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Supplemental Information

**Atractylodinol prevents pulmonary fibrosis
through inhibiting TGF- β receptor 1 recycling
by stabilizing vimentin**

Mengjiao Hao, Zhuoji Guan, Zhikang Zhang, Haopeng Ai, Xing Peng, Huihao Zhou, Jun Xu, and Qiong Gu

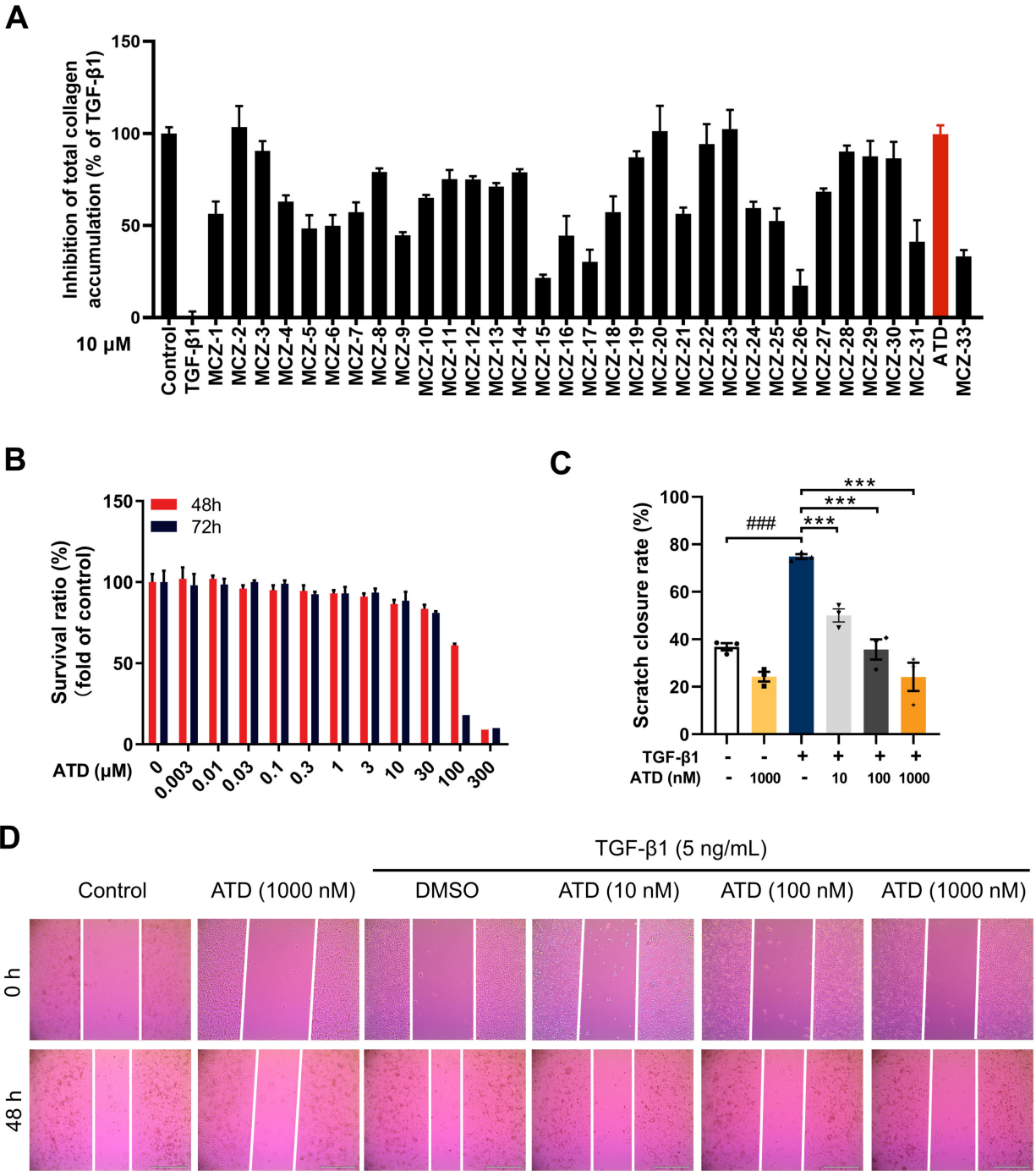


Figure S1. Screening to identify ATD with anti-PF.

(A) Picosirius red staining of HFL1 cells showed collagen accumulation after treated with 10 μM compounds. Triplicates were performed. (B) Relative viability measurements of the HFL1 cells after 48 hours or 72 hours treatment with ATD ($n = 3$). (C) Quantification of scratch closure rate ($n = 3$). (D) Scratch recorded after exposing to ATD in A549 cell wound healing assay. Scale bar: 400 μm . The data are presented as the mean \pm SEM. # $P < 0.05$, ## $P < 0.01$, ### $P < 0.001$ compared

to control group; * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ compared to TGF- β 1 group. ns: no statistical difference.

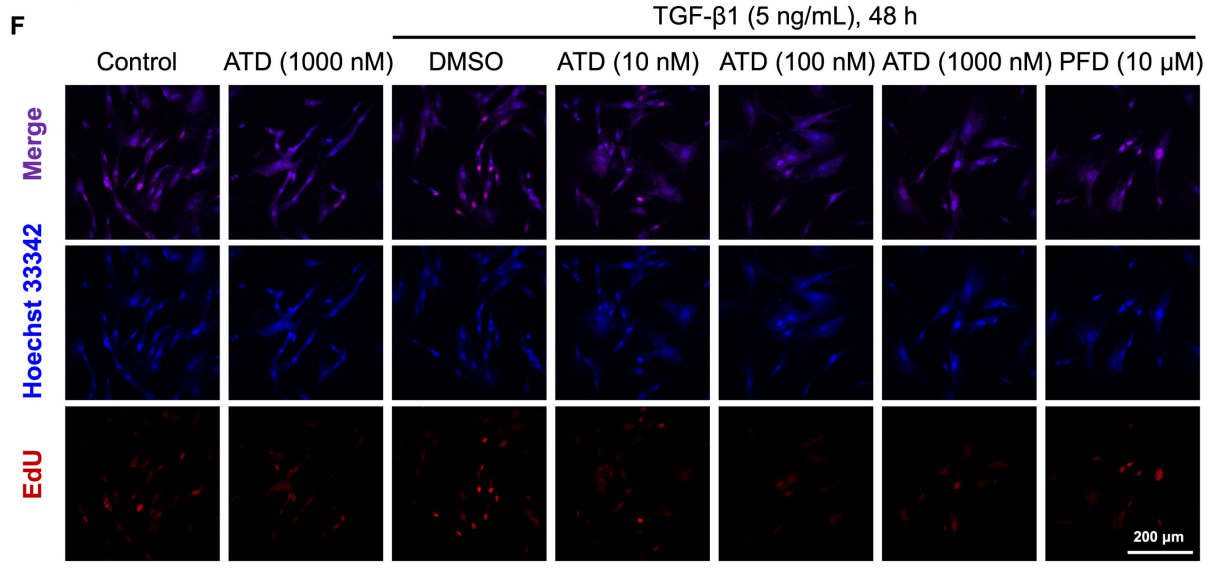
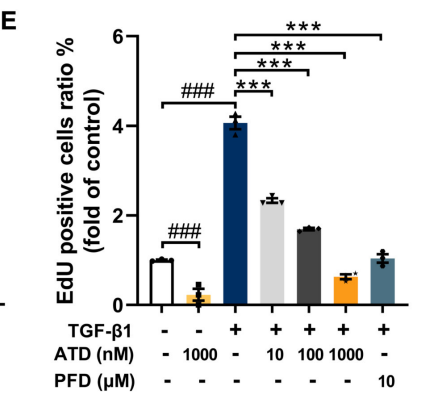
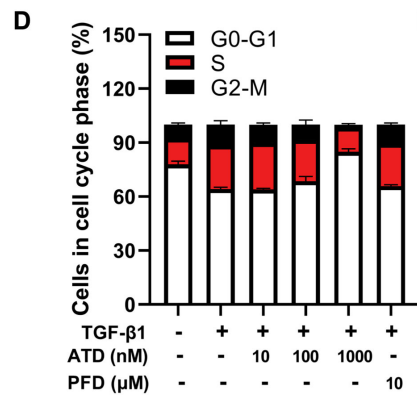
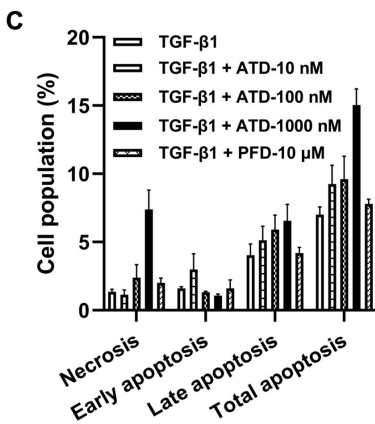
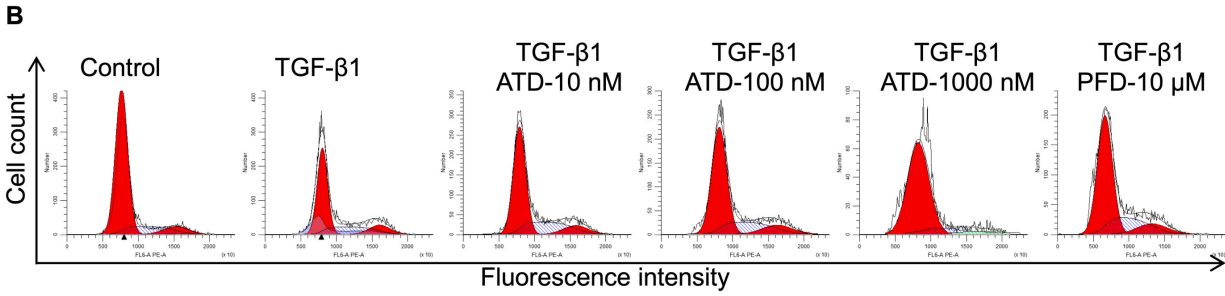
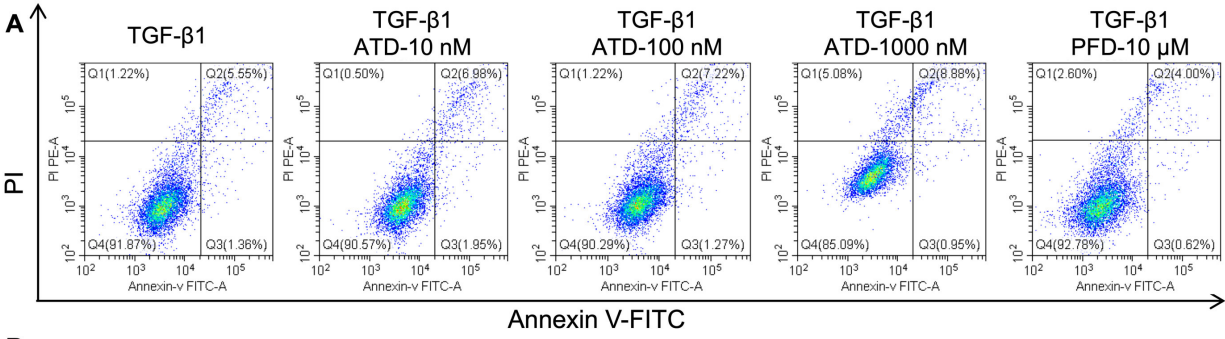


Figure S2. ATD promotes apoptosis and inhibits excessive proliferation of HFL1 cells.

(A) HFL1 cells were treated with different concentrations of ATD for 48 hours, and then the apoptotic cells were assessed by Annexin V Alexa Fluor 488/PI apoptosis detection kit. (B) HFL1 cells were treated with different concentrations of ATD for 48 hours, and then the cells cycle were assessed by PI staining. (C) The percentage of apoptotic HFL1 cells was measured with flow cytometry ($n = 3$). (D) The distribution of HFL1 cells (%) treated with ATD in each cell-cycle phase ($n = 3$). (E) The EdU positive cells ratio of the HFL1 cells after 48 hours treatment with ATD ($n = 3$). (F) The HFL1 cells were incubated with different concentrations of ATD in the presence or absence of TGF- β 1 stimulation for 48 hours, and were detected by the EdU staining kit. Scale bar: 200 μ m. The data are presented as the mean \pm SEM. # $P < 0.05$, ## $P < 0.01$, ### $P < 0.001$ compared to control group; * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ compared to TGF- β 1 group. ns: no statistical difference.

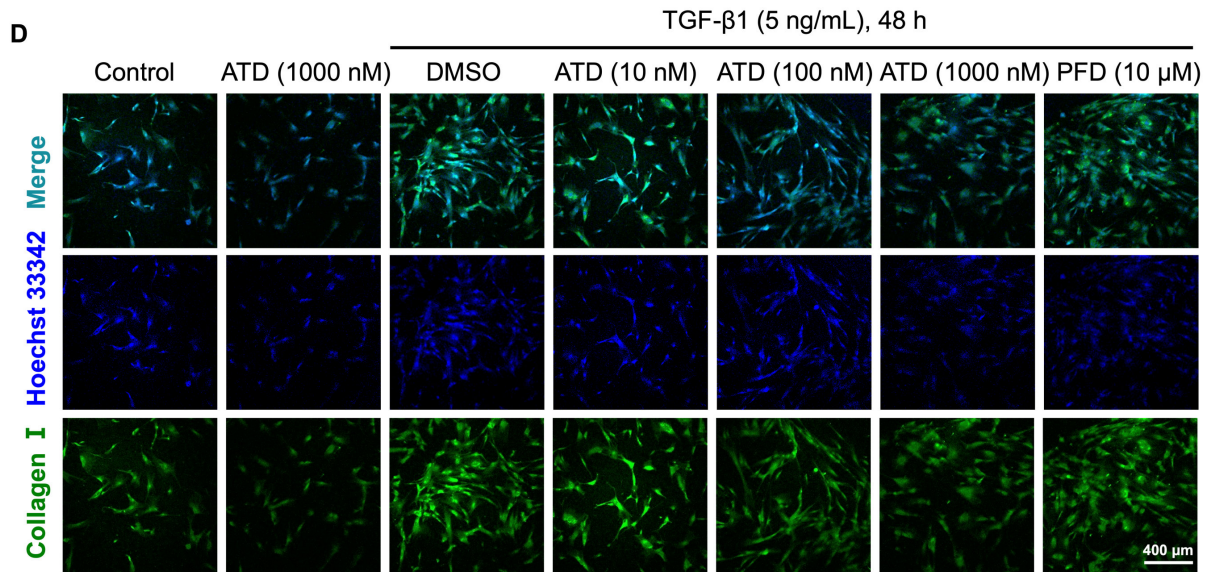
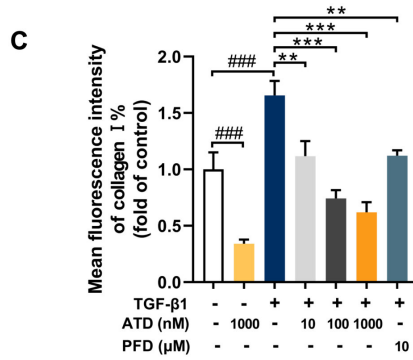
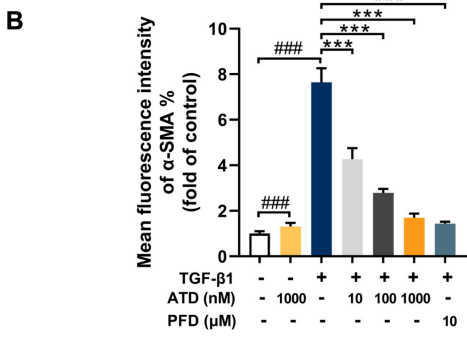
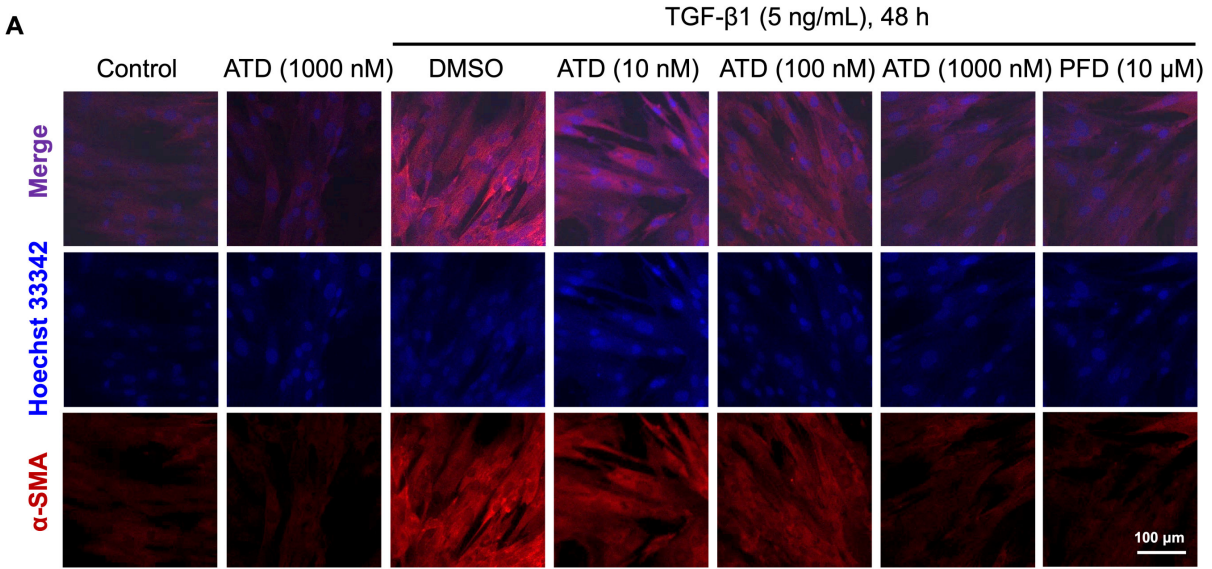


Figure S3. ATD inhibits the expression of α -SMA and collagen I in HFL1 cells to improve PF.

(A) The HFL1 cells were incubated with different concentrations of ATD in the presence or absence of TGF- β 1 stimulation for 48 hours. The expression of α -SMA was observed by immunofluorescence microscopy. Scale bar: 100 μ m. (B) Quantification of the fluorescence intensity of α -SMA ($n = 3$). (C) The expression of collagen I was observed by immunofluorescence microscopy. Scale bar: 400 μ m. (D) Quantification of the fluorescence intensity of collagen I ($n = 3$). The data are presented as the mean \pm SEM. # $P < 0.05$, ## $P < 0.01$, ### $P < 0.001$ compared to control group; * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ compared to TGF- β 1 group.

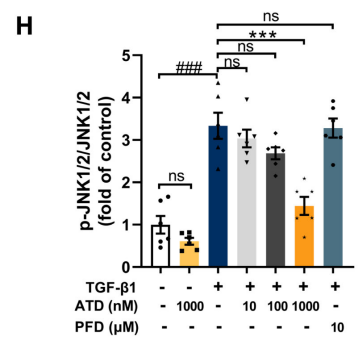
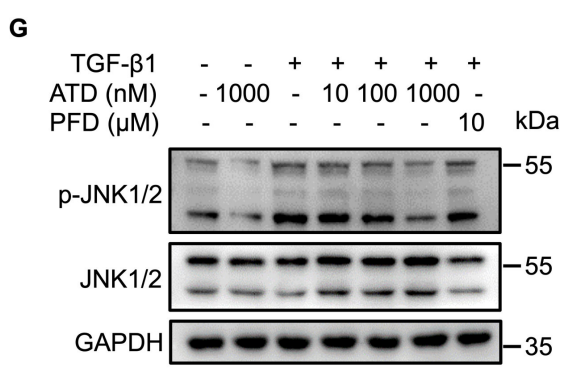
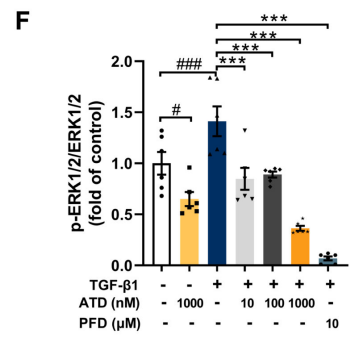
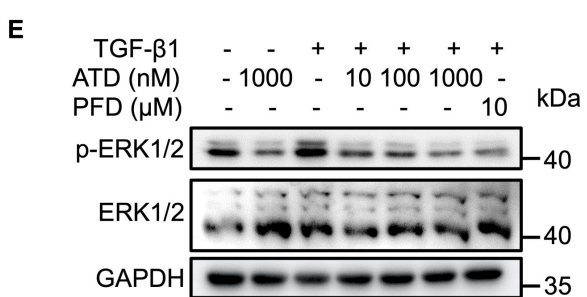
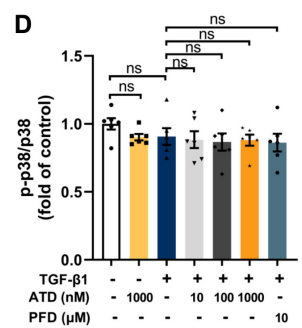
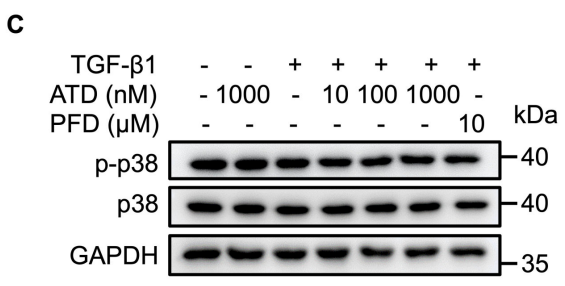
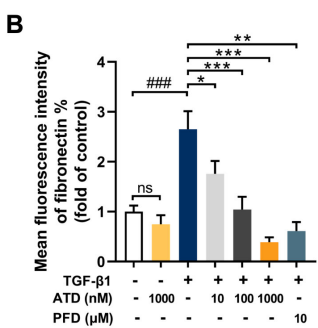
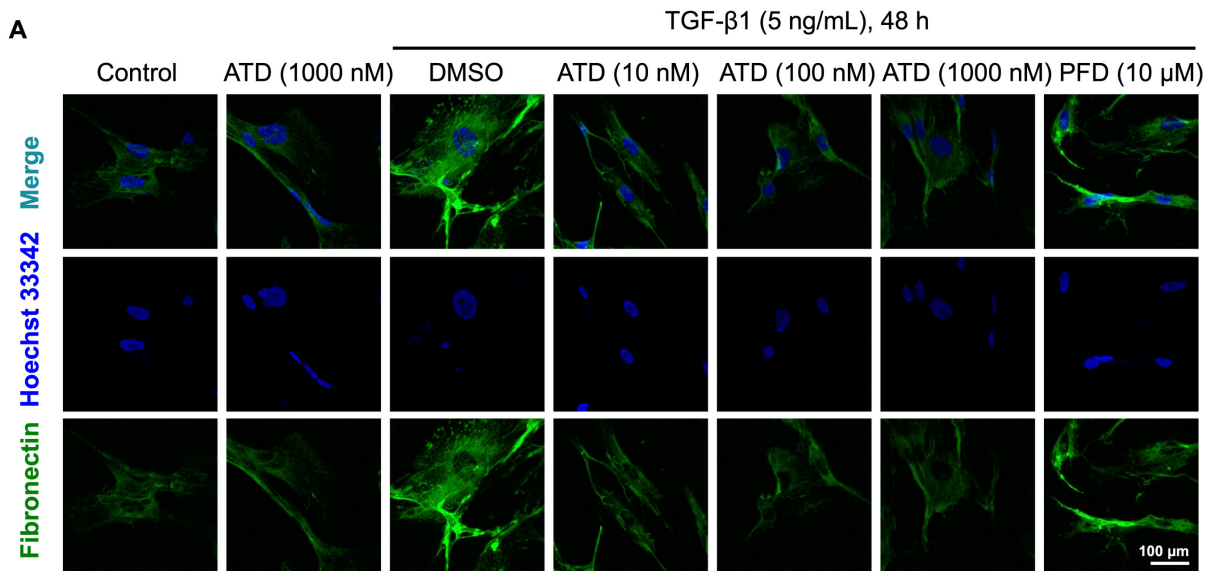
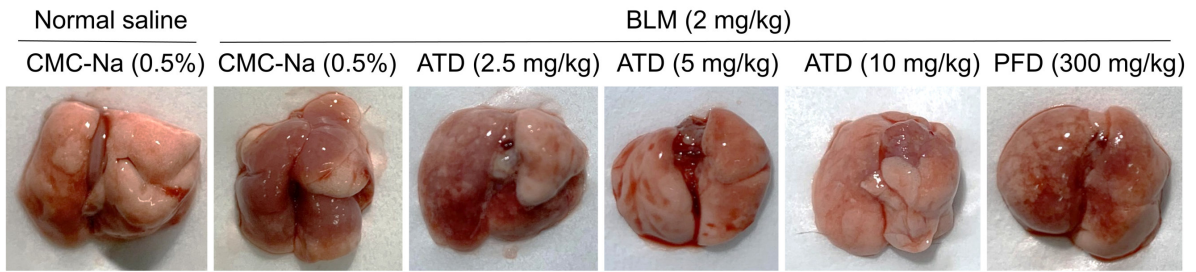


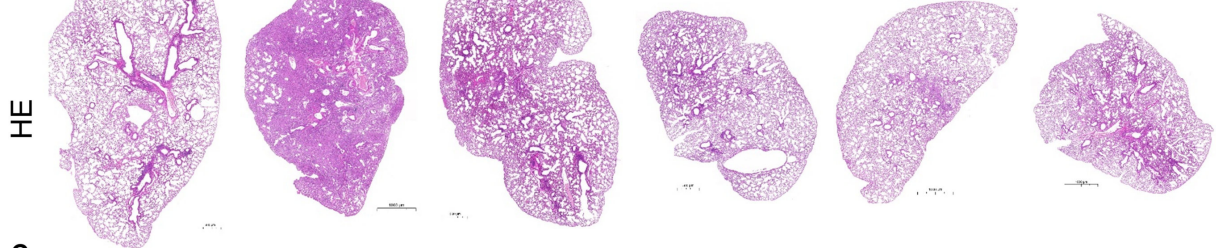
Figure S5. ATD prevents PF *via* inhibition ERK1/2 and JNK1/2 phosphorylation.

(A) The expression of fibronectin was observed by immunofluorescence microscopy. Scale bar: 100 μm . (B) Quantification of the fluorescence intensity of fibronectin ($n = 3$). (C) The protein expression of p-p38 and p38 was analyzed by Western blotting analysis. (D) Quantification of the phosphorylation level of p-p38/p38. ($n = 6$). (E) The protein expression of p-ERK1/2 and ERK1/2 was analyzed by Western blotting analysis. (F) Quantification of the phosphorylation level of p-ERK1/2 / ERK1/2. ($n = 6$). (G) The protein expression of p-JNK1/2 and JNK1/2 was analyzed by Western blotting analysis. (H) Quantification of the phosphorylation level of p-JNK1/2 / JNK1/2. ($n = 6$). The data are presented as the mean \pm SEM. # $P < 0.05$, ## $P < 0.01$, ### $P < 0.001$ compared to control group; * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ compared to TGF- β 1 group. ns: no statistical difference.

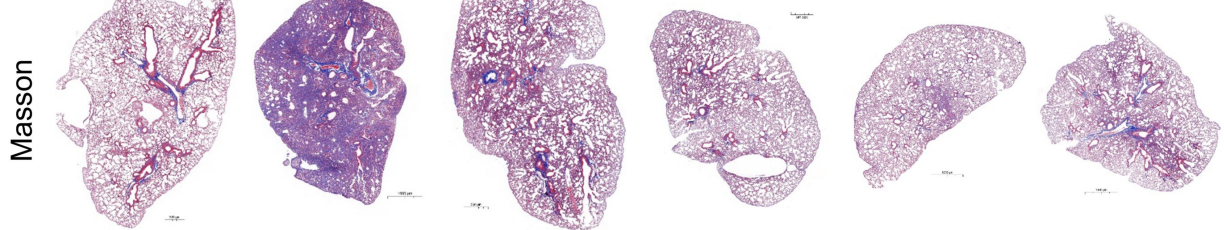
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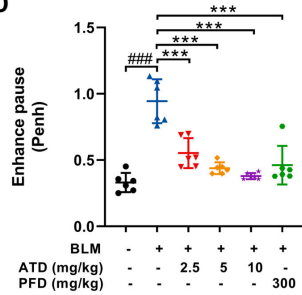
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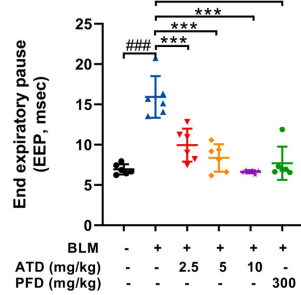
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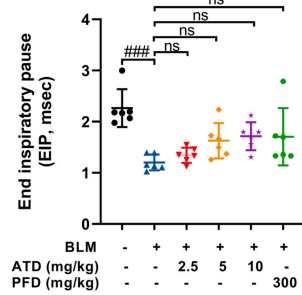
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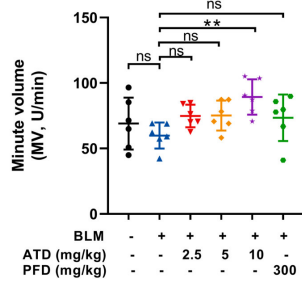
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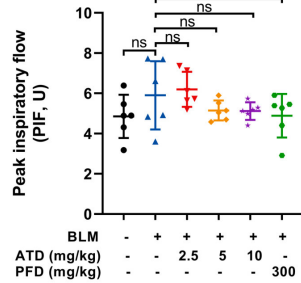
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I

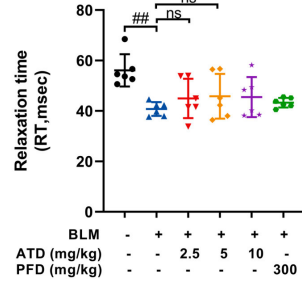


Figure S6. ATD protected against PF induced by bleomycin (BLM) in C57BL/6 mice.

(A) Representative images of lung tissue. (B) Representative images of HE staining. (C) Representative images of Masson staining. Representative pulmonary function parameters: (D) enhance pause (Penh), (E) end expiratory pause dynamic (EEP), (F) end inspiratory pause (EIP), (G) minute volume (MV), (H) peak inspiratory flow (PIF) and (I) relaxation time (RT) ($n = 6$). The data are presented as the mean \pm SEM. # $P < 0.05$, ## $P < 0.01$, ### $P < 0.001$ compared to control group; * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ compared to bleomycin group. ns: no statistical difference.

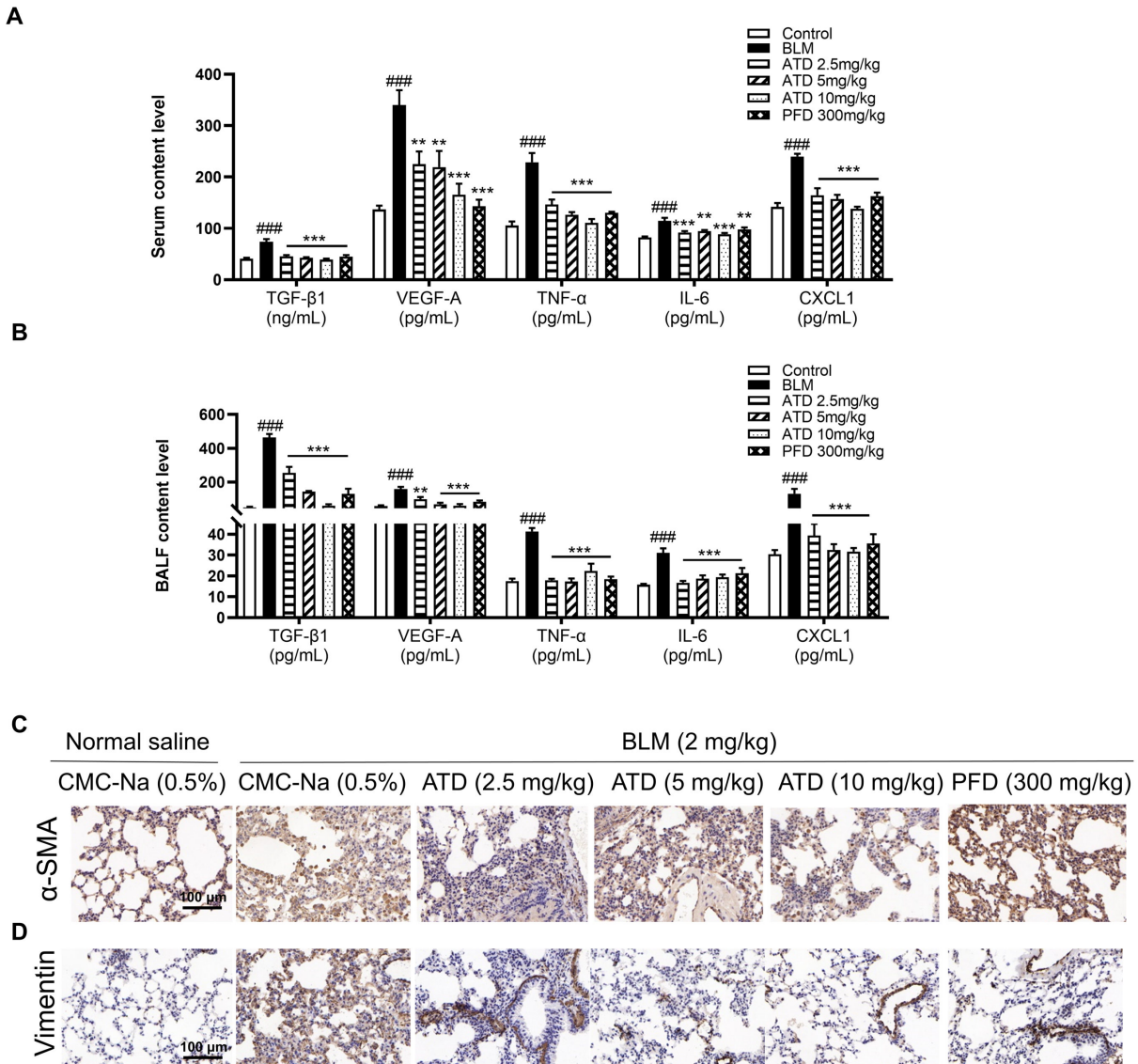
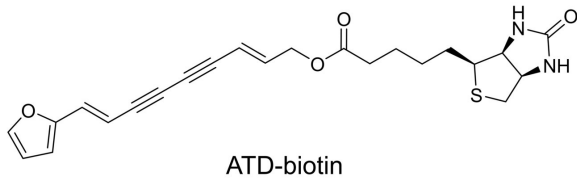
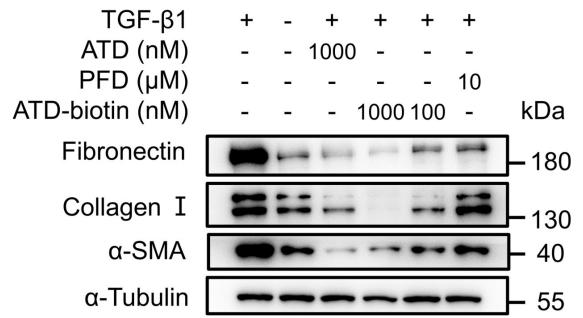
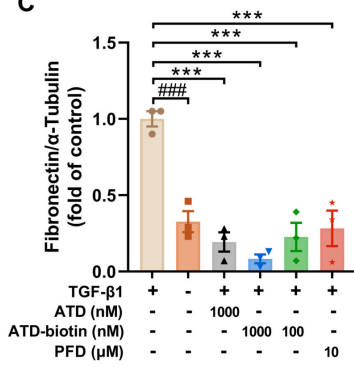
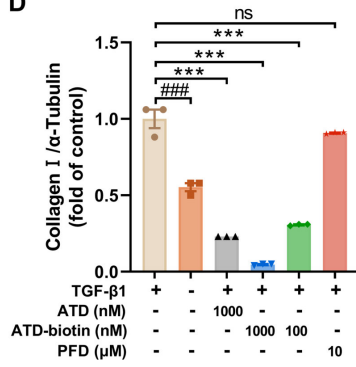
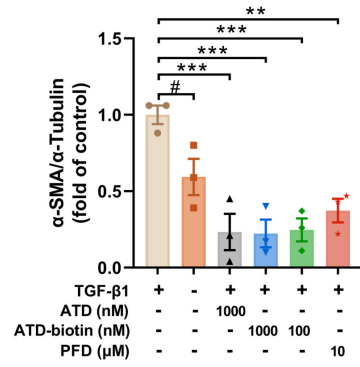
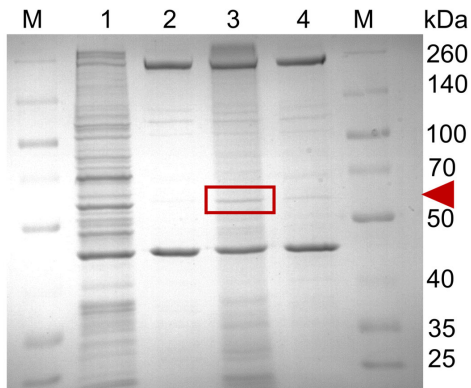
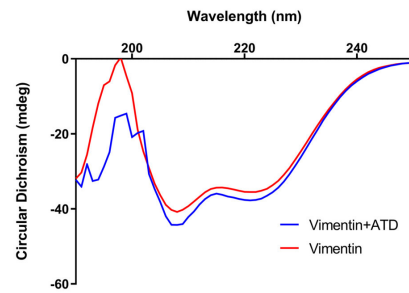
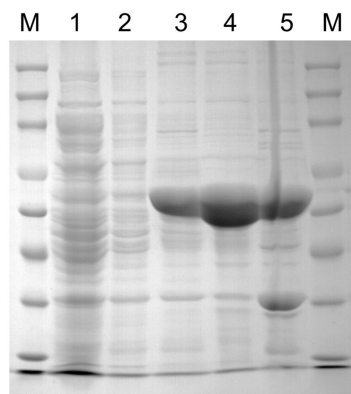


Figure S7. ATD alleviates inflammation and fibrosis induced by bleomycin in C57BL/6 mice.

(A) Secretion levels of transforming growth factor β 1 (TGF- β 1), vascular endothelial growth factor A (VEGF-A), tumor necrosis factor α (TNF- α), interleukin 6 (IL-6), and chemokine (CXCL1) in serum quantified by enzyme-linked immunosorbent assay (ELISA) kits ($n = 6$). (B) Secretion levels of TGF- β 1, VEGF-A, TNF- α , IL-6, and CXCL1 in bronchoalveolar lavage fluid (BALF) quantified by ELISA kits ($n = 6$). Representative immunohistochemistry images of (C) α -SMA and (D) vimentin in lung tissue. Scale bar: 100 μ m. The data are presented as the mean \pm SEM. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ compared to bleomycin group; # $P < 0.05$, ### $P < 0.01$, ### $P < 0.001$ compared to control. ns: no statistical difference.

A**B****C****D****E****F****G****H****I**

| | | | | | | | | | | | | |
|---|----------------|----|----|----|----|----|----|-----|-----|-----|-----|---|
| M | Load | FT | W1 | W2 | W3 | W4 | W5 | E1 | E2 | E3 | E4 | M |
| | Imidazole (mM) | - | 5 | 10 | 20 | 40 | 80 | 100 | 200 | 500 | 500 | |
| | Urea (8 M) | + | + | + | + | + | + | + | + | + | - | |

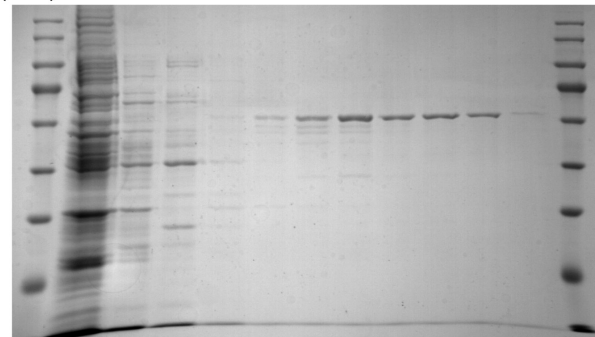


Figure S8. Target identification of ATD.

(A) Structure of atractyloidinol-biotin (ATD-biotin). (B) The protein expression of fibronectin, collagen I, and α -SMA in HFL1 cells was examined by Western blotting analysis ($n = 3$). Quantification of the protein expression of (C) fibronectin, (D) collagen I and (E) α -SMA. (F) TGF- β 1-induced HFL1 cell lysates (lane 1), were incubated overnight at 4 °C with biotin (20 μ M, lane 2), ATD-biotin (20 μ M, lane 3), or ATD-biotin (10 μ M, lane 4). Streptavidin agarose beads were used to capture ATD-biotin-protein complexes. Proteins were run on tris-glycine gel and visualized using coomassie blue stain. (G) CD spectra of VIM (5 μ M) and the mixture of VIM and ATD (5 μ M). (H) Protein expression and purification. soluble fraction after cell disruption (lane 1); soluble fraction after repeated disruption (lane 2); soluble fraction after treatment with 2 M urea (lane 3); soluble fraction after treatment with 8 M urea (lane 4); insoluble fraction after treatment with 8 M urea (lane 5); M: Molecular weight marker. (I) FT: flow-through; 100 mM to 500 mM imidazole elution fraction is purified vimentin. The data are presented as the mean \pm SEM. # $P < 0.05$, ## $P < 0.01$, ### $P < 0.001$ compared to control group; * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ compared to TGF- β 1 group. ns: no statistical difference.

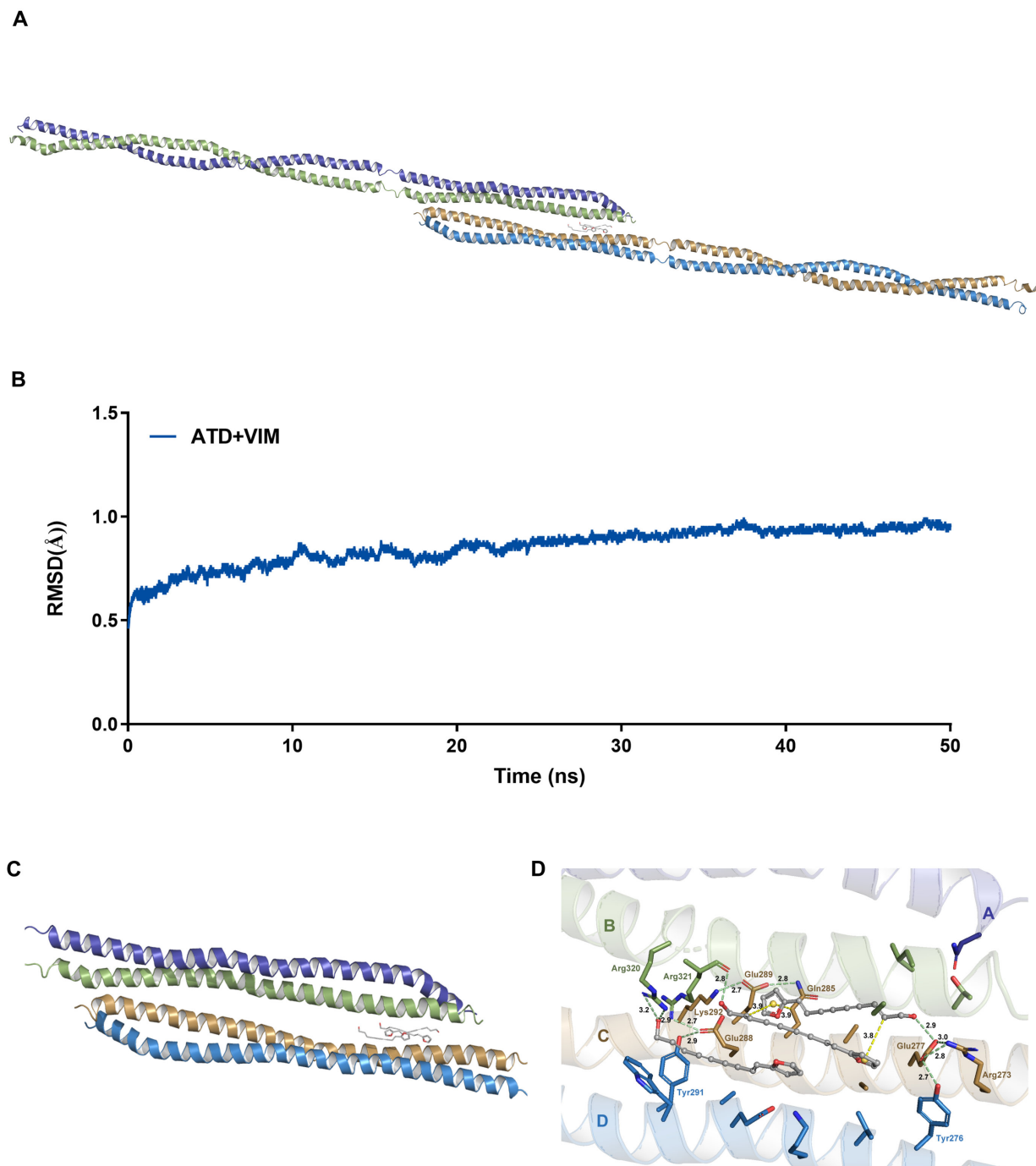


Figure S9. Molecular model of ATD binding site in tetrameric VIM.

(A) A snapshot of the MD-simulated solvent-accessible surface area binding structure showing ATD binding in the cleft between the B and C α helices of the VIM tetramer. (B) Time-series of RMSD of backbone atoms from the starting structures for the complexes over 50 ns of MD simulations. The equilibration phase is not included. (C) A snapshot of the MD-simulated solvent-accessible surface area binding structure showing ATD binding in the cleft between the

B and C α helices of the VIM tetramer. (D) This model shows the interaction between VIM and ATD.

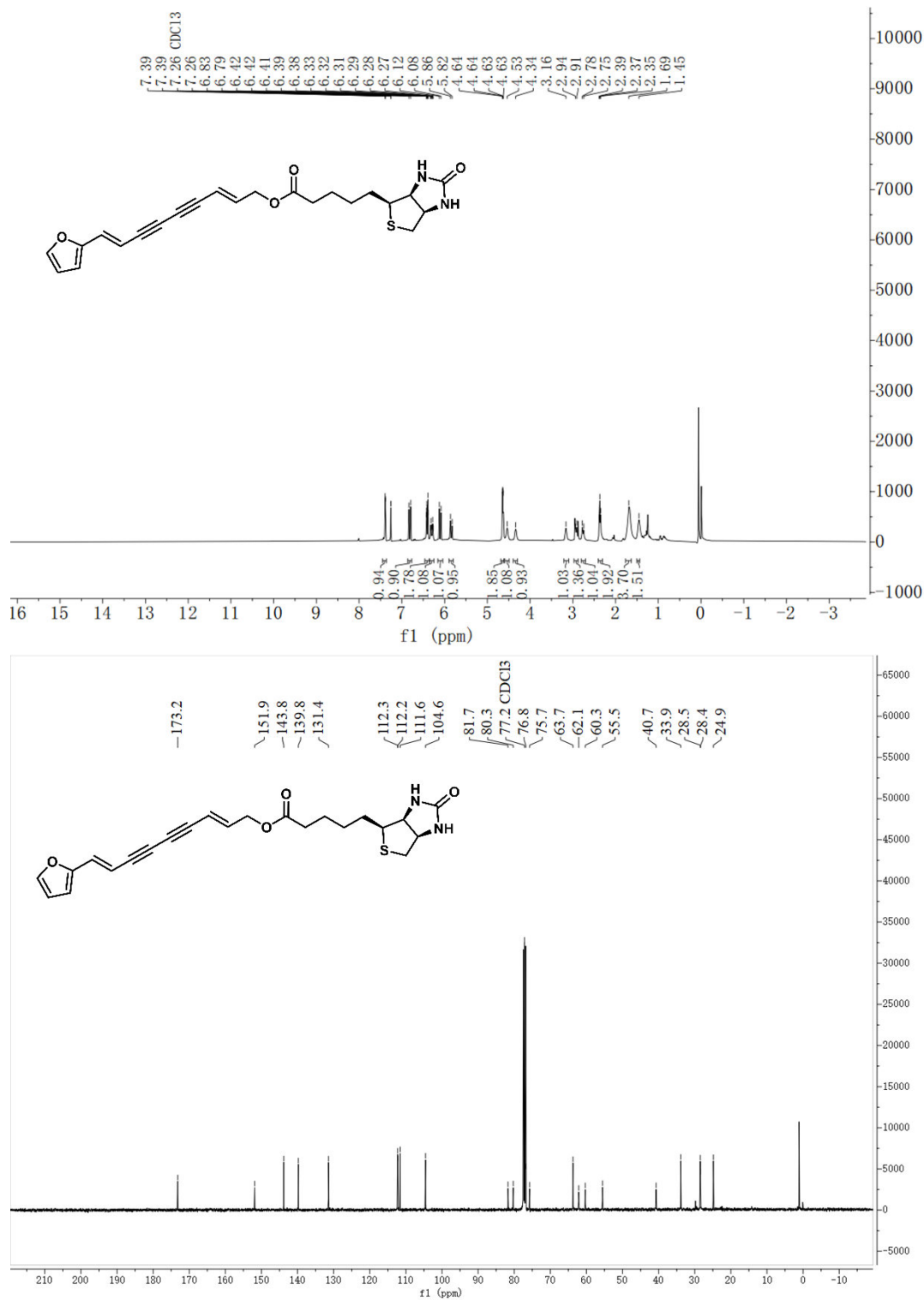
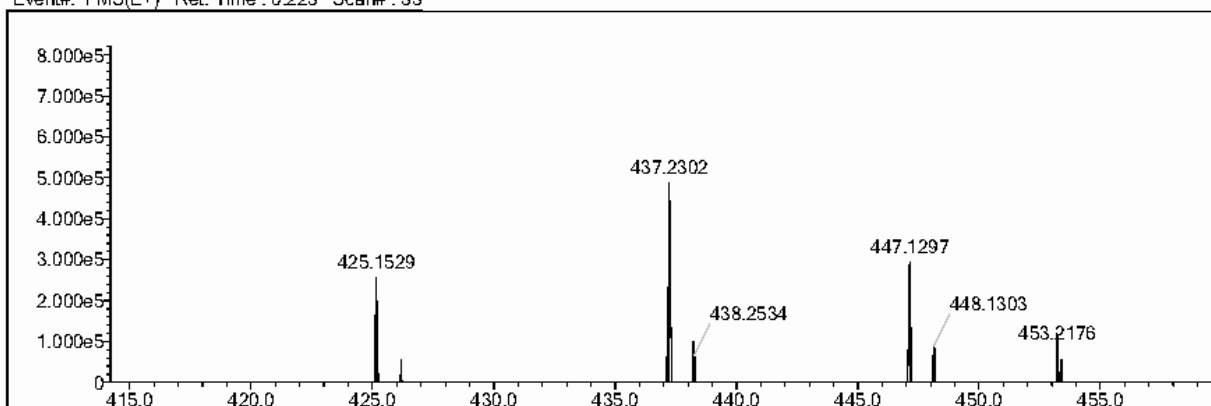
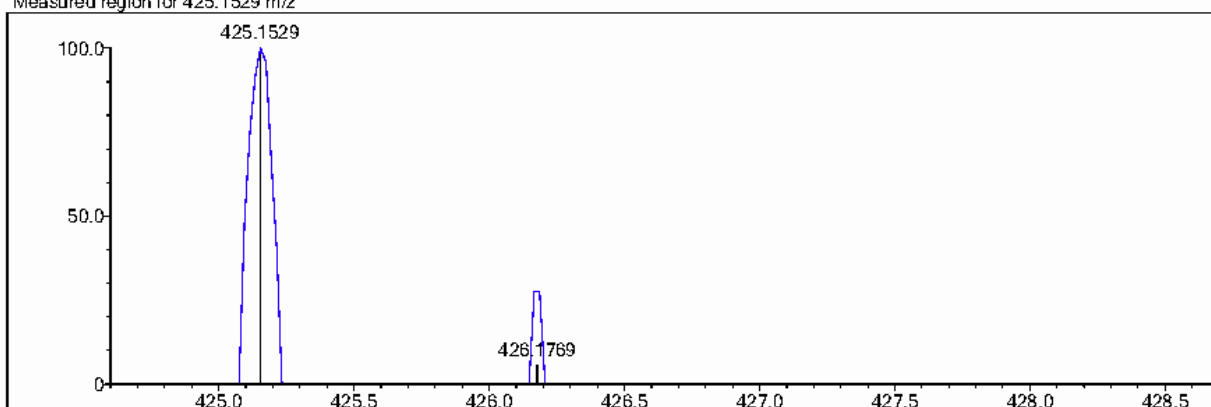


Figure S10. ¹H and ¹³C NMR spectra of ATD-biotin in chloroform-*d*.

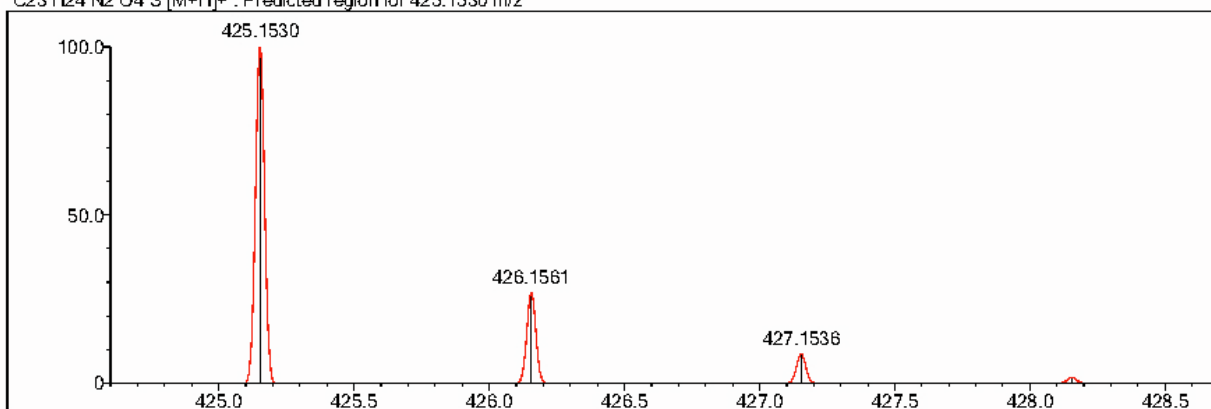
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Measured region for 425.1529 m/z



C23 H24 N2 O4 S [M+H]⁺ : Predicted region for 425.1530 m/z



| Formula (M) | Ion | Meas. m/z | Pred. m/z | Df. (mDa) | Df.(ppm) | DBE |
|-----------------|--------------------|-----------|-----------|-----------|----------|------|
| C23 H24 N2 O4 S | [M+H] ⁺ | 425.1529 | 425.1530 | -0.1 | -0.24 | 13.0 |

Figure S11. HRMS spectrum of ATD-biotin.

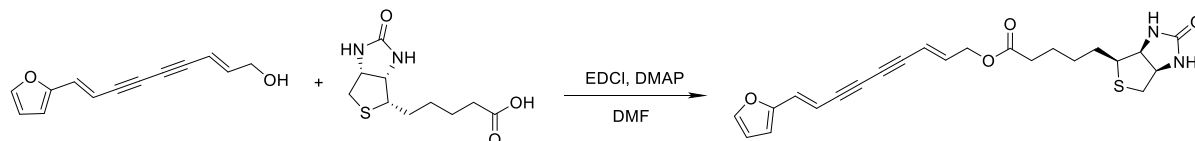


Figure S12. Synthesis of ATD-biotin.

D-Biotin (122.4 mg, 0.5 mmol), DMAP (63.7 mg, 0.5 mmol), and EDCI (75.7 mg, 0.4 mmol) were dissolved in DMF (8.0 mL). The mixture was stirred at room temperature for 30 min. Atractylodinol (73.2 mg, 0.4 mmol) was dissolved in DMF (2.0 mL), then added to the mixture. The reaction mixture was stirred at room temperature for 18 hours under N₂ environment and protected from light. And then water (20.0 mL) was added and the mixture was extracted with CH₂Cl₂ (3 ×). The combined organic layer was washed with saturated NH₄Cl (aq), water, and saturated NaCl (aq) in turn, dried over Na₂SO₄, and concentrated under reduced pressure. The residue was purified by silica gel chromatography, eluting with a gradient of 0 to 100% MeOH in CH₂Cl₂, to provide ATD-biotin (26.5 mg, 16.9 % yield) as a brown solid.

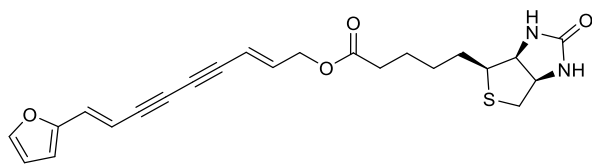


Figure S13. ATD-biotin chemical structure.

ATD-biotin: brown solid, 38 %. ^1H NMR (400 MHz, Chloroform-*d*) δ_{H} 7.39 (br s, 1H), 6.81 (d, $J = 16.0$ Hz, 1H), 6.44 – 6.37 (m, 2H), 6.30 (dt, $J = 16.0, 5.7$ Hz, 1H), 6.10 (d, $J = 16.0$ Hz, 1H), 5.84 (d, $J = 16.0$ Hz, 1H), 4.67 – 4.60 (m, 2H), 4.53 (br s, 1H), 4.34 (br s, 1H), 3.16 (br s, 1H), 2.96 – 2.85 (m, 2H), 2.71 – 2.79 (m, 1H), 2.37 (t, $J = 7.3$ Hz, 2H), 1.77 – 1.59 (m, 4H), 1.42 – 1.48 (m, 2H). ^{13}C NMR (100 MHz, Chloroform-*d*) δ_{C} 24.9, 28.4, 28.5, 33.9, 40.7, 55.5, 60.3, 62.1, 63.7, 75.7, 76.8, 80.3, 81.7, 104.6, 111.6, 112.2, 112.3, 131.4, 139.8, 143.8, 151.9, 173.2. HRMS (ESI): calcd for $\text{C}_{23}\text{H}_{25}\text{N}_2\text{O}_4\text{S}$ $[\text{M}+\text{H}]^+$ 425.1530, found 425.1529.

Table S1. Acute toxicity in mice by up-and-down method.

| Group | Dose (mg/kg) | Log Dose | Mortality rates (%) | Deaths (n) | Survivals (n) |
|--------------|---------------------|-----------------|----------------------------|-------------------|----------------------|
| 1 | 175 | 2.2 | 0 | 0 | 2 |
| 2 | 550 | 2.7 | 0 | 0 | 2 |
| 3 | 1750 | 3.2 | 0 | 0 | 6 |
| 4 | 5000 | 3.7 | 100 | 6 | 0 |

Estimated LD₅₀ = 3129 mg/kg.

95% confidence interval = 1750 - 5000 mg/kg.

Table S2. Organ weights were relative to body weight (percentage body weight). The organ coefficients was calculated as body weight (g) divided by organ weight (g). $n = 8$. Data were presented as the mean \pm SEM. # $P < 0.05$, ## $P < 0.01$, ### $P < 0.001$ compared to the control group. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ compared to the bleomycin group.

| Organs | Control | BLM | ATD (2.5 mg/kg) | ATD (5 mg/kg) | ATD (10 mg/kg) | PFD (300 mg/kg) |
|--------------------|------------------|---------------------|---------------------|---------------------|---------------------|---------------------|
| Body weight (g) | 23.10 \pm 1.41 | 13.41 \pm 2.02### | 20.55 \pm 3.07*** | 21.22 \pm 0.70*** | 22.14 \pm 1.27*** | 20.18 \pm 3.65*** |
| Lung (% BW) | 0.93 \pm 0.01 | 1.60 \pm 0.06## | 1.08 \pm 0.03* | 0.91 \pm 0.02*** | 0.84 \pm 0.01*** | 0.84 \pm 0.01* |
| Heart (% BW) | 0.59 \pm 0.07 | 0.60 \pm 0.08 | 0.60 \pm 0.03 | 0.58 \pm 0.06 | 0.57 \pm 0.08 | 0.93 \pm 0.01 |
| Liver (% BW) | 4.44 \pm 0.06 | 4.14 \pm 0.05 | 4.09 \pm 0.05 | 4.34 \pm 0.06 | 4.15 \pm 0.04 | 4.97 \pm 0.05* |
| Kidney (% BW) | 0.62 \pm 0.01 | 0.64 \pm 0.04 | 0.66 \pm 0.01 | 0.68 \pm 0.07 | 0.66 \pm 0.06 | 0.65 \pm 0.01 |
| Spleen (% BW) | 0.27 \pm 0.06 | 0.28 \pm 0.06 | 0.27 \pm 0.05 | 0.27 \pm 0.03 | 0.25 \pm 0.05 | 0.24 \pm 0.06 |

Table S3. Serum biochemical in mice. $n = 8$. Data were presented as the mean \pm SEM. $^{\#}P < 0.05$, $^{\#\#}P < 0.01$, $^{\#\#\#}P < 0.001$ compared to the control group. $^*P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$ compared to the bleomycin group.

| Blood parameters | Control | BLM | ATD (2.5 mg/kg) | ATD (5 mg/kg) | ATD (10 mg/kg) | PFD (300 mg/kg) |
|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|-------------------------------|
| ALP (U/L) | 116.00 \pm 3.65 | 134.00 \pm 6.56 | 133.60 \pm 6.40 | 128.00 \pm 2.31 | 142.00 \pm 5.72 | 137.20 \pm 8.80 |
| ALT (U/L) | 30.67 \pm 2.67 | 34.80 \pm 2.53 | 37.20 \pm 2.07 | 37.14 \pm 3.87 | 34.86 \pm 3.46 | 39.00 \pm 3.00 |
| AST (U/L) | 112.00 \pm 8.33 | 124.00 \pm 7.17 | 121.78 \pm 8.14 | 126.00 \pm 7.04 | 117.71 \pm 9.39 | 106.80 \pm 9.11 |
| CREA (μ mol/L) | 14.00 \pm 0.89 | 17.20 \pm 0.85 | 16.80 \pm 1.16 | 18.22 \pm 0.97 | 18.00 \pm 1.37 | 20.00 \pm 1.79 [#] |
| BUN (mmol/L) | 16.91 \pm 1.38 | 17.36 \pm 1.00 | 16.06 \pm 0.47 | 15.03 \pm 0.58 | 17.62 \pm 0.89 | 15.61 \pm 0.71 |
| CK (U/L) | 1084.67 \pm 99.84 | 1284.00 \pm 95.51 | 1128.00 \pm 99.95 | 1184.00 \pm 94.23 | 1078.29 \pm 98.82 | 1157.60 \pm 91.25 |
| CHO (mmol/L) | 2.71 \pm 0.14 | 2.44 \pm 0.05 | 2.46 \pm 0.09 | 2.65 \pm 0.09 | 2.74 \pm 0.07 | 2.65 \pm 0.06 |
| TG (mmol/L) | 0.66 \pm 0.07 | 0.78 \pm 0.05 | 0.56 \pm 0.04 | 0.61 \pm 0.08 | 0.75 \pm 0.09 | 0.79 \pm 0.09 |
| LDH (U/L) | 575.33 \pm 39.52 | 586.80 \pm 53.85 | 462.00 \pm 30.237 | 456.50 \pm 18.09 | 472.00 \pm 33.76 | 432.67 \pm 41.97 |
| GLU (mmol/L) | 5.69 \pm 0.18 | 5.87 \pm 0.15 | 5.98 \pm 0.14 | 5.67 \pm 0.17 | 5.94 \pm 0.13 | 6.05 \pm 0.11 |
| TBA (mmol/L) | 0.667 \pm 0.16 | 2.17 \pm 0.55 | 2.00 \pm 0.50 | 1.80 \pm 0.32 | 1.38 \pm 0.46 | 1.33 \pm 0.67 |

Table S4. Mass Spectroscopy analysis of proteins bound to ATD-biotin in HFL1.

| Protein | Accession no. | Coverage % | Peptides | Molecular mass (kDa) |
|--|----------------------|-------------------|-----------------|-----------------------------|
| Vimentin | P08670 | 71 | 41 | 53.6 |
| Keratin, type II cytoskeletal 1 | P04264 | 41 | 28 | 66 |
| Tubulin beta chain | P07437 | 30 | 11 | 49.8 |
| Pyruvate kinase PKM | P14618 | 35 | 16 | 57.9 |
| ATP synthase subunit alpha, mitochondrial | P25705-1 | 28 | 15 | 59.7 |
| Perilipin-3 | O60664-1 | 21 | 7 | 47 |
| Actin, aortic smooth muscle | P62736 | 23 | 8 | 42 |
| Hornerin | Q86YZ3 | 12 | 8 | 282.2 |
| Isoform 2 of Keratin, type II cytoskeletal 8 | P05787-2 | 13 | 10 | 56.6 |
| Histone H4 | P62805 | 50 | 5 | 11.4 |

Table S5. Primer sequences for real-time Q-PCR.

| Abbreviations | Gene | Forward Primer | Reverse Primer |
|----------------------|--|-------------------------------|------------------------------|
| COL1A1 | Collagen type I alpha 1 chain | GCGAGAGCATGACCGATGG ATTC | GCCTTCTTGAGGTTGCCAGTCT G |
| FN1 | Fibronectin 1 | ATGCAACGATCAGGACACA AGGAC | TGCCTCTCACACTTCCACTCTCC |
| ACTA2 | Actin alpha 2, smooth muscle | CTCTGGACGCACAACCTGGCA TC | CACGCTCAGCAGTAGTAACGAA GG |
| VIM | Vimentin | CCTTCGTGAATACCAAGACC TGCTC | AATCCTGCTCTCCTCGCCTTCC |
| TGFBR1 | Transforming growth factor beta receptor 1 | CTCTTCAAAAACCTGGGTCTG TG | CATCAACATGAGTGAGATGCAG |
| GAPDH | Glyceraldehyde-3-phosphate dehydrogenase | AGAAGGCTGGGGCTCATTG | AGGGGCCATCCACAGTCTTC |

Table S6. Target sequences of shRNAs.

| Name | Sequences (5' to 3') |
|--------------------|-----------------------------|
| h-Vimentin shRNA#1 | 5'-GCTAACTACCAAGACACTATT-3' |
| h-Vimentin shRNA#2 | 5'-CTCTGGTTGATACCCACTCAA-3' |
| h-Vimentin shRNA#3 | 5'-GCAGGATGAGATTCAGAATAT-3' |
| h-Vimentin shRNA#4 | 5'-CGCCATCAACACCGAGTTCAA-3' |

Table S7. Antibodies used for Western blotting and immunofluorescence assay.

| Antibody | Species | Catalog Number | Supplier |
|-------------------------------|----------------|-----------------------|-----------------------------|
| Vimentin | Rabbit | 10366-1-AP | Proteintech |
| Fibronectin | Rabbit | 15613-1-AP | Proteintech |
| Collagen Type I | Mouse | 66761-1-Ig | Proteintech |
| E-cadherin | Rabbit | 20874-1-AP | Proteintech |
| alpha smooth muscle Actin | Mouse | ab7817 | Abcam |
| TGFβ Receptor I | Mouse | sc-518018 | Santa |
| TGFβ Receptor II | Mouse | sc-17792 | Santa |
| Phospho-Smad2 (Ser255) | Rabbit | ab188334 | Abcam |
| Phospho-Smad2 (Ser465/Ser467) | Rabbit | 18338 | Cell Signaling Technologies |
| Smad2 | Rabbit | ab40855 | Abcam |
| Phospho-Smad3 (Ser465/Ser467) | Rabbit | Ab52903 | Abcam |
| Phospho-Smad3 (Ser204) | Rabbit | Ab63402 | Cell Signaling Technologies |
| Smad3 | Rabbit | ab40854 | Abcam |
| Smad7 | Mouse | sc-365846 | Santa |
| Smad4 | Mouse | sc-7966 | Santa |
| TGFβ 1 | Rabbit | ab215715 | Abcam |
| Erk1/2 | Rabbit | 4695 | Cell Signaling Technologies |
| Phospho-Erk1/2 | Rabbit | 4370 | Cell Signaling Technologies |
| JNK | Rabbit | 9252 | Cell Signaling Technologies |
| phospho-JNK | Rabbit | 9255 | Cell Signaling Technologies |
| p38 | Rabbit | 8690 | Cell Signaling Technologies |
| Phospho-p38 | Rabbit | 4511 | Cell Signaling Technologies |
| Phospho-Vimentin (Ser39) | Rabbit | 13614 | Cell Signaling Technologies |
| Phospho-Vimentin (Ser56) | Rabbit | ab217673 | Abcam |
| Phospho-Vimentin (Ser83) | Rabbit | 3878 | Cell Signaling Technologies |