

CLAIMS

WHAT IS CLAIMED IS:

1. A method of identifying fibrotic agents capable of modulating a fibrotic process, comprising:
 - a) contacting a plurality of immortalized or transformed fibroblasts with a test compound;
 - b) determining a level of activity of a collagen inhibiting gene of the fibroblasts contacted with the test compound;
 - c) comparing the level of activity of the collagen inhibiting gene to a control; and
 - d) identifying the test compound as a fibrotic agent capable of modulating a fibrotic process when the activity of the collagen inhibiting gene indicates an upregulation or downregulation of the collagen inhibiting gene relative to the controlwherein the activity of the collagen inhibiting gene is determined by at least one of protein quantitation and transcriptomic analysis.
2. The method according to claim 1, wherein a gene product of the collagen inhibiting gene is druggable.
3. The method according to claim 1 or 2, wherein the level of activity of two or more collagen inhibiting genes is determined.
4. The method according to claim 3, wherein the two or more collagen inhibiting genes are from the same gene family.
5. The method according to any of the previous claims, wherein the test compound is ribonucleic acid (RNA) selected from the group consisting of small interfering RNA, micro RNA, and small activating RNA.
6. The method according to claim 1, wherein the activity of the collagen inhibiting gene is determined by measuring reporter gene activity, and wherein the protein is a fluorescent protein coded by a reporter gene inserted downstream of an endogenous promoter for the collagen inhibiting gene in the fibroblasts.
7. The method according to claim 6, wherein the fluorescent protein is a red fluorescent protein selected from the group consisting of mCherry, mStrawberry, mOrange, and dTomato.
8. The method according to claim 1, wherein the activity of the collagen inhibiting gene is measured by transcriptomic analysis, the transcriptomic analysis comprising:

- a) generating a transcriptional profile for the plurality of fibroblasts contacted with the test compound, wherein the transcriptional profile comprises data related to the transcription of a collagen inhibiting gene,
 - b) comparing the transcriptional profile of the fibroblasts to a control, and
 - c) identifying the test compound as a fibrotic agent capable of modulating a fibrotic process when the transcriptional profile for the fibroblasts, relative to the control, indicates an upregulation or downregulation of the collagen inhibiting gene.
9. The method according to claim 8, wherein the transcriptomic analysis further comprises isolating RNA from the fibroblasts, creating labeled cRNA or cDNA from the isolated RNA, and hybridizing the labeled cRNA or cDNA to a microarray comprising a probe for the collagen inhibiting gene.
10. The method according to any one of the preceding claims, wherein collagen inhibiting gene is selected from the list comprising BZW1, STKLD1, RAB2A, ZNF567, ACBD6, ATMIN, FNDC11, CCD57, CCL27, DNAJC1, EEF1D, FAIM, FAM107A, FAM171A2, NXPE2, FPR2, GPN3, HDAC3, HIVEP2, ISTS1, ITGB1BP2, L3MBTL2, LILRB3, LRRIQ4, OSCAR, PFKL, PSMB4, PTAFR, RIPK3, SNTN, SGK3, SLC6A20, SMAD4, SNAP47, FGF18, FGL1, FHL2, FOXP2, FOXRED2, FSD2, GAS2L2, GDP4, GFI1, GFRA1, U2AF2, UMODL1, USH1G, WDR34, ZFP91, ZNF584, A1CF, AAMP, ADRA1B, ANKLE1, AQP12A, ASCC1, ATOH7, ATOX1, ATP2C2, BCL7B, BMP8B, TSPO2, BBOF1, CBARP, TANGO2, CADPS, CBR4, CCDC130, CENPK, CETN1, CHD2, CHTF18, COLEC10, CYP4F22, ECHDC2, EMP1, UBALD1, KDM5D, KCNE1, KLHL33, LILRA5, IGSF23, LRRN4CL, MYCBPAP, MYLK4, NDUFA1, NEURL2, NPIPA1, GNRHR, GP1BB, ADGRF5, GTPBP6, LAMTOR5, HIPK2, ING5, INHBC, INSL5, IPP, DVL1, SGCG, ZNF16, ZNF17, CYP39A1, ERCC5, INHBA, NCAM1, PCCA, QPCT, TGFBI, RBSN, ZNF583, ZNF655, GPR18, ZNF764, ADAMTS5, TNFRSF17, NSMCE4A, OVOL1, PDE1C, PNLOP, RCBTB1, SCARF1, SDCBP2, DERP1B7, ARHGEF26, SLIT3, SMURF1, SPACA3, SPATA17, SSX2IP, STX10, TAS2R1, THOP1, TMEM102, TMEM14A, TMEM26, TNFRSF9, TPRKB, TPST2, TRAPPC6B, TRIM29, TRIM65, RNF103 and TTC23L.