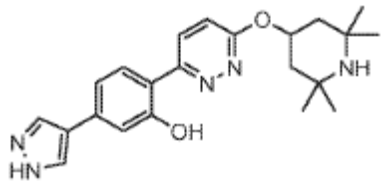
What is claimed is:

1. A method for modulating the amount of a mature mRNA transcript comprising an intronic exon (iExon), wherein the mature mRNA transcript is produced from a pre-mRNA transcript, the method comprising contacting 5-(1H-pyrazol-4-yl)-2-(6-((2,2,6,6-tetramethylpiperidin-4-yl)oxy)pyridazin-3-yl)phenol compound having the formula:



or a salt, hydrate, solvate, clathrate, isotopologue, racemate, enantiomer, diastereomer, stereoisomer, polymorph, tautomer form thereof, with a cell containing the pre-mRNA transcript in cell culture, or a cell lysate containing the pre-mRNA transcript, wherein the pre-mRNA transcript comprises two exons and an intron, wherein a first exon is upstream of the intron and a second exon is downstream of the intron, wherein the intron comprises a RNA nucleotide sequence comprising in 5' to 3' order: an intronic recognition element for splicing modifier (iREMS), a branch point, and a 3' splice site, wherein the iREMS comprises an RNA sequence GAgurngn, wherein r is adenine or guanine and n is any nucleotide,

wherein the pre-mRNA transcript is a pre-mRNA transcript of a gene selected from the group consisting of:

(a) ADAL, ADAMTS19, AGPS, AKAP8L, ANKRD13C, ANXA11, ARL15, ARSJ, BECN1, BIN3, BTBD10, C11orf30, C12orf4, C1orf27, C2orf47, CACNB1, CACNB4, CADM2, CDH18, CEP162, CEP170, CEP192, CHEK1, CHRM2, CMAHP, CNRIP1, CNTN1, CUX1, DAAM1, DCAF17, DCUN1D4, DDX42, DENND1A, DENND4A, DENND5A, DGKI, DHFR, DIAPH3, DLG5, DYRK1A, DZIP1L, ELMO2, ENAH, ENOX1, EVC, FAM162A, FAM174A, FAM208B, FAM69B, FBXL16, FGD4, FHOD3, GALC, GOLGB1, GXYLT1, HDAC5, HDX, HTT, IFT57, INO80, INVS, KDM6A, KIDINS220, KIF21A, L3MBTL2, LINCR-0002, LINGO2, LOC400927, LPHN1, LRRC1, LRRC42, LYRM1, MACROD2, MAPK10, MARCH8,

MDN1, MEAF6, MEMO1, MFN2, MLLT10, MRPL39, MRPL45, MRPS28, MTMR3, MYB, MYCBP2, NSUN4, NUPL1, OSBPL3, PAPD4, PCDH10, PDE3A, PDE7A, PDXDC1, PDXDC2P, PELI1, PITPNB, PMS1, POMT2, PSMA4, RAB23, RAF1, RCOR3, RERE, RNF130, RNF144A, RNF213, RPF2, RPS10, SCO1, SENP6, SF3B3, SGMS1, SGPL1, SLC25A16, SLC25A17, SNX24, SNX7, SORCS1, SPIDR, SPRYD7, SREK1, SSBP1, STRADB, SUPT20H, TAF2, TARBP1, TASP1, TBCA, TCF4, TET1, TIAM1, TJP2, TMEM214, TNRC6A, TRAF3, TRIM65, TSPAN7, UBN2, URGCP-MRPS24, UVRAG, WDR27, WDR90, WNK1, XRN2, ZFP82, ZMIZ2, ZNF138, ZNF208, ZNF212, ZNF280D, ZNF37BP, ZNF426, ZNF618, ZNF680, ZNF730, ZNF836, ZSCAN25; or

(b) ABHD10, ADAM17, AGPAT4, AGPS, AKT1, ANKRD13C, ANXA11, APIP, APPL2, ARHGAP1, ARHGAP5, ARL15, ARL5B, ASAP1, ATF6, BECN1, BHMT2, BIN3, BNC2, BTBD10, C10orf76, C11orf30, C11orf73, C12orf4, C1orf27, C1QTNF9B-AS1, CCNL2, CDH18, CENPI, CEP57, CMSS1, CNOT7, COPS7B, CRISPLD2, CUX1, DCAF17, DDX42, DENND4A, DENND5A, DET1, DLG5, DMXL1, DNAJA4, DNMBP, ENAH, EP300, ERC1, EVC, EXOC3, EXOC6B, FAM162A, FAM174A, FAM208B, FAM49B, FBN2, GBP1, GNG12, GXYLT1, HDX, HMGXB4, HOXB3, HSD17B4, IFT57, IKBKAP, INO80, INPP4B, ITCH, IVD, KDM6A, KDSR, KIAA1524, KIAA1715, KIDINS220, L3MBTL2, LGALS3, LOC400927, LRRC42, LYRM1, MACROD2, MANEA, MARCH7, MARCH8, MEAF6, MEMO1, MFN2, MMS19, MORF4L1, MRPL39, MRPL45, MRPS28, MYCBP2, MYLK, MZT1, NEDD4, NFASC, NGF, NIPA1, NLN, NREP, NUPL1, OSBPL3, PAPD4, PBX3, PDE7A, PIGN, PITPNB, PNISR, POMT2, PPARG, PPFIBP1, PRPF31, PSMA4, PXK, RAB23, RAF1, RAPGEF1, RBBP8, RERE, RGL1, RPF2, SAMD4A, SCO1, SENP6, SF3B3, SGIP1, SH2B3, SKP1, SLC12A2, SLC25A17, SMOX, SNAP23, SNX24, SNX7, SOCS6, SOGA2, SPIDR, SSBP1, STRADB, STXBP6, SUPT20H, TAF2, TASP1, TBCA, TBL1XR1, TCF4, TJAP1, TJP2, TMEM214, TMX3, TNRC6A, TXNL4B, UBE2D3, UBE2L3, UNC13B, URGCP-MRPS24, VDAC2, WHSC2, WNK1, XRN2, ZFP82, ZNF138, ZNF350, ZNF37BP, ZNF618, ZNF680, ZNF777, ZNF804A, ZSCAN25.

2. The method of claim 1, wherein the method leads to an increase in the production of a mature mRNA transcript comprising an intronic exon (iExon).

3. The method of claim 1, wherein the intron further comprises in 5' to 3' order: a 5' splice site, a branch point, and a 3' splice site, wherein the 5' splice site, the branch point, and the 3' splice site are upstream of the iREMS.

4. The method of any one of claims 1 to 3, wherein the pre-mRNA transcript is a pre-mRNA transcript of a gene selected from the group consisting of:
   (a) C12orf4, CDH18, CHEK1, DHFR, DHFR, HDX, LOC400927, LRRC42, MEAF6, MYCBP2, PAPD4, PDE7A, POMT2, TAF2, TRIM65, WDR27; or
   (b) ADAMTS19, BECN1, CACNB4, CADM2, CHEK1, CHRM2, CMAHP, DENND4A, DHFR, DHFR, EVC, GXYLT1, MEMO1, MYCBP2, NUPL1, PDXDC1, SENP6, SPIDR, TNRC6A, TRIM65, URGCP-MRPS24, WDR90, ZFP82, ZNF618, ZNF680, or
   (c) AGPS, AKT1, ANXA11, ARHGAP5, ARL15, ATF6, BIN3, C11orf30, C11orf73, CDH18, CENPI, DCAF17, DENND4A, EXOC6B, FAM162A, FAM174A, FAM208B, HOXB3, IFT57, IVD, KIAA1715, KIDINS220, MYCBP2, MYCBP2, SLC25A17, SNX24, SNX7, SPIDR, STRADB, TASP1, TCF4, TMEM214, UBE2D3, XRN2, ZNF618, ZNF777.

5. The method of any one of claims 1 to 3, wherein the pre-mRNA transcript is a pre-mRNA transcript of a gene selected from the group consisting of:
   (a) ARL15, PDXDC2P, ZNF37BP; or
   (b) ERC2, FHOD3, HDX, HTT, KDM6A, LOC400927, LRRC42, MACROD2, MEAF6, PAPD4, PDE7A, TAF2, TET1, TIAM1, WDR27; or
   (c) BECN1, BHMT2, C1orf27, ENAH, KIAA1524, LOC400927, LRRC42, LYRM1, MFN2, MORF4L1, NGF, NUPL1, PAPD4, PDE7A, RERE, SF3B3, STXBP6, TAF2, URGCP-MRPS24, WNK1, ZNF350, ZNF680.

6. The method of any one of claims 1 to 3, wherein the pre-mRNA transcript is a pre-mRNA transcript of a gene selected from the group consisting of:
   (a) ELMO2; or

(b) ARL15, C12orf4, CDH18, PDXDC2P, POMT2, RASIP1, ZNF37BP; or

(c) ARL15, ASAP1, C12orf4, EVC, GXYLT1, HDX, KDM6A, MACROD2, MEAF6, MEMO1, POMT2, SENP6, TBCA, TNRC6A, UBE2L3, VDAC2, ZFP82, ZNF138, ZNF37BP.

7. The method of any one of claims 1 to 3, wherein the iREMS comprises an RNA sequence GAguragu, and wherein r is adenine or guanine.

8. The method of any one of claims 1 to 3, wherein the iREMS comprises an RNA sequence NNGAgurngn (SEQ ID NO: 1), wherein r is adenine or guanine and n or N is any nucleotide, and wherein the RNA sequence NNGAgurngn (SEQ ID NO: 1) is selected from the group consisting of ANGAgurngn (SEQ ID NO: 4), CNGAgurngn (SEQ ID NO: 5), GNGAgurngn (SEQ ID NO: 6), UNGAgurngn (SEQ ID NO: 7), NAGAgurngn (SEQ ID NO: 8), NCGAgurngn (SEQ ID NO: 9), NGGAgurngn (SEQ ID NO: 10), NUGAgurngn (SEQ ID NO: 11), AAGAgurngn (SEQ ID NO: 12), ACGAgurngn (SEQ ID NO: 13), AGGAgurngn (SEQ ID NO: 14), AUGAgurngn (SEQ ID NO: 15), CAGAgurngn (SEQ ID NO: 16), CCGAgurngn (SEQ ID NO: 17), CGGAgurngn (SEQ ID NO: 18), CUGAgurngn (SEQ ID NO: 19), GAGAgurngn (SEQ ID NO: 20), GCGAgurngn (SEQ ID NO: 21), GGGAgurngn (SEQ ID NO: 22), GUGAgurngn (SEQ ID NO: 23), UAGAgurngn (SEQ ID NO: 24), UCGAgurngn (SEQ ID NO: 25), UGGAgurngn (SEQ ID NO: 52), and UUGAgurngn (SEQ ID NO: 53), wherein r is adenine or guanine and n or N is any nucleotide.

9. The method of any one of claims 1 to 3, wherein the iREMS comprises an RNA sequence NNGAguragu (SEQ ID NO: 2), wherein r is adenine or guanine and N is any nucleotide, and wherein the RNA sequence NNGAguragu (SEQ ID NO: 2) is selected from the group consisting of ANGAguragu (SEQ ID NO: 28), CNGAguragu (SEQ ID NO: 29), GNGAguragu (SEQ ID NO: 30), UNGAguragu (SEQ ID NO: 31), NAGAguragu (SEQ ID NO: 32), NCGAguragu (SEQ ID NO: 33), NGGAguragu (SEQ ID NO: 34), NUGAguragu (SEQ ID NO: 35), AAGAguragu (SEQ ID NO: 36), ACGAguragu (SEQ ID NO: 37), AGGAguragu (SEQ ID NO: 38), AUGAguragu (SEQ ID NO: 39), CAGAguragu (SEQ ID NO: 40), CCGAguragu (SEQ ID NO: 41), CGGAguragu (SEQ ID NO: 42), CUGAguragu (SEQ ID NO: 43), GAGAguragu (SEQ ID NO: 44), GCGAguragu (SEQ ID NO: 45), GGGAguragu (SEQ ID NO: 46),

GUGAguragu (SEQ ID NO: 47), UAGAguragu (SEQ ID NO: 48), UCGAguragu (SEQ ID NO: 49), UGGAguragu (SEQ ID NO: 489) and UUGAguragu (SEQ ID NO: 508), wherein r is adenine or guanine, and N is any nucleotide.

10. The method of any one of claims 1 to 3, wherein the pre-mRNA transcript is a pre-mRNA transcript of a gene selected from the group consisting of: ARL15, C12orf4, CDH18, CHEK1, DHFR, ELMO2, HDX, LOC400927, LRRC42, MEAF6, MYCBP2, PAPD4, PDE7A, PDXDC2P, POMT2, TAF2, TRIM65, WDR27, ZNF37BP, ADAMTS19, BECN1, CACNB4, CADM2, CHRM2, CMAHP, DENND4A, ERC2, EVC, FHOD3, GXYLT1, HTT, KDM6A, MACROD2, MEMO1, NUPL1, PDXDC1, RASIP1, SENP6, SPIDR, TET1, TIAM1, TNRC6A, URGCP-MRPS24, WDR90, ZFP82, ZNF618, ZNF680 , AGPS, AKT1, ANXA11, ARHGAP5, ATF6, ASAP1, BHMT2, BIN3, C11orf30, C11orf73, C1orf27, CENP1, DCAF17, ENAH, EXOC6B, FAM162A, FAM174A, FAM208B, HOXB3, IFT57, IVD, KIAA1524, KIAA1715, KIDINS220, LYRM1, MFN2, MORF4L1, NGF, RERE, SF3B3, SLC25A17, SNX24, SNX7, STRADB, STXBP6, TASP1, TBCA, TCF4, TMEM214, TNRC6A, UBE2D3, UBE2L3, VDAC2, WNK1, XRN2, ZFP82, ZNF138, ZNF350, and ZNF777.

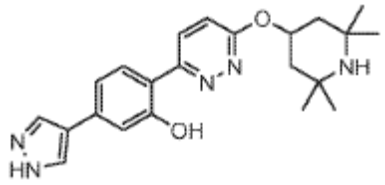
11. The method of any one of claims 1 to 3, wherein the pre-mRNA transcript is a pre-mRNA transcript of a gene selected from the group consisting of DIAPH3, NIPA1, RAF1, DCAF17, GNG12, HMGXB4, MRPL45, NSUN4, DMXL1, GALC, GBP1, SSBP1, CTNS, DENND5A, DGK1, GTSF1, L3MBTL2, MMS19, PMS1, PRPF31, SKP1, and SUPT20H.

12. The method of any one of claims 1 to 3, wherein the pre-mRNA transcript is a pre-mRNA transcript of the HTT gene.

13. The method of any one of claims 1 to 12, wherein the cell containing the pre-mRNA transcript in cell culture is contacted with 5-(1H-pyrazol-4-yl)-2-(6-((2,2,6,6-tetramethylpiperidin-4-yl)oxy)pyridazin-3-yl)phenol compound or a salt, hydrate, solvate, clathrate, isotopologue, racemate, enantiomer, diastereomer, stereoisomer, polymorph, or tautomer form thereof.

14. The method of any one of claims 1 to 12, wherein the cell lysate containing the pre-mRNA transcript is contacted with 5-(1H-pyrazol-4-yl)-2-(6-((2,2,6,6-tetramethylpiperidin-4-yl)oxy)pyridazin-3-yl)phenol compound or a salt, hydrate, solvate, clathrate, isotopologue, racemate, enantiomer, diastereomer, stereoisomer, polymorph, or tautomer form thereof.

15. A method for regulating the amount of a functional protein produced in a cell transfected by an artificial gene construct or a vector comprising the artificial gene construct, wherein the method comprises contacting in cell culture 5-(1H-pyrazol-4-yl)-2-(6-((2,2,6,6-tetramethylpiperidin-4-yl)oxy)pyridazin-3-yl)phenol compound having the formula



or a salt, hydrate, solvate, clathrate, isotopologue, racemate, enantiomer, diastereomer, stereoisomer, polymorph, or tautomer form thereof, with the cell, wherein the artificial gene construct comprises an RNA sequence comprising exons and one or more introns, wherein at least one intron comprises an iREMS that is downstream of a branch point and a 3’ splice site, and wherein the iREMS comprises an RNA sequence GAgurngn, wherein r is adenine or guanine and n is any nucleotide.

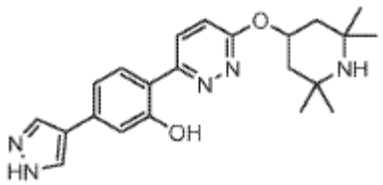
16. The method of claim 15, wherein the artificial gene construct comprises an RNA sequence comprising two exons and an intron, wherein a first exon is upstream of the intron and a second exon is downstream of the intron, wherein the RNA nucleotide sequence of the intron comprises in 5' to 3' order: a first 5' splice site, a first branch point, a first 3' splice site, an iREMS, a second branch point and a second 3' splice site, wherein the iREMS comprises an RNA sequence GAgurngn, and wherein r is adenine or guanine and n is any nucleotide.

17. The method of claim 15, wherein the artificial gene construct comprises an RNA sequence comprising two exons and an intron, wherein a first exon is upstream of the intron and a second exon is downstream of the intron, wherein the RNA nucleotide

sequence of the intron comprises in 5' to 3' order: an iREMS, a branch point and a 3' splice site, wherein the iREMS comprises an RNA sequence GAgurngn, and wherein r is adenine or guanine and n is any nucleotide.

18. The method of claim 15, wherein the artificial gene construct comprises an RNA sequence comprising three exons and two introns, wherein a first exon is upstream of a first intron, a second exon, a second intron, and a third exon, wherein the first intron is upstream of the second exon, the second intron and the third exon, wherein the second intron is upstream of the third exon, wherein the RNA sequence of the first intron comprises in 5’ to 3’ order: a first 5’ splice site, a first branch point, a first 3’ splice site, and the RNA sequence of the second intron comprises in 5’ to 3’ order: a second 5’ splice site, an iREMS, a second branch point and a second 3’ splice site, wherein the iREMS comprises an RNA sequence GAgurngn, wherein r is adenine or guanine and n is any nucleotide.

19. A method for regulating the amount of a functional protein produced by a cell expressing a pre-mRNA transcript encoded by an artificial gene construct, wherein the method comprises contacting in cell culture 5-(1H-pyrazol-4-yl)-2-(6-((2,2,6,6-tetramethylpiperidin-4-yl)oxy)pyridazin-3-yl)phenol compound having the formula



or a salt, hydrate, solvate, clathrate, isotopologue, racemate, enantiomer, diastereomer, stereoisomer, polymorph, or tautomer form thereof, with the cell, wherein the artificial gene construct comprises a DNA sequence encoding exons and one or more introns, wherein the nucleotide sequence encoding at least one intron comprises a nucleotide sequence encoding an iREMS that is downstream of the nucleotide sequence encoding a branch point and the nucleotide sequence encoding a 3’ splice site, and wherein the iREMS is encoded by a nucleotide sequence comprising a DNA sequence GAgtrngn, wherein r is adenine or guanine and n is any nucleotide.

20. The method of claim 19, wherein the artificial gene construct comprises a DNA sequence encoding two exons and an intron, wherein a nucleotide sequence encoding a first exon is upstream of a nucleotide sequence encoding the intron and a nucleotide sequence encoding a second exon is downstream of the nucleotide sequence encoding the intron, wherein the nucleotide sequence encoding the intron comprises in 5’ to 3’ order: a nucleotide sequence encoding a first 5’ splice site, a nucleotide sequence encoding a first branch point, a nucleotide sequence encoding a first 3’ splice site, a nucleotide sequence encoding an iREMS, a nucleotide sequence encoding a second branch point and a nucleotide sequence encoding a second 3’ splice site, wherein the nucleotide sequence encoding the iREMS comprises a DNA sequence GAgtrngn, wherein r is adenine or guanine and n is any nucleotide.

21. The method of claim 19, wherein the artificial gene construct comprises a DNA sequence encoding two exons and an intron, wherein the nucleotide sequence encoding a first exon is upstream of the nucleotide sequence encoding the intron and the nucleotide sequence encoding a second exon is downstream of the nucleotide sequence encoding the intron, wherein the nucleotide sequence encoding the intron comprises in 5' to 3' order: a nucleotide sequence encoding an iREMS, a nucleotide sequence encoding a branch point and a nucleotide sequence encoding a 3' splice site, wherein the nucleotide sequence encoding the iREMS comprises an DNA sequence GAgtrngn, wherein r is adenine or guanine and n is any nucleotide.

22. The method of claim 19, wherein the artificial gene construct comprises a DNA sequence encoding three exons and two introns, wherein a nucleotide sequence encoding a first exon is upstream of a nucleotide sequence encoding a first intron, a nucleotide sequence encoding a second exon, a nucleotide sequence encoding a second intron, and a nucleotide sequence encoding a third exon, wherein the nucleotide sequence encoding the first intron is upstream of the nucleotide sequence encoding the second exon, the nucleotide sequence encoding the second intron and the nucleotide sequence encoding the third exon, wherein the nucleotide sequence encoding the second intron is upstream of the nucleotide sequence encoding the third exon, wherein the nucleotide sequence encoding the first intron comprises in 5’ to 3’ order: a nucleotide sequence encoding a first 5’ splice site, a nucleotide sequence encoding a first branch point, a nucleotide sequence encoding a first 3’ splice site, and the

nucleotide sequence encoding the second intron comprises in 5’ to 3’ order: a nucleotide sequence encoding a second 5’ splice site, a nucleotide sequence encoding an iREMS, a nucleotide sequence encoding a second branch point and a nucleotide sequence encoding a second 3’ splice site, wherein the iREMS is encoded by a nucleotide sequence comprising a DNA sequence GAgtrngn, wherein r is adenine or guanine and n is any nucleotide.

23. The method of any one of claims 19 to 22, wherein the cell is transfected with the artificial gene construct or a vector comprising the artificial gene construct.

24. The method of any one of claims 15 to 23, wherein the cell is a patient cell.

25. The method of claim 24, wherein the patient is human.

26. The method of any one of claims 15 to 18, wherein the vector is a viral vector selected from the group consisting of an adeno-associated virus (AAV), a self-complimentary adeno-associated virus (scAAV), an adenovirus, a retrovirus, a lentivirus, a Newcastle disease virus (NDV), a herpes virus, an alphavirus, and a vaccinia virus.

27. The method of any one of claims 23 to 25, wherein the artificial gene construct is present in a vector.

28. The method of claim 27, wherein the vector is a viral vector selected from the group consisting of an adeno-associated virus (AAV), a self-complimentary adeno-associated virus (scAAV), an adenovirus, a retrovirus, a lentivirus, a Newcastle disease virus (NDV), a herpes virus, an alphavirus, and a vaccinia virus.