-like protein subunit p38 OS=Homo sapiens OX=9606 GN=RPP38 PE=1 SV=2	0.504	0.468	0.481	0.447
MP2K2	P36507	Dual specificity mitogen-activated protein kinase 2 OS=Homo sapiens OX=9606	0.482	0.486	0.462	0.466
DNM1L	O00429	Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L PE=1 SV=2	0.43	0.435	0.51	0.517
2A5D	Q14738	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo	0.474	0.49	0.456	0.471
ESF1	Q9H501	ESF1 homolog OS=Homo sapiens OX=9606 GN=ESF1 PE=1 SV=1	0.518	0.394	0.552	0.419
RPAC1	O15160	DNA-directed RNA polymerases I and III subunit RPAC1 OS=Homo sapiens OX=9606	0.375	0.514	0.419	0.574
PICAL	Q13492	Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens OX=9606	0.493	0.48	0.46	0.447
DDX23	Q9BUQ8	Probable ATP-dependent RNA helicase DDX23 OS=Homo sapiens OX=9606 GN=DDX23	0.436	0.493	0.443	0.501
TOPK	Q96KB5	Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens OX=9606	0.362	0.366	0.569	0.575
ACPH	P13798	Acylamino-acid-releasing enzyme OS=Homo sapiens OX=9606 GN=APEH PE=1 SV=4	0.412	0.488	0.444	0.527
UGPA	Q16851	UTP-glucose-1-phosphate uridylyltransferase OS=Homo sapiens OX=9606 GN=UGP2 PE=1	0.452	0.506	0.426	0.477
AP3M1	Q9Y2T2	AP-3 complex subunit mu-1 OS=Homo sapiens OX=9606 GN=AP3M1 PE=1 SV=1	0.456	0.408	0.524	0.468
ZC11A	O75152	Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens OX=9606	0.43	0.48	0.446	0.498
LICH	P38571	Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens OX=9606 GN=LIPA	0.451	0.41	0.516	0.469
NVL	O15381	Nuclear valosin-containing protein-like OS=Homo sapiens OX=9606 GN=NVL PE=1 SV=1	0.458	0.47	0.45	0.463

MBD3	O95983	Methyl-CpG-binding domain 3 OS=Homo sapiens OX=9606 GN=MBD3 PE=1 SV=1	0.47	0.47	0.45	0.45
NDUA9	Q16795	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Homo	0.442	0.441	0.478	0.476
LRBA	P50851	Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens OX=9606	0.432	0.447	0.462	0.478
ARP2C	O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens OX=9606 GN=ARP2C PE=1	0.508	0.436	0.463	0.397
NRDC	O43847	Nardilysin OS=Homo sapiens OX=9606 GN=NRDC PE=1 SV=3	0.391	0.441	0.455	0.513
RAP2C	Q9Y3L5	Ras-related protein Rap-2c OS=Homo sapiens OX=9606 GN=RAP2C PE=1 SV=1	0.452	0.381	0.521	0.439
GNP11	P46926	Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens OX=9606 GN=GNDPA1 PE=1	0.436	0.428	0.468	0.459
CDK6	Q00534	Cyclin-dependent kinase 6 OS=Homo sapiens OX=9606 GN=CDK6 PE=1 SV=1	0.501	0.451	0.44	0.396
NAMPT	P43490	Nicotinamide phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=NAMPT PE=1	0.392	0.465	0.425	0.504
COQ8A	Q8N160	Atypical kinase COQ8A, mitochondrial OS=Homo sapiens OX=9606 GN=COQ8A PE=1	0.392	0.48	0.41	0.503
GCN1	Q92616	eIF-2-alpha kinase activator GCN1 OS=Homo sapiens OX=9606 GN=GCN1 PE=1 SV=6	0.454	0.435	0.458	0.438
GLE1	Q53GS7	Nucleoporin GLE1 OS=Homo sapiens OX=9606 GN=GLE1 PE=1 SV=2	0.383	0.427	0.461	0.513
PAPS1	O43252	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Homo sapiens OX=9606	0.413	0.501	0.392	0.477
GNL3	Q9BV2P	Guanine nucleotide-binding protein-like 3 OS=Homo sapiens OX=9606 GN=GNL3 PE=1	0.439	0.456	0.435	0.451
BACH	O00154	Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens OX=9606 GN=ACOT7	0.423	0.439	0.445	0.462
RL9	P32969	60S ribosomal protein L9 OS=Homo sapiens OX=9606 GN=RPL9 PE=1 SV=1	0.437	0.428	0.454	0.445
DYN1	Q05193	Dynamin-1 OS=Homo sapiens OX=9606 GN=DNM1 PE=1 SV=2	0.447	0.437	0.438	0.428
SNR40	Q96D17	U5 small nuclear ribonucleoprotein 40 kDa protein OS=Homo sapiens OX=9606	0.449	0.413	0.462	0.425
GLSK	Q94925	Glutaminase kidney isoform, mitochondrial OS=Homo sapiens OX=9606 GN=GLS	0.389	0.405	0.466	0.485
LRC40	Q9H9A6	Leucine-rich repeat-containing protein 40 OS=Homo sapiens OX=9606 GN=LRC40 PE=1	0.4	0.485	0.385	0.467
PLOD2	O00469	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens OX=9606 GN=PLOD2	0.416	0.461	0.397	0.441
CUL3	Q13618	Cullin-3 OS=Homo sapiens OX=9606 GN=CUL3 PE=1 SV=2	0.417	0.457	0.4	0.438
STRBP	Q96S19	Spermatid perinuclear protein STRBP OS=Homo sapiens OX=9606 GN=STRBP PE=1	0.4	0.428	0.425	0.455
NMD3	Q96D46	60S ribosomal export protein NMD3 OS=Homo sapiens OX=9606 GN=NMD3 PE=1 SV=1	0.479	0.398	0.452	0.376
MEP50	Q9BQA1	Methylome protein 50 OS=Homo sapiens OX=9606 GN=WDR77 PE=1 SV=1	0.394	0.426	0.425	0.432
UTRO	P46939	Urothrin OS=Homo sapiens OX=9606 GN=UTRN PE=1 SV=2	0.419	0.451	0.4	0.432
FLNC	Q14315	Filamin-C OS=Homo sapiens OX=9606 GN=FLNC PE=1 SV=3	0.369	0.434	0.411	0.483
KC1D	P48730	Casein kinase I isoform delta OS=Homo sapiens OX=9606 GN=CSNK1D PE=1 SV=2	0.455	0.384	0.461	0.389
B3A2	P04920	Anion exchange protein 2 OS=Homo sapiens OX=9606 GN=SLC4A2 PE=1 SV=4	0.378	0.429	0.413	0.468
MSH6	P52701	DNA mismatch repair protein Msh6 OS=Homo sapiens OX=9606 GN=MSH6 PE=1 SV=2	0.422	0.419	0.424	0.421
RL11	P62913	60S ribosomal protein L11 OS=Homo sapiens OX=9606 GN=RPL11 PE=1 SV=2	0.401	0.49	0.357	0.436
ULA1	Q13564	NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens OX=9606 GN=NAE1	0.439	0.414	0.426	0.402
DMTF1	Q9Y222	WD repeat-containing protein 26 OS=Homo sapiens OX=9606 GN=WDR26 PE=1 SV=1	0.39	0.453	0.367	0.426
H4	P62805	Histone H4 OS=Homo sapiens OX=9606 GN=H4C1 PE=1 SV=2	0.394	0.388	0.447	0.44
STK25	O00506	Serine/threonine-protein kinase 25 OS=Homo sapiens OX=9606 GN=STK25 PE=1 SV=1	0.363	0.408	0.421	0.473
THOC6	Q86W42	THO complex subunit 6 homolog OS=Homo sapiens OX=9606 GN=THOC6 PE=1 SV=1	0.396	0.423	0.407	0.436
SYLC	Q9P215	Leucine-tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=LARS PE=1 SV=2	0.405	0.398	0.423	0.416
EIF3F	O00303	Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens OX=9606 GN=EIF3F	0.407	0.39	0.431	0.413
WDR26	Q9HT7D	WD repeat-containing protein 26 OS=Homo sapiens OX=9606 GN=WDR26 PE=1 SV=				

20.2 Full Protein Lists Identified by isx10

Protein IDs	Enrichment Ratio (isx10/DSMO)			Enrichment Ratio (isx10/isx10+Luminespib)		
	1st	2nd	3rd	1st	2nd	3rd
sp P08238 HS90B_HUMAN	4.395	4.27	4.509	5.485	5.073	5.036
sp Q9Y399 RT02_HUMAN	0	5.859	5.834	0	5.017	5.348
sp Q6GYQ0 RGP1_HUMAN	1.448	1.492	1.516	2.42	2.538	2.286
sp P28072 PSB6_HUMAN	2.23	1.899	2.225	2.299	2.048	2.334
sp Q9NQ29 LUC7L_HUMAN	2.448	2.902	2.316	2.1	2.396	2.079
sp P05556 ITB1_HUMAN	1.481	1.339	1.392	2.131	1.743	1.671
sp P10599 THIO_HUMAN	1.183	1.21	1.16	1.582	1.587	1.556
sp Q15102 PAIB3_HUMAN	2.354	0.97	0.924	2.853	0.916	0.897
sp Q9BQE3 TBA1C_HUMAN	0.918	0.898	1.44	0.801	0.819	3.014
sp O60716 CTND1_HUMAN	0.881	0.989	2.015	1.111	1.152	2.343
sp P49321 NASP_HUMAN	1.448	1.487	1.473	1.371	1.647	1.503
sp Q9H0U4 RAB1B_HUMAN	0.79	0.718	0.782	1.381	1.653	1.477
sp P27824 CALX_HUMAN	1.081	1.147	1.13	1.339	1.62	1.438
sp P08174 DAF_HUMAN	1.281	1.289	1.278	1.362	1.483	1.426
sp Q8TCT9 HM13_HUMAN	1.054	1.023	1.121	1.181	1.207	1.763
sp Q14847 LASP1_HUMAN	0.923	0.922	0.939	1.343	1.382	1.415
sp P56537 IF6_HUMAN	0.853	0.836	0.835	1.445	1.383	1.3
sp P53990 IST1_HUMAN	0.971	0.926	1.002	1.541	1.222	1.328
sp Q5JNZ5 RS26L_HUMAN	0.671	0.658	0.713	1.344	1.398	1.325
sp O15020 SPTN2_HUMAN	0.659	0.788	0.752	1.223	1.364	1.408
sp P27797 CALR_HUMAN	1.384	1.314	1.265	1.389	1.304	1.282
sp P19338 NUCL_HUMAN	0.957	0.93	0.979	1.36	1.18	1.373
sp P20042 IF2B_HUMAN	0.933	0.915	1.036	1.412	1.291	1.209
sp P43487 RANG_HUMAN	1.057	1.089	1.092	1.284	1.315	1.279
sp O43852 CALU_HUMAN	0.932	0.919	1.958	1.212	1.18	1.484
sp P45880 VDAC2_HUMAN	1.061	1.12	1.115	1.281	1.319	1.27
sp Q86YB8 ERO1B_HUMAN	1.255	1.233	1.147	1.342	1.372	1.15
sp Q14444 CAPR1_HUMAN	1.198	1.207	1.107	1.219	1.352	1.274
sp P49207 RL34_HUMAN	0.778	0.747	0.804	1.27	1.133	1.407
sp Q9NQC3 RTN4_HUMAN	1.546	1.432	1.228	1.479	1.28	1.049
sp P61604 CH10_HUMAN	0.974	1.075	1.124	1.211	1.454	1.138
sp P10809 CH60_HUMAN	1.13	1.154	1.146	1.252	1.281	1.257
sp P07237 PDIA1_HUMAN	1.193	1.235	1.249	1.154	1.311	1.323
sp Q7L1Q6 BZW1_HUMAN	0.978	1.003	0.981	1.26	1.293	1.221
sp Q86YZ3 HORN_HUMAN	1.167	1.123	1.118	1.346	1.33	1.092
sp O95816 BAG2_HUMAN	0.879	0.965	0.966	1.155	1.359	1.25
sp P62937 PP1A_HUMAN	0.563	0.489	0.369	0.992	0.825	1.942
sp P61201 CSN2_HUMAN	0.902	0.869	0.877	1.292	1.247	1.218
sp Q9Y266 NUDC_HUMAN	1.156	1.198	1.258	1.187	1.268	1.294
sp P34932 HSPT4_HUMAN	0.924	1.001	0.986	1.309	1.226	1.203
sp Q9H2H9 S38A1_HUMAN	0.987	0.906	0.958	1.259	1.214	1.264
sp Q9ULF5 S39AA_HUMAN	0.991	0.906	0.953	1.328	1.273	1.134
sp Q15084 PDIA6_HUMAN	1.093	1.069	1.085	1.225	1.277	1.218
sp P36873 PP1G_HUMAN	0.945	0.867	0.867	1.299	1.275	1.143
sp P62820 RAB1A_HUMAN	1.119	1.014	1.024	1.28	1.201	1.227
sp Q14974 IMB1_HUMAN	0.925	0.922	0.916	1.23	1.244	1.233
sp P47756 CAPZB_HUMAN	0.826	0.81	0.87	1.243	1.251	1.211
sp P05165 PCCA_HUMAN	1.276	1.232	1.218	1.272	1.188	1.241
sp Q8NBS9 TXND5_HUMAN	1.223	1.244	1.22	1.248	1.255	1.197
sp Q9HB96 FANCE_HUMAN	0.489	0.47	0.497	1.203	1.243	1.237
sp P51148 RAB5C_HUMAN	1.029	0.966	1.019	1.326	1.21	1.145

sp Q9H7Z7 PGES2_HUMAN	3.377	3.407	3.838	1.195	1.248	1.235
sp Q8WTV0 SCRB1_HUMAN	0	1.766	1.534	0	2.053	1.619
sp Q9H6W3 RIOX1_HUMAN	0.837	1.028	0.803	0.913	1.908	0.844
sp O95373 IPO7_HUMAN	0.93	0.91	0.899	1.254	1.254	1.14
sp P04083 ANXA1_HUMAN	1.026	1.111	1.087	1.13	1.243	1.272
sp P05023 AT1A1_HUMAN	1.01	0.995	1.012	1.259	1.244	1.139
sp P55072 TERA_HUMAN	1.036	1.04	1.026	1.24	1.21	1.191
sp P16403 H12_HUMANS	1.27	1.4	1.362	1.192	1.154	1.294
sp P13073 COX41_HUMAN	0.819	0.825	0.809	1.335	1.275	1.022
sp P17174 AAC7_HUMAN	0.977	1.061	0.928	1.232	1.249	1.145
sp P08865 RSSA_HUMAN	0.936	0.981	0.94	1.056	1.366	1.19
sp P00367 DHE3_HUMAN	0.75	0.769	0.734	1.199	1.235	1.166
sp P08670 VIME_HUMAN	1.208	1.16	1.19	1.204	1.216	1.174
sp P11498 PYC_HUMAN	1.021	1.022	1.002	1.229	1.168	1.191
sp Q9UKK9 NUDT5_HUMAN	1.153	1.066	1.159	1.222	1.19	1.173
sp P31641 SC6A6_HUMAN	1.106	1.132	0.99	1.22	1.132	1.231
sp P32119 PRDX2_HUMAN	1.152	1.205	1.17	1.149	1.223	1.201
sp Q15365 PCBP1_HUMAN	1.001	0.972	0.967	1.223	1.199	1.14
sp Q8NC51 PAIRB_HUMAN	1.217	1.243	1.207	1.099	1.273	1.189
sp O95831 AIFM1_HUMAN	0.927	0.944	0.965	1.163	1.19	1.207
sp P16152 CBR1_HUMAN	1.199	1.237	1.259	1.165	1.199	1.182
sp Q9Y4E8 UBP15_HUMAN	0.857	0.808	0.912	1.273	1.018	1.252
sp Q9UQ90 PA2G4_HUMAN	0.94	0.885	0.941	1.203	1.224	1.115
sp Q86TC9 MYPN_HUMAN	0.895	0.849	0.985	1.089	1.158	1.293
sp Q92878 RAD50_HUMAN	0.893	0.928	0.888	1.173	1.234	1.13
sp Q02790 FKBP4_HUMAN	1.183	1.237	1.068	1.212	1.259	1.057
sp Q8IV08 PLD3_HUMAN	1.131	1.227	1.304	1.206	1.237	1.079
sp P42166 LAP2A_HUMAN	1.029	1.117	1.038	1.164	1.235	1.117
sp P20020 AT2B1_HUMAN	0.866	0.824	0.869	1.073	1.281	1.159
sp Q43719 HTSF1_HUMAN	0.879	0.799	0.867	1.095	1.14	1.276
sp A6NHQ2 FBLL1_HUMAN	1.028	0.824	1.014	1.076	1.087	1.348
sp P00558 PGK1_HUMAN	1.002	1.03	1.02	1.185	1.189	1.13
sp P30626 SORCN_HUMAN	1.041	1.013	1.047	1.045	1.207	1.243
sp Q9BU2 HNRL1_HUMAN	0.815	0.867	0.837	1.252	1.154	1.084
sp P35659 DEK_HUMAN	1.195	1.185	1.123	1.17	1.174	1.144
sp P06396 GEEL_HUMAN	0.859	0.956	0.879	1.094	1.297	1.095
sp Q99497 PARK7_HUMAN	1.07	1.192	1.095	1.14	1.22	1.119
sp P61978 HNRPK_HUMAN	0.926	0.998	0.956	1.189	1.162	1.124
sp Q13576 IQGA2_HUMAN	0.792	0.769	0.862	1.146	1.177	1.151
sp P50402 EMD_HUMAN	1.35	1.012	1.453	1.35	1.023	1.101
sp Q9C0E8 LNP_HUMAN	1.101	1.125	1.175	1.145	1.15	1.157
sp Q96T37 RBM15_HUMAN	0.739	0.757	0.835	1.087	1.09	1.268
sp Q9H9A5 CNO10_HUMAN	0.903	0.803	0.866	1.048	1.173	1.223
sp P13667 PDIA4_HUMAN	0.952	0.947	0.985	1.15	1.132	1.161
sp O15355 PPM1G_HUMAN	1.044	1.068	1.152	1.127	1.099	1.215
sp P27816 MAP4_HUMAN	1.091	1.064	1.025	1.191	1.174	1.07
sp Q99632 PHB2_HUMAN	1.236	1.361	1.348	1.056	1.175	1.202
sp P24752 THIL_HUMAN	0.93	0.965	0.956	1.166	1.068	1.198
sp P11310 ACADM_HUMAN	0.755	0.848	0.858	1.182	1.071	1.173
sp P16070 CD44_HUMAN	1.079	1.066	1.163	1.218	1.109	1.099
sp Q8N8S7 ENAH_HUMAN	1.008	1.023	1.004	1.143	1.187	1.096
sp Q06830 PRDX1_HUMAN	1.147	1.105	1.136	1.148	1.172	1.105
sp P61106 RAB14_HUMAN	1.15	1.156	1.047	1.11	1.321	0.993
sp P15170 ERF3A_HUMAN	0.943	0.916	0.984	1.184	1.077	1.161
sp P13861 KAP2_HUMAN	1.034	1.153	1.192	0.981	1.16	1.28
sp Q92994 TF3B_HUMAN	0.908	0.863	0	1.707	1.713	0
sp P31483 TIA1_HUMAN	0.88	1.012	0.979	1.129	1.21	1.078
sp P09923 PPB1_HUMAN	1.002	0.992	0.978	1.106	1.149	1.161

sp P46940 IQGA1_HUMAN	0.823	0.811	0.841	1.112	1.144	1.16
sp P30048 PRDX3_HUMAN	1.239	1.193	1.331	1.067	1.102	1.246
sp Q5VWQ0 RSBN1_HUMAN	0.738	0.682	0.716	1.318	0.969	1.126
sp P04264 K2C1_HUMAN	0.921	0.918	0.991	1.122	1.126	1.165
sp Q94826 TOM70_HUMAN	1.103	1.072	1.042	1.13	1.153	1.13
sp Q8Y150 S35F3_HUMAN	1.053	1.045	1.034	1.164	1.16	1.084
sp P45974 UBP5_HUMAN	1.076	0.945	1.159	1.141	1.119	1.144
sp P08195 4P2_HUMAN	0.898	0.899	0.917	1.156	1.173	1.075
sp Q96S55 WRIP1_HUMAN	0.85	0.931	0.908	1.092	1.196	1.113
sp P48739 PIPNB_HUMAN	1.043	1.012	1.166	1.042	1.153	1.189
sp P31040 SDHA_HUMAN	1.062	0.903	0.858	1.305	1.106	0.962
sp Q9BTX1 NDC1_HUMAN	0.628	0.713	0.615	1.141	1.148	1.081
sp Q16543 CDC37_HUMAN	0.881	0.792	0.912	1.061	1.119	1.187
sp Q96AG4 LRC59_HUMAN	1.524	1.293</				

sp P30101 PDIA3_HUMAN	1.063	1.077	1.109	1.073	1.066	1.092
sp P42766 RL35_HUMAN	0.935	0.978	0.953	0.968	1.174	1.085
sp P04844 RPN2_HUMAN	0.902	0.907	0.918	1.115	1.01	1.101
sp P37837 TALDO_HUMAN	1.009	1.014	1.029	1.084	1.07	1.073
sp Q15428 SF3A2_HUMAN	0.728	0.744	0.727	0.996	1.165	1.063
sp P48643 TCPE_HUMAN	0.904	0.901	0.928	1.071	1.07	1.079
sp Q9UQ35 SRRM2_HUMAN	0.664	0.772	0.761	1.129	1.118	0.97
sp P62633 CNBP_HUMAN	0.887	0.864	0.794	1.026	1.092	1.097
sp P48047 ATPO_HUMAN	0.991	0.941	1.041	1.052	1.063	1.099
sp P62249 RS16_HUMAN	0.504	0.466	0.489	0.958	1.143	1.111
sp P26599 PTBP1_HUMAN	0.942	0.947	0.937	1.055	1.11	1.045
sp Q14694 UBP10_HUMAN	0.797	0.825	0.806	1.074	1.076	1.058
sp Q15029 U551_HUMAN	0.722	0.723	0.746	1.06	1.064	1.081
sp O43583 DENR_HUMAN	0.749	0.775	0.784	1.072	1.058	1.075
sp O15226 NKRF_HUMAN	0.77	0.757	0.786	1.15	1.046	1.007
sp Q13177 PAK2_HUMAN	1.253	1.223	0.97	1.039	1.162	1.002
sp Q86UP2 KTN1_HUMAN	0.785	0.897	0.865	1.129	1.055	1.014
sp Q9Y5B9 SP16H_HUMAN	0.735	0.756	0.732	1.076	1.035	1.088
sp P21399 ACOC_HUMAN	0.827	0.816	0.803	1.036	1.072	1.089
sp P37802 TAGL2_HUMAN	1.25	1.222	1.165	1.125	1.084	0.988
sp P50452 SPB8_HUMAN	0.831	0.789	0.808	1.054	1.028	1.111
sp P63010 AP2B1_HUMAN	0.864	0.872	0.85	1.094	1.019	1.079
sp Q14203 DCTN1_HUMAN	0.767	0.752	0.784	1.108	1.146	0.936
sp Q9P2E9 RBBP1_HUMAN	0.86	1.001	0.889	1.004	1.128	1.057
sp Q9Y6E2 BZW2_HUMAN	0.943	0.968	0.943	1.059	1.079	1.05
sp O15067 PUR4_HUMAN	0.924	0.89	0.887	1.082	1.019	1.086
sp O75396 SC22B_HUMAN	1.056	0.966	1.021	1.09	1.018	1.077
sp Q92544 TM9S84_HUMAN	0.953	0.926	0.956	1.081	1.059	1.04
sp P62258 I433E_HUMAN	1.1	1.062	1.094	1.084	1.048	1.048
sp O14617 AP3D1_HUMAN	0.827	0.805	0.856	1.052	1.078	1.047
sp P50395 GDB_HUMAN	0.903	0.89	0.907	1.079	1.058	1.039
sp O94905 ERLN2_HUMAN	0.975	0.957	1.014	1.016	0.99	1.17
sp P29401 TKT_HUMAN	0.891	0.904	0.899	1.024	1.076	1.074
sp Q15008 PSMD6_HUMAN	0.849	0.83	0.837	1.115	1.088	0.97
sp Q15155 NOMO1_HUMAN	1.01	0.882	0.861	1.062	1.134	0.974
sp P33176 KINH_HUMAN	0.93	0.881	0.971	1.068	1.015	1.087
sp O00400 ACATN_HUMAN	0.903	1.368	1.132	1.043	1.099	1.027
sp Q92896 GSLG1_HUMAN	0.95	0.91	0.914	1.109	1.019	1.041
sp P22234 PUR6_HUMAN	0.875	0.931	0.902	1.062	1.03	1.076
sp Q02750 MP2K1_HUMAN	0.97	0.957	0.833	1.03	1.071	1.067
sp P13987 CD59_HUMAN	0.93	0.992	0.993	1.038	1.079	1.05
sp P28070 PSB4_HUMAN	0.941	0.976	0.915	1.068	1.073	1.026
sp P33992 MCM5_HUMAN	0.764	0.826	0.781	1.017	1.059	1.09
sp P83881 RL36A_HUMAN	0.65	0.617	0.638	1.087	1.017	1.06
sp Q9UBU9 NXFL1_HUMAN	0.895	0.903	0.864	1.07	0.987	1.107
sp P14923 PLAK_HUMAN	0.755	0.771	0.756	1.021	1.066	1.076
sp Q9HCE1 MOV10_HUMAN	0.68	0.901	0.895	0.95	1.08	1.131
sp P49419 AL7A1_HUMAN	0.845	0.911	0.905	1.055	0.989	1.117
sp P53618 COPB_HUMAN	0.906	0.856	0.92	1.074	1.032	1.054
sp P06737 PYGL_HUMAN	0.833	0.827	0.823	1.042	1.061	1.056
sp P07355 ANXA2_HUMAN	1.122	1.111	1.116	1.017	1.053	1.089
sp Q9UM00 TMCO1_HUMAN	0.931	0.95	1.071	1.027	1.03	1.099
sp Q9NUU6 F105A_HUMAN	0.838	0.776	0.84	1.115	1.028	1.013
sp P16615 AT2A2_HUMAN	0.979	0.989	1.04	1.033	1.074	1.048
sp P35249 RFC4_HUMAN	1.023	1.071	1.104	1.004	1.091	1.06
sp P09874 PARP1_HUMAN	0.922	0.845	0.863	1.065	1.053	1.037
sp Q01813 PFKAP_HUMAN	0.949	0.952	0.949	1.077	1.021	1.055
sp O43681 ASNA_HUMAN	0.882	0.81	0.879	0.994	1.136	1.024

sp Q16799 RNT1_HUMAN	0	1.517	1.5	0	1.556	1.596
sp Q99878 H2A11_HUMAN	0.819	0.811	0.818	0.949	1.104	1.098
sp Q99798 ACON_HUMAN	0.821	0.813	0.805	0.992	1.035	1.12
sp P13639 EF2_HUMAN	0.829	0.815	0.818	1.04	1.047	1.056
sp P62987 RL40_HUMAN	1.133	1.127	1.017	0.962	1.089	1.093
sp P16192 STA5B_HUMAN	0.9	0.901	0.902	1.012	1.132	0.999
sp Q9HC35 EMAL4_HUMAN	0.795	0.817	0.791	1.107	0.978	1.056
sp Q9HC38 GLOD4_HUMAN	0.979	0.993	1.012	1.122	1.06	1.058
sp O96005 CLPT1_HUMAN	0.932	0.951	0.997	1.023	1.094	1.022
sp Q72417 NUFP2_HUMAN	0.947	0.893	0.764	0.977	1.074	1.083
sp O00203 AP3B1_HUMAN	0.77	0.771	0.883	0.904	1.076	1.154
sp Q71UM5 RS27L_HUMAN	1.006	0.976	1.046	1.047	1.037	1.05
sp P56192 SYMC_HUMAN	0.891	0.896	0.915	1.029	1.036	1.068
sp P07437 TBBS5_HUMAN	1.135	1.167	1.088	1.252	0.972	0.905
sp Q15185 TEBP_HUMAN	1.253	1.476	1.254	0.982	1.26	0.887
sp P0972 ALDOC_HUMAN	1.067	0.982	1.006	1.092	1.04	0.996
sp Q9NX63 MIC19_HUMAN	1.153	1.137	1.07	1.046	1.1	0.978
sp P21291 CSRPI1_HUMAN	1.183	1.249	1.254	1.033	1.1	0.989
sp P31944 CASPE1_HUMAN	0.857	0.938	0.839	1.028	1.12	0.97
sp Q687X5 STE4A_HUMAN	0.982	0.901	0.909	1.056	1.014	1.047
sp O95785 WIZ_HUMAN	0.909	0.842	0.909	1.04	1.02	1.053
sp Q14676 MDC1_HUMAN	0.893	0.962	0.969	1.045	0.997	1.07
sp Q16501 LAT1_HUMAN	0.992	1.09	1.054	0.992	1.052	1.068
sp Q13085 ACACA_HUMAN	0.953	1.035	0.97	1.08	1.027	1.004
sp Q99714 HCD2_HUMAN	0.926	0.902	0.919	1.073	1.012	1.024
sp P35606 COPB2_HUMAN	0.833	0.849	0.818	1.048	1.04	1.019
sp Q9HAB3 S52A2_HUMAN	0.948	0.981	0.961	1.043	1.025	1.038
sp Q99733 NP1L4_HUMAN	0.976	0.991	0.982	1.035	1.058	1.012
sp P49915 GUAA_HUMAN	0.957	1.016	0.848	1.078	1.063	0.962
sp P49721 PSB2_HUMAN	0.938	0.908	0.918	1.034	1.058	1.01
sp P50991 TCPD_HUMAN	0.875	0.906	0.913	1.09	1.041	0.971
sp P22314 UBA1_HUMAN	0.899	0.901	0.891	1.033	1.011	1.057
sp Q99567 NUP88_HUMAN	0.813	0.762	0.747	1.074	1.06	0.965
sp P27694 RFA1_HUMAN	0.927	1.009	0.946	0.885	1.211	1.002
sp P78344 IF4G2_HUMAN	0.865	0.822	0.838	1.134	0.84	1.123
sp Q92945 FBP2_HUMAN	0.911	0.954	0.918	0.976	1.044	1.075
sp Q9BXT2 CCG4_HUMAN	0.762	0.746	0.726	1.039	1.047	1.005
sp Q4G0N4 NAKD2_HUMAN	1.064	0.935	0.952	0.857	1.226	1.007
sp P13010 XRCC5_HUMAN	0.841	0.793	0.793	0.98	1.049	1.059
sp Q92597 NDRG1_HUMAN	0	2.514	2.355	0	1.554	1.533
sp P26038 MOES_HUMAN	0.856	0.874	0.843	1.051	1.005	1.03
sp Q9Y4LJ HYOU1_HUMAN	0.903	0.926	0.929	1.051	1	1.035
sp P40925 MDHC_HUMAN	1.097	1.11	1.07	1.013	1.013	1.058
sp Q04695 K1C17_HUMAN	0.812	0.839	0.84	1	1.058	1.027
sp Q08257 QOR_HUMAN	1.014	1.012	0.982	1.074	0.908	1.102
sp P62995 TRA2B_HUMAN	1.192	1.357	0.752	1.092	1.28	0.71
sp P31939 PUR9_HUMAN	0.809	0.773	0.762	1.006	1.037	1.039
sp Q9BXJ9 NAA15_HUMAN	0.842	0.972	0.995	1.031	1.002	1.049
sp P07814 SYEP_HUMAN	0.871	0.869	0.854	0.963	1.07	1.047
sp O00151 PDLII_HUMAN	0.981	0.954	1.017	1.044	1.004	1.031
sp Q96RS6 NUDC1_HUMAN	0.977	1.022	1.034	1.028	0.987	1.062
sp P13489 RINI_HUMAN	0.948	0.97	0.953	1.045	0.998	1.032
sp Q15637 SF01_HUMAN	0.744	0.763	0.784	1.001	1.028	1.046
sp Q14566 MCM6_HUMAN	0.831	0.808	0.791	1.021	1.022	1.03
sp P04179 SODM_HUMAN	1.012	1.079	0.915	0.917	0.98	1.175
sp P11766 ADHX_HUMAN	0.935	0.869	0.877	1.082	0.992	0.999
sp Q15397 PUM3_HUMAN	0.787	0.964	0.922	1.03	1.049	0.992
sp P40939 ECHA_HUMAN	0.863	0.858	0.888	0.996	1.011	1.064

sp Q95365 1B38_HUMAN	0.969	0.92	1.019	1.052	0.989	1.028
sp Q8FY81 SPB1_HUMAN	0.813	0.788	0.791	1.055	1.144	0.871
sp Q13451 FKBP5_HUMAN	1.112	0.988	0.98	1.157	0.899	1.012
sp P55265 DSRAD_HUMAN	0.894	0.901	0.904	1.035	0.987	1.045
sp Q75323 NIPS2_HUMAN	0.953	0.925	0.969	1.021	0.998	1.049
sp Q9BSJ8 ESYT1_HUMAN	0.949	0.92	0.873	1.003	0.984	1.08
sp P61927 RL37_HUMAN	0.769	0.702	0.709	1.158	0.922	0.986
sp Q96AC1 FERM2_HUMAN	0.889	0.833	0.754	1.061	0.936	1.067
sp P31327 CPSM_HUMAN	0.799	0.797	0.803	1.024	1.016	1.022
sp Q9UKM9 RALLY_HUMAN	1.019	0.835	0.968			

sp P52597 HNRPF_HUMAN	0.894	0.962	0.887	0.988	1.008	1.01
sp O60934 NBN_HUMAN	0.941	0.901	0.839	1.062	1.015	0.927
sp P46063 RECC1_HUMAN	0.907	0.851	0.883	1.057	0.919	1.026
sp Q15005 SPCS2_HUMAN	1.035	1.052	0.974	0.976	1.018	1.006
sp P35998 PRS7_HUMAN	0.853	0.882	0.865	1.001	0.99	1.009
sp P54819 KAD2_HUMAN	1.031	0.919	1.035	0.904	1.053	1.042
sp P02545 LMNA_HUMAN	0.859	0.837	0.867	1.036	0.96	1.002
sp O00469 PLOD2_HUMAN	0.849	0.848	0.853	0.993	0.981	1.023
sp P62136 PP1A_HUMAN	0.825	0.798	0.879	1.024	0.98	0.991
sp O60763 USO1_HUMAN	0.951	0.88	0.926	1.056	0.993	0.944
sp O15533 TPSN_HUMAN	0.994	0.973	1.02	0.916	1	1.076
sp P15311 EZRI_HUMAN	0.831	0.828	0.86	1.005	0.988	0.998
sp Q9Y265 RUVB1_HUMAN	0.954	0.908	0.946	0.966	1.003	1.022
sp P30153 2AAA_HUMAN	0.945	0.996	0.96	0.994	0.997	1
sp P41250 GARS_HUMAN	0.931	1.008	0.891	0.924	1.037	1.028
sp O43592 XPOT_HUMAN	0.983	0.916	1.016	0.986	0.982	1.022
sp Q9Y446 PKP3_HUMAN	0.763	0.816	0.796	0.927	1.068	0.988
sp P13647 K2C5_HUMAN	0.933	0.957	1.012	1.009	0.99	0.984
sp Q92499 DDX1_HUMAN	0.8	0.823	0.811	0.975	1.013	0.995
sp P43243 MATR3_HUMAN	0.77	0.804	0.814	0.984	0.991	1.007
sp P49916 DNL13_HUMAN	0.84	0.8	0.865	0.996	0.993	0.991
sp P13797 PLST_HUMAN	1.053	1.001	0.996	1.005	0.998	0.977
sp P62829 RL23_HUMAN	0.303	0.294	0.519	1.087	1.078	0.814
sp O43175 SERA_HUMAN	0.88	0.931	0.861	0.983	1.01	0.986
sp P07910 HNRPC_HUMAN	0.894	0.911	0.851	0.946	1.007	1.025
sp Q06203 PUR1_HUMAN	0.866	1.042	0.936	0.922	1.016	1.039
sp P04075 ALDOA_HUMAN	0.928	0.941	0.93	0.985	1.009	0.979
sp P52292 IMAI1_HUMAN	0.858	0.853	0.861	0.988	0.943	1.041
sp P46977 STT3A_HUMAN	0.832	0.85	0.825	0.968	1.03	0.973
sp P23284 PPIB_HUMAN	0.991	0.948	0.982	1.005	1.007	0.958
sp Q96HC4 PDIL5_HUMAN	0.771	0.573	0.803	0.853	1.021	1.096
sp Q27J81 INF2_HUMAN	0.873	0.725	0.78	1.023	0.955	0.991
sp Q8WX93 PALLD_HUMAN	0.868	0.851	0.761	1.017	0.991	0.962
sp P00492 HPRT_HUMAN	0.932	0.884	0.796	1.137	0.913	0.919
sp Q96AE4 FUBP1_HUMAN	0.929	0.943	0.957	0.989	0.964	1.014
sp O60841 IF2P_HUMAN	0.869	0.863	0.736	0.991	1.023	0.942
sp Q9NUU7 DDI19A_HUMAN	0.996	0.951	1.016	1.021	0.933	1.008
sp Q8IX12 CCAR1_HUMAN	0.741	0.811	0.807	0.948	0.971	1.042
sp Q9Y230 RUVB2_HUMAN	1.011	1.004	1.003	1.007	0.999	0.955
sp P60174 PTIS_HUMAN	0.925	0.953	0.955	0.968	0.973	1.019
sp P35268 RL22_HUMAN	0.557	0.515	0.597	1.011	0.915	1.032
sp Q86VP6 CAND1_HUMAN	0.883	0.843	0.88	0.983	1.027	0.948
sp O75367 H2AY_HUMAN	0.793	0.843	0.824	0.929	1.041	0.988
sp P08237 PFKAM_HUMAN	0.863	0.827	0.928	1.003	0.955	0.999
sp Q8GW50 MET16_HUMAN	0.942	0.916	0.921	0.987	0.958	1.008
sp P42704 LPPRC_HUMAN	0.863	0.887	0.874	1.023	0.951	0.979
sp P48637 GSHB_HUMAN	1.041	1.023	1.102	0.975	0.913	1.065
sp Q96GQ7 DDX27_HUMAN	0.937	0.833	0.848	1.019	0.985	0.948
sp Q9Y263 PLAP_HUMAN	0.826	0.855	0.787	0.99	0.983	0.978
sp Q13310 PABP4_HUMAN	0.746	0.69	0.742	1.002	0.936	1.012
sp P38159 RBMX_HUMAN	0.961	1.023	0.917	0.903	1.091	0.955
sp Q9BZZ5 API5_HUMAN	0.978	1.007	0.913	1.024	1.067	0.856
sp P23786 CPT2_HUMAN	0.824	0.879	0.931	0.957	1.016	0.972
sp P28340 DPD01_HUMAN	0.694	0.724	0.921	0.869	0.97	1.105
sp Q16881 TRXR1_HUMAN	0.907	0.887	0.95	0.953	0.986	1.005
sp O95399 UTS2_HUMAN	1.002	0.944	1.002	0.999	0.971	0.972
sp O00629 IMA3_HUMAN	0.961	0.876	0.896	1.01	0.969	0.963
sp Q9UQE7 SMC3_HUMAN	0.77	0.813	0.796	0.985	0.96	0.996

sp Q9UHX1 PUF60_HUMAN	0.888	0.916	0.874	0.963	0.995	0.983
sp Q99715 COCA1_HUMAN	1.077	1.049	0.979	0.876	1.074	0.99
sp Q04828 AK1C1_HUMAN	0.912	0.946	0.917	0.997	0.988	0.954
sp P18077 RL35A_HUMAN	0.531	0.542	0.511	1.001	0.95	0.988
sp O00303 EIF3F_HUMAN	0.815	0.817	0.904	0.926	1.021	0.989
sp P49368 TCPG_HUMAN	0.821	0.843	0.84	0.965	0.975	0.996
sp P78371 TCPB_HUMAN	0.92	0.917	0.923	0.98	0.948	1.006
sp Q00610 CLH1_HUMAN	0.881	0.883	0.896	0.972	0.984	0.977
sp P53621 COPA_HUMAN	0.834	0.81	0.816	0.995	1.003	0.934
sp Q9H73 SIL1_HUMAN	0.894	0.849	0.858	0.983	0.976	0.974
sp P26639 SYTC_HUMAN	0.697	0.754	0.741	1.003	0.937	0.992
sp P21266 GSTM3_HUMAN	0.923	0.975	0.966	0.929	1.007	0.995
sp Q7L2H7 EIF3M_HUMAN	1.884	1.466	2.129	1.036	0.901	0.993
sp Q96T76 MMS19_HUMAN	0.811	0.792	0.734	0.974	0.981	0.974
sp Q14692 BMS1_HUMAN	0.55	0.501	0.528	0.815	1.021	1.094
sp Q96B11 S22A1_HUMAN	1.173	1.1	1.03	0.933	1.108	0.887
sp Q12849 GRSF1_HUMAN	0.87	0.81	0.834	1.032	0.92	0.977
sp Q14204 DYHC1_HUMAN	0.955	0.918	0.909	0.968	0.939	1.022
sp Q99436 PSB7_HUMAN	0.949	0.945	1.158	0.922	0.884	1.121
sp P17066 HSP76_HUMAN	0.96	0.908	0.963	1.087	0.925	0.914
sp Q14247 SRC8_HUMAN	0.991	0.955	0.937	0.962	0.979	0.983
sp Q15393 SF3B1_HUMAN	0.763	0.778	0.791	0.955	0.983	0.987
sp O95433 AHSA1_HUMAN	0.91	0.899	0.926	1.001	0.945	0.978
sp Q12770 SCAP_HUMAN	0.717	0.772	0.762	1.035	0.928	0.96
sp Q9BTW9 TBCD_HUMAN	0.9	0.773	0.862	1.038	0.918	0.966
sp P40227 TCPZ_HUMAN	0.909	0.969	0.869	0.926	1.028	0.966
sp P61803 DAD1_HUMAN	0.891	0.947	0.951	1.011	0.967	0.94
sp Q9UHB6 LIMA1_HUMAN	0.76	0.993	0.864	0.937	1.061	0.92
sp Q53EL6 PDCD4_HUMAN	1.053	1.006	0.995	0.965	0.943	1.01
sp P62750 RL23A_HUMAN	0.885	0.929	1.004	0.939	0.976	1.002
sp Q12797 ASPH_HUMAN	0.894	0.874	0.957	1.017	0.895	1.004
sp P38646 GRP75_HUMAN	0.873	0.883	0.873	0.972	0.971	0.973
sp P21796 VDAC1_HUMAN	0.934	0.945	0.872	0.964	1.002	0.949
sp Q13620 CUL4B_HUMAN	0.748	0.774	0.854	0.997	0.968	0.951
sp Q96TA1 NIBL1_HUMAN	0.8	0.768	0.807	0.955	0.955	1.006
sp P49189 AL9A1_HUMAN	0.879	0.927	0.957	0.944	0.956	1.014
sp P30086 PEBP1_HUMAN	0.941	0.871	0.984	0.986	0.957	0.97
sp Q13435 SF3B2_HUMAN	0.814	0.794	0.795	0.982	0.965	0.966
sp Q13423 INTM_HUMAN	0.788	0.788	0.839	0.963	0.914	1.035
sp Q8WWMT ATX2L_HUMAN	0.851	0.817	0.815	1.007	0.938	0.966
sp Q9NTJ3 SMC4_HUMAN	0.835	0.894	0.777	0.947	1.019	0.944
sp P09960 LKAH4_HUMAN	0.865	0.87	0.884	0.949	0.974	0.986
sp P22102 PUR2_HUMAN	0.89	0.881	0.894	0.99	0.956	0.963
sp P47897 SYQ_HUMAN	0.82	0.764	0.818	0.913	1.023	0.971
sp P30041 PRDX6_HUMAN	1.032	1	1.008	1.006	0.93	0.972
sp Q5T4S7 UBR4_HUMAN	0.857	0.915	0.886	0.914	1.128	0.863
sp P05198 IF2A_HUMAN	0.81	0.892	0.888	0.943	0.946	1.016
sp Q15205 SART3_HUMAN	0.9	0.876	0.945	0.946	0.897	1.063
sp P21333 FLNA_HUMAN	0.88	0.882	0.877	0.958	0.965	0.982
sp Q8TBX8 PI42C_HUMAN	0.703	0.716	0.732	0.931	1.068	0.904
sp P30740 ILEU_HUMAN	0.98	0.947	0.942	0.988	0.947	0.969
sp O60264 SMCA5_HUMAN	0.83	0.848	0.848	0.932	1.01	0.961
sp O94979 SC31A_HUMAN	0.784	0.789	0.781	1.021	0.946	0.936
sp P24298 RPB1_HUMAN	0.952	0.874	1.46	0.79	0.785	1.326
sp Q96A65 EXOC4_HUMAN	0.893	1.062	0.914	1.009	0.828	1.066
sp O00422 SAP18_HUMAN	0.945	0.988	0.893	0.959	1.114	0.829
sp P43686 PRS6B_HUMAN	0.9	0.944	0.922	1.027	0.924	0.95
sp P41252 SYIC_HUMAN	0.869	1.064	0.942	0.909	0.937	1.054

sp P26641 EF1G_HUMAN	0.885	0.854	0.865	0.986	0.947	0.967
sp P17987 TCPA_HUMAN	0.886	0.874	0.872	0.962	1.031	0.907
sp P27708 PYR1_HUMAN	0.936	0.948	1.037	0.956	0.976	0.967
sp P49748 ACADV_HUMAN	0.835	0.842	0.872	1.022	0.9	0.977
sp Q13247 SRSF6_HUMAN	0.778	0.786	0.828	1.017	1.063	0.817
sp P08779 K1C16_HUMAN	0.384	0.348	0.323	0.902	0.809	1.186
sp Q9BXP5 SRRT_HUMAN	0.784	0.757	0.778	0.974	0.941	0.981
sp Q15366 PCBP2_HUMAN	0.926	0.936	0.916	0.972	0.952	0.972
sp P49792 RBP2_HUMAN	0.933	0.707	0.719	0.808	1.052	1.035
sp Q9NL29 MAT2B_HUMAN</						

sp P62333 PRS10_HUMAN	0.886	0.934	0.904	0.938	0.995	0.915
sp Q9NRW1 RAB6B_HUMAN	1.002	1.102	1.124	0.898	0.937	1.013
sp P11413 G6PD_HUMAN	0.84	0.821	0.809	0.915	0.959	0.973
sp P52209 PGD_HUMAN	0.843	0.8	0.791	0.945	0.976	0.926
sp Q16555 DPYL2_HUMAN	0.768	1.021	0.914	0.764	1.025	1.058
sp Q71D13 H32_HUMANS	0.462	0.467	0.471	0.97	0.953	0.921
sp Q75821 EIF3G_HUMAN	0.978	1.111	0.957	0.994	0.96	0.889
sp P22695 QCR2_HUMAN	0.746	0.78	0.749	0.955	0.971	0.914
sp P61221 ABC1_HUMAN	0.889	0.898	0.873	0.95	0.939	0.95
sp Q99613 EIF3C_HUMAN	0.714	0.768	0.867	0.904	0.957	0.977
sp Q96P70 IPO9_HUMAN	0.883	0.879	0.894	0.943	0.943	0.95
sp O75369 FLNB_HUMAN	0.804	0.802	0.838	0.951	0.931	0.954
sp P12814 ACTN1_HUMAN	0.862	0.832	0.854	0.864	1.006	0.963
sp O14744 ANM5_HUMAN	0.866	0.881	0.819	0.889	0.927	1.016
sp P21980 TGM2_HUMAN	0.976	0.977	0.971	0.978	0.903	0.952
sp P11387 TOP1_HUMAN	0.766	0.818	0.804	0.917	0.913	1.001
sp O94855 SC24D_HUMAN	0.837	0.76	0.855	0.967	0.935	0.93
sp P49720 PSB3_HUMAN	0.837	0.744	0.837	0.922	0.952	0.957
sp P12268 IMDH2_HUMAN	0.968	0.951	0.964	0.959	0.935	0.937
sp P49959 MRE11_HUMAN	0.934	0.832	0.904	0.885	0.942	1.003
sp P25705 ATPA_HUMAN	0.914	0.919	0.915	0.947	0.942	0.94
sp Q15459 SF3A1_HUMAN	0.826	0.806	0.802	0.957	0.964	0.907
sp Q13428 TCOF_HUMAN	0.958	0.949	0.977	0.964	0.964	0.901
sp Q8TEM1 PO210_HUMAN	0.724	0.702	0.665	0.845	1.043	0.937
sp P63104 I43S2_Z_HUMAN	0.964	0.935	0.937	0.971	0.902	0.95
sp Q9NYU2 UGGG1_HUMAN	0.778	0.806	0.817	0.966	0.957	0.899
sp Q08211 DHX9_HUMAN	0.818	0.815	0.808	0.956	0.926	0.938
sp P47712 PA24A_HUMAN	0.763	0.757	0.781	0.953	0.961	0.906
sp P02786 TFR1_HUMAN	0.776	0.781	0.76	0.903	0.973	0.944
sp P62495 ERF1_HUMAN	0.866	0.808	0.888	0.868	0.95	1
sp P23526 SAHH_HUMAN	0.852	0.826	0.834	0.902	0.968	0.948
sp Q5SSJ5 HP1B3_HUMAN	0.891	0.83	0.822	0.997	0.938	0.882
sp Q7Z2W4 ZCCHV_HUMAN	0.892	0.824	0.873	0.97	0.989	0.856
sp P06744 G6PL_HUMAN	0.899	0.896	0.895	0.945	0.991	0.88
sp P63244 RACK1_HUMAN	1.022	0.957	0.944	0.923	0.941	0.951
sp P14324 FPFS_HUMAN	0.857	0.86	0.841	0.965	0.931	0.919
sp P23246 SFPQ_HUMAN	0.815	0.813	0.797	0.947	0.937	0.931
sp Q8TEX9 IPO4_HUMAN	0.853	0.993	0.948	0.873	0.964	0.978
sp Q9NQX3 GEPH_HUMAN	0.893	0.885	0.857	0.864	1.001	0.948
sp P25205 MCM3_HUMAN	0.776	0.78	0.751	0.934	0.935	0.944
sp P06733 ENO4_HUMAN	1.033	1.069	1.074	0.965	0.915	0.931
sp Q13151 ROAO_HUMAN	1.03	1.017	0.97	0.911	0.951	0.946
sp Q92841 DDX17_HUMAN	0.815	0.828	0.842	0.932	0.92	0.954
sp Q9Y5K5 UCHL5_HUMAN	1.003	0.967	1.015	0.871	0.926	1.009
sp Q07954 LRP1_HUMAN	0.888	0.798	0.897	1.036	0.809	0.959
sp Q9UXJ4 APC5_HUMAN	0.84	0.885	0.845	0.893	0.904	1.007
sp Q15006 EMC2_HUMAN	1.028	0.817	0.969	0.92	0.797	1.086
sp P05388 RLA0_HUMAN	0.914	0.96	0.998	0.906	0.935	0.962
sp Q8TEQ6 GEMI5_HUMAN	0.844	0.863	0.823	0.958	0.935	0.909
sp P11142 HSP7C_HUMAN	0.981	0.965	0.991	0.945	0.93	0.926
sp O43818 U3IP2_HUMAN	0.836	0.933	0.93	0.928	0.843	1.03
sp Q9Y3F4 STRAP_HUMAN	0.892	0.895	0.928	0.941	0.935	0.924
sp O96019 ACL6A_HUMAN	0.936	0.904	0.906	0.911	0.954	0.934
sp Q92616 GCN1_HUMAN	0.845	0.873	0.898	0.912	0.908	0.979
sp Q9NR30 DDX21_HUMAN	0.752	0.781	0.783	0.868	0.997	0.933
sp P48444 COPD_HUMAN	0.879	0.848	0.888	0.88	1.053	0.864
sp P51648 AL3A2_HUMAN	1.014	1.002	0.917	0.824	1.003	0.97
sp Q13200 PSMD2_HUMAN	0.752	0.777	0.794	0.975	0.849	0.972

sp P35579 MYH9_HUMAN	0.756	0.797	0.758	0.926	0.929	0.941
sp Q13813 SPTN1_HUMAN	0.878	0.889	0.889	0.947	0.933	0.916
sp P07741 APT_HUMAN	0.918	0.945	0.911	0.934	0.949	0.912
sp P54886 PCSS_HUMAN	0.8	0.805	0.809	0.952	0.927	0.915
sp O43760 SNG2_HUMAN	1.036	1.092	1.039	1.241	0.718	0.835
sp P49589 SYCC_HUMAN	0.902	0.88	0.889	0.893	0.924	0.977
sp P31930 QCR1_HUMAN	0.842	0.854	0.885	0.956	0.949	0.889
sp Q04446 GLGB_HUMAN	0.729	0.746	0.752	0.864	0.932	0.997
sp P21964 COMT_HUMAN	1.043	0.963	0.971	1.027	0.873	0.893
sp O60488 ACSL4_HUMAN	0.874	0.815	0.825	0.967	0.931	0.894
sp Q98T78 CSN4_HUMAN	0.971	0.956	0.953	0.94	0.958	0.893
sp O43390 HNRPR_HUMAN	0.797	0.869	0.84	0.98	0.941	0.869
sp P07737 PROF1_HUMAN	0.517	0.832	0.543	0.86	1.102	0.827
sp Q5JTH9 RPR12_HUMAN	0.81	0.862	0.795	0.927	0.992	0.871
sp P14735 IDE_HUMAN	0.751	0.989	0.816	0.937	0.924	0.927
sp Q12906 ILF3_HUMAN	0.748	0.739	0.749	0.926	0.929	0.931
sp Q93052 LPP_HUMAN	0.825	0.773	0.865	0.922	0.937	0.925
sp O14980 XP01_HUMAN	0.817	0.788	0.793	0.947	0.915	0.922
sp P31947 I433S_HUMAN	0.911	0.952	0.954	0.938	0.905	0.941
sp O15427 MOT4_HUMAN	0.943	0.959	1.002	0.909	0.948	0.925
sp P60228 EIF3E_HUMAN	0.761	0.759	0.764	0.899	0.959	0.923
sp Q12931 TRAP1_HUMAN	0.786	0.814	0.811	0.953	0.92	0.908
sp P12956 XRCC6_HUMAN	0.861	0.897	0.868	0.911	0.915	0.955
sp P43304 GPDM_HUMAN	0.862	0.811	0.859	0.903	0.907	0.97
sp P84098 RL19_HUMAN	0.858	0.82	0.842	0.984	0.909	0.887
sp Q9NSD9 SYFB_HUMAN	0.856	0.838	0.83	0.92	0.931	0.927
sp P20073 ANXA7_HUMAN	0.904	0.968	0.918	0.93	0.993	0.854
sp P06865 HEXA_HUMAN	0.888	0.925	0.928	0.92	0.959	0.897
sp Q8N127 THOC2_HUMAN	0.842	0.806	0.814	1.021	0.824	0.928
sp Q13642 FH1L_HUMAN	0.834	0.819	0.889	0.914	0.874	0.984
sp Q94973 AP2A2_HUMAN	0.771	0.816	0.836	0.929	0.908	0.934
sp P30520 PURA2_HUMAN	0.827	0.855	0.861	0.879	0.968	0.922
sp Q15149 PLEC_HUMAN	0.882	0.875	0.853	0.923	0.918	0.927
sp Q04726 TLE3_HUMAN	0.792	0.802	0.756	1.01	0.753	1.005
sp Q96EP5 DAZP1_HUMAN	0.872	0.804	0.901	0.888	0.839	1.04
sp P51610 HCFC1_HUMAN	0.907	0.846	0.832	0.867	0.872	1.028
sp Q9Y490 TLN1_HUMAN	0.817	0.789	0.851	0.894	0.948	0.922
sp Q00625 PIR_HUMAN	1.194	1.176	1.217	0.903	0.921	0.94
sp O75306 NDUS2_HUMAN	0.877	0.823	0.846	0.926	0.876	0.96
sp P78527 PRKDC_HUMAN	0.875	0.87	0.879	0.899	0.924	0.937
sp P61254 RL26_HUMAN	0.891	0.934	0.955	0.954	0.896	0.91
sp Q0VDF9 HSP7E_HUMAN	0.956	1.039	1.041	0.981	0.947	0.827
sp Q8IWS0 PHF6_HUMAN	0.991	0.935	0.911	0.861	0.87	1.022
sp P08651 NFIC_HUMAN	0.819	0.733	0.76	0.879	0.958	0.914
sp P12081 SYHC_HUMAN	0.892	0.918	0.889	0.857	0.923	0.971
sp O43660 PLRG1_HUMAN	0.772	0.755	0.811	0.909	0.936	0.905
sp O43670 ZN207_HUMAN	0.952	0.846	0.955	1.004	0.798	0.948
sp Q34795 MYO1B_HUMAN	0.767	0.754	0.787	0.947	0.921	0.881
sp Q16790 CAH9_HUMAN	0.969	1.016	1.053	0.863	0.86	1.026
sp Q00796 DHSO_HUMAN	0.847	1.078	0.842	0.915	1.01	0.822
sp Q14C86 GAPD1_HUMAN	0.857	0.862	0.842	0.937	0.895	0.914
sp Q13616 CUL1_HUMAN	0.864	0.851	0.849	1.019	0.915	0.811
sp P23528 COF1_HUMAN	0.799	0.83	0.78	0.901	0.985	0.859
sp P62888 RL30_HUMAN	0.426	0.443	0.521	0.926	0.957	0.861
sp Q96I59 SYNM_HUMAN	1.001	0.949	0.947	0.932	0.911	0.899
sp O15042 SR140_HUMAN	0.759	0.817	0.823	0.978	0.887	0.876
sp Q13724 MOGS_HUMAN	0.739	0.823	0.738	0.909	0.929	0.903
sp P62424 RL7A_HUMAN	0.716	0.733	0.737	0.902	0.948	0.89

sp P50454 SERPH_HUMAN	0.955	0.916	0.991	0.907	0.945	0.889
sp P07195 LDHB_HUMAN	1.024	1.014	1.053	0.911	0.915	0.914
sp P00505 AATM_HUMAN	0.9	0.903	0.921	0.918	0.921	0.901
sp P30043 BLVRB_HUMAN	0.897	0.833	0.846	0.953	0.869	0.916
sp Q9BP6 DPYL5_HUMAN	0.567	0.552	0.564	0.903	0.904	0.931
sp Q99832 TCPH_HUMAN	0.794	0.784	0.801	0.931	0.898	0.91
sp P63261 ACTG_HUMAN	0.764	0.795	0.783	0.902	0.925	0.909
sp P48147 PPCE_HUMAN	0.944	1.024	0.929	0.912	0.939	0.88
sp Q9BT2C DIDO1_HUMAN	0.82	0.704	0.844	0.935	0.858	0.937

sp Q9UMS4 PRP19_HUMAN	0.844	0.861	0.864	0.887	0.896	0.916
sp POCW18 PRSS6_HUMAN	0.639	0.679	0.661	0.823	0.958	0.918
sp P17676 CEPB_HUMAN	0.915	0.947	0.946	0.928	0.89	0.88
sp P35573 GDE_HUMAN	0.986	0.918	0.928	0.902	0.898	0.895
sp Q9Y6M1 IF2B2_HUMAN	0.749	0.792	0.842	0.826	0.952	0.916
sp P61081 UBC12_HUMAN	0.99	0.912	0.958	0.887	0.883	0.925
sp Q13838 DX39B_HUMAN	0.894	0.929	0.885	0.883	0.917	0.895
sp Q7Z2K6 ERMP1_HUMAN	0.797	0.82	0.787	0.871	0.911	0.91
sp Q99879 H2B1M_HUMAN	0.723	0.766	0.741	0.88	0.903	0.909
sp Q9NR45 SIAS_HUMAN	0.929	0.967	0.96	0.837	0.943	0.912
sp P29692 EF1D_HUMAN	1.025	1.006	1.046	0.92	0.829	0.942
sp Q9NNW7 TRXR2_HUMAN	0.902	0.916	0.883	0.981	0.911	0.799
sp O15260 SURF4_HUMAN	0.76	0.883	1.02	0.762	0.804	1.125
sp Q7OUQ0 IKIP_HUMAN	1.443	0	1.302	1.429	0	1.261
sp P51659 DHB4_HUMAN	0.879	0.808	0.868	0.918	0.799	0.97
sp Q9BTE3 MCMBP_HUMAN	0.935	0.896	0.92	0.864	0.91	0.911
sp O14776 TCRG1_HUMAN	0.875	0.823	0.85	0.925	0.742	1.017
sp Q14152 EIF3A_HUMAN	0.758	0.734	0.771	0.873	0.893	0.919
sp O15371 EIF3D_HUMAN	0.828	0.849	0.882	0.875	0.934	0.874
sp P61981 I433G_HUMAN	0.826	0.879	0.825	0.892	0.871	0.919
sp A6NDG6 PGP_HUMAN	0.935	0.931	0.88	0.899	0.885	0.897
sp Q8WUM0 NU133_HUMAN	0.802	0.685	0.765	0.953	0.849	0.88
sp Q15424 SAFB1_HUMAN	0.846	0.831	0.836	0.955	0.812	0.912
sp O95470 SGPL1_HUMAN	1.071	0.933	1.046	0.927	0.841	0.91
sp Q9ULT8 HECD1_HUMAN	0.783	0.66	0.655	0.96	0.853	0.866
sp P82675 RT05_HUMAN	0.783	0.793	0.808	0.974	0.89	0.814
sp Q15942 ZYX_HUMAN	0.822	0.749	0.797	0.936	0.845	0.895
sp Q7L2J0 MEPC1_HUMAN	0.874	0.862	0.857	0.972	0.861	0.843
sp P08758 ANXA5_HUMAN	1.085	1.091	1.072	0.873	0.935	0.866
sp P21283 VATC1_HUMAN	0.81	0.852	0.883	0.866	0.784	1.024
sp Q7Z739 YTHD3_HUMAN	0.784	0.956	0.783	0.862	0.92	0.891
sp Q13547 HDAC1_HUMAN	0.82	0.787	0.725	0.913	0.866	0.894
sp P07954 FUMH_HUMAN	0.932	0.825	0.888	0.937	0.822	0.913
sp Q8TCS8 PNPT1_HUMAN	0.876	0.832	0.826	0.906	0.845	0.919
sp P19525 E2AK2_HUMAN	0.942	0.906	0.835	0.891	0.951	0.829
sp Q9UHD8 SEPT9_HUMAN	0.825	0.83	0.829	0.966	0.83	0.874
sp P52564 MP2K6_HUMAN	0.77	0.805	0.784	0.852	0.914	0.902
sp P34896 GLYC_HUMAN	1.031	0.959	0.88	0.933	0.876	0.859
sp Q08J23 INSN2_HUMAN	0.851	0.821	0.82	0.77	0.959	0.939
sp Q8NDH3 PEPL1_HUMAN	0.799	0.828	0.804	0.904	0.858	0.905
sp Q7KZF4 SNDF1_HUMAN	0.798	0.779	0.779	0.876	0.876	0.915
sp O60832 DKC1_HUMAN	0.913	0.934	0.856	0.916	0.935	0.812
sp Q05397 FAK1_HUMAN	0.759	0.73	0.828	0.886	0.827	0.949
sp Q13217 DNJC3_HUMAN	0.957	0.931	0.92	0.906	0.915	0.841
sp P26640 SYVC_HUMAN	0.823	0.785	0.79	0.917	0.874	0.871
sp O00429 DNM1L_HUMAN	0.834	0.837	0.885	0.876	0.844	0.94
sp Q9Y3I0 RTCB_HUMAN	0.871	0.848	0.858	0.904	0.839	0.917
sp Q9ULV4 COR1C_HUMAN	0.783	0.822	0.793	0.906	0.825	0.93
sp P50416 CPT1A_HUMAN	0.856	0.871	0.806	0.871	0.892	0.896
sp Q16181 SEPT7_HUMAN	0.859	0.801	0.815	0.921	0.865	0.872
sp Q9UN86 G3BP2_HUMAN	0.904	0.85	0.84	0.886	0.852	0.921
sp Q96CW1 AP2M1_HUMAN	0.806	0.844	0.785	0.903	0.855	0.9
sp P11940 PABP1_HUMAN	0.705	0.708	0.725	0.917	0.851	0.89
sp Q9HAV0 GBB4_HUMAN	0.94	0.995	0.962	0.847	0.945	0.865
sp Q9BPX3 CND3_HUMAN	0.799	0.785	0.802	0.904	0.909	0.844
sp Q9Y2W1 TR150_HUMAN	0.718	0.753	0.732	0.805	0.93	0.921
sp P52701 MSH6_HUMAN	0.808	0.839	0.768	0.904	0.971	0.78
sp Q9UJS0 CMC2_HUMAN	0.88	0.887	0.917	0.879	0.874	0.903

sp Q93008 USP9X_HUMAN	0.94	0.847	0.781	0.928	0.878	0.849
sp P61163 ACTZ_HUMAN	0.687	0.799	0.722	0.909	0.841	0.904
sp Q9UNF1 MAGD2_HUMAN	0.822	0.779	0.82	0.857	0.872	0.925
sp P68371 TB4B4_HUMAN	0.808	0.874	0.855	0.871	0.901	0.882
sp P07942 LAMB1_HUMAN	0.779	0.664	0.896	0.953	0.832	0.867
sp Q9UBQ0 VPS29_HUMAN	0.828	0.918	0.931	0.891	0.909	0.85
sp Q9BP2/GNL3_HUMAN	0.824	0.833	0.842	0.869	0.871	0.909
sp Q8N1F7 NUP93_HUMAN	0.784	0.766	0.734	0.871	0.928	0.851
sp Q9Y295 DRG1_HUMAN	0.914	0.763	0.809	0.938	0.859	0.852
sp Q9NTZ6 RBM12_HUMAN	0.776	0.71	0.691	0.913	0.818	0.918
sp Q9NXF1 TEX10_HUMAN	0.769	0.746	0.737	0.859	0.947	0.842
sp Q8ND83 SLAI1_HUMAN	0.843	0.817	0.84	0.866	0.872	0.909
sp Q16576 RBBP7_HUMAN	0.881	0.686	0.501	1.062	0.92	0.665
sp P52294 IMA5_HUMAN	0.866	0.848	0.878	0.87	0.887	0.889
sp O60568 PLOD3_HUMAN	0.788	0.813	0.861	0.885	0.838	0.921
sp P84095 RHOQ_HUMAN	0.949	0.931	0.926	0.832	0.951	0.862
sp P62899 RL31_HUMAN	0.508	0.61	0.705	0.842	0.843	0.96
sp P62805 H4_HUMAN	0.929	0.92	0.982	0.861	0.873	0.91
sp Q9PLO0 VAPA_HUMAN	0.932	0.913	0.969	0.919	0.855	0.869
sp O95163 ELP1_HUMAN	0.829	0.87	0.813	0.901	0.933	0.809
sp Q9H583 HEAT1_HUMAN	0.785	0.815	0.767	0.868	0.932	0.842
sp P46087 NOP2_HUMAN	0.742	0.768	0.757	0.837	0.913	0.891
sp P55809 SCOT1_HUMAN	0.858	0.91	0.867	0.862	0.828	0.95
sp Q02878 RL6_HUMAN	0.925	0.958	0.913	0.848	0.903	0.889
sp P52948 NUP98_HUMAN	0.779	0.792	0.754	0.918	0.813	0.909
sp Q99848 EBP2_HUMAN	0.891	0.868	0.821	0.882	0.889	0.868
sp P10155 RO60_HUMAN	0.961	0.949	0.899	0.915	0.855	0.869
sp P60660 MYL6_HUMAN	0.526	0.492	0.465	0.833	0.979	0.826
sp Q14978 NOLC1_HUMAN	0.795	0.741	0.695	0.878	0.88	0.879
sp P35555 FBN1_HUMAN	0.86	0.853	0.884	0.935	0.917	0.784
sp Q01433 AMPD2_HUMAN	0.834	0.824	0.798	0.934	0.857	0.845
sp Q14157 UBP2L_HUMAN	1.113	0.976	0.98	0.897	0.88	0.859
sp Q15233 NONO_HUMAN	0.862	0.85	0.887	0.89	0.865	0.881
sp P50552 VASP_HUMAN	0.91	0.816	0.844	0.9	0.836	0.895
sp Q9U4L6 PSME2_HUMAN	0.633	0.963	0.7	0.861	0.839	0.931
sp Q9N56 MBNL1_HUMAN	0.829	0.858	0.857	1.068	0.79	0.773
sp P61011 SRP54_HUMAN	0.901	0.928	0.875	0.794	0.883	0.951
sp Q86X55 CARM1_HUMAN	1.299	1.266	0.83	0.638	1.087	0.903
sp P49327 FAS_HUMAN	0.814	0.844	0.798	0.867	0.908	0.853
sp P33991 MCM4_HUMAN	0.776	0.815	0.839	0.847	0.891	0.888
sp P14868 SYDC_HUMAN	0.971	0.95	0.973	0.878	0.907	0.839
sp P52888 THOP1_HUMAN	0.834	0.837	0.866	0.911	0.843	0.869
sp P00338 LDHA_HUMAN	1.056	1.064	0.929	0.783	0.834	1.004
sp Q9Y262 EIF3L_HUMAN	0.729	0.727	0.735	0.897	0.847	0.876
sp O43776 SYNC_HUMAN	0.79	0.886	0.925	0.814	0.91	0.894
sp P36957 ODO2_HUMAN	0.849	0.803	0.885	0.806	0.868	0.944
sp Q9NY33 DPP3_HUMAN	0.864	0.868	0.853	0.865	0.863	0.888
sp P35610 SOAT1_HUMAN	0.791	0.965	0.844	0.774	0.951	0.89
sp Q13185 CBX3_HUMAN	0.834	0.867	0.883	0.832	0.912	0.871
sp P22626 ROA2_HUMAN	1.057	1.064	1.078	0.859	0.874	0.881
sp Q93009 UBP7_HUMAN	0.83	0.849	0.911	0.904	0.821	0.888
sp P61313 JRL15_HUMAN	0.819	0.81	0.817	0.867	0.889	0.856
sp O76003 GLRX3_HUMAN	1.04	0.998	1.013	0.855	0.865	0.893
sp Q09666 AHNK_HUMAN	0.74	0.739	0.712	0.864	0.87	0.878
sp Q8TDD1 DDX54_HUMAN	0.769	0.869	0.806	0.848	0.909	0.854
sp Q8TAQ2 SMRC2_HUMAN	0.75	0.876	0.762	0.809	0.907	0.894
sp P46459 NSF_HUMAN	0.894	0.936	0.934	0.868	0.893	0.847
sp P49411 EFTU_HUMAN	0.818	0.831	0.845	0.883	0.867	0.857

sp Q12788 TBL3_HUMAN	0.783	0.768	0.752	0.887	0.83	0.891
sp P51532 SMCA4_HUMAN	0.723	0.70	0.755	0.839	0.888	0.88
sp O60884 DNJA2_HUMAN	0.868	0.85	0.797	0.891	0.838	0.878
sp Q9HCD5 NCOA5_HUMAN	0.827	0.921	0.887	0.826	0.916	0.862
sp Q9V838 WDR18_HUMAN	0.804	0.853	0.781	0.931	0.804	0.868
sp Q01518 CAP1_HUMAN	0.884	0.878	0.981	0.891	0.89	0.821
sp Q92552 RT27_HUMAN	0.811	0.822	0.835	0.884	0.862	0.857
sp Q86TX2 ACOT1_HUMAN	0.853	0.826	0.936	0.851	0.837	0.914
sp Q8NB5 GT251_HUMAN	0.964	0.788	0.81	0.977	0.817	0.808
sp Q8NE71 ABC1_HUMAN	0.933	0.				

sp Q96PU4 UHRF2_HUMAN	1.04	0.847	0.785	0.655	0.981	0.934
sp P43897 EFTS_HUMAN	1.087	1.093	1.077	0.862	0.894	0.815
sp Q6P1A2 MBOA5_HUMAN	0.762	0.869	0.745	0.88	0.857	0.833
sp P15927 RFA2_HUMAN	1.03	0.938	1.023	0.847	0.848	0.873
sp Q9Y2Z0 NGT1_HUMAN	0.89	1.11	1.003	0.697	0.863	1.008
sp O75694 NU155_HUMAN	0.682	0.745	0.727	0.862	0.853	0.851
sp Q9BY44 EIF2A_HUMAN	0.765	0.809	0.786	0.842	0.88	0.843
sp P46781 IRS9_HUMAN	0.793	0.79	0.793	0.85	0.86	0.854
sp P60842 IF4A1_HUMAN	0.794	0.841	0.849	0.813	0.876	0.874
sp P49591 SYSCE_HUMAN	0.853	0.82	0.909	0.914	0.893	0.754
sp Q13630 FCL_HUMAN	0.828	0.798	0.923	0.865	0.844	0.851
sp Q7L2E3 DXH30_HUMAN	0.807	0.853	0.78	0.815	0.954	0.791
sp P60953 CDC42_HUMAN	1.021	0.976	1.024	0.891	0.824	0.844
sp Q13393 PLD1_HUMAN	0.855	0.736	0.856	0.909	0.819	0.83
sp P31942 HNRRH3_HUMAN	0.974	0.959	0.988	0.895	0.835	0.828
sp P62263 RS14_HUMAN	0.498	0.378	0.359	0.803	0.802	0.951
sp Q9BW60 ELOV1_HUMAN	0.861	0.873	0.954	0.767	0.893	0.895
sp Q92890 UFD1_HUMAN	0.841	0.911	0.879	0.886	0.821	0.848
sp O60437 PEPL_HUMAN	0.763	0.816	0.83	0.825	0.795	0.935
sp P00403 COX2_HUMAN	0.895	0.845	0.944	0.887	0.825	0.841
sp Q9NZ01 TECR_HUMAN	0.819	0.796	0.81	0.906	0.754	0.893
sp Q9H2P0 ADNP_HUMAN	0.77	0.893	0.842	0.919	0.757	0.876
sp Q99805 TM9S2_HUMAN	0.846	0.687	0.953	0.87	0.915	0.768
sp P98175 RBM10_HUMAN	1.01	0.83	1.005	0.898	0.749	0.902
sp Q86U42 PABP2_HUMAN	0.891	0.792	0.802	0.826	0.858	0.863
sp Q969V3 NCLN_HUMAN	0.817	0.902	0.809	0.885	0.861	0.8
sp P26358 DNMT1_HUMAN	0.792	0.806	0.791	0.851	0.87	0.825
sp O75663 TIPRL_HUMAN	0.971	0.991	0.895	0.915	0.795	0.836
sp Q12905 ILF2_HUMAN	0.843	0.815	0.772	0.901	0.791	0.852
sp Q9GZR7 DDX24_HUMAN	0.766	0.796	0.692	0.825	0.816	0.901
sp P27105 STOM_HUMAN	0.748	0.717	0.688	0.847	0.828	0.866
sp P46779 RL28_HUMAN	0.704	0.698	0.695	0.837	0.864	0.84
sp O43684 BUB3_HUMAN	0.856	0.854	0.885	0.791	0.882	0.868
sp Q99459 CDC5L_HUMAN	0.691	0.679	0.681	0.907	0.77	0.863
sp P00571 DDX3X_HUMAN	0.75	0.732	0.745	0.833	0.846	0.86
sp P25786 PSA1_HUMAN	0.841	0.74	0.827	0.862	0.843	0.834
sp Q96T58 MINT_HUMAN	0.65	0.661	0.714	0.786	0.896	0.857
sp P62140 PP1B_HUMAN	0.885	0.875	0.693	0.902	0.918	0.718
sp Q6ZSZ5 ARHGI_HUMAN	0.789	0.81	0.829	0.857	0.822	0.856
sp Q5RKV6 EXOS6_HUMAN	0.875	0.905	0.866	0.794	0.888	0.852
sp Q14690 RRP5_HUMAN	0.797	0.855	0.8	0.82	0.887	0.827
sp P23219 PGH1_HUMAN	0.825	0.802	0.817	0.863	0.824	0.846
sp Q9UBM7 DHCR7_HUMAN	0.757	0.873	0.807	0.985	0.794	0.753
sp Q9UHR6 ZNH12_HUMAN	0.774	0.834	0.775	0.898	0.797	0.833
sp P04792 HSBP1_HUMAN	0.858	0.829	0.798	0.877	0.838	0.811
sp O75643 U520_HUMAN	0.8	0.799	0.799	0.812	0.873	0.843
sp Q9BX55 AP1M1_HUMAN	0.85	0.883	0.838	0.803	0.887	0.835
sp Q8NFW8 NEUEA_HUMAN	0.884	0.854	0.863	0.841	0.86	0.823
sp P63000 RAC1_HUMAN	1.004	0.948	0.974	0.75	0.798	0.976
sp P34897 GLYM_HUMAN	0.95	0.947	0.939	0.857	0.827	0.838
sp Q8IXB1 DJC10_HUMAN	0.858	0.87	0.858	0.796	0.824	0.901
sp Q9UBT2 SAE2_HUMAN	0.871	0.78	0.826	0.852	0.828	0.841
sp Q92979 NEP1_HUMAN	0.844	0.808	0.958	0.841	0.811	0.868
sp P11172 UMPS_HUMAN	0.893	0.918	0.877	0.83	0.788	0.903
sp Q15437 SC23B_HUMAN	0.846	0.659	0.786	0.931	0.758	0.829
sp Q8WVM8 SCFD1_HUMAN	0.803	0.775	0.749	0.796	0.816	0.905
sp Q96T88 UHRF1_HUMAN	0.773	0.687	0.751	0.908	0.763	0.845
sp Q969X5 ERGI1_HUMAN	0.888	0.872	0.904	0.847	0.831	0.837

sp Q01082 SPTB2_HUMAN	0.831	0.832	0.804	0.842	0.832	0.84
sp P15559 NQO1_HUMAN	0.745	0.794	0.697	0.799	0.916	0.797
sp Q13409 DC112_HUMAN	0.753	0.758	0.736	0.842	0.855	0.815
sp P51991 ROA3_HUMAN	0.918	0.949	0.966	0.837	0.829	0.844
sp Q92922 SMRC1_HUMAN	0.779	0.837	0.781	0.832	0.87	0.808
sp Q13155 AIMP2_HUMAN	0.953	0.853	0.829	0.843	0.819	0.848
sp P30876 RPB2_HUMAN	0.676	0.707	0.766	0.846	0.854	0.81
sp O14732 IMP2A_HUMAN	0.831	0.805	0.808	0.807	0.844	0.858
sp Q9Y305 ACOT9_HUMAN	0.859	0.856	0.849	0.822	0.856	0.831
sp O60701 UGDH_HUMAN	0.889	0.964	0.965	0.706	0.891	0.912
sp Q9BS8 ERP44_HUMAN	0.873	0.868	0.852	0.819	0.844	0.844
sp Q29RF7 PDS5A_HUMAN	0.891	0.757	0.69	0.801	0.844	0.86
sp Q9UNM6 PSD13_HUMAN	0.836	0.829	0.87	0.829	0.8	0.873
sp Q9Y3U8 RL36_HUMAN	0.621	0.608	0.612	0.807	0.889	0.804
sp O95202 LETM1_HUMAN	0.8	0.839	0.843	0.862	0.797	0.841
sp Q9BW92 SYTM_HUMAN	0.72	0.813	0.75	0.849	0.837	0.814
sp Q9Y606 TRUA_HUMAN	0.944	1.019	0.897	0.843	0.861	0.796
sp Q9H4A4 AMPB_HUMAN	0.85	0.821	0.827	0.849	0.814	0.837
sp Q8N163 CCAR2_HUMAN	0.728	0.701	0.735	0.853	0.756	0.89
sp O75027 ABC7_HUMAN	0.701	0.655	0.846	0.84	0.906	0.752
sp Q5VTE0 EF1A3_HUMAN	0.926	0.9	0.916	0.784	0.867	0.846
sp Q01780 EXOSX_HUMAN	0.815	0.811	0.79	0.826	0.873	0.799
sp O60563 CCNT1_HUMAN	0.812	0.815	0.838	0.816	0.855	0.826
sp P17931 LEG3_HUMAN	0.757	0.799	0.726	0.827	0.804	0.865
sp Q15418 KS6A1_HUMAN	0.761	0.78	0.747	0.865	0.811	0.82
sp Q15019 SEPT2_HUMAN	0.796	0.84	0.783	0.837	0.857	0.802
sp P83731 RL24_HUMAN	0.858	0.839	0.834	0.829	0.86	0.806
sp Q8IY67 RAVR1_HUMAN	0.738	0.763	0.566	0.816	0.841	0.838
sp Q15293 RNC1_HUMAN	0	1.14	1.313	0	1.072	1.422
sp P29144 TPP2_HUMAN	0.825	0.804	0.758	0.899	0.807	0.787
sp Q32CQ8 TIM50_HUMAN	0.85	0.838	0.829	0.806	0.812	0.873
sp P36915 GNL1_HUMAN	0.849	0.959	0.889	0.858	0.894	0.739
sp Q6UB35 C1TM_HUMAN	0.868	0.742	0.857	0.723	0.779	0.99
sp P62191 PRSA4_HUMAN	0.868	0.838	0.875	0.807	0.836	0.848
sp Q9BQG0 MBB1A_HUMAN	0.843	0.797	0.69	0.776	0.797	0.918
sp P39023 RL3_HUMANs	0.776	0.795	0.776	0.818	0.844	0.827
sp P24534 EF1B_HUMAN	1.033	1.051	1.094	0.813	0.837	0.838
sp Q15629 TRAM1_HUMAN	0.87	0.837	0.887	0.829	0.788	0.872
sp Q96IU4 ABHEB_HUMAN	0.791	0.926	0.875	0.696	1.042	0.748
sp P08243 ASNS_HUMAN	0.883	0.885	0.836	0.822	0.83	0.834
sp Q02809 PLOD1_HUMAN	0.834	0.85	0.832	0.807	0.848	0.829
sp P30050 RL12_HUMAN	0.831	0.831	0.823	0.834	0.834	0.816
sp P62906 RL10A_HUMAN	0.892	0.762	0.797	0.805	0.843	0.835
sp Q14527 HLTF_HUMAN	0.765	0.794	0.818	0.776	0.863	0.841
sp Q92538 GBFL1_HUMAN	0.858	0.926	0.81	0.795	0.893	0.792
sp P49257 LMAN1_HUMAN	0.814	0.825	0.854	0.715	0.951	0.814
sp P62910 RL32_HUMAN	0.782	0.74	0.69	0.818	0.831	0.83
sp P04843 RPN1_HUMAN	0.761	0.786	0.745	0.851	0.803	0.824
sp Q3SXMS5 HSDL1_HUMAN	0.931	1.01	0.911	0.822	0.824	0.832
sp Q00325 MPCP_HUMAN	0.862	0.866	0.874	0.816	0.836	0.824
sp O15269 SPTC1_HUMAN	0.768	0.866	0.769	0.804	0.908	0.764
sp Q9NTK5 OLA1_HUMAN	0.847	0	0.82	1.266	0	1.207
sp O00567 NOP56_HUMAN	0.809	0.813	0.868	0.802	0.8	0.869
sp Q9Y285 SYFA_HUMAN	0.816	0.808	0.779	0.83	0.84	0.799
sp P30419 NM1T1_HUMAN	0.829	0.774	0.781	0.84	0.792	0.836
sp Q9NVET7 PANK4_HUMAN	0.71	0.825	0.818	0.831	0.825	0.811
sp Q7L8L6 FAKD5_HUMAN	0.83	0.813	0.848	0.864	0.822	0.781
sp Q16719 KYNU_HUMAN	0.871	0.847	0.884	0.819	0.797	0.85

sp P36507 MP2K2_HUMAN	0.717	0.492	0.65	0.96	0.725	0.779
sp Q99700 ATX2_HUMAN	0.993	0.965	0.93	0.849	0.824	0.791
sp Q07065 CKAP4_HUMAN	1.124	0	1.168	1.218	0	1.243
sp O43837 IDH3B_HUMAN	0.925	0.856	0.824	0.852	0.775	0.835
sp P26373 RL13_HUMAN	0.783	0.807	0.756	0.786	0.899	0.775
sp P09651 ROA1_HUMAN	0.923	0.817	0.933	0.809	0.812	0.838
sp Q9BQ04 RBM4B_HUMAN	0.848	0.861	0.873	0.822	0.829	0.808
sp Q53GS9 SNUT2_HUMAN	0.867	0.708	0.808	0.881	0.78	0.794
sp P62280 RS11_HUMAN	0.806	0.807	0.803	0.812	0.818	0.824
sp Q9UBC5 MY01A_HUMAN	0.761	0.758				

sp Q6P2Q9 PRPS_HUMAN	0.764	0.749	0.764	0.753	0.826	0.804
sp Q04917 I433F_HUMAN	0.782	0.835	0.911	0.811	0.817	0.754
sp P62266 RS23_HUMAN	0.546	0.565	0.614	0.793	0.77	0.814
sp Q15392 DH24_HUMAN	0.846	0.864	0.864	0.785	0.764	0.827
sp Q9Y5S9 RBM8A_HUMAN	0.861	0.85	0.867	0.793	0.775	0.807
sp P08621 RU17_HUMAN	0.901	0.928	0.942	0.734	0.795	0.843
sp Q07955 SRSF1_HUMAN	0.853	0.773	0.836	0.806	0.778	0.785
sp P62913 RL11_HUMAN	0.82	0.827	0.836	0.793	0.775	0.801
sp Q14166 TTL12_HUMAN	0.794	0.797	0.816	0.803	0.737	0.828
sp Q02543 RL18A_HUMAN	0.916	0.906	0.901	0.773	0.787	0.809
sp Q9UBK8 MTRR_HUMAN	0.792	0.784	0.78	0.828	0.758	0.782
sp P28482 MK01_HUMAN	0.79	0.796	0.787	0.773	0.797	0.798
sp Q5VV41 ARHGG_HUMAN	0.963	0.825	0.833	0.794	0.808	0.765
sp P68036 UB2L3_HUMAN	0.491	0.476	0.523	0.786	0.82	0.759
sp Q9BZE4 NOG1_HUMAN	0.723	0.69	0.705	0.801	0.764	0.798
sp Q96G03 PGM2_HUMAN	0.845	0.765	0	1.184	1.178	0
sp P06703 S10A6_HUMAN	1.056	1.063	0	1.232	1.13	0
sp P38117 ETFB_HUMAN	0.869	0.929	0.896	0.779	0.815	0.767
sp P50750 CDK9_HUMAN	0.811	0.732	0.816	0.787	0.745	0.827
sp P07384 CAN1_HUMAN	0.85	0.846	0.928	0.82	0.812	0.724
sp P46379 BAG6_HUMAN	0.671	0.606	0.659	0.829	0.75	0.776
sp Q9UG63 ABCF2_HUMAN	0.698	0.71	0.738	0.82	0.754	0.781
sp O75533 SF3B1_HUMAN	0.771	0.765	0.749	0.787	0.773	0.791
sp Q15181 IPYR_HUMAN	1.089	1.078	1.073	0.822	0.838	0.691
sp P62241 RS8_HUMAN	0.786	0.76	0.803	0.801	0.741	0.808
sp P05455 LA_HUMAN	0	1.156	1.149	0	1.135	1.214
sp Q13617 CUL2_HUMAN	0.681	0.676	0.687	0.758	0.809	0.782
sp P27554 VE5_HPV41	1.138	1.08	0	1.207	1.138	0
sp Q15645 PCH2_HUMAN	0.916	0.892	0.877	0.756	0.782	0.806
sp Q5IPH6 SYEM_HUMAN	0.728	0.738	0.689	0.776	0.766	0.801
sp Q9NQW7 XPP1_HUMAN	0.851	0.867	0.846	0.762	0.794	0.786
sp Q7KZ85 SPT6_HUMAN	0.862	0.833	0.826	0.76	0.823	0.755
sp O76021 RL1D1_HUMAN	0.75	0.773	0.777	0.797	0.798	0.743
sp Q08379 GOGA2_HUMAN	0.926	0	0.868	1.163	0	1.174
sp P31946 I433B_HUMAN	0.892	0.868	0.906	0.741	0.754	0.84
sp O75794 CD123_HUMAN	0.844	0.838	0.877	0.754	0.774	0.807
sp P07099 HYEP_HUMAN	0.796	0.791	0.709	0.734	0.76	0.839
sp P17844 DDX5_HUMAN	0.683	0.707	0.7	0.729	0.801	0.803
sp Q15436 SC23A_HUMAN	0.835	0.878	0.771	0.76	0.755	0.816
sp Q6NU3 MSF12_HUMAN	0.744	0.888	0.895	0.95	0.702	0.677
sp P27144 KAD4_HUMAN	0.78	0.744	0.888	0.757	0.692	0.876
sp Q8TAT6 NPL4_HUMAN	0.774	0.807	0.874	0.856	0.834	0.634
sp Q9NUQ3 TXLNG_HUMAN	0	0.918	1.063	0	1.057	1.263
sp Q13242 SRSF9_HUMAN	0.789	0.82	0.823	0.77	0.759	0.79
sp Q9YSQ0 FADS3_HUMAN	0.929	0.86	0.861	0.739	0.884	0.694
sp O43488 ARK72_HUMAN	0.846	0.818	0.783	0.805	0.797	0.714
sp P42345 MTOR_HUMAN	0.884	0.856	0.596	0.868	0.832	0.615
sp Q9Y224 RTRAF_HUMAN	0.748	0.788	0.776	0.793	0.761	0.761
sp P50213 IDH3A_HUMAN	0	0.885	0.885	0	1.137	1.175
sp O60547 GMDS_HUMAN	0.775	0.754	0.829	0.75	0.762	0.796
sp O43292 GPAA1_HUMAN	0.762	0.8	0.822	0.766	0.688	0.853
sp P35232 PHB_HUMAN	0.743	0.732	0.717	0.751	0.696	0.859
sp Q9NVP1 DDX18_HUMAN	0.744	0.761	0.687	0.721	0.826	0.758
sp Q8NFH5 NUP35_HUMAN	0.877	0	0.858	1.159	0	1.141
sp P21912 SDHB_HUMAN	0.664	0.749	0.701	0.722	0.796	0.782
sp Q8N684 CPSF7_HUMAN	0.741	0.744	0.788	0.728	0.775	0.798
sp Q86V8 RTTN_HUMAN	0.661	0.682	0.681	0.755	0.77	0.77
sp Q8TB61 S35B2_HUMAN	0.768	0.78	0.842	0.78	0.707	0.808

sp Q13769 THOC5_HUMAN	0.786	0.841	0	1.055	1.235	0
sp Q07666 KHDR1_HUMAN	0.72	0.68	0.73	0.78	0.764	0.743
sp Q9BY32 ITPA_HUMAN	0	1.153	1.209	0	1.091	1.193
sp P67870 CSK2B_HUMAN	0.788	0.805	0.849	0.768	0.676	0.839
sp O75153 CLU_HUMAN	0.731	0.738	0.756	0.796	0.733	0.754
sp P25325 THTM_HUMAN	0.839	0.91	0.942	0.712	0.725	0.845
sp O14735 CDIPT_HUMAN	0.878	0.806	0.952	0.775	0.821	0.686
sp Q9H2U2 IPYR2_HUMAN	1.131	1.124	0.972	0.759	0.809	0.713
sp Q16186 ADRM1_HUMAN	0.944	0	0.898	1.115	0	1.162
sp Q72Z7T HWE1_HUMAN	1.036	0.803	0.794	0.493	0.809	0.975
sp P62701 RS4X_HUMAN	0.721	0.705	0.705	0.779	0.741	0.755
sp Q9NZB2 F120A_HUMAN	0.704	0.745	0.813	0.66	0.855	0.76
sp Q9NXW2 DJB12_HUMAN	0.902	0.877	0.878	0.738	0.799	0.738
sp P18669 PGAM1_HUMAN	0.918	0.909	0.892	0.748	0.745	0.778
sp P52594 AGFG1_HUMAN	1.29	1.055	1.122	0.784	0.694	0.79
sp Q32P28 P3H1_HUMAN	0.877	0	0.981	1.099	0	1.169
sp P43490 NAMP1_HUMAN	0.868	0.853	0.835	0.747	0.749	0.771
sp O43172 PRP4_HUMAN	0.796	0.82	0.82	0.761	0.759	0.746
sp Q13459 MYOB_HUMAN	0.728	0.726	0.849	0.641	0.788	0.835
sp Q05513 KPCZ_HUMAN	0.899	0.797	0.746	0.707	0.759	0.796
sp Q99575 POP1_HUMAN	0.755	0.833	0.741	0.7	0.821	0.739
sp Q9873 ANM1_HUMAN	0.827	0.731	0.711	0.782	0.763	0.714
sp P25788 PSA3_HUMAN	0.774	0.76	0.769	0.756	0.758	0.741
sp Q9BRX2 PELO_HUMAN	0.841	0.799	0.799	0.727	0.78	0.744
sp Q92626 PXDN_HUMAN	0.643	0.627	0.69	0.76	0.731	0.76
sp Q5BKZ1 ZN326_HUMAN	0.849	0.822	0.817	0.779	0.741	0.731
sp P36405 ARL3_HUMAN	1.002	1.068	0	1.083	1.167	0
sp O15213 WDR46_HUMAN	0.834	0.824	0.816	0.733	0.783	0.733
sp Q9Y4G6 TLN2_HUMAN	0.875	0.844	0.839	0.758	0.754	0.737
sp P32969 RL9_HUMAN	0.855	0.881	0.915	0.739	0.778	0.732
sp Q9UKN8 TF3C4_HUMAN	1.069	0.951	0.833	0.788	0.761	0.696
sp P15880 RS2_HUMAN	0.846	0.866	0.848	0.756	0.732	0.755
sp O60427 FADS1_HUMAN	0.809	0.612	0.674	0.853	0.691	0.698
sp P62442 RS15A_HUMAN	0	0.599	0.518	0	0.996	1.245
sp P36542 ATPG_HUMAN	0.915	0.971	0.945	0.726	0.771	0.742
sp P04040 CATA_HUMAN	0.677	0.629	0.591	0.75	0.759	0.729
sp Q8WWC4 MAIP1_HUMAN	0	0.969	1.015	0	1.087	1.148
sp Q03252 LMNB2_HUMAN	0.887	0.841	0.784	0.809	0.739	0.68
sp Q9Y6C9 MTCH2_HUMAN	0.856	0.831	0.831	0.797	0.787	0.642
sp Q969N2 PIGT_HUMAN	0.788	0.818	0.789	0.723	0.705	0.797
sp Q14197 ICT1_HUMAN	1.023	1.11	0	1.033	1.188	0
sp P00387 NB5R3_HUMAN	0.872	0.862	0.888	0.753	0.697	0.769
sp P30622 CLIP1_HUMAN	0	1.002	0.917	0	1.157	1.063
sp Q14997 PSME4_HUMAN	0.807	0.743	0.769	0.771	0.771	0.676
sp Q16229 SRSF7_HUMAN	0.943	0.962	0.933	0.832	0.644	0.743
sp P05141 ADT2_HUMAN	0.738	0.72	0.739	0.78	0.705	0.734
sp O43242 PSMD3_HUMAN	0.782	0.759	0.75	0.734	0.75	0.731
sp O60678 ANM3_HUMAN	0.85	0.954	0.942	0.604	0.773	0.837
sp O15460 P4HA2_HUMAN	0	1.018	1.049	0	1.132	1.081
sp Q9NV06 DCA13_HUMAN	0.789	0.848	0.744	0.764	0.686	0.758
sp P31689 DNJA1_HUMAN	0.954	1.054	1.094	0.817	0.736	0.654
sp P78347 GTF2L_HUMAN	0	0.87	0.866	0	1.122	1.084
sp P62753 RS6_HUMAN	0.774	0.792	0.779	0.71	0.737	0.759
sp Q9YSJ1 UTP18_HUMAN	0.673	0.785	0.869	0.596	0.75	0.857
sp P00264 PGRC1_HUMAN	1.203	1.194	0	1.134	1.067	0
sp Q75844 FACE1_HUMAN	0.667	0.787	0.717	0.689	0.767	0.745
sp Q969Z0 FAKD4_HUMAN	0.761	0.683	0.709	0.749	0.735	0.714
sp Q92504 S39A7_HUMAN	0.683	0.664	0.792	0.701	0.715	0.781

sp Q12769 NU160_HUMAN	0.694	0.692	0.788	0.721	0.655	0.814
sp Q9UK59 DBR1_HUMAN	0.868	0.795	0.768	0.79	0.735	0.665
sp Q15370 ELOB_HUMAN	0.853	0.86	0	1.13	1.058	0
sp P43121 MUC18_HUMAN	1.035	0	1.052	1.06	0	1.123
sp Q49A26 GLYR1_HUMAN	0.698	0.897	0.719	0.707	0.763	0.71
sp P23581 SYWC_HUMAN	0.861	0.703	0.73	0.723	0.712	0.744
sp Q9UBQ5 EIF3K_HUMAN	1.026	0.988	0	1.056	1.12	0
sp Q9EB1 ELP4_HUMAN	0.835	0.869	0.813	0.76	0.733	0.683
sp Q9NYF8 BCLF1_HUMAN	0.824	0	0.831	1.044	0	1.132
sp P60762 DPM1_HUMAN	0.732	0.725	0.72	0.716	0.716	0.733
sp Q99543 DNJC2_HUMAN	0.824	0.841	0.868	0.834	0.612	0.718
sp Q9HA64 KT3K_HUMAN	0.93					

sp Q16630 CPSF6_HUMAN	0.854	0.849	0.911	0.634	0.681	0.713
sp Q9H074 PAIP1_HUMAN	0	1.05	1.163	0	0.929	1.097
sp P50995 ANX11_HUMAN	0	0.906	0.912	0	1.001	1.02
sp P30533 AMRP_HUMAN	0.965	0	0.91	1.043	0	0.977
sp Q9H09J PAR12_HUMAN	0.862	0.826	0.804	0.642	0.672	0.702
sp O43395 PRPF3_HUMAN	0	0.862	0.834	0	1.007	1.006
sp Q8TDN6 BRX1_HUMAN	0.742	0.708	0.751	0.667	0.669	0.676
sp P19623 SPEE_HUMAN	0.806	0.96	0.966	0.651	0.621	0.736
sp Q9H845 ACAD9_HUMAN	1.024	0.93	0.895	0.92	0.467	0.617
sp Q5S007 LRRK2_HUMAN	0.274	0.268	0	1.036	0.963	0
sp Q9H98S L2HDH_HUMAN	0	0.857	0.962	0	0.965	1.034
sp O60684 IMA7_HUMAN	0.919	0.86	0	1.067	0.927	0
sp O14979 HNRLD_HUMAN	0.928	0	0.855	0.982	0	1.011
sp O43491 E4I1L2_HUMAN	0	0.911	0.896	0	0.936	1.056
sp Q9NUL7 DDX28_HUMAN	0.793	0.806	0.827	0.656	0.658	0.678
sp P41227 NAA10_HUMAN	0.697	0.792	0.759	0.657	0.642	0.692
sp Q15417 CNN3_HUMAN	0	0.875	1.126	0	0.927	1.063
sp Q8EW42 THOC6_HUMAN	0.916	0	0.9	1.064	0	0.924
sp O75439 MPPB_HUMAN	0.87	0	0.908	0.97	0	1.016
sp P61289 PSME3_HUMAN	0.509	1.224	0	0.861	1.124	0
sp O00116 ADAS_HUMAN	1.222	0	1.02	1.067	0	0.916
sp Q9NVA1 UQCQC1_HUMAN	0	0.9	0.927	0	0.949	1.022
sp P06493 CDK1_HUMAN	0.549	0.67	0.547	0.607	0.777	0.585
sp Q92615 LAR4B_HUMAN	0.82	0	0.837	0.999	0	0.967
sp P18124 RL7_HUMAN	0.659	0.654	0.645	0.653	0.649	0.663
sp O94822 LTN1_HUMAN	0	0.88	0.978	0	0.917	1.045
sp Q96C19 EFHD2_HUMAN	0.948	0	0.777	0.981	0	0.978
sp Q68DH5 LMBD2_HUMAN	0	0.776	0.843	0	0.983	0.971
sp Q96RQ3 MCCA_HUMAN	0	1.227	1.077	0	0.967	0.975
sp Q9UNX4 WDR3_HUMAN	0.835	0.914	0	1.012	0.93	0
sp Q99816 TS101_HUMAN	0	1.106	0.938	0	0.948	0.992
sp P09543 CN37_HUMAN	0.91	0.856	0	0.98	0.957	0
sp Q9H3U5 MFSD1_HUMAN	0	1.076	0.944	0	1.047	0.888
sp P85037 FOKK1_HUMAN	0	0.757	0.77	0	0.937	0.997
sp Q03154 ACY1_HUMAN	0.897	0.78	0	0.992	0.932	0
sp P51665 PSMD7_HUMAN	0	0.792	0.901	0	0.94	0.981
sp Q9UNH7 SNX6_HUMAN	1.174	1.096	0	0.947	0.972	0
sp P49821 NDUV1_HUMAN	0.87	0	0.813	0.933	0	0.987
sp Q13045 FLI1_HUMAN	0.845	0	0.804	0.922	0	0.997
sp O95478 NSA2_HUMAN	0.759	0.755	0.741	0.636	0.638	0.644
sp Q7Z434 MAVS_HUMAN	0	1.296	1.237	0	0.986	0.929
sp P62081 R57_HUMAN	1.002	0	1.256	0.987	0	0.923
sp Q6DKJ4 NXN_HUMAN	0.995	0.981	0	0.908	1	0
sp Q96PZ0 PUS7_HUMAN	0	0.82	0.952	0	0.883	1.025
sp Q9P035 HACD3_HUMAN	1.126	0	0.596	1.057	0	0.846
sp P53595 MOT1_HUMAN	0.569	0.673	0.574	0.653	0.601	0.645
sp P43034 LIS1_HUMAN	0.881	0.917	0	0.89	1.007	0
sp Q8N1G4 LRC47_HUMAN	0.548	0.641	0.517	0.609	0.679	0.606
sp Q01581 HMCS1_HUMAN	0.949	0	0.921	0.928	0	0.963
sp O60216 RAD21_HUMAN	0	0.825	0.784	0	0.954	0.937
sp Q9BV55 TR61B_HUMAN	0.7	0.664	0.675	0.598	0.663	0.629
sp Q9C0J8 WDR33_HUMAN	0.753	0.633	0	0.916	0.966	0
sp Q15003 CND2_HUMAN	0	0.904	0.861	0	0.976	0.907
sp Q94888 UBXN7_HUMAN	0.844	1.029	0	0.916	0.965	0
sp Q9BUQ8 DDX23_HUMAN	0	0.807	0.798	0	0.926	0.952
sp Q96KA5 CLPIL_HUMAN	0	0.918	0.889	0	0.953	0.925
sp Q6F81 CPIN1_HUMAN	0.986	0	0.84	0.895	0	0.977
sp Q68CQ4 DIEFX_HUMAN	0	0.345	0.512	0	0.891	0.981

sp Q9UG18 TES_HUMAN	0.894	0.944	0	0.954	0.918	0
sp Q6NXE6 ARMC6_HUMAN	0.717	0.792	0	0.914	0.957	0
sp Q14160 SCRIB_HUMAN	0.858	0	0.731	0.97	0	0.901
sp P30260 CDC27_HUMAN	0.778	0	0.8	0.975	0	0.894
sp P59989 ARPC4_HUMAN	0.601	0.497	0.833	0.715	0.476	0.678
sp P0914 RL14_HUMAN	1.127	0.892	0.778	0.619	0.572	0.677
sp Q16795 NDUA9_HUMAN	0	0.692	0.483	0	0.86	1.006
sp Q13011 ECH1_HUMAN	0.947	0	1.018	0.91	0	0.953
sp Q6Y7W6 GGYF2_HUMAN	0.797	0.803	0	0.974	0.887	0
sp Q9P2T1 GMPR2_HUMAN	0.923	1.012	0	0.934	0.926	0
sp Q9H4V9 XPO5_HUMAN	0	0.832	0.907	0	1.002	0.852
sp Q14929 HAT1_HUMAN	0.955	0.766	0	0.925	0.928	0
sp P50570 DYN2_HUMAN	0	0.785	0.797	0	0.904	0.948
sp P22059 OSBP1_HUMAN	0.922	0	0.825	0.904	0	0.949
sp Q14739 LBR_HUMAN	0.77	0.83	0.83	0.515	0.635	0.697
sp O43813 LANC1_HUMAN	0.921	0	0.858	0.887	0	0.958
sp Q8N239 KLH34_HUMAN	0	1.004	0.876	0	0.931	0.909
sp Q6PI48 SYDM_HUMAN	0.908	0	0.862	0.946	0	0.891
sp Q96B26 EXOS8_HUMAN	0.897	0	0.904	0.902	0	0.932
sp P00267 SPT5H_HUMAN	0	0.86	0.882	0	0.887	0.941
sp P15924 DESP_HUMAN	0.791	0.785	0	0.892	0.936	0
sp O00425 IF2B3_HUMAN	0	0.892	0.828	0	0.953	0.875
sp Q9BQ1 MEP50_HUMAN	0	0.781	0.855	0	0.841	0.985
sp Q9HD45 TM9S3_HUMAN	0.866	0	0.816	0.978	0	0.847
sp Q16836 HCDH_HUMAN	0.754	0.841	0	0.924	0.897	0
sp Q9UIGO BAZ1B_HUMAN	0	0.908	0.941	0	0.913	0.904
sp P61006 RAB8A_HUMAN	0	0.89	0.792	0	0.936	0.874
sp Q92785 REQU_HUMAN	0.958	0	0.568	0.987	0	0.823
sp Q68D10 SPT2_HUMAN	0.78	0.844	0	0.863	0.946	0
sp P53004 BIEA_HUMAN	0	0.505	0.717	0	0.916	0.891
sp Q9NQT4 EXOS3_HUMAN	0	0.894	0.814	0	0.95	0.856
sp Q9Y697 NFS1_HUMAN	0.859	0.894	0	0.852	0.948	0
sp P09525 ANXA4_HUMAN	0.906	0.932	0	0.891	0.907	0
sp Q9HC57 SYF1_HUMAN	0	0.82	0.819	0	0.909	0.884
sp Q16740 CLPP_HUMAN	0	1.008	0.911	0	0.918	0.875
sp Q13033 STRN3_HUMAN	0	0.749	0.803	0	0.92	0.866
sp Q86XP3 DDX42_HUMAN	0	0.78	0.77	0	0.886	0.898
sp Q658Y4 F91A1_HUMAN	0	0.761	0.716	0	0.9	0.884
sp Q9GZT8 NIF3L_HUMAN	0.81	0.813	0	0.897	0.885	0
sp P22694 KAPCB_HUMAN	0.997	0	0.973	0.898	0	0.881
sp P83111 LACTB_HUMAN	0	0.852	0.859	0	0.84	0.939
sp Q9H078 CLPB_HUMAN	0	0.984	0.974	0	0.916	0.863
sp Q86UK7 ZN598_HUMAN	0	0.878	0.887	0	0.837	0.939
sp Q9BXW7 HDHD5_HUMAN	0.868	0	0.873	0.867	0	0.906
sp Q9BWS9 CHID1_HUMAN	0.874	0	0.797	0.946	0	0.823
sp Q9UN37 VPS4A_HUMAN	0	0.908	0.915	0	0.872	0.897
sp P49755 TMEDA_HUMAN	0	0.993	1.383	0	1.103	0.665
sp Q9H8H0 NOL11_HUMAN	0	0.731	0.831	0	1.068	0.698
sp Q99962 SH3G2_HUMAN	0	0.992	0.916	0	0.852	0.914
sp Q15843 NEDD8_HUMAN	0.817	0.818	0	0.836	0.927	0
sp P32993 G3_VAR67	0.299	0	0.303	0.88	0	0.883
sp Q7Z5L9 L2BP2_HUMAN	0	0.813	0.893	0	0.851	0.909
sp O75152 ZC11A_HUMAN	0.983	0.947	0	0.935	0.82	0
sp P00374 DYR_HUMAN	0	0.911	0.829	0	0.897	0.858
sp P00568 KAD1_HUMAN	0	0.822	0.915	0	0.811	0.942
sp Q86T12 DPP9_HUMAN	0	0.902	0.837	0	0.868	0.885
sp Q96RP9 EFGM_HUMAN	0.854	0.852	0	0.937	0.815	0
sp P09884 DPOLA_HUMAN	0	0.895	0.828	0	0.944	0.806

sp Q9NQ55 SSF1_HUMAN	0	0.792	0.815	0	0.839	0.904
sp Q9HL43 SENP3_HUMAN	0.72	0.78	0	0.832	0.911	0
sp P58107 EPIPL_HUMAN	0.856	0.945	0	0.849	0.893	0
sp P32004 L1CAM_HUMAN	0.792	0	0.712	0.847	0	0.895
sp O60343 TBCCD4_HUMAN	0	0.897	0.786	0	0.826	0.91
sp P61086 UBE2K_HUMAN	0	1.005	1.207	0	0.767	0.966
sp Q9NP58 ABC6_HUMAN	0.947	0	0.994	0.873	0	0.859
sp Q96I25 SPF45_HUMAN	0.882	0	0.915	0.88	0	0.849
sp Q5T8P6 RBM26_HUMAN	0.84	0.792	0	0.893	0.83	0
sp O60831 PRAF2_HUMAN	0	0.922	1.152	0	0.781	0.938
sp Q4KMK1 QCCT_HUMAN	0.854	0	0.828	0.837	0	0.881
sp P38606 VATA_HUMAN	0.88	0	0.854	0.751	0	0.965
sp Q9HCC0 MCCB_HUMAN	0.81	0	0.805	0.867	0	0.847
sp Q969S3 ZN622_HUMAN	0.926	0	1.015	0.789	0	0.922
sp Q9NXS2 QPCTL_HUMAN	0.77	0	0.769	0.84	0	0.868
sp Q9ULC4 MCTS1_HUMAN	0	0.9	0.836	0	0.872	0.834
sp Q9UJ5 TRM6_HUMAN	0.666	0.694	0.748	0.549	0.555	0.601
sp Q09161 NCBP1_HUMAN	0	0.805	0.796	0	0.862	0.836
sp Q9B4V44 THUM3_HUMAN	0.749	0	0.898	0.76	0	0.938
sp Q53H96 P5CR3_HUMAN	0.788	0	0.796	0.835	0	0.86
sp Q6L8Q7 PDE12_HUMAN	0	0.864	0.829	0		

sp Q99447 PCY2_HUMAN	0.743	0	0.764	0.838	0	0.761
sp Q96S52 PIGS_HUMAN	0.701	0.711	0	0.773	0.822	0
sp Q86UY5 FA83A_HUMAN	0.718	0	0.845	0.688	0	0.907
sp Q86YM7 HOME1_HUMAN	0	0.856	0.931	0	0.867	0.717
sp Q81VT2 MISP_HUMAN	0.826	0.816	0	0.819	0.763	0
sp Q96BP3 PPWD1_HUMAN	0.798	0.975	0	0.882	0.698	0
sp Q81ZL8 PELP1_HUMAN	0	0.806	0.825	0	0.78	0.8
sp P13804 ETFA_HUMAN	1.337	1.261	1.072	0.442	0.565	0.572
sp P51812 KS6A3_HUMAN	0	0.805	0.773	0	0.867	0.712
sp Q96IR7 HPDL_HUMAN	0	0.62	0.84	0	0.74	0.837
sp Q9UNS2 CSN3_HUMAN	0	0.911	0.822	0	0.799	0.77
sp P49750 YLPM1_HUMAN	0.742	0.801	0	0.802	0.762	0
sp P04818 TYSY_HUMAN	0.912	0.921	0	0.766	0.798	0
sp Q99986 VRK1_HUMAN	0.829	0	0.837	0.697	0	0.855
sp Q7Z460 CLAP1_HUMAN	0.871	0.925	0	0.826	0.722	0
sp Q8WYA6 CTBL1_HUMAN	0.704	0.762	0	0.77	0.778	0
sp Q9Y2S7 PDIP2_HUMAN	0	0.859	0.903	0	0.741	0.803
sp Q9NVX2 NLE1_HUMAN	0.885	0.819	0	0.776	0.761	0
sp Q13492 PICAL_HUMAN	0.932	0	0.739	0.895	0	0.639
sp Q2NL82 TSR1_HUMAN	0.759	0.803	0	0.758	0.773	0
sp Q8N5M9 JAGN1_HUMAN	0.689	0.941	0.952	0.539	0.471	0.493
sp Q14181 DPQA2_HUMAN	0	0.767	0.722	0	0.802	0.694
sp Q14117 DPYS_HUMAN	0.721	0	0.925	0.541	0	0.952
sp Q9Y5A9 YTHD2_HUMAN	0	0.995	0.83	0	0.921	0.548
sp P12236 ADT3_HUMAN	0.775	0.82	0	0.712	0.755	0
sp Q13509 TBB3_HUMAN	0	0.869	1.005	0	0.711	0.748
sp P30084 ECHM_HUMAN	0.961	0	0.918	0.666	0	0.789
sp P22087 FBRL_HUMAN	0	0.828	0.82	0	0.707	0.74
sp Q8IZH2 XRN1_HUMAN	0.818	0.824	0	0.714	0.729	0
sp O75616 ERAL1_HUMAN	0.796	0.771	0	0.781	0.66	0
sp Q8WVJ2 NUDC2_HUMAN	0.698	0	0.667	0.719	0	0.711
sp O75116 ROCK2_HUMAN	0.91	0	0.858	0.961	0	0.468
sp P52907 CAZA1_HUMAN	0	0.771	0.829	0	0.66	0.769
sp P33897 ABCD1_HUMAN	0	0.851	0.914	0	0.705	0.703
sp Q15477 SKIV2_HUMAN	1.067	1.219	0	0.711	0.68	0
sp P48729 KC1A_HUMAN	0.924	0.726	0	0.711	0.676	0
sp Q9NYJ8 TAB2_HUMAN	0	0.798	0.678	0	0.698	0.685
sp P08708 RS17_HUMAN	0.548	0.487	0	0.699	0.661	0
sp Q6Y1H2 HACD2_HUMAN	0	0.987	1.139	0	0.773	0.585
sp Q9GZZ1 NAAS0_HUMAN	0	0.59	0.897	0	0.539	0.817
sp Q2TAY7 SMU1_HUMAN	0	0.754	0.823	0	0.603	0.752
sp Q99729 ROAA_HUMAN	0.823	0	0.77	0.696	0	0.637
sp Q9NVS2 RT18A_HUMAN	0	0.608	0.759	0	0.625	0.656
sp O60476 MA1A2_HUMAN	0.682	0	0.694	0.667	0	0.584
sp Q9NU11 DECRR2_HUMAN	0.62	0	0.534	0.653	0	0.553
sp Q96ER9 CCDS1_HUMAN	0	1.099	0.926	0	0.507	0.604
sp Q9UEG4 ZN629_HUMAN	0	0.884	0.811	0	0.479	0.455
sp Q5TSP2 SKT_HUMAN	0.781	0	0.883	0.206	0	0.439
sp Q9BX40 LS14B_HUMAN	0.694	0.685	0.746	0.083	0.067	0.077